2016 TECHNICAL SUMMARIES.

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Conferences & Courses
27 February–3 March 2016

RETURNING TO SAN DIEGO IN 2016
Town & Country Resort and Convention Center
San Diego, California, USA
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SPIE would like to express its deepest appreciation to the symposium chairs, conference chairs, program committees, session chairs, and authors who have so generously given their time and advice to make this symposium possible.

The symposium, like our other conferences and activities, would not be possible without the dedicated contribution of our participants and members. This program is based on commitments received up to the time of publication and is subject to change without notice.
9783-1, Session 1

Quantification of resolution in multiplanar reconstructions for digital breast tomosynthesis

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Multiplanar reconstruction (MPR) in digital breast tomosynthesis (DBT) allows for tomographic images to be portrayed in any orientation. We have conducted research to determine the resolution of tomosynthesis MPR. We built a phantom that houses a star test pattern to measure resolution. This phantom provides three rotational degrees of freedom. The design consists of two hemispheres with longitudinal and latitudinal grooves that reference angular increments. When joined together, the hemispheres form a dome that sits inside a cylindrical encasement. The cylindrical encasement contains reference notches to match the longitudinal and latitudinal grooves that guide the phantom's rotations. With this design, any orientation of the star-pattern can be analyzed. Images of the star-pattern were acquired using a DBT mammography system at the Hospital of the University of Pennsylvania. Images taken were reconstructed and analyzed by two different methods. First, the maximum visible frequency (in line pairs per millimeter) of the star test pattern was measured. Then, the contrast was calculated at a fixed spatial frequency. These analyses confirm that resolution decreases with tilt relative to the breast support. They also confirm that resolution in tomosynthesis MPR is dependent on object orientation. Current results verify that the existence of super-resolution depends on the orientation of the frequency; the direction parallel to x-ray tube motion shows super-resolution. In conclusion, this study demonstrates that the direction of the spatial frequency relative to the motion of the x-ray tube is a determinant of resolution in MPR for DBT.

9783-2, Session 1

Tomosynthesis for coronary artery calcium scoring

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Coronary artery calcium score (CACS) measures the buildup of calcium on the coronary artery wall and has been shown to be an important predictor of the risk of coronary artery diseases (CAD). Currently CACS is measured using CT, though the relatively high cost and high radiation dose has limited its adoption as a routine screening procedure. Tomosynthesis, which uses limited number of projection images for 3D reconstruction, is potentially a low dose and low cost alternative to CT. Commercial mechanical scanning tomosynthesis scanner requires long scanning time, and cannot be easily gated to cardiac cycles, necessary for CACS. The carbon nanotube (CNT) based field emission x-ray allows high-resolution prospectively gated imaging. Here we report preliminary results of estimating CACS using a prototype CNT x-ray based stationary chest tomosynthesis (s-DCT) system. A human coronary calcifications heart model placed inside a chest phantom was developed and scanned by the s-DCT system and a clinical CT. The adapted fan-beam iterative volume reconstruction method, developed specifically for stationary tomosynthesis systems, is used to obtain high resolution tomosynthesis images. A trained cardiologist segmented out the calcifications and the CACS was obtained. We observed a good correlation between the tomosynthesis derived CACS and CT CACS ($r = 0.89$). Our result shows s-DCT imaging has the potential to estimate CACS, thus providing a possible low cost and low dose imaging protocol for screening and monitoring CAD.

9783-3, Session 1

A new generation of stationary digital breast tomosynthesis system with wider angular span and faster scanning time

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Using a CNT X-ray source array we have developed a clinically ready first generation stationary breast tomosynthesis system (s-DBT). In the s-DBT system, the focus spot blur associated with x-ray source motion is completely eliminated, and it allows for rapid acquisition of projection images over different angular span without changing the acquisition time. In the phantom studies the 1st Gen s-DBT system has demonstrated 30% higher spatial resolution than the corresponding continuous motion DBT systems. The system is currently installed at UNC hospital and is being evaluated for its diagnostic performance in 100 patient clinical evaluation against the current gold standard, FFDM. Initial clinical results indicate that the s-DBT system can produce increased lesion conspicuity and comparable MC visibility. However due to the limitation in x-ray flux, certain large size patients have to be excluded. In addition both ours and other group's recent studies have shown that increasing the angular span beyond 30 degree can be beneficial for enhance depth resolution.

Here we report the preliminary characterization of 2nd Gen s-DBT system with a new CNT x-ray source array with increased tube flux and a larger angular span. Increasing x-ray tube flux allows for a larger patient population, as well as allow for dual energy imaging. Initial results indicate that 2nd Gen s-DBT system delivers more than twice the flux, which allows for imaging of all size patients with acquisition time less than 4 seconds.

9783-4, Session 1

Detection of microcalcification clusters by 2D-mammography and narrow and wide angle digital breast tomosynthesis

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The aim of this study was to compare the detection of microcalcification clusters by human observers in breast images using 2D-mammography and narrow (15°/15 projections) and wide (50°/25 projections) angle digital breast tomosynthesis (DBT). Simulated microcalcification clusters with a range of microcalcification diameters (100 μm-500 μm) were inserted into 6 cm thick simulated compressed breasts. Breast images were produced with and without inserted microcalcification clusters using a set of image modelling tools, which were developed to represent clinical imaging by mammography and tomosynthesis. Commercially available software was used for the image processing and image reconstruction. The images were
then used in a series of 4-alternative forced choice (4AFC) human observer experiments conducted for signal detection with the microcalcification clusters as targets. For each of the three imaging modalities the threshold diameter required for microcalcification detection was determined. Results showed that 2D-mammography has a lower threshold diameter for microcalcification detection than both DBT imaging modalities and that narrow angle DBT has a lower threshold diameter than wide angle DBT.

9783-5, Session 1

Feasibility of reduced-dose 3D/4D-DSA using a weighted edge preserving filter
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A conventional 3D/4D digital subtraction angiogram (DSA) requires two rotational acquisitions (mask and fill) to compute the log-subtracted projections that are used to reconstruct a 3D/4D volume. Since all of the vascular information is contained in the fill acquisition, it is hypothesized that it is possible to dramatically reduce the x-ray dose of the mask acquisition and still obtain subtracted projections adequate to reconstruct a 3D/4D volume with comparable noise variance to a full dose acquisition. A full dose mask and fill acquisition were acquired from a clinical study to provide a known full dose reference reconstruction. Gaussian noise was added to the mask acquisition to simulate a mask acquisition acquired at 10% relative dose. Noise in the low-dose mask projections was reduced with a weighted edge preserving (WEP) filter designed to preserve bony edges while suppressing noise. 2D log-subtracted projections were computed from the filtered low-dose mask and full-dose fill projections, and then 3D/4D-DSA reconstruction algorithms were applied. Additional bilateral filtering was applied to the 3D volumes. The signal-to-noise ratio measured in the filtered 3D/4D-DSA volumes was compared to the full dose case. The average ratio of filtered low-dose SNR to full dose SNR across a set of VOIs was 0.9979 for the 3D-DSA and 1.1040 for the 4D-DSA, indicating the method is a feasible approach to restoring SNR in DSA scans acquired with a low-dose mask.

9783-6, Session 2

Simulation of 3D synthetic breast blocks
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Virtual clinical trials (VCTs) are an emergent approach for the rapid evaluation and comparison of various imaging techniques and technologies. A fundamental requirement of this approach is the use of realistic looking breast anatomy in the studies to produce clinically relevant results. In this work, a biologically inspired approach has been used to simulate realistic synthetic breast blocks for use in virtual clinical trials. A variety of high and low frequency features (including Cooper’s ligaments, blood vessels and glandular tissue) have been extracted from clinical digital breast tomosynthesis (DBT) images to simulate synthetic breast blocks. In a pilot validation study, a selection of simulated 2D and DBT images interleaved with real images was presented to an experienced radiologist for rating. The results of the study were promising with the radiologist rating 90% of simulated 2D images and 77% of simulated DBT images as real. This motivates a full validation study, the results of which will be included in the extended version of this paper.

9783-7, Session 2

Rayleigh imaging in spectral mammography
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Spectral imaging is the acquisition of multiple images of an object at different energy spectra. In mammography, dual-energy imaging (spectral imaging with two energy levels) has been investigated for several applications, in particular material decomposition, which allows for quantitative analysis of breast composition. Material decomposition with dual-energy imaging is based on the assumption that there are two dominant photon interaction effects that determine linear attenuation: the photoelectric effect and Compton scattering. This assumption limits the number of basis materials, i.e. the number of materials that are possible to differentiate between, to two. However, Rayleigh scattering may account for more than 10% of the linear attenuation in the mammography energy range. In this work, we show that a modified version of a scanning multi-slit spectral photon-counting mammography system is able to simultaneously acquire three images at different spectra and can be used for triple-energy imaging. We further show that triple-energy imaging in combination with the efficient scatter rejection of the system enables measurement of Rayleigh scattering, which adds an additional energy dependency to the linear attenuation and enables material decomposition with three basis materials. Three available basis materials have the potential to improve virtually all applications of spectral imaging.

9783-8, Session 2

Reproducing 2D breast mammography images with 3D printed phantoms
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Mammography is currently the standard imaging modality used to screen women for breast abnormalities and, as a result, it is a tool of great importance for the early detection of breast cancer. Physical phantoms are commonly used as surrogates of breast tissue to evaluate some aspects of the performance of mammography systems. However, most phantoms do not reproduce the anatomic heterogeneity of real breasts. New fabrication technologies have created the opportunity to build more complex, anatomically realistic breast phantoms that could potentially assist in the evaluation of mammography systems. The primary objective of this work is to present a simple, easily reproducible methodology to design and print 3D objects that replicate the attenuation profile observed in real 2D mammograms. The secondary objective is to evaluate the capabilities and limitations of the competing 3D printing technologies, and characterize the x-ray properties of the different materials they use. Printable phantoms can be created using the open-source code introduced in this work, which processes a raw mammography image to estimate the amount of x-ray attenuation at each pixel, and outputs a triangle mesh object that encodes the observed attenuation map. The conversion from the observed pixel gray value to a column of printed material with equivalent attenuation requires certain assumptions and knowledge of multiple imaging system parameters, such as x-ray energy spectrum, source-to-object distance, compressed breast thickness, and average breast material attenuation. A detailed description of the new software, a characterization of the printed materials using x-ray spectroscopy, and an evaluation of the realism of the sample printed phantoms are presented.
Breast ultrasound tomography with two parallel transducer arrays
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Ultrasound tomography is a new imaging modality to reconstruct the sound speed, density, and ultrasound attenuation of the breast in addition to reflection images for breast cancer characterization. We design and manufacture a new synthetic-aperture breast ultrasound tomography system with two parallel transducer arrays consisting of a total of 768 transducer elements. The transducer arrays are translated vertically to scan the breast in a water tank from the chest wall/axillary region to the nipple region to acquire ultrasound transmission and reflection data for whole-breast ultrasound tomography imaging. We use the system to acquire in vivo patient data to study the clinical feasibility of ultrasound tomography for breast cancer characterization. We apply our recently developed ultrasound imaging and tomography algorithms to both ultrasound transmission and reflection data acquired using our breast ultrasound tomography system. Our results demonstrate that using multiple physical parameters and images obtained with breast ultrasound tomography has great potential to improve characterization of breast cancers.

A new open-source multi-modality digital breast phantom
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An anthropomorphic digital breast phantom has been developed with the goal of generating random voxelized breast models that capture the anatomic variability observed in vivo. This is a new phantom and is not based on existing digital breast phantoms or patient images. It has been designed at the outset to be modality agnostic (i.e., suitable for use in modeling x-ray based imaging systems, magnetic resonance imaging, and potentially other imaging systems) and open source so that users may freely modify the phantom to suit a particular study. In this work we describe the modeling techniques that have been developed, the capabilities and novel features of this phantom, and study the realism of simulated images produced from it. Starting from a base quadric, a series of deformations are performed to create a breast with a particular volume and shape. Initial glandular compartments are generated using a Voronoi technique and a ductal tree structure with terminal duct lobular units is grown from the nipple into each compartment. An additional step involving the creation of fat and glandular lobules using a Perlin noise function is performed to create more realistic glandular/fat tissue interfaces and generate a Cooper’s ligament network. A vascular tree is grown from the chest muscle into the breast tissue. Breast compression is performed using a neo-Hookean elasticity model. We show simulated mammographic and T2-weighted MRI images and study the properties of the these images.

Dictionary-based image denoising for dual-energy computed tomography
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Compared to conventional computed tomography (CT), dual energy CT allows for improved material decomposition by conducting measurements at two distinct energy spectra. Since radiation exposure is a major concern in clinical CT, there is a need for tools to reduce the noise level in images while preserving diagnostic information. One way to achieve this goal is the application of image-based denoising algorithms after an analytical reconstruction has been performed. We have developed a modified dictionary denoising algorithm for dual energy CT aimed at exploiting the high spatial correlation between between images obtained from different energy spectra. Both the low- and high energy image are partitioned into small patches which are subsequently normalized. Combined patches with improved signal-to-noise ratio are formed by a weighted addition of corresponding normalized patches from both images. Assuming that corresponding low- and high energy image patches are related by a linear transformation, the signal in both patches is added coherently while noise is neglected. Conventional dictionary denoising is then performed on the combined patches. Compared to conventional dictionary denoising and bilateral filtering, our algorithm achieved superior performance in terms of qualitative and quantitative image quality measures. We demonstrate, in
9783-14, Session 3
Reconstruction of limited-angle multi-energy CT using joint clustering prior and sparsity regularization
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In this article we present an easy-to-implement Multi-energy CT scanning strategy and a corresponding reconstruction algorithm, which facilitate projection data downsampling by the number of energy channel fold and mitigate the limited-angle artifacts caused by the downsampling. Leveraging the structure coherence at different energies, we first pre-reconstruct a prior structure information image using the projection data at all energy channels. Then we perform a k-means clustering on the prior image to generate a sparse dictionary representation for the image, which serves as a structural information constraint. We combine this constraint with the conventional compressed sensing method and proposed a new model called Joint Clustering Prior and Sparsity Regularization (CPSR). CPSR is a convex programming problem and solved by Alternating Direction Method of Multipliers (ADMM).

We verify our CPSR method with a numerical simulation experiment. The object is a dental phantom and X-ray beams at three different energies (120kVp, 90kVp, 60kVp) are used. We pick up only 75 views projection data at each energy for reconstruction. Independent reconstruction at each energy will cause limited-angle artifacts even with compressed sensing, while CPSR is free from limited-angle artifacts, keeping nearly all the edge details.

9783-15, Session 4
Multipurpose robotic x-ray system for 2D radiographic and 3D cone-beam CT imaging
Andreas Fieselm, Jan Steinbrener, Anna K. Jerebko, Thomas Mertelmeier, Siemens AG (Germany)

In this work, we present a novel multi-purpose robotic X-ray system. It has two motor-driven telescopic arms for the X-ray tube and detector. 2D radiographs can be acquired from different angles. Projection data for 3D cone-beam CT reconstruction can be acquired during simultaneous movement of the arms along dedicated scanning trajectories. We provide an initial evaluation of the 3D image quality based on phantom and cadaver scans. High spatial resolution enables adequate visualization of bones. The novel system allows 3D X-ray scanning of patients in the standing and weight-bearing position. This system could enable new 2D/3D imaging work flows in musculoskeletal imaging and improve diagnosis of musculoskeletal disorders.

9783-16, Session 4
Image-based motion compensation for high-resolution extremities cone-beam CT
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Purpose: Cone-beam CT (CBCT) of the extremities provides high spatial resolution, but its quantitative accuracy may be challenged by involuntary sub-mm motions that cannot be controlled with patient immobilization. We investigate a two-step iterative motion compensation based on a multi-component metric of image sharpness.

Methods: The motion was assumed to be locally rigid and estimated by maximizing a cost function with three components: a gradient metric encouraging image sharpness, an entropy term that favored high contrast and penalized streaks, and a penalty term encouraging smooth motion. The compensation involved initial coarse estimation of gross motion followed by estimation of fine-scale displacements using high resolution reconstructions. The method was evaluated in simulations with synthetic motion (1-4 mm) applied to a wrist volume obtained on a CMOS-based CBCT testbench. Structural similarity index (SSIM) quantified the agreement between motion-compensated and static data. The algorithm was also tested on a motion contaminated patient scan from dedicated extremities CBCT.

Results: Excellent correction was achieved for the investigated range of displacements, indicated by good visual agreement with the static data. 10-15% improvement in SSIM was attained for 2-4 mm motions. The compensation was robust against increasing motion (4% decrease in SSIM across the investigated range, compared to 14% with no compensation). Consistent performance was achieved across a range of noise levels. Significant mitigation of artifacts was shown in patient data.

Conclusion: The results indicate feasibility of image-based motion correction in extremities CBCT without the need for a priori motion models, external trackers, or fiducials.

9783-17, Session 4
Striped ratio grids for scatter estimation
Scott S. Hsieh, Stanford Univ. (United States); Adam S. Wang, Josh M. Star-Lack, Varian Medical Systems, Inc. (United States)

Striped ratio grids are a new concept for scatter management in cone-beam CT. These grids are a modification of conventional anti-scatter grids and consist of stripes which alternate between high grid ratio and low grid ratio. Such a grid is related to existing hardware concepts for scatter estimation such as blocker-based or primary modulation, but rather than modulating the primary, the striped ratio grid modulates the scatter. The transitions between adjacent stripes can be used to estimate and subtract the remaining scatter. However, these transitions could be contaminated by variation in the primary radiation. We describe a simple nonlinear image processing algorithm to estimate scatter, and proceed to validate the striped ratio grid on experimental data of a pelvic phantom. The striped ratio grid is emulated by combining data from two scans with different grids. Preliminary results are encouraging and show a significant reduction of scatter artifact. Some artifacts are introduced by the striped ratio grid and may need to be addressed with more sophisticated image processing.

9783-18, Session 4
Five-dimensional motion compensation for respiratory and cardiac motion with cone-beam CT of the thorax region
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We propose an adapted method of our previously published five-dimensional motion compensation algorithm that targets sub-mm motion patterns not possible with current patient immobilization techniques. The method is iterative and uses a warped image representation for closed form optimization. The algorithm is tested on simulation data and clinical 4D CBCT scans. Significant mitigation of artifacts was shown in patient data.
dimensional (5D) motion compensation (MoCo) algorithm, developed for micro-CT imaging of small animals, to provide for the first time motion artifact-free 5D CBCT images from a conventional flat detector-based CBCT scan of clinical patients. Image quality of retrospectively respiratory- and cardiac-gated volumes from flat detector CBCT scans is deteriorated by severe sparse projection artifacts. These artifacts further complicate motion estimation, as it is required for MoCo image reconstruction. For high quality 5D CBCT images at the same x-ray dose and the same number of projections as todays 3D CBCT we developed a double MoCo approach based on motion vector fields (MVF) for respiratory and cardiac motion. In a first step we already published a four-dimensional (4D) artifact-specific cyclic motion-compensation (acMoCo) approach to compensate for the respiratory patient motion. With this information a cyclic phase-gated deformable heart registration algorithm is applied to the respiratory motion-compensated 4D CBCT data, thus resulting in cardiac MVFs. We apply these MVFs on double-gated images and thereby respiratory and cardiac motion-compensated 5D CBCT images are obtained. Our 5D MoCo approach processing patient data acquired with the TrueBeam® 4D CBCT system (Varian Medical Systems). Our double MoCo approach turned out to be very efficient and removed nearly all streak artifacts due to making use of 100% of the projection data for each reconstructed frame. The 5D MoCo patient data show fine details and no motion blurring, even in regions close to the heart where motion is fastest.

9783-19, Session 4

Over-exposure correction in knee cone-beam CT imaging with automatic exposure control using a partial low-dose scan

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C-arm-based cone-beam CT (CBCT) systems with flat-panel detectors are suitable for diagnostic knee imaging due to their potentially flexible selection of CT trajectories and wide volumetric beam coverage. In knee CT imaging, over-exposure artifacts can occur because of limitations in the dynamic range of the flat panel detectors present on most CBCT systems. We developed a straightforward but effective method for correction and detection of over-exposure for an Automatic Exposure Control (AEC)-enabled standard knee scan incorporating a prior considerably low dose scan. The radiation dose associated with the low dose scan was negligible (0.0042mSv, 2.8% increase) which was enabled by partially sampling the projection images considering the geometry of the knees and lowering the dose further to be able to just see the skin-air interface. We combined the line integrals from the AEC and low dose scans after detecting over-exposed regions by comparing the line profiles of the two scans detector row-wise. The combined line integrals were reconstructed into a volumetric image using filtered back projection. We evaluated our method using in vivo human subject knee data. The proposed method effectively corrected and detected over-exposure, and thus recovered the visibility of exterior tissues (e.g., the shape and density of the patella, and the patellar tendon), incorporating a prior low dose scan with a negligible increase in radiation exposure.

9783-20, Session 4

Offset detector super short scan reconstruction for the rotate-plus-shift trajectories and its application to C-arm CT systems

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Mobile and compact C-arm systems are routinely used in interventional procedures for fluoroscopic CT imaging. The mechanical requirements guarantee for a maximum of flexibility and mobility but restrict the mechanical rotation range (e.g. 165°) and the lateral size of the field of measurement (FOM), typically about 160 mm. While the rotate-plus-shift trajectory for the acquisition of full datasets with 180° minus fan-angle has been recently published, an offset detector approach for a fully motorized C-arm system is presented in the current manuscript. As the isocenter in non-centric C-arms can be freely chosen, the offset detector can be equally well absorbed with an offset of the C parallel to the transaxial detector direction. The typical rotation range of 360° used in offset detector trajectories is replaced by a double rotate-plus-shift scan requiring a rotation range of at least 180° minus fan-angle. The trajectory increasing the diameter of the FOM by up to a factor of two is presented and the practical application of variations with an asymmetric FOM is shown. Filtered backprojection using a modified FDK algorithm with an universal redundancy weight is used for the reconstruction of the acquired data. The presented trajectory can increase the applicability and flexibility of C-arm systems and has the potential to perform intra-operative large volume control or overview scans and thus reduce the patient’s risk.

9783-21, Session 5

Single-shot x-ray phase contrast imaging with an algorithmic approach using spectral detection

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X-ray phase contrast imaging has been investigated during the last two decades for potential benefits in soft tissue imaging. Long imaging time, high radiation dose and general measurement complexity involving motion of x-ray components has prevented the clinical translation of these methods. In all the popular phase contrast imaging methods, multiple measurements per projection angle involving motion of optical components are required to achieve quantitatively accurate estimation of absorption, phase and differential phase. Recently we proposed an algorithmic approach to use spectral detection data in a phase contrast imaging setup to obtain absorption, phase and differential phase in a single-step. Our generic approach has been shown via simulations in all three types of phase contrast imaging; propagation, coded aperture and grating interferometry. While other groups have used spectral detector in phase contrast imaging setups, our proposed method is unique in outlining an approach to use this spectral data to simplify phase contrast imaging. In this abstract we show the first experimental proof of our single-shot phase retrieval using a Medipix3RX photon counting detector (with only 2 energy bins) in a coded aperture phase contrast setup.
9783-22, Session 5

X-ray differential phase contrast imaging using a Talbot-Lau interferometer and a photon-counting detector
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The noise performance of a grating interferometer based x-ray differential phase contrast (DPC) imaging system is strongly dependent on both the visibility of the interferometer and the total number of photons used to extract the DPC signal. Since the interferometer is designed to perform best, i.e., with the highest visibility, for a specific x-ray energy, deviations from this designed energy lead to a drop in visibility. The incorporation of a photon counting detector in a DPC imaging system has the potential to selectively use photons in an energy window matching the design energy of the interferometer. However, this strategy requires discarding x-ray photons at other energies received by the detector, potentially leading to a degradation of radiation dose efficiency in the DPC imaging system. In this paper, a novel method was developed and validated to leverage all incident x-ray photons in DPC imaging to achieve a high contrast-to-noise ratio for all energy bins, enabling energy independent performance for the DPC imaging system. Experimental phantom studies have demonstrated that the proposed method is able to increase the image contrast to noise ratio by at least 43.6% for the least noisy energy bin and as much as 542.4% for the noisiest energy bin.

9783-23, Session 5

Potential use of microbubbles (MBs) as contrast material in x-ray dark field (DF) imaging: How does the DF signal change with the characteristic parameters of the MBs?
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One of the most exciting aspects of a grating based x-ray differential phase contrast (DPC) acquisition method is the concurrent generation of the so-called dark field (DF) signal along with the well-known absorption and DPC signals. The DF signal is associated with local distribution of small angle scatterers in a relatively uniform background, while the DPC signal is used to characterize the relatively uniform structure of the image object. Besides the endogenous image contrast, exogenous contrast media are often used to locally enhance the image signal. This paper proposes a potential contrast medium for DF signal enhancement: microbubbles (MBs). MBs have already been developed for clinical use in ultrasound imaging. However, recent experimental observations have shown that a MB solution also has the potential to enhance the DF signal, although it remains unclear how the characteristics of the MBs impact the DF signal. In this paper, a systematic study was performed to investigate the impact of the following characteristics on x-ray DF signal: size, concentration, shell thickness, size uniformity, and having gold nanoparticles attached. The results of this systematic study provide the critical information needed for further optimization of use of MBs in x-ray DF imaging. The experimental results demonstrate that an increased MB size (about 4 microns) may generate a stronger DF signal; additionally, a moderately increased shell thickness, the use of gold nanoparticles on the shell surface, and careful refinement of the MBs also result in further enhancement of DF signal.

9783-24, Session 5

Phase contrast imaging with a dual-phase grating interferometer
Matias E. Kagias, Zhentian Wang, Marco F. M. Stampanoni, Paul Scherrer Institut (Switzerland) and ETH Zürich (Switzerland)

Hard X-ray grating interferometry has shown a great potential for medical and industrial applications. The method is capable of recording simultaneously three complementary contrasts: absorption, differential phase and scattering. Currently, the wide applicability of the method is restricted due to dose efficiency and manufacturing challenges of large, high quality absorption gratings. The authors propose a single-shot grating interferometer for phase contrast imaging. The proposed system does not require absorption gratings and therefore utilize all the photons for imaging. This opens the way to higher energies where the main technical limitation consists of the fabrication of high aspect ratio absorption gratings. The system requires only two phase gratings of small pitch (~1 μm) (easier to produce that absorption gratings). The interference fringe generated from the first phase grating acts as a structured illumination for the second. This configuration generates an interference fringe at the detector plane with a much larger pitch than the grating periods, which can be recorded directly without an absorption grating or high-resolution detectors. Two identical gratings of period 1.27 μm where fabricated in house. The gratings where etched to a depth producing a phase shift at 17keV. The feasibility of the proposed method was demonstrated on a compact imaging setup with a micro-focal tube by comparing the flat grating images with only one and both gratings in the beam. As expected a large pitch fringe only appeared with both gratings in the beam. Finally, absorption and differential phase images of a plastic tube were retrieved using Fourier analysis.

9783-25, Session 5

High-energy x-ray grating-based phase-contrast radiography of human anatomy
Florian Horn, Christian Hauke, Sebastian Lachner, Veronica Ludwig, Georg Pelzer, Jens Rieger, Max Schuster, Maria Seiffert, Johannes Wandner, Andreas Wolf, Thilo Michel, Gisela Anton, Friedrich-Alexander-Univ. Erlangen-Nürnberg (Germany)

X-ray grating-based phase-contrast Talbot-Lau interferometry is a promising imaging technology that has the potential to raise soft tissue contrast in comparison to conventional attenuation-based imaging. Additionally, it is sensitive to attenuation, refraction and scattering of the radiation and thus provides complementary and otherwise inaccessible information due to the dark-field image, which shows the sub-pixel size granularity of the measured object.

Until recent progress the method has been mainly limited to photon energies below 40 keV. Scaling the method to photon energies that are sufficient to pass large and spacious objects represents a challenging task. This is caused by increasing demands regarding the fabrication process of the gratings and the broad spectra that come along with the use of polychromatic X-ray sources operated at high acceleration voltages.

We designed a setup that is capable to reach high visibilities in the range from 50 to 120 kV. Therefore, spacious and dense parts of the human body with high attenuation can be measured such as a human knee.

The authors will show investigations on the resulting attenuation, differential phase-contrast and dark-field images concerning contrast-to-noise and similarity of information. The images experimentally show that X-ray grating-based phase-contrast radiography is feasible with highly absorbing parts of the human body containing massive bones that will not destroy soft tissue contrast.
9783-26, Session 6

Design and characterization of a dedicated cone-beam CT scanner for detection of acute intracranial hemorrhage

Jennifer Xu, Alejandro Sisniega, Wojciech Zbijewski, Hao Dang, Joseph W. Stayman, Johns Hopkins Univ. (United States); Xiaohui Wang, David H. Foos, Carestream Health, Inc. (United States); Nafi Aygun, Vassili E. Koliatsos, Jeffrey H. Siewerdsen, Johns Hopkins Univ. (United States)

Purpose: Prompt and reliable detection of intracranial hemorrhage (ICH) has substantial clinical impact in diagnosis and treatment of stroke and traumatic brain injury. This paper describes the design, development, and preliminary performance characterization of a dedicated cone-beam CT (CBCT) head scanner prototype for imaging of acute ICH.

Methods: A task-based image quality model was used to compute the detectability index as a function of system configuration; hardware design was guided by the results of this model-based optimization. A robust artifact correction pipeline was developed using GPU-accelerated Monte Carlo (MC) scatter simulation, beam hardening corrections, and detector veiling glare and lag deconvolution. An iterative penalized weighted least-squares (PWLS) reconstruction framework with weights adjusted for artifact-corrected projections was developed. Various bowtie filters were investigated for potential dose and image quality benefits, with a MC-based tool providing estimates of spatial dose distribution.

Results: The initial prototype will feature a source-detector-distance of 1000 mm and source-axis-distance of 550 mm, a 43x43 cm2 flat panel detector, and a 15° rotating anode x-ray source with 15 kW power and 0.6 focal spot size. Artifact correction reduced image nonuniformity by ~250 HU and improve CNR by 25%.

Conclusions: A dedicated CBCT system capable of imaging millimeter-scale acute ICH was designed; preliminary findings support feasibility of point of care applications in TBI and stroke imaging, with clinical studies beginning on a prototype.

9783-27, Session 6

Intravenous 3D digital subtracted angiography (IV 3D-DSA) from a single sweep C-arm cone beam CT (CBCT) acquisition

Yinsheng Li, Kai Niu, Pengfei Yang, Beverly D. Aagaard-Kienitz, David B. Niemann, Azam S. Ahmed, Charles M. Strother, Guang-Hong Chen, Univ. of Wisconsin-Madison (United States)

Currently, clinical acquisition of IV 3D-DSA requires two separate scans: one mask scan without contrast medium and a filled scan with contrast injection. Having two separate scans adds radiation dose to the patient and increases the likelihood of suffering inadvertent patient motion induced mis-registration and the associated mis-registration artifacts in IV 3D-DSA images. In this paper, a new technique is introduced to generate IV 3D-DSA images from a single Cone Beam CT (CBCT) acquisition to eliminate the mask scan for reduction in both radiation dose and patient motion artifacts. To achieve this purpose, a new reconstruction method was used to generate three image volumes from one short scan range. These three image volumes can have significantly different contrast enhancement and thus a subtraction between the two image volumes with the largest difference enables us to generate the desired IV 3D DSA angiograms. The technical foundation of this work is our recently published iterative image reconstruction algorithm: Synchronized MultiArtifact Reduction with Tomographic reconstruction (SMART-RECON). Both a numerical phantom study and in vivo human subject data were used to validate the algorithm in terms of contrast recoverability and the ability to mitigate artifacts.

9783-28, Session 6

C-arm cone-beam CT perfusion imaging using SMART-RECON method to improve temporal sampling density and temporal resolution

Kai Niu, Yinsheng Li, Univ. of Wisconsin-Madison (United States); Sebastian Schafer, Kevin L. Royalty, Siemens Medical Solutions USA, Inc. (United States); Charles M. Strother, Guang-Hong Chen, Univ. of Wisconsin-Madison (United States)

In this work we applied a newly developed reconstruction algorithm, Synchronized MultiArtifact Reduction with Tomographic reconstruction (SMART-RECON), to C-arm cone beam CT perfusion (CBCTP). This algorithm contains a special rank regularizer, designed to reduce limited view artifacts associated with super-short scan reconstructions. As a result, high temporal sampling and temporal resolution image reconstructions are achievable using a C-arm gantry. This algorithm can be directly used to solve the problems associated with current CBCTP acquisitions, namely, low temporal sampling and temporal resolution and inferior contrast to noise ratio (CNR) compared with CT perfusion (CTP). The algorithm was evaluated in terms of reconstruction accuracy, temporal sampling/resolution improvement, and noise reduction on both reconstructed CBCTP images and calculated perfusion maps in a simulated phantom study. The algorithm was also applied to an in vivo human dataset to compare the CBCTP maps with clinical CTP maps. Using SMART-RECON, the temporal curve can be accurately recovered (error is within 5% compared with 22% for FBP) and the temporal sampling and temporal resolution of CBCTP dataset can be improved from 4-5 seconds to 1-2 seconds. In addition, the CNR can be boosted dramatically. For the in vivo human dataset, the CBCTP maps calculated with SMART-RECON image quality equivalent to the clinical CTP maps in terms of differentiating gray and white matter as well as identifying the relevant abnormality’s shape and location.

9783-29, Session 6

Nonlinear statistical reconstruction for flat-panel cone-beam CT with blur and correlated noise models

Steven W. Tilley II, Jeffrey H. Siewerdsen, Wojciech Zbijewski, Joseph W. Stayman, Johns Hopkins Univ. (United States)

Flat-panel cone-beam CT (FP-CBCT) is a promising imaging modality, partly due to its potential for high spatial resolution reconstructions in relatively compact scanners. Despite this potential, FP-CBCT can face difficulty resolving important fine scale structures (e.g. trabecular details in dedicated extremities scanners and microcalcifications in dedicated CBCT mammography). Model-based methods offer one opportunity to improve high-resolution performance without any hardware changes. Previous work, based on a linearized forward model, demonstrated improved performance when both system blur and spatial correlations characteristics of FP-CBCT systems are modeled. Unfortunately, the linearized model relies on a staged processing approach that complicates tuning parameter selection and can limit the finest achievable spatial resolution. In this work, we present an alternative scheme that leverages a full nonlinear forward model with both system blur and spatially correlated noise. A likelihood-based objective function is derived from this forward model and we derive an iterative optimization algorithm for its solution. The proposed approach is evaluated in simulation studies using a digital extremities phantom and resolution-noise tradeoffs are quantitatively evaluated. The correlated nonlinear model...
outperformed both the uncorrelated nonlinear model and the staged linearized technique with up to a 300% reduction in variance at matched spatial resolution. Additionally, the correlated nonlinear model could achieve finer spatial resolution (as low as 0.1 mm) than the nonlinear uncorrelated model (0.14 mm), the linear correlated model (0.15 mm), and traditional FBP (0.4 mm). This suggests the proposed nonlinear approach may be an important tool in improving performance for high-resolution clinical applications.

9783-30, Session 6
Automatic intrinsic cardiac and respiratory gating from cone-beam CT scans of the thorax region
Andreas Hahn, Sebastian Sauppe, Deutsches Krebsforschungszentrum (Germany); Michael Lell, Friedrich-Alexander-Univ. Erlangen-Nürnberg (Germany); Marc Kachelriess, Deutsches Krebsforschungszentrum (Germany)

We present a new algorithm that allows for raw data-based automated cardiac and respiratory intrinsic gating in cone-beam CT scans. It can be summarized in three steps:

First, a median filter is applied to an initially reconstructed volume. The forward projection of this volume contains no more motion information but only blurred projections. Subtracting the original and the blurred projections results in new raw data that contain only moving and not static anatomy like bones, that would otherwise impede the cardiac or respiratory signal acquisition. All further steps are applied to these modified raw data.

Second, the raw data are cropped to a region of interest (ROI). The ROI in the raw data is determined by the forward projection of a binary volume of interest (VOI) that includes the diaphragm for respiratory gating and most of the edge of the heart for cardiac gating.

Third, the mean gray value in this ROI is calculated for every projection and the respiratory/cardiac signal is acquired using a bandpass filter.

Steps two and three are carried out simultaneously for 64 overlapping VOI inside the body. The signals acquired from each ROI are compared and the most consistent one is chosen as the desired cardiac or motion signal. Consistency is assessed by the standard deviation of the time between two maxima.

The robustness and efficiency of the method is evaluated using simulated and measured patient data by computing the standard deviation of the mean signal difference between the ground truth and the intrinsic signal.

9783-31, Session 6
Reduction of beam hardening artifacts in cone-beam CT imaging via SMART-RECON algorithm
Yinsheng Li, John Garrett, Guang-Hong Chen, Univ. of Wisconsin-Madison (United States)

When an Automatic Exposure Control (AEC) is introduced in C-arm cone beam CT data acquisition, the spectral inconsistencies between acquired projection data are exacerbated. Hence, conventional water/bone correction schemes are not as effective as in conventional diagnostic x-ray CT acquisitions with a fixed tube potential. In this paper, a new method was proposed to reconstruct several images with different degree of spectral consistency and thus different level of beam hardening artifacts. In this paper, the recently developed Synchronized Multi-Artifact Reduction with Tomographic RECONstruction (SMART-RECON) algorithm will be used to cope with the highly spectrally inconsistent data acquired from a C-arm cone beam CT system with tube potential modulation due to the use of AEC. As a result, several images can be reconstructed from a spectrally mixed data set. These images demonstrate different levels of beam hardening artifacts and thus any with significantly reduced beam hardening artifacts can be selected for clinical use. The new method relies on neither on prior knowledge of the x-ray beam spectrum nor prior compositional information of the imaging object. Both numerical simulations and in vivo human subject studies have been performed to validate the proposed strategy.

9783-32, Session 7
Development of a realistic dynamic digital brain phantom for CT perfusion validation
Sarah E. Divel, Stanford Univ. (United States); W. Paul Segars, Duke Univ. Medical Ctr. (United States); Soren Christensen, Max Wintermark, Maarten G. Lansberg, Stanford Univ. Medical Ctr. (United States); Norbert J. Pelc, Stanford Univ. (United States)

Physicians rely on CT Perfusion (CTP) images and quantitative image data, including cerebral blood flow, cerebral blood volume, and bolus arrival delay, to diagnose and treat stroke patients. However, the quantification of these metrics may vary depending on the computational method used. Therefore, we have developed a dynamic and realistic digital brain phantom upon which CTP scans can be simulated based on a set of ground truth scenarios. Building upon the previously developed 4D extended cardiac-torso (XCAT) phantom containing a highly detailed brain model, this work consisted of expanding the intricate vasculature by semi-automatically segmenting existing MRA data and fitting nonuniform rational B-spline surfaces to the new vessels. Using time attenuation curves input by the user as reference, the contrast enhancement in the vessels changes dynamically. At each time point, the iodine concentration in the arteries and veins is calculated from the curves and the material composition of the blood changes to reflect the expected values. CatSim, a CT system simulator, generates simulated data sets of this dynamic digital phantom which can be further analyzed to validate CTP studies and post-processing methods. The development of this dynamic and realistic digital phantom provides a valuable resource with which current uncertainties and controversies surrounding the quantitative computations generated from CTP data can be examined and resolved.

9783-33, Session 7
Fluence-field modulated x-ray CT using multiple aperture devices
Joseph W. Stayman, Aswin J. Mathews, Wojciech Zbijewski, Grace J. Gang, Jeffrey H. Siewerdsen, Satomi Kawamoto, Johns Hopkins Univ. (United States); Ira Blevis, Reuven Levinson, Philips Medical Systems Technologies Ltd. (Israel)

We introduce a novel strategy for fluence field modulation (FFM) in x-ray CT using multiple aperture devices (MADs). MAD filters permit FFM by blocking or transmitting the x-ray beam on a fine (0.1-1 mm) scale. The filters have a number of potential advantages over other beam modulation strategies including the potential for a highly compact design, modest actuation speed and acceleration requirements, and spectrally neutral filtration due to their essentially binary action. In this paper, we present the underlying MAD filtration concept including a design process to achieve a specific class of FFM patterns. A set of MAD filters is fabricated using a tungsten laser sintering process and integrated into an x-ray CT test bench. A characterization of the MAD filters is conducted and compared to traditional attenuating bowtie filters and the ability to flatten the fluence profile for a 32 cm acrylic phantom is demonstrated. MAD-filtered tomographic data was acquired on the CT test bench and reconstructed without artifacts associated with the MAD filter. These initial studies suggest that MAD-based FFM is appropriate for integration in clinical CT system to create patient-specific fluence field profile and reduce radiation exposures.
Accuracy of patient specific organ-dose estimates obtained using an automated image segmentation algorithm

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The overall goal of this work is to develop a rapid, accurate and fully automated software tool to estimate patient-specific organ doses from computed tomography (CT) scans using a deterministic Boltzmann Transport Equation solver and automated CT segmentation algorithms. This work quantified the accuracy of organ dose estimates obtained by an automated segmentation algorithm. The investigated algorithm uses a combination of feature-based and atlas-based methods. A multi-atlas approach was also investigated. We hypothesize that the autosegmentation algorithm is sufficiently accurate to provide organ dose estimates since random errors at the organ boundaries will average out when computing the total organ dose. To test this hypothesis, twenty head-neck CT scans were expertly segmented into 13 regions. A leave-one-out validation study was performed, where every case was automatically segmented with each of the remaining cases used as the expert atlas, resulting in nineteen automated segmentations for each of the twenty datasets. The segmented regions were applied to gold-standard Monte Carlo dose maps to estimate mean and peak organ doses. The results demonstrated that the fully automated segmentation algorithm estimated the mean and peak CT organ dose to within 10% of the expert segmentation for non-bone regions in head/neck CT scans. The error in bone regions ranged from 13% to 30%. The multiple-case atlas reduced the error and variation in the dose estimates and additional improvements may be possible with more robust multi-atlas approaches. Overall, the results support potential feasibility of an automated segmentation algorithm to provide accurate organ dose estimates.

Noise characteristics of CT perfusion imaging: How does noise propagate from source images to final perfusion maps?

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Cerebral CT perfusion (CTP) imaging is playing an increasingly important role in the diagnosis and treatment of acute ischemic strokes. Meanwhile, the reliability of CTP-based ischemic lesion detection has been challenged due to the noisy appearance and low signal-to-noise ratio of CTP maps. To reduce noise and improve image quality, a rigorous study on the noise transfer properties of CTP systems is highly desirable to provide the needed scientific guidance. This paper concerns how noise in the CTP source images propagates to the final CTP maps. Both theoretical deviations and subsequent validation experiments demonstrated that, the noise level of background frames plays a dominant role in the noise level of the cerebral blood volume (CBV) maps. This is in direct contradiction with the general belief that noise of non-background image frames is of greater importance in CTP imaging. The study found that when radiation doses delivered to the background frames and to all non-background frames are equal, lowest noise variance is achieved in the final CBV maps. This novel equality condition provides a practical means to optimize radiation dose delivery in CTP data acquisition: radiation exposures should be modulated between background frames and non-background frames so that the above equality condition is satisfied. For two typical CTP acquisition protocols of our clinical institution, numerical simulations demonstrated approximate threefold reduction in noise variance using the proposed exposure modulation method, which was qualitatively confirmed through an in vivo animal experiment.

Experimental characterization of extra-focal radiation in CT scanners

Bruce R. Whiting, Univ. of Pittsburgh (United States); Joshua D. Evans, Mariela A. Porras-Chaverri, Jeffrey F. Williamson, Virginia Commonwealth Univ. (United States)

Quantitative computed tomography (CT) applications based on statistical iterative reconstruction algorithms require accurate models for all aspects of the CT signal formation process, including contributions to the collimated detector array from scattered as well as primary photons produced by the x-ray fan beam. We present a method to experimentally determine the extra-focal radiation profile measured by individual CT detectors. Using a tungsten cylinder as a knife edge, the trajectory of the edge was computed and used to form a super-sampled signal from sinogram data. This signal traces the “eclipse” of the x-ray source as seen from a detector. By differentiating this signal and correcting for finite detector size and motion blur, the effective source profile can be recovered. Extra-focal scatter was found to be on the order of several percent of the focal beam intensity, with symmetric lower relative magnitude near isocenter and increasing towards the edge of the fan beam, with its profile becoming asymmetric at large angles. The implications for reconstruction algorithms and QCT applications will be discussed.
questionable assumptions are addressed: (1) the need for regular breathing patterns and (2) a constant correlation between the external breathing signal acquired for image/projection sorting and internal motion patterns. To counteract (1), a patient-specific upper breathing signal amplitude threshold is introduced to avoid artifacts due to unusual deep inspiration (helpful for both amplitude- and phase-based reconstruction). In addition, a projection data-binning algorithm based on a statistical analysis of the patient’s breathing signal is proposed to stabilize phase-based sorting. To further alleviate the need for (2), an image artifact metric is incorporated into and minimized during the reconstruction process. The optimized reconstruction is evaluated using 30 clinical 4DCT data sets and demonstrated to significantly reduce motion artifacts.

To facilitate rigorous virtual clinical trials for breast imaging optimization and evaluation, we demonstrated a method of defining statistical models, based on 200 breast CT patient data, in order to generate tens of thousands of unique digital breast phantoms.

Variations in breast shape, size, or compressed thickness can be introduced by mapping to different atlas geometries. But to simplify we removed the variation in breast shape by deforming the phantom population to one atlas compressed geometry. Principal component analysis (PCA) was then performed on the shape-matched breast CT volumes to capture the variation of patient breast textures. PCA decomposes the training set of N breast CT volumes into an N-dimensional space of eigenvectors, which we call eigenbreasts. By summing weighted combinations of eigenbreasts, a large ensemble of different breast phantoms can be newly created.

Different training sets can be used in eigenbreast analysis for designing basis models to target sub-populations defined by breast characteristics, such as size or density. In this work, we plan to generate ensembles of 30,000 new phantoms based on glandularity for an upcoming virtual trial of lesion detectability in digital breast tomosynthesis.

Our method extends our series of digital and physical breast phantoms based on the human subject anatomy, providing a capability to generate new, unique ensembles consisting of tens of thousands or more virtual subjects. This work represents an important step towards conducting future virtual trials for tasks-based assessment of breast imaging, where it is vital to have a large ensemble of realistic phantoms for statistical power as well as clinical relevance.

9783-500, Session PL

The evolution of medical imaging from qualitative to quantitative: opportunities, challenges, and approaches
Edward F. Jackson, Univ. of Wisconsin School of Medicine and Public Health (United States)

No Abstract Available

9783-81, Session PS1

Conceptual detector development and Monte Carlo simulation of a novel 3D breast computed tomography system
Jens Ziegle, Christoph Hoeschen, Bernhard H. Müller, Bernd Neumann, Otto-von-Guericke Univ. Magdeburg (Germany)

A new 3D breast computed tomography (CT) system is under development enabling imaging of microcalcifications in a fully uncompressed breast including posterior chest wall tissue. The system setup uses a steered electron beam impinging on small tungsten targets surrounding the breast to emit X-rays. A realization of the detector concept is presented in this work and it is modeled through Monte Carlo simulations in order to quantify first characteristics of transmitted and scattered photons. The modeled system comprises a vertical alignment of linear detectors hold by a case that also hosts the breast. Detectors are separated by gaps to allow the passage of X-rays towards the breast volume. The detectors located directly on the opposite side of the gaps detect incident X-rays. Mechanically moving parts in an imaging system increase the duration of image acquisition and thus can cause motion artifacts. So, a major advantage of the presented system design is the combination of the fixed detectors and the fast steering electron beam which enable a greatly reduced scan time. Thereby potential motion artifacts are reduced so that the visualization of small structures such as microcalcifications is improved. The result of the simulation of a single projection shows high attenuation by parts of the detector electronics causing low signal levels at the opposing detectors which would require a flat field correction. However the ratio of scattering to the overall counted X-rays is less than 1 percent.

9783-82, Session PS1

Eigenbreasts for statistical breast phantoms
Gregory M. Sturgeon, Duke Univ. (United States); Daniel J. Tward, Johns Hopkins Univ. (United States); Subok Park, U.S. Food and Drug Administration (United States); W. Paul Segars, Joseph Y. Lo, Duke Univ. (United States)

9783-83, Session PS1

Optimal exposure techniques for iodinated contrast-enhanced breast CT
Stephen J. Glick, Andrey V. Makeev, Ctr. for Devices and Radiological Health, U.S. Food and Drug Administration (United States)

Screening for breast cancer using mammography has been very successful in the effort to reduce breast cancer mortality, and its use has largely resulted in the 30% reduction in breast cancer mortality observed since 1990. However, diagnostic mammography, defined as a separate procedure from screening where supplemental mammographic views are acquired to assist radiologists in the evaluation of an area of clinical or radiographic concern remains an area of breast imaging that is in great need for improvement. One imaging modality proposed for improving the accuracy of diagnostic workup is iodinated contrast-enhanced breast CT. In this study, a mathematical framework is used to evaluate optimal exposure techniques for contrast-enhanced breast CT. The ideal observer signal-to-noise ratio (i.e., d’) figure-of-merit is used to provide a task performance based assessment of optimal acquisition parameters under the assumptions of a linear, shift-invariant imaging system. A parallel-cascade model was used to estimate signal and noise propagation through the detector, and a realistic lesion model with iodine uptake was embedded into a structured breast background. Ideal observer performance was investigated across kVp settings, filter materials, filter thickness, breast size and radiation dose. Results indicated many kVp spectra/filter combinations can perform well, however, if x-ray tube heat loading limitations are considered, there are only a few kVp spectra/filter combinations that provide superior performance.

9783-84, Session PS1

Simulation of spiculated breast lesions
Premkumar Elangovan, Faisal Alrehily, Rafael F. Pinto, Univ. of Surrey (United Kingdom); Alaleh Rashid Nasab, Univ. College London (United Kingdom); David R. Dance, Kenneth C. Young, The Royal Surrey County Hospital NHS Trust (United Kingdom); Kevin Wells, Univ. of Surrey (United Kingdom)
Virtual clinical trials are a promising new approach increasingly used for the evaluation and comparison of breast imaging modalities. A key component in such an assessment paradigm is the use of simulated pathology, in particular, simulation of lesions. Breast mass lesions can be generally classified into two categories based on the appearance; non-spiculated masses and spiculated masses. In our previous work, we have successfully simulated non-spiculated masses using a fractal growth process known as diffusion limited aggregation (DLA). In this new work, we have extended the DLA model to simulate spiculated lesions by using features extracted from patient DBT images containing spiculated lesions. The features extracted include spicule length, width, curvature and distribution. This information was used to simulate realistic looking spicules which were attached to the surface of a DLA mass to produce a spiculated mass. A batch of simulated spiculated masses was inserted into normal patient images and presented to an experienced radiologist for review. The study yielded promising results with 33% detection of this disease is possible via mammography. A photon-counting mammography technique is the ability to discriminate using three energy ranges. Therefore we proposed a method of estimating the composition of the mammary gland using a CdTe series detector as a photon-counting detector in this study. An important advantage of our proposed photon-counting mammography technique is the ability to discriminate using three energy bins. We designed the CdTe series detector system in a MATLAB simulation. The phantom, a 3 cm x 3 cm rectangular parallelepiped, was divided into nine sections, with the ratio of glandular tissue and adipose tissue varied in increments of 10%. The attenuation coefficient for each bin’s energy was calculated from the number of input and output photons each possessed. The results of evaluations conducted by plotting the attenuation coefficient ? in a three-dimensional (3D) scatter plot showed that the plots had a regular composition order congruent with that of the mammary gland. Consequently, we believe that our proposed method can be used to estimate the composition of the mammary gland.

**9783-85, Session PS1**

**Estimation of mammary gland composition using CdTe series detector developed for photon-counting mammography**

Akito Ihori, Chizuru Okamoto, Nagoya Univ. (Japan); Tsutomu Yamakawa, Shuichi Yamamoto, Masahiro Okada, JOB Corp. (Japan); Ai Nakajima, Misa Kato, Yoshie Kodera, Nagoya Univ. (Japan)

Breast cancer is one of the most common cancers in Japan. Early detection of this disease is possible via mammography. A photon-counting mammography is a new technology, and it counts the number of photons that passes through an object, and presents it as a pixel value in an image of the object. Silicon semiconductor detectors are already used in commercial mammography. However, the disadvantage of silicon is the low absorption efficiency for high photon energies. The cadmium telluride (CdTe) series detector has high absorption efficiency over a wide energy range. Therefore we proposed a method of estimating the composition of the mammary gland using a CdTe series detector as a photon-counting detector in this study. An important advantage of our proposed photon-counting mammography technique is the ability to discriminate using three energy bins. We designed the CdTe series detector system in a MATLAB simulation. The phantom, a 3 cm x 3 cm rectangular parallelepiped, was divided into nine sections, with the ratio of glandular tissue and adipose tissue varied in increments of 10%. The attenuation coefficient for each bin’s energy was calculated from the number of input and output photons each possessed. The results of evaluations conducted by plotting the attenuation coefficient ? in a three-dimensional (3D) scatter plot showed that the plots had a regular composition order congruent with that of the mammary gland. Consequently, we believe that our proposed method can be used to estimate the composition of the mammary gland.

**9783-86, Session PS1**

**Modeling and dimensioning a novel tissue-specific breast imaging system using spectral x-ray coherent scattering**

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Mammography is currently one of the most demanding imaging techniques due to a persistent difficulty to detect small microcalcifications and distinguish masses, benign or malign, from fibro-glandular tissue. This latter issue seems to be solvable thanks to x-ray coherent scattering. Indeed, some previous studies have shown that this technique can provide a better contrast between these tissues than classical x-ray absorption. The ultimate goal of our work is to develop a system based on this technique usable in medical condition, in or ex vivo. For that we chose to use a specific technique of scattering measurement called Energy-Dispersive X-Ray Diffraction (EDXRD); or spectral x-ray coherent scattering which combines the use of an x-ray tube and a spectrometric detector. Therefore, this paper presents the modeling of an EDXRD device as a way to identify and image materials for a medical application. This model is based on an analytic direct model which combines all the different factors involved in the system such as incident spectrum, attenuation, x-ray scattering, collimations and detection. Then, a series of processing is used to extract the signatures of the materials from the detected spectrum. This is aimed to optimize energy-dispersive x-ray scattering experimental setup for medical application, namely breast imaging. The results presented here shows the capability of our modeling to get the material-specific image of a given object viewed by an EDXRD system.

**9783-87, Session PS1**

**Reduction of artifacts in computer simulation of breast Cooper’s ligaments**

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Anthropomorphic software breast phantoms have been introduced as a tool for quantitative validation of breast imaging systems. Efficacy of the validation results depends on the realism of phantom images. The recursive partitioning algorithm based upon the octree simulation has been demonstrated as versatile and capable of efficiently generating large number of phantoms to support virtual clinical trials of breast imaging. Previously, we have observed specific artifacts, (here labeled “dents”) on the boundaries of simulated Cooper’s ligaments. In this work, we have demonstrated that these “dents” result from the existing approximate determination of the closest simulated ligament to an examined subvolume (i.e., octree node) of the phantom. We propose a modification of the algorithm that determines the closest ligament by considering a pre-specified number (3-4) of neighboring ligaments selected based upon the functions that govern the shape of ligaments simulated in the subvolume. We have qualitatively and quantitatively demonstrated that the modified algorithm can lead to elimination or reduction of dent artifacts in software phantoms. In a proof-of-concept example, we simulated a 450ml phantom with 333 compartments at 100 micron resolution. After the proposed modification, we corrected 148,105 dents, with an average size of 5.27 voxels (5.27nl). We have also qualitatively analyzed the corresponding improvement in the appearance of simulated mammographic images. The proposed algorithm leads to reduction of linear and star-like artifacts in simulated phantom projections, which can be attributed to dents. Analysis of a larger number of phantoms is ongoing.

**9783-88, Session PS1**

**Analysis of the scatter effect on detective quantum efficiency of digital mammography**

Jiwoong Park, Pusan National Univ. (Korea, Republic of); Seungman Yun, SAMSUNG Electronics Co., Ltd. (Korea, Republic of); Dong Woon Kim, Pusan National Univ. (Korea, Republic of); Cheol-Ha Baek, Dongseo Univ. (Korea, Republic of); Hanbeun Yun, Hosang Jeon, Pusan National Univ. Yangsan Hospital (Korea, Republic of) and
It is a question whether removal of an antiscatter grid would be beneficial to the lower patient dose without losing contrast-detail performance in digital mammography. In this study, we investigate the scatter effect on the Jacobian matrix (J) for each energy window using a Monte Carlo method. For the quantitative comparison, we used the homogeneous cylindrical breast phantom as a reference and the heterogeneous XCAT breast phantom. To evaluate the J matrix, we obtained images according to the energy windows based on the energy absorption efficiency over a wide energy range. In a previous study, we showed that the use of high X-ray energy in digital mammography is useful for reducing the scatter effect. In this work, we present the MAMMOCARE prototype, a dedicated breast PET-guided biopsy system which allows real-time 3D visualization of the lesion position and needle motion. Two PET detector rings and their associated electronics, a complete biopsy system, two transparent polycarbonate pallets to hold the breast during the biopsy procedure, and the engines required to move the system comprise the prototype. The detector system is formed by two rings of twelve modules based on continuous LYSO crystals and PSPMTs that can move axially to explore up to 170mm of FOV. To enable the biopsy procedure, the detectors are separable up to 60mm in the transaxial direction to allow the passage of the biopsy needle.

The biopsy protocol includes the generation of high quality images with the closed detector configuration for the lesion identification and then the online generation of images with the open configuration to allow the user to monitor the procedure and modify the trajectory if it is needed. The image quality has been measured by means of the spatial resolution, uniformity, and sensitivity for both configurations. Uniformity has been found below 15%, and the sensitivity up to 4% in the closed configuration. The resolution degrades off-center from closed (2.5mm FWHM) to open configuration (5.9mm), but still is more than sufficient for performing safely the biopsy monitoring.
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Tendency for the distribution to depend on the thickness of the tumor tissue. Thinner tumor tissues were shown to be closer in appearance to normal breast tissue. This study also demonstrated that the difference between them can be made obvious by using a CdTe series detector. We believe that the differentiation shown is important and therefore expect this technology to be applied to new systems in the future.

9783-92, Session PS1

Grid-less imaging with anti-scatter correction software in 2D mammography: the effects on image quality and MGD under a virtual clinical validation study

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This work investigated the effect of the grid-less acquisition mode with scatter correction software developed by Siemens Healthcare (PRIME mode) on image quality and mean glandular dose (MGD). Image quality was technically quantified with contrast-detail (c-d) analysis on the CDMAM test object and by calculating detectability indices (d’) using a non-prewhitening eye filter observer (NPWE). MGD was estimated technically using slabs of PMMA and clinically on a set of patient images. The c-d analysis gave similar results for all mammographic systems examined, although the d’ values were slightly lower for the system using PRIME mode when compared to the same system in standard mode; a reduction of 2.9% to 5.9% was seen, depending on the PMMA thickness. The MGD values calculated from the PMMA measurements indicated a dose reduction from 11.4% to 27.3% for the system with PRIME mode. The largest dose reduction was found for the smallest indicated breast thickness. The results from the clinical dosimetry study showed an overall population-averaged (breast thicknesses from 20 to 69 mm) dose reduction of 5.9% and 6.8%, respectively, when comparing the system with PRIME mode to the two systems that operated in standard mode. The image quality results will be further investigated, in term of detectability with a virtual clinical trial study by using simulated lesions of microcalcification clusters and masses inserted in patient images.

9783-93, Session PS1

Estimation of adipose compartment volumes in CT images of a mastectomy specimen

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Anthropomorphic software breast phantoms have been utilized for quantitative validation of breast imaging systems. Efficacy of the validation results depends on the realism of phantom images. Our phantom generation method uses the anatomy description based upon the number of adipose compartments and their orientation, thickness of Cooper's ligaments, and the volumetric distribution of these parameters. The realistic values of those anthropometric parameters, however, cannot in general be found in the literature.

In this study, we assess the statistics of adipose compartments from 3D images of a mastectomy specimen of a normal breast. The specimen was preserved in formalin and imaged using a body CT scanner. The 3D images were obtained using a standard CT reconstruction technique. A human operator identified individual adipose compartment by manual segmentation of the specimen reconstructed images. The volume of such segmented compartments was computed using ITK-SNAP software, and its variations throughout the specimen were analyzed. We tracked the time needed for manual segmentation of individual compartments, and examined the relationship between the estimated volumes, segmentation time, and operator’s confidence in the segmentation results.

Preliminary analysis of 27 adipose compartments yielded the average adipose volume of 1.5±0.88ml. The average time needed for manually segmenting average of 23 reconstructed CT slices per compartment was 14.6 minutes. The compartment volume is correlated with manual segmentation time but does not influence the segmentation confidence. The analysis of the intra- and inter-operator variability is ongoing.

9783-94, Session PS1

Feasibility of generating quantitative composition images in dual energy mammography: a simulation study

Donghoon Lee, Ye-seul Kim, Sunghoon Choi, Haenghwa Lee, Seungyeon Choi, Hee-Joung Kim, Yonsei Univ. (Korea, Republic of)

Breast cancer is one of the most common causes of death for women aged 50-69. Thus, it is important to finding breast cancer at early stage before it starts to cause symptoms. X-ray mammography has been a gold standard for breast cancer screening in normal risk women for early breast cancer detection [1]. Mammography has an excellent diagnosis capability especially for women from 50 to 70 year old while the detectability of cancer drops significantly for young women who have dens breasts. Therefore, it is important to identify the presence of cancer in dense breast. Dual energy mammography is recently developed imaging technique that can resolve poor sensitivity in dense breast. However conventional dual energy technique can decompose breast into only two materials. To resolve this problem, we tested capability of three materials decomposition in digital mammography by using simulation study. The GATE v6 (Geant4 application for tomographic emission) and XASMP code were used for simulation study and simulated cylinder shape phantom consisted of 9 inner cylinder which were composed of different composition of water, lipid and protein. The results showed that three materials can be decomposed effectively by using dual energy mammography system. The results of quantitative analysis of three materials showed that water and lipid had relatively high accuracy of materials decomposition comparing to protein. In conclusion, this study can help improving diagnosis efficiency in dual energy mammography by decomposing three kinds of materials which are mainly composed of human breast.

9783-95, Session PS1

A new paradigm of dielectric relaxation spectroscopy for non-invasive detection of breast abnormalities: a preliminary feasibility analysis

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In order to improve efficacy of screening mammography, in recent years, we investigated the feasibility of applying resonance-frequency based electrical impedance spectroscopy (REIS) to non-invasively detect breast abnormalities that may lead to the development of cancer in the near-term. Despite promising study-results, we found that REIS suffered from relatively poor reproducibility due to perturbations in electrode placement, contact pressure variation on the breast, as well as variation of the resonating inductor. To overcome this limitation, in this study, we propose and analyze a new paradigm of Dielectric Relaxation Spectroscopy (DRS) that measures polarization-lag of dielectric signals in breast-capacitance when excited by the pulses or sine waves. Unlike conventional DRS that operates using the
signals at very high frequencies (GHz) to examine changes in polarization, our new method detects and characterizes the dielectric properties of tissue at low frequencies (≤10 MHz) due to the advent of inexpensive oscillators that are accurate to 1 pico-second (used in GPS receivers) as well as measurement of amplitudes of 1 ppm or better. From theoretical analysis, we have proved that the sensitivity of new DRS in detecting permittivity of water increased by ≥80 times as compared to conventional DRS, operated at frequency around 4GHz. By analyzing and comparing the relationship between the new DRS and REIS, we found that this DRS has advantages in enhancing repeatability from various readings, including temperature-insensitive detection, and yielding higher resolution or sensitivity (up to 100 Femtofardads).

9783-96, Session PS1

**DICOM organ dose does not accurately represent calculated dose in mammography**

Moayyad E. Suleiman, Patrick C. Brennan, Lucy Cartwright, The Univ. of Sydney (Australia); Jennifer Diffey, The Univ. of Sydney (Australia); Mark F. McEntee, The Univ. of Sydney (Australia)

This study aims to analyze the agreement between doses estimated within the mammography unit (DICOM dose) and doses calculated using published methods (calculated dose). Anonymised digital mammograms from 50 BreastScreen NSW centers were downloaded and exposed information related to the calculation of dose were extracted along with the DICOM dose estimated by the system. Data from quality assurance annual tests for the included centers were collected and used to calculate the mean glandular dose for each mammogram. Bland-Altman analysis and a two-tailed paired t-test were used to study the agreement between calculated and DICOM dose and the significance of any differences. A total of 27,869 dose points from 40 centers were included in the study, mean DICOM dose and mean calculated dose were 1.47 (±0.66) and 1.38 (±0.56) mGy. A statistically significant 0.09 mGy bias (t = 69.25; p<0.0001) with 95% limits of agreement between calculated and DICOM doses ranging from -0.336 to 0.517 were shown by Bland-Altman analysis, which indicates a small yet highly significant difference between the two means. The use of DICOM dose for dose audits is done at the risk of over or underestimating the calculated dose, hence, further work is needed to identify the causal agents for differences between DICOM and calculated doses and to generate a correction factor for DICOM dose.

9783-97, Session PS1

**Radiation dose differences between digital mammography and digital breast tomosynthesis are dependent on breast thickness**

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Purpose: To evaluate the radiation dose derived from digital mammography (DM) and digital breast tomosynthesis (DBT) at different tube current-exposure time product (mAs) and at 6 phantom thicknesses from 10 to 60 mm. Materials and Methods: A total of 240 DM and DBT cranio-caudal (CC) phantom images were acquired at each thickness and at four exposure levels (the baseline mAs, 50%, 25% and 12.5% the baseline mAs). The mean glandular dose (MGD) was measured using a solid state dosimeter. MGD values were reported for both modalities (DM and DBT). Results: DBT dose was greater than that of DM for all mAs at each phantom thickness. For a breast thickness of 50 mm (close to average sized breast), the current study shows that the dose for DBT (2.32 mGy) was 1.3% higher than that for DM (2.05 mGy). The results also show that the difference in MGD between DM and DBT at 100% mAs was less for the thinner compared with the thinner phantom, this difference being approximately a factor of 2.6 at 10 mm compared with a factor of 1.0 at 60 mm. While the MGD increased with increasing phantom thickness for both modalities, the dose increase with DBT was less than for DM, with the difference between 10 and 60 mm being a factor of 1.0 for DM and 3 for DBT. Conclusion: The radiation dose from DBT was higher than that of DM and that the difference in dose between DM and DBT becomes less for thicker phantoms.

9783-98, Session PS2

**Ring artifacts removal via spatial sparse representation in cone beam CT**

Zhongyuan Li, Guang Li, Yi Sun, Shouhua Luo, Southeast Univ. (China)

This paper is about the ring artifacts removal method in cone beam CT. Cone beam CT images often suffer from disturbance of ring artifacts which caused by the non-uniform responses of the elements in detectors. Conventional ring artifacts removal methods focus on the correlation of the elements and the ring artifacts’ structural characteristics in either sinogram domain or cross-section image. The challenge in the conventional methods is how to distinguish the artifacts from the intrinsic structures; hence they often give rise to the blurred image results due to over processing. In this paper, we investigate the characteristics of the ring artifacts in spatial space, different from the continuous essence of 3D texture feature of the scanned objects, the ring artifacts are displayed discontinuously in spatial space, specifically along z-axis. Thus we can easily recognize the ring artifacts in spatial space than in cross-section. As a result, we choose dictionary representation for ring artifacts removal due to its high sensitivity to structural information. We verified our theory both in spatial space and coronal-section, the experimental results demonstrate that our methods can remove the artifacts efficiently while maintaining image details.

9783-99, Session PS2

**Library based x-ray scatter correction for dedicated cone beam breast CT**

Lei Zhu, Linxi Shi, Georgia Institute of Technology (United States)

Purpose: Scatter contamination is a fundamental limitation of cone-beam breast CT (CBBCT) image quality, obscuring the conspicuity of calcification and soft-tissue lesion. We propose to pre-compute a scatter library for high efficiency of scatter correction on CBBCT with no requirements of additional scans, hardware modifications or repeated scatter simulation. Method: We use a simplified empirical model to generate a library of scatter maps with varying breast sizes and the CBBCT geometry, using Monte-Carlo (MC) simulation. Breasts are approximated as ellipsoid shapes, filled with homogeneous glandular/adipose tissue mixture. To accelerate the computation of the scatter library, a small number of photons are used in the MC simulation. A 2D Gaussian fitting method is then applied on the simulated scatter to suppress noise. The Geant4 software is chosen in the MC simulation. A 2D Gaussian fitting method is then applied on the simulated scatter to suppress noise. The Geant4 software is chosen for differences between DICOM and calculated doses and to generate a correction factor for DICOM dose.
tissue is enhanced by a factor of 2 on average.

Conclusion: The proposed library-based method shows great promise for effective scatter correction on clinical CBCT, with attractive features of implementation simplicity and high computational efficiency.

9783-100, Session PS2
Properties of the ellipse-line-ellipse trajectory with asymmetrical variations
Zijia Guo, Frédéric Noo, The Univ. of Utah (United States); Guenter Lauritsch, Siemens Healthcare GmbH (Germany)

Three-dimensional cone-beam (CB) imaging using a mounted C-arm system has become an important tool in interventional radiology. This success motivates new developments to improve image quality. One direction in which advancement is sought is the data acquisition geometry and related CB artifacts. Currently, data acquisition is performed using the circular short-scan trajectory, which yields limited axial coverage and also provides incomplete data for accurate reconstruction. To improve the image quality, as well as to increase the coverage in the longitudinal direction of the patient, we recently introduced the ellipse-line-ellipse trajectory and showed that this trajectory provides full R-line coverage within the FOV, which is a key property for accurate reconstruction from truncated data. An R-line is any segment of line that connects two source positions. Here, we examine how the application of asymmetrical variations to the definition of the ELE trajectory impacts the R-line coverage. This question is significant to understand how much flexibility can be used in the implementation of the ELE trajectory, particularly to adapt the scan to patient anatomy and imaging task of interest. Two types of asymmetrical variations, called axial and angular variations, are investigated.

9783-101, Session PS2
Lens of the eye dose calculation for neuro-interventional procedures and CBCT scans of the head
Zhenyu Xiong, Sarath Vijayan, Vijay K. Rana, Amit Jain, Stephen Rudin, Daniel R. Bednarek, Toshiba Stroke and Vascular Research Ctr., Univ. at Buffalo (United States)

The aim of this work is to develop a method to calculate lens dose for fluoroscopically-guided neuro-interventional procedures and for CBCT scans of the head. EGSnrc Monte Carlo software is used to determine the dose to the lens of the eye for the projection geometry and exposure parameters used in these procedures. This information is provided by a digital CAN bus on the Toshiba Infinix C-Arm system which is saved in a log file by the real-time skin-dose tracking system (DTS) we previously developed. The x-ray beam spectra on this machine were simulated using BEAMnrc. These spectra were compared to those determined by SpekCalc and validated through measured percent-depth-dose (PDD) curves and HVL measurements. We simulated CBCT procedures in DOSXYZnrc for a CTDI head phantom and compared the surface dose distribution with that measured with Gafchromic film, and for an SK150 head phantom and compared the lens dose with that measured with an ionization chamber. Both methods demonstrated good agreement. Organ dose calculated for a simulated neuro-interventional procedure using DOSXYZnrc with the Zubal CT voxel phantom agreed within 10% with that calculated by PCXMC code for most organs. To calculate the lens dose in a neuro-interventional procedure, we developed a library of normalized lens dose values for different projection angles and kVp's. The total lens dose is then calculated by summing the values over all beam projections and can be included on the DTS report at the end of the procedure.

9783-102, Session PS2
A system to track skin dose for neuro-interventional cone-beam computed tomography (CBCT)
Zijia Guo, Frédéric Noo, The Univ. of Utah (United States); Guenter Lauritsch, Siemens Healthcare GmbH (Germany)

The skin-dose tracking system (DTS) provides a color-coded illustration of the cumulative skin-dose distribution on a closely-matching 3D graphic of the patient during fluoroscopic interventions in real-time for immediate feedback to the interventionist. The skin-dose tracking utility of DTS has been extended to include cone-beam computed tomography (CBCT) of neurointerventions. While the DTS was developed to track the entrance skin dose including backscatter, a significant part of the dose in CBCT is contributed by exit primary radiation and scatter due to the many overlapping projections during the rotational scan. The variation of scatter inside and outside the collimated beam was measured with radiochromic film and a curve was fit to obtain a scatter spread function that could be applied in the DTS. Likewise, the exit dose distribution was measured with radiochromic film for a single projection and a correction factor was determined as a function of path length through the head. Both of these sources of skin dose are added for every projection in the CBCT scan to obtain a total dose mapping over the patient graphic. Results show the backscatter to follow a sigmoidal falloff near the edge of the beam, extending outside the beam as far as 8 cm. The exit dose measured for a cylindrical CTDI phantom was nearly 10% of the entrance peak skin dose for the central ray. The dose mapping performed by the DTS for a CBCT scan was compared to that measured with radiochromic film and a CTDI-head phantom with good agreement.

9783-103, Session PS2
Regularization design for high-quality cone-beam CT of intracranial hemorrhage using statistical reconstruction
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Intracranial hemorrhage (ICH) is associated with pathologies such as hemorrhagic stroke and traumatic brain injury. More dedicate CT is the current front-line imaging modality for detecting ICH (fresh blood contrast 30-50 HU, down to 1 mm). Flat-panel detector (FPD) cone-beam CT (CBCT) offers a potential alternative with a smaller scanner footprint, greater portability, and lower cost. Previous studies have suggested reliable detection of ICH down to 3 mm in CBCT using high-fidelity artifact correction and penalized weighted least-squared (PWLS) image reconstruction with a post-artifact-correction noise model. However, ICH reconstructed by traditional image regularization exhibits nonuniform spatial resolution and noise due to interaction between the statistical weights and regularization, which potentially degrades the detectability of ICH. In this work, we propose three regularization methods designed to overcome these challenges. The first two compute spatially varying certainty for uniform spatial resolution and noise compared to traditional regularization. The third exhibits the highest uniformity in detectability among all methods and best overall image quality. The proposed regularization provides a valuable means to achieve uniform image quality in CBCT of ICH and is being incorporated in a CBCT prototype for ICH imaging.
A fast GPU-based approach to branchless distance-driven projection and back-projection in cone beam CT

Daniel E. Schlifske, Marquette Univ. (United States)

Modern image reconstruction algorithms rely on projection and back-projection operations to refine an image estimate in iterative image reconstruction. A widely-used state-of-the-art technique is distance-driven projection and back-projection. While the distance-driven technique yields superior image quality in iterative algorithms, it is a computationally demanding process. This has a detrimental effect on the relevance of the algorithms in clinical settings. A few methods have been proposed for enhancing the distance-driven technique in order to take advantage of modern computer hardware. This paper explores a two-dimensional extension of the branchless method that does not compromise image quality. The extension of the branchless method is named “pre-projection integration” because it gets a performance boost by integrating the data before the projection and back-projection operations. It was written with NVIDIA’s CUDA platform and carefully designed for massively parallel GPUs. The performance and the image quality of the pre-projection integration method were analyzed. Both projection and back-projection are significantly faster with pre-projection integration. The image quality was analyzed using cone beam image reconstruction algorithms within Jeffrey Fessler’s Image Reconstruction Toolbox. Images produced from regularized, iterative image reconstruction algorithms using the pre-projection integration method show no significant artifacts.

Scatter correction in CBCT with an offset detector through a deconvolution method using data consistency

Changhwan Kim, Miran Park, Hoyeon Lee, Seungryong Cho, KAIST (Korea, Republic of)

Our earlier work has demonstrated that the data consistency condition can be used as a criterion for scatter kernel optimization in deconvolution methods in a full-fan mode cone-beam CT. However, this scheme cannot be directly applied to a half-fan mode because of transverse data truncation in projections. In this study, we proposed a modified scheme of the scatter kernel optimization method that can be used in a half-fan mode cone-beam CT, and have successfully shown its feasibility. Using the first-reconstructed volume image from half-fan projection data, we acquired full-fan projection data by forward projection synthesis. The synthesized full-fan projections were partly used to fill the truncated regions in the half-fan data. By doing so, we were able to utilize the existing data consistency-driven scatter kernel optimization method. The proposed method was validated by a simulation study using the XCAT numerical phantom.

Imaging characteristics of distance-driven method in a prototype cone-beam computed tomography (CBCT)

Sunghoon Choi, Ye-seul Kim, Haenghwa Lee, Donghoon Lee, Chang-Woo Seo, Hee-Joung Kim, Yonsei Univ. (Korea, Republic of)

Cone-beam computed tomography (CBCT) presents an innovative role in both medical imaging and radiation therapy. The aim of this study was to evaluate our newly developed CBCT system by implementing a distance-driven system modeling technique in order to produce excellent and accurate cross-sectional images. For the purpose of comparing the performance of the distance-driven methods, we also performed pixel-driven and ray-driven techniques when conducting forward- and back-projection schemes. We conducted the Feldkamp-Davis-Kress (FDK) algorithm and simultaneous algebraic reconstruction technique (SART) to retrieve a volumetric information of scanned chest phantom. The results indicated that contrast-to-noise (CNR) of the reconstructed images by using FDK and SART showed 8.02 and 15.78 for distance-driven, whereas 4.02 and 5.16 for pixel-driven scheme and 7.81 and 13.01 for ray-driven scheme. This could demonstrate that distance-driven more closely described the chest phantom compared to pixel- and ray-driven. However, both elapsed time for modeling a system matrix and reconstruction time took longer time when performing the distance-driven scheme. Therefore, future works will be directed toward reducing computational cost to reasonable limits.

Deblurring in iterative reconstruction of half CBCT for image guided brain radiosurgery

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A high spatial resolution iterative reconstruction algorithm is proposed for half cone beam CT (H-CBCT). The proposed algorithm improves spatial resolution by explicitly accounting for image blurriness caused by different factors, such as extended X-ray source, detectors, etc. We model blur with a shift invariant Gaussian kernel measured in x and y direction using a Catphan phantom. The proposed algorithm is specifically optimized for the new Leksell Gamma Knife Icon, Elekta AB, Stockholm, Sweden, which incorporates a H-CBCT geometry to accommodate the existing treatment couch while covering down to the base-of-skull in the reconstructed field-of-view. However, this geometry reduces the sampling rate of the scanned object, which in turn affects the quality of the reconstructed images. Image reconstruction involves a Fourier-based scaling simultaneous algebraic reconstruction technique (SART) coupled with total variation (TV) minimization, solved using a split Bregman separation technique that splits the reconstruction problem into a gradient based updating step and a TV based deconvolution algorithm. This formulation preserves edges and reduces the staircase effect caused by regular TV penalized iterative algorithms. GPU implementation is utilized to handle the computational load of the proposed algorithm. A Catphan phantom and an anatomical brain phantom were used to compare the performance of in-house Feldkamp-Davis-Kress (FDK), TV penalized SART, and the proposed algorithm (TV+Blurring effect). Our experiments indicate that our proposed method outperforms FDK and TV-SART in terms of line pair resolution and retains the favorable properties of the popular TV penalized reconstruction.

Reduction in x-ray scatter and beam hardening for low-dose cone-beam CT

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Purpose: Although cone-beam computed tomography (CBCT) has wide applications in medicine, CBCT does suffer from substantial degrading effects due to scatter on the overall image quality. Meanwhile beam hardening is non-ignorable, as well as the x-ray radiation. Considering the advantages of the Compressed sensing (CS) based reconstruction in sparse-view reconstruction, in this paper, we combined scatter suppression with beam hardening correction for sparse-view CT reconstruction to reduce CT radiation and improve CT image quality.

Methods: First, We distribute blocked areas on the top and bottom of the detector, where primary signals are considered redundant in a full scan. Scatter distribution is estimated by interpolating measured scatter samples inside blocked areas. Second, the attenuation coefficient of each voxel at different energies is linearly modeled and estimated as an equivalent attenuation coefficient at the effective energy, and integrated into the forward projector of the algebraic reconstruction technique (ART). Finally the CS-based iterative reconstruction can recover images when only a limited number of projections are available.

Results: Preliminary validation using Monte Carlo simulations indicates that the with only about 25% of conventional dose, our method reduces the magnitude of cupping artifact by a factor of 6.1, increase the contrast by a factor of 1.8 and the CNR by a factor of 12.

Conclusion: The proposed method can provide relatively good reconstructed images from sparse-view projection data, with effective suppression of artifacts caused by scatter and beam hardening. With the proposed framework and appropriate modeling of other degrading effects, it may provide a new way for low-dose CT imaging.

9783-109, Session PS3

Beam hardening and motion artifacts in cardiac CT: Evaluation and iterative correction method

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For myocardial perfusion CT exams, beam hardening (BH) artifacts may degrade the accuracy of myocardial perfusion defect detection. Meanwhile, cardiac motion may make BH process inconsistent, which makes conventional BH correction (BHC) methods ineffective.

In this study, four sets of forward projection data were first acquired using both cylindrical phantoms and cardiac images as objects: (1) with monochromatic x-rays without motion; (2) with polychromatic x-rays without motion; (3) with monochromatic x-rays with motion; and (4) with polychromatic x-rays with motion. From each dataset, images were reconstructed using filtered back projection; for datasets 2 and 4, one of the following BH correction (BHC) methods was also performed: (A) no BHC; (B) BHC that concerns water only; and (C) BHC that takes both water and iodine into account, which is an iterative method we developed in this work. Biases of images were quantified by the mean absolute difference (MAD).

The MAD of images with BH artifacts alone (dataset 2, without BHC) was comparable or larger than that of images with motion artifacts alone (dataset 3). In the study of cardiac image, BH artifacts account for over 80% of the total artifacts. The use of BhC was effective: with dataset 4, MAD values were 170 HU with no BHC, 54 HU with water BHC, and 42 HU with the proposed BHC. Qualitative improvements in image quality were also noticeable in reconstructed images.

9783-110, Session PS3

MADR: metal artifact detection and reduction

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Metal in CT-imaged objects drastically reduces the quality of these images due to the severe artifacts it can cause. Most metal artifacts reduction (MAR) algorithms consider the metal-affected sinogram portions as the corrupted data and replace them via sophisticated interpolation methods. While these schemes are successful in removing the metal artifacts, they fail to recover some of the edge information. To address these problems, the frequency shift metal artifact reduction algorithm (FSMAR) was recently proposed. It exploits the information hidden in the uncorrected image and combines the high frequency (edge) components of the uncorrected image with the low frequency components of the corrected image. Although this can effectively transfer the edge information of the uncorrected image, it also introduces some of its unwanted artifacts. The essential problem of these algorithms is that they lack the capability of detecting the artifacts and as a result cannot discriminate between desired and undesired edges. We propose a scheme that does better in these respects. Our Metal Artifact Detection and Reduction (MADR) scheme constructs a weight map which stores whether a pixel in the uncorrected image belongs to an artifact region or a non-artifact region. This weight matrix is optimal in the Linear Minimum Mean Square Sense (LMMSE). Our results demonstrate that MADR outperforms the existing algorithms and ensures that the anatomical structures close to metal implants are better preserved.

9783-111, Session PS3

Metal artifact reduction in CT via ray profile correction

Sungsoo Ha, Klaus D. Mueller, Stony Brook Univ. (United States) and SUNY Korea (Korea, Republic of)

In computed tomography (CT), metal implants increase the inconsistencies between the measured data and the linear assumption made by the analytical CT reconstruction algorithm. The inconsistencies appear in the form of dark and bright bands and streaks in the reconstructed image, collectively called metal artifacts. The standard method for metal artifact reduction (MAR) replaces the inconsistent data with the interpolated data. However, sinogram interpolation not only introduces new artifacts but it also suffers from the loss of detail near the implanted metals. With the help of a prior image that is usually estimated from the metal-artifact-degraded image via computer vision techniques, improvements are feasible but still no MAR method exists that is widely accepted and utilized. We propose a technique that utilizes a prior image from a CT scan taken of the patient before implanting the metal objects. Hence there is a sufficient amount of structural similarity to cover the loss of detail around the metal implants. Using the prior scan and a segmentation or model of the metal implant our method then replaces sinogram interpolation with ray profile matching and estimation which yields much more reliable data estimates for the affected sinogram regions. As preliminary work, we built a new MAR framework on fan-beam geometry and tested it to remove simulated metal artifacts on a thorax phantom. The comparison with two representative sinogram correction based MAR methods shows very promising results.

9783-112, Session PS3

Line-ratio based ring artifact correction method using transfer function

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Computed tomography (CT) has been used for various purpose. Especially CT is used for diagnosis of diseases therefore accurate image is very important for that purpose. However, there are many types of CT artifacts and that degrade image quality. Ring artifact is one of the artifacts which is cause by different sensitivity of detectors. Traditional sinogram-domain ring artifact correction method is mean curve based method using...
moving average (MA) filter or median filter. However those methods often make distortion because mean curve not always demonstrate sensitivity difference. Therefore, line-ratio method was proposed to overcome the problem by calculating relative sensitivity ratio of nearest detector. The quality and correction effectiveness of Line-ratio method outperforms mean curve base method without making other artifacts. However, previous line-ratio method could not correct ring properly when some circular object is inside which is centered at isocenter. Proposed method use simple transfer function when calculating relative sensitivity ratio to deal with abnormal case. Such a process makes it possible to correct only ring artifact without distorting circular object. Therefore line-ratio method using transfer function is superior to previous line-ratio method so it can remove ring artifact from CT images properly.

9783-128, Session PS5

Quantitative comparison using generalized relative object detectability (G-ROD) metrics of an amorphous selenium microangiographic fluoroscopes (MAF) and standard flat panel detectors (FPD)

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A novel amorphous selenium (a-Se) direct detector with CMOS readout has been designed, and relative detector performance investigated. The detector features include a 25µm pixel pitch, and 1000µm thick a-Se layer operating at 10V/µm bias field. A simulated detector QE was determined, and used in comparative calculations of the Relative Objective Detectability (ROD) family of prewhitened matched-filter (PWMF) observer and non-prewhitened matched-filter (NPWMF) observer model metrics to gauge a-Se detector performance against existing high resolution microangiographic fluoroscopic (MAF) detectors and a standard flat panel detector (FPD). The PWMF-ROD or RODP metric compares two x-ray imaging detectors in their relative abilities in imaging a given object by taking the integral over spatial frequencies of the Fourier transform of the detector QE weighted by an object function, divided by the comparable integral for a different detector. The generalized-ROD (G-ROD) metric incorporates clinically relevant parameters (focal-spot size, magnification, and scatter) to show the degradation in imaging performance for detectors that are part of an imaging chain. Previous RODP calculations using simulated spheres as the object predicted superior imaging performance by the a-Se detector as compared to existing detectors. New PWMF-G-ROD and NPWMF-G-ROD results still indicate better performance by the a-Se detector in an imaging chain over all sphere sizes for various focal spot sizes and magnifications, although a-Se performance advantages were degraded by focal spot blurring. Nevertheless, the a-Se technology has great potential to provide break-through abilities such as visualization of fine details including neuro-vascular perforator vessels and small vascular devices.

9783-129, Session PS5

Exploration of maximum count rate capabilities for large-area photon counting arrays based on polycrystalline silicon thin-film transistors

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Pixelated photon counting detectors with energy discrimination capabilities are of increasing clinical interest for x-ray imaging. Such detectors, presently in clinical use for mammography and under development for breast tomosynthesis and spectral CT, usually employ in-pixel circuits based on crystalline silicon – a semiconductor material that is generally not well-suited for economic manufacture of large-area devices. One interesting alternative material is polycrystalline silicon (poly-Si), a thin-film technology capable of creating large-area, monolithic devices. Similar to crystalline silicon, poly-Si allows the implementation of the type of fast, complex, in-pixel circuitry required for photon counting – operating at processing speeds that are not possible with amorphous silicon (the material currently used for large-area flat-panel imagers). The pixel circuits of two-dimensional photon counting arrays are generally comprised of four stages: amplifier, comparator, clock-generator and counter. The analog front-end (in particular, the amplifier) strongly influences performance and is therefore of interest to study for purpose of optimization. In this presentation, the relationship between incident and output count rates of the analog front-end is explored for a number of poly-Si based photon counting array designs under diagnostic imaging conditions. The input to the amplifier is modeled in the time domain assuming realistic input x-ray spectra and a cadmium zinc telluride converter. Simulations of circuits based on poly-Si thin-film transistors are used to determine the resulting output count rate as a function of x-ray fluence, energy discrimination threshold and operating conditions. This research was partially supported by NIH grant ROI-EB000558.

9783-130, Session PS5

Indirect-detection single photon-counting x-ray detector for breast tomosynthesis

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X-ray mammography is a crucial screening tool available to modern medicine for early identification of breast cancer. However, the confusing overlap of anatomical features present in projection images often complicate the task of correctly identifying suspicious masses. As a result, there has been increasing interest in acquisition of volumetric information through digital breast tomosynthesis (DBT) which, compared to mammography, offers the advantage of depth information. Since DBT requires acquisition of many projection images, it is desirable that the noise in each projection image be dominated by the statistical noise of the incident x-ray quanta and not by the additive noise of the imaging system (referred to as quantum-limited imaging) and that the cumulative dose be as low as possible (e.g., no more than for a mammogram). Unfortunately, the electronic noise (~ 2000 electrons) present in current DBT systems based on active matrix, flat-panel imagers (AMFPIS) is still relatively high compared with modest x-ray sensitivity of the a-Se and CsI:Tl x-ray converter systems often used. To overcome the modest signal-to-noise ratio (SNR) limitations of current DBT systems, we have developed a large-area x-ray imaging detector with the combination of an extremely low noise (~20 electron) active-pixel CMOS and a specially designed high resolution scintillator. The high sensitivity of such system provides better SNR by an order of magnitude than current state-of-art AMFPIS systems and enables x-ray indirect-detection single photon counting (SPC) at mammographic energies with the potential of dose reduction.
SWAD: inherent photon counting performance of amorphous selenium multi-well avalanche detector

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Photon counting detectors (PCDs) have the potential to improve x-ray imaging, however they are still hindered by several performance limitations and high cost. By using amorphous Selenium (a-Se) the cost of PCD can be significantly reduced compared to crystalline materials and enable large area detectors. To overcome the problem of low carrier mobility and low charge conversion gain in a-Se, we are developing a novel direct conversion a-Se field-Shaping multi-Well Avalanche Detector (SWAD). SWAD circumvents the charge transport limitation by Frisch grid built within the readout circuit, reducing charge collection time to ~200 ns. Field shaping permits depth independent avalanche gain in wells, resulting in total conversion gain that is comparable to Si and CdTe. In the present work we investigate the effects of charge sharing and energy loss to understand the inherent photon counting performance for SWAD at x-ray energies used in breast imaging applications (20-50keV). The energy deposition profile for each interacting x-ray was determined with Monte-Carlo simulation and a charge transport model was developed to simulate the charge collection process for SWAD. For the energy ranges we are interested in, photoelectric interaction dominates, with a K-fluorescence yield of approximately 60%. Using a monoenergetic 45 keV beam incident on a target pixel in 400um of a-Se, our results show that only 4.2% and 3.1% of escaped k-fluorescence emissions are reabsorbed in neighboring pixels for 100um and 85um pixel sizes respectively, demonstrating SWAD’s potential for high spatial resolution applications.

Both QLD and DQE proposed for flat panel detector characterization

Sarah J. Boyce, Michael J. Petrillo, Isaias D. Job, Kungang Zhou, Varian Medical Systems, Inc. (United States)

In general, DQE(0) is the standard metric for assessing image quality of a flat panel detector (FPD); however, a single descriptor is insufficient for describing the image quality of an FPD and clinical imaging tasks involve complex anatomical structures. Most clinical imaging applications study anatomy with varying x-ray attenuation properties. For example, in the lung, attenuation differences are as high as two orders of magnitude. This paper seeks to demonstrate DQE(0) usually presented at optimal exposure levels does not describe the working range of the FPD. For the energy ranges we are interested in, photoelectric interaction dominates, with a K-fluorescence yield of approximately 60%. Using a monoenergetic 45 keV beam incident on a target pixel in 400mu of a-Se, our results show that only 4.2% and 3.1% of escaped k-fluorescence emissions are reabsorbed in neighboring pixels for 100mu and 85mu pixel sizes respectively, demonstrating SWAD’s potential for high spatial resolution applications.

Focal spot deblurring for high-resolution direct conversion x-ray detectors

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Small pixel high resolution direct x-ray detectors have the advantage of higher spatial sampling and decreased blurring characteristic. The limiting factors for such systems becomes the degradation due to limited size of the focal spot.

One solution is a smaller focal spot; however, this can limit the output of the tube. Here a software solution of deconvoluring with an estimated focal spot blur is presented.

To simulate images from a direct detector affected with focal-spot blur, first a set of high-resolution stent images (FRED from Microvention, Inc.) were acquired using a 75um pixel size Dexcela-Perkin-Elmer detector and frame averaged to reduce quantum noise. Then the averaged image was blurred with a known Gaussian blur. To add noise to the blurred image a flat-field image was multiplied with the blurred image. Both the ideal and the noisy-blurred images were then deconvoluled with the known Gaussian function using either threshold-based inverse filtering or Weiner deconvolution. The blur in the ideal image was removed and the details were recovered successfully. However, the inverse filtering deconvolution process is extremely susceptible to noise. The Weiner deconvolution process was able to recover some of the details of the stent from the noisy-blurred image, but for noisier images, stent details are lost in the recovery process.

For CBCT applications, the magnification of specific objects can be obtained using initial reconstructions then corrected for focal-spot blurring to improve resolution. Similarly, if object magnification can be determined such correction may be applied in angiography.

Noise power spectrum measurements under nonuniform gains and their compensations

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The fixed pattern noise, which is due to the x-ray source heel effect and the nonuniform amplifier gains, should be alleviated in radiography imaging and have less influence on measuring the noise power spectrum (NPS) of the radiography detector. In order to reduce the influence, background trend removing methods, which are based on low-pass filtering, polynomial fitting, and subtracting averaged images, are traditionally employed in the literature. In terms of removing the fixed pattern noise, the subtracting method shows a good performance. However, the number of images to be averaged is practically finite and thus the noise contained in the averaged image contaminates the image difference and increases the NPS curve from the true one. In this paper, an image formation model considering the nonuniform gain is constructed and two measuring methods, which are based on the gain map and image difference, respectively, are proposed. In order to accurately measure a normalized NPS (NNPS) in the proposed algorithms, the number of images to be averaged is considered for NNPS compensations. For several radiography detectors, the NNPS measurements are conducted and compared with conventional approaches. Through experiments it is shown that the proposed algorithms can provide accurate NNPS measurements less influenced by the fixed pattern noise.
A comparison of quantum limited dose and noise equivalent dose
Sarah J. Boyce, Isaías D. Job, Michael J. Petrillo, Kungang Zhou, Varian Medical Systems, Inc. (United States)

Quantum limited dose (QLD) and noise equivalent dose (NED) are often used interchangeably. Although the metrics are related, they are not equivalent. QLD and NED are becoming more important metrics for understanding the limitations of flat panel detectors (fpd) at low dose. This paper seeks to demonstrate the theoretical differences between these metrics as well as the different measurement techniques used to obtain these metrics. Measurement techniques include acquisition of data at different exposures and using a step wedge to simulate different exposures, with scatter correction applied as necessary. Different methods of calculation are also examined. Two of the methods examined resulted in an approximately 7% difference in QLD. The investigation will also relate QLD and NED to clinical images.

Optimizing the CsI thickness for chest dual-shot dual-energy detectors
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Dual-energy imaging technique is to be used to improve conspicuity of abnormalities in radiographs. Commercial DEI systems usually employ a same detector and use a dual-shot approach that acquires low- and high-energy projections in successive x-ray exposures by rapidly switching the kilovoltage (kV) applied to the x-ray tube. However, it is typically known that there exists an optimal detector thickness regarding specific imaging tasks or energies used. In this study, we develop a theoretical model describing the energy-dependent detector signal and noise, and apply the developed model to the cost-benefit analysis on the use of dual detectors for DEI. Otherwise, we suggest the optimal thickness of the signle detector for DEI.

Physical properties of a new flat panel detector with cesium-iodide technology
Andreas Hahn, Petar Penchev, Martin Fiebich, Technische Hochschule Mittelhessen (Germany)

Flat panel detectors have become the standard technology in projection radiography. Further progress in detector technology will result in an improvement of MTF and DQE. The new detector (DX-D45C; Agfa, Mortsel/ Belgium) is based on cesium-iodine crystals and has a change in the detector material and the readout electronics. The detector has a size of 30 cm x 24 cm and a pixel matrix of 2560 x 2048 with a pixel pitch of 124 μm. The system includes an automatic exposure detectors, which enables the use of the detector without a connection to the x-ray generator. The physical properties of the detector were determined following IEC 62220-1-1 in a laboratory setting. The MTF showed an improvement compared to the previous version of cesium-iodine based flat-panel detectors. Thereby the DQE is also improved especially for the higher frequencies. The new detector showed an improvement in the physical properties compared to the previous versions. This enables a potential for further dose reductions in clinical imaging.
A geometric calibration method for inverse geometry computed tomography using P-matrices

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Accurate and artifact free reconstruction of tomographic images requires the imaging system geometry be precisely known. This work proposes a novel projection matrix based calibration method to enable C-arm inverse geometry CT (IGCT). The proposed method is evaluated for scanning-beam digital x-ray (SBDX), a C-arm mounted inverse geometry fluoroscopic technology. A known helical configuration of fiducials is imaged at each gantry angle in a rotational acquisition. For each gantry angle, digital tomosynthesis is performed at multiple planes and then a composite image analogous to a cone-beam projection is generated from the plane stack. The geometry of the C-arm, source array, and detector array is determined at each angle by constructing a parameterized 3D-to-2D projection matrix that minimizes the sum-of-squared deviations between measured and projected fiducial coordinates. Simulations were used to evaluate calibration performance with translations and rotations of the source and detector. In a geometry with 1 mm translation of the central ray relative to the axis-of-rotation and 1 degree yaw of the detector and source arrays, the maximum error in the recovered translational parameters was 0.4 mm and maximum error in the rotation parameter was 0.02 degrees. The relative root mean square error in a reconstruction of a numerical thorax phantom was 0.4% using the proposed calibration method, versus 7.7% without calibration. Changes in SDD were the most challenging to estimate. The proposed IGCT geometric calibration method reduces image artifacts when uncertainties exist in system geometry.

CT dose minimization using personalized protocol optimization and aggressive bowtie

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Computerized Tomography (CT) is a powerful imaging technology but the potential health risk due to the exposure of x-ray radiation has drawn wide concerns. In this study, we propose to use patient-specific x-ray fluence control to reduce the radiation dose to sensitive organs without degrading the image quality (IQ) in the region of interest (ROI). The mA-modulation profile could be optimized via back-projection, based on a low dose volumetric CT scout [1], where both sensitive organs and ROI can be defined. A set of clinical chest scans is used to demonstrate the feasibility of the proposed concept, where the breast region is selected as sensitive organs while the cardiac region is selected as IQ ROI. Three groups of simulations are performed for comparison: (1) Constant mA scan adjusted based on the patient attenuation (120 kVp, 300 mA), which serves as baseline; (2) ROI centering followed by patient-specific mA-modulation; (3) aggressive bowtie and ROI centering followed by patient-specific mA-modulation. The results show that with combination of aggressive bowtie, centered ROI and patient-specific mA-modulation, over 50% of dose reduction can be achieved in the breast region compared to a constant mA baseline while the IQ in the cardiac region is maintained.

Segmentation-free x-ray energy spectrum estimation for computed tomography

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X-ray energy spectrum plays an essential role in imaging and related tasks. Due to the high photon flux of clinical CT scanners, most of spectrum estimation methods are indirect and are usually suffered from various limitations. The recently proposed indirect transmission measurement-based method requires at least the segmentation of one material, which is insufficient for CT images of highly noisy and with artifacts. To combat for the bottleneck of spectrum estimation using segmented CT images, in this study, we develop a segmentation-free indirect transmission measurement based energy spectrum estimation method using dual-energy material decomposition.

Noise power spectrum studies of CT systems with off-centered image object and bowtie filter

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Noise power spectrum (NPS) has fundamental impact on the diagnostic performance for a given CT imaging task and thus has been extensively investigated in the past several decades. In these previous studies, image objects were placed at the iso-center of the scanning field of view. In this case, the impact of the bowtie filter is primarily on the noise amplitude, not the topology of the NPS. However, in many clinical applications, the targeted region of interest (ROI) may be located at off-centered positions. In this case, the interplay of the geometrical location of the ROI and the bowtie filter become intricate. As a result of this interplay, the topology of the NPS may change drastically, which may have a significant impact on the diagnostic performance of CT imaging tasks for the off-centered ROIs. This work presents the first numerical simulation and experimental studies on the NPS of CT systems with off-centered image objects and bowtie filter. It was found that when the object goes out of the designed compensation zone of the bowtie filter, the NPS shows a peculiar anisotropic topology that may profoundly influence the diagnostic performance of certain low contrast detection tasks.

Prototype adaptive bow-tie filter based on spatial exposure time modulation

Andreu Badal, U.S. Food and Drug Administration (United States)
In recent years, there has been an increased interest in the development of dynamic bow-tie filters that are able to provide patient-specific x-ray beam shaping. We introduce the first physical prototype of a new adaptive bow-tie filter design based on the concept of “spatial exposure time modulation.” While most existing bow-tie filters operate by attenuating the radiation beam differently in different locations using partially attenuating objects, the presented filter shapes the radiation field using two movable completely radio-opaque collimators. The aperture and speed of the collimators is modulated in synchrony with the x-ray exposure to selectively block the radiation emitted to different parts of the object. This mode of operation does not allow the reproduction of every possible attenuation profile, but it can reproduce the profile of any object with an attenuation profile monotonically decreasing from the center to the periphery, such as an object with an elliptical cross section. Therefore, the new adaptive filter provides the same advantages as the currently existing static bow-tie filters, which are typically designed to work for a pre-determined cylindrical object at a fixed distance from the source, and provides the additional capability to adapt its performance at image acquisition time to better compensate for the actual diameter and location of the imaged object. A detailed description of the prototype filter, the implemented control methods, and a preliminary experimental validation of its performance are presented.

9783-118, Session PS4

Evaluation of the dose reduction potential using a breast positioning technique for organ-based tube current modulated CT examinations

Wanyi Fu, Xiaoyu Tian, W. Paul Segars, Duke Univ. (United States); Mitchell M. Goodsitt, Ella A. Kazerooni, Univ. of Michigan (United States); Ehsan Samei, Duke Univ. (United States)

The purpose of this work was to investigate the breast dose saving potential of a designed breast positioning technique (BP) for thoracic CT examinations with organ-based tube current modulation (OTCM). The study included 13 female patient models (XCAT, age range: 27-65 y.o., weight range: 52 to 105.8 kg). Each model was modified to simulate 3 breast sizes and positions reflective of standard supine geometry. The modeled breasts were further deformed, emulating a BP that would constrain the breasts within 120° anterior tube current (mA) reduction zone. The tube current value of the CT examination was modeled using an attenuation-based program which reduces the radiation dose to 20% in the anterior region and increases the dose to maintain corresponded dose level in the posterior region. A validated Monte Carlo program was used to estimate organ doses with a typical clinical system (SOMATOM Definition Flash, Siemens Healthcare). The simulated breast and other organ doses were compared with attenuation-based tube current modulation (ATCM), OTCM, and OTCM with BP (OTCMPB). On average, compared to TCM, OTCM reduced the breast dose by 27.7±5%. With OTCMPB, the breast dose reduces by an additional 25.4±12% to 46.3±9%. The dose saving was more significant for larger breasts (on average 39, 50, and 59% reduction for 0.5, 1.5, and 2.5 kg breasts, respectively). Compared to TCM, OTCMPB also reduced thyroid and heart dose with 15.7±9% and 15.2±4%, respectively. OTCM with BP can remarkably reduce breast dose on thoracic CT examinations, particularly for female patients with large breast size.

9783-119, Session PS4

Robust dynamic myocardial perfusion CT deconvolution using adaptive-weighted tensor total variation regularization

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Dynamic myocardial perfusion computed tomography (MPCT) is a promising technique for diagnosis and risk stratification of coronary artery disease by assessing the myocardial perfusion hemodynamic maps (MPHM). Meanwhile, the repeated scanning of the same region results in a relatively large radiation dose to patients potentially. In this work, we develop a robust MPCT deconvolution algorithm with adaptive-weighted tensor total variation regularization to estimate residue function accurately under the low-dose context, which is termed ‘MPD-AwTTV.’ More specifically, the AwTTV regularization takes into account the anisotropic edge property of the MPCT images compared with the conventional total variation (TV) regularization, which can mitigate the drawbacks of TV regularization. Subsequently, an effective iterative algorithm was adopted to minimize the associative objective function. Experimental results on a modified XCAT phantom demonstrated that the present MPD-AwTTV algorithm outperforms and is superior to other existing deconvolution algorithms in terms of noise-induced artifacts suppression, edge details preservation and accurate MPHM estimation.

9783-120, Session PS4

Estimation of organ dose under tube current modulated CT for 58 patients across diverse protocols

Wanyi Fu, Xiaoyu Tian, Pooyan Sahbaee, Yakun Zhang, W. Paul Segars, Ehsan Samei, Duke Univ. (United States)

Organ dose requires explicit modeling of the scan protocol and patient anatomy. Organ dose further depends on how tube current is modulated in response to the patient attenuation. This study aimed to provide an extensive organ dose database for routine body CT examinations with tube current modulation (TCM). 58 XCAT phantoms (age range: 18-78 y.o., weight range: 52 to 117 kg) were included, with most of the radiosensitive organs. The CTDivol normalized organ dose coefficients were calculated from protocol groups (Chest-abdomen-pelvis, Chest, Abdomen-pelvis, Abdomen, Pelvis, Adrenals, Liver, Kidneys, Liver-to-kidneys, and Kidneys-to-bladder). For each examination, four modulation strengths (β=0.25, 0.5, 0.75, 1) were simulated representing various manufacture dependency on body attenuations. The attenuation of the body was calculated by a ray-tracing program. A validated Monte Carlo program was used to estimate organ doses with a typical clinical system and CT technique (Definition Flash, Siemens Healthcare, 120 kVp, helical scan). The organ dose was fitted against averaged body diameter in exponential functions. The organ dose decreased with increased body size. This relationship is more prominent for organs within scan coverage. The dose dependency on body size is weaker with larger modulation strength. Based on this mathematical model, a dose estimation iPhone operating system application was designed and developed to be used as a tool to estimate dose to the patients for a variety of routinely used CT examinations.

9783-121, Session PS4

A technique for multi-dimensional optimization of radiation dose, contrast dose, and image quality in CT imaging

Pooyan Sahbaee, Duke Univ. Medical Ctr. (United States); Ehsan Abadi, Duke Univ. School of Medicine (United States); Greeshma Agasthya, Yakun Zhang, Marc Becchetti, W. Paul Segars, Ehsan Samei, Duke Univ. Medical Ctr. (United States)

The purpose of this study was to substantiate the interdependency of image quality, radiation dose, and contrast material dose in CT towards the patient-specific optimization of the imaging protocols. The study deployed two
phantom platforms. First, a variable sized phantom containing an iodinated inert was imaged on a representative CT scanner at multiple CTDI values. The contrast and noise were measured from the reconstructed images for each phantom diameter. Linearly related to iodine-concentration, contrast to noise ratio (CNR), was calculated for different iodine-concentration levels. Second, the analysis was extended to a recently developed suit of 58 virtual human models (5D-XCAT) with added contrast dynamics. Emulating a contrast-enhanced abdominal image procedure and targeting a peak-enhancement in aorta, each XCAT phantom was “imaged” using a CT simulation platform. 3D surfaces for each patient/size established the relationship between iodine-concentration, dose, and CNR. The Sensitivity of Ratio (SR), defined as ratio of change in iodine-concentration versus dose to yield a constant change in CNR was calculated and compared at high and low radiation dose for both phantom platforms. The results show that sensitivity of CNR to iodine concentration is larger at high radiation dose (up to 73%). The SR results were highly affected by radiation dose metric; CTDI or organ dose. Furthermore, results showed that the presence of contrast material could have a profound impact on optimization results (up to 45%).

9783-122, Session PS4
Experimental demonstration of a dynamic bowtie for region-based CT fluence optimization
Vance S. Robinson, Walter J. Smith, Zhye Yin, Mingye Wu, Paul F. Fitzgerald, Bruno De Man, GE Global Research (United States)

Technology development in Computed Tomography (CT) Imaging is driven by the need to balance minimizing patient dose and maximizing feature detectability. One approach to managing dose without compromising resolution is to spatially vary the x-ray flux such that regions of high interest receive more radiation while regions of low importance or regions sensitive to the radiation damage receive less dose. If the region of interest (ROI) is centered in the bore of the CT system, a simple stationary bowtie or fixed hardware filter, could be mounted between the x-ray tube and the patient to reduce the signal everywhere except in the center. If the ROI is off centered then a dynamic bowtie that can track the ROI is necessary. We experimentally demonstrate the concept of a dynamic bowtie using a design that is relatively simple, low cost, requires no auxiliary power supply and was retrofitted to an existing commercial CT scanner. We will build a prototype dynamic bowtie, install it on a GE Lightspeed VCT scanner and acquire scans of a phantom with an off-centered ROI. Reconstructed images will illustrate the resulting image noise distribution and dose estimation will demonstrate the corresponding dose reduction of an ROI-focused dynamic bowtie filter.

9783-123, Session PS4
Hybrid deterministic and stochastic x-ray transport simulation for transmission computed tomography with advanced detector noise model
Lucretiu M. Popescu, U.S. Food and Drug Administration (United States)

In this paper we present a model for simulation of noisy X-ray computed tomography data sets. The model is made of two main components, a photon transport simulation component that generates the noiseless photon field incident on the detector, and a detector response model that is taking as input the incident photon field parameters and given the X-ray source intensity and exposure time can generate noisy data sets, accordingly. The photon transport simulation component combines direct ray-tracing of polychromatic X-rays for calculation of transmitted data, with Monte Carlo simulation for calculation of the scattered-photon data. The Monte Carlo scatter simulation is accelerated by implementing particle splitting and importance sampling variance reduction techniques. The detector-incident photon field data are stored as energy expansion coefficients on a refined grid that covers the detector area. From these data the detector response model is able to generate noisy detector data realizations, by reconstituting the main parameters that describe each detector element response in statistical terms, including spatial correlations. The model is able to generate very fast, on the fly, CT data sets corresponding to different radiation doses, as well as detector response characteristics, facilitating data management in extensive optimization studies by reducing the computation time and storage space demands.

9783-124, Session PS4
An automated technique for estimating patient-specific regional imparted energy in TCM CT exams
Jeremiah Sanders, Xiaoyu Tian, W. Paul Segars, Duke Univ. (United States); John M. Boone, Univ. of California, Davis (United States); Ehsan Samei, Duke Univ. (United States)

Currently computed tomography (CT) dosimetry relies on CT dose index (CTDI) and size specific dose estimates (SSDE). Organ dose is a better metric of radiation burden. However, organ dose estimation requires precise knowledge of organ locations. Regional imparted energy and dose can offer an advantage as they do not require precise estimates of the organ size or location. In this work, an automated technique for estimating the imparted energy from chest and abdomenopelvic CT exams was investigated. Monte Carlo simulations of chest and abdomenopelvic CT examinations were performed on 58 computation XCAT phantoms to develop relationships between scanned mass and the normalized imparted energy from ionizing radiation exposure. An automated algorithm for calculating the scanned patient volume was developed using an open-source MATLAB based mesh generation toolbox. The scanned patient volume was then used to estimate the scanned patient mass. The scanned patient mass and CTDIvol from the scan were used to estimate the imparted energy to the patient using the lendielines found from the Monte Carlo simulations. Imparted energy estimates were made from 20 chest and abdomenopelvic CT exams. Results indicate that the average imparted energy is 153 ± 26 mJ and 346 ± 60 mJ for the chest and abdomenopelvic exams, respectively.

9783-125, Session PS4
A framework for analytical estimation of patient-specific CT dose
Hanbeau Yoon, Hosang Jeon, Jiho Nam, Jin Woo Kim, Pusan National Univ. (Korea, Republic of); Seungman Yun, Min Kook Cho, SAMSUNG Electronics Co., Ltd. (Korea, Republic of); Ho Kyung Kim, Pusan National Univ. (Korea, Republic of)

The authors introduce an algorithm to estimate the spatial dose distributions in CT images. The algorithm calculates dose distributions due to the primary and scattered photons separately. The algorithm only requires the CT dataset that includes the patient CT images and the scanner acquisition parameters. Otherwise the scanner acquisition parameters are extracted from the CT images. The estimated dose distributions are validated in comparisons with the experimental measurements and the Monte Carlo simulations. The strategy to accelerate the computation time for the real-time patient-specific dose estimation is discussed.
9783-126, Session PS4

Modulation transfer function determination using the edge technique for cone-beam micro-CT

Junyan Rong, Wen Lei Liu, Peng Gao, Qimei Liao, Hongbing Lu, Fourth Military Medical Univ. (China)

Evaluating spatial resolution is an essential work for cone-beam computed tomography (CBCT) manufacturer, prototype designer or equipment users. To investigate the cross-sectional spatial resolution for different transaxial slices with CBCT, the slanted edge technique with a 5D slanted edge phantom are proposed and implemented on a prototype cone-beam micro-CT. Three transaxial slices with different cone angles are under investigation. An over-sampled edge response function (ERF) is firstly generated from the intensity of the slightly tilted air to plastic edge in each row of the transaxial reconstruction image. Then the oversampled ERF is binned and smoothed. The derivative of the binned and smoothed ERF gives the line spread function (LSF). At last the presampled modulation transfer function (MTF) is calculated by taking the modulus of the Fourier transform of the LSF. The spatial resolution is quantified with the spatial frequencies at 10% MTF level and FWHM value. The spatial frequencies 10% of MTFs are 3.1±0.08mm-1, 3.0±0.05mm-1, and 3.2±0.04mm-1 for the three transaxial slices at cone angles of 3.8°, 0°, and -3.8° respectively. The corresponding FWHMs are 252.8µm, 261.7µm and 253.6µm. Results indicate that cross-sectional spatial resolution has no much differences when transaxial slices being 3.8° away from z=0 plane for the prototype cone-beam micro-CT.

9783-127, Session PS4

An approach for quantitative image quality analysis for CT

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An objective and standardized approach to assess image quality of CT systems is required in a wide variety of imaging processes to identify CT systems appropriate for a given application. We present an overview of the framework we have developed to help standardize and to objectively assess CT image quality for different models of CT scanners used for security applications. Within this framework, we have developed methods to quantitatively assess feature identification, detection accuracy and precision, and image registration capabilities of CT machines and to identify strengths and weaknesses in different CT imaging technologies in transportation security. To that end we have designed, developed and constructed phantoms that allow for systematic and repeatable measurements of over 100 image quality metrics, representing modulation transfer function, noise equivalent quanta, noise power spectra, slice sensitivity profiles, streak artifacts, CT number uniformity, CT number consistency, object length accuracy, CT number path length consistency, and object registration. Furthermore, we have developed a sophisticated MATLAB based image analysis tool kit to analyze the CT generated images and report these metrics in a format that is standardized across the considered models of CT scanners allowing for comparative image quality analysis within a CT model or between different CT models. In addition, we have developed a modified sparse component analysis (SCPA) method to generate a modified set of PCA components as compared to the standard principal component analysis (PCA) with sparse loadings in conjunction with Hotelling T2 statistical analysis method to compare, qualify, and detect faults in the tested systems.

9783-234, Session PS4

Low dose CT perfusion using k-means clustering

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We aim at improving low dose CT perfusion functional parameters maps and CT images quality, preserving quantitative information. In a dynamic CT perfusion dataset, each voxel is measured T times, where T is the number of acquired time points. In this sense, we can think of a voxel as a point in a T-dimensional space, where the coordinates of the voxel would be the values of its time attenuation curve (TAC). Starting from this idea, a k-means algorithm was designed to group voxels in K classes. A modified guided time-intensity profile similarity (gTIPS) filter was implemented and applied only for those voxels belonging to the same class (k-gTIPS). The approach was tested on a digital brain perfusion phantom as well as on clinical brain and body perfusion datasets, and compared to the original TIPS implementation.

The TIPS filter showed the highest CNR improvement, but lowest spatial resolution. gTIPS proved to have the best combination of spatial resolution and CNR improvement for CT images, while k-gTIPS was superior to both gTIPS and TIPS in terms of perfusion maps image quality. We demonstrate k-means clustering analysis can be applied to de-noise dynamic CT perfusion data and to improve functional maps. Beside the promising results, this approach has the major benefit of being independent from the perfusion model employed for functional parameters calculation. No similar approaches were found in literature.
Theoretical and Monte Carlo optimization of a stacked three-layer flat-panel x-ray imager for applications in multi-spectral diagnostic medical imaging

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We propose a new design of a stacked three-layer flat-panel x-ray detector for dual-energy (DE) imaging. Each layer consists of its own scintillator of individual thickness and an underlying thin-film transistor (TFT) based flat-panel. Three images are obtained simultaneously in the detector during the same x-ray exposure, thereby eliminating any motion artifacts. The detector operation is two-fold: a conventional radiography image can be obtained by combining all three layer images, while a DE subtraction image can be obtained from the front and back layer images where the middle layer acts as a mid-filter that helps achieve spectral separation. We proceed to optimize the detector parameters for a sample imaging task of energy subtraction angiography to obtain the best possible signal to noise ratio per root entrance exposure using well-established theoretical models adapted to fit our new design. These results are compared to a conventional DE temporal subtraction detector and a single-shot DE subtraction detector with a copper mid-filter, both of which underwent the same theoretical optimization. The findings are then validated using advanced Monte Carlo simulations for all optimized detector setups. Given the performance expected from initial results and the recent decrease in price for digital x-ray detectors, the simplicity of the three-layer stacked imager approach appears promising to usher in a new generation of multi-spectral digital x-ray diagnostics.

A novel scatter correction method for multi-energy x-ray imaging

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The emergence of energy-resolved photon counting detectors opens up new perspectives in x-ray imaging. This includes the ability to differentiate material components and estimate their equivalent thicknesses or relative ratios by processing a single shot acquisition image. However, such techniques require highly accurate images, especially for materials close in terms of attenuation. The presence of scattered radiation leads to a loss of contrast and, more importantly, a bias in radiographic material imaging and artefacts in computed tomography (CT). The aim of the present study was to introduce and evaluate a physical measurement based scatter correction approach adapted for multi-energy imaging. This evaluation was carried out with the aid of numerical simulations provided by an internal simulation tool, Sindbad-SFFD. A simplified numerical thorax phantom placed in a CT geometry was used. The projection image visualized after correction proved to be almost scatter free: bias has been reduced and contrast recovered. Average relative error between the corrected total and primary projection images was below 1%. Qualitative evaluation of several control point spectra from primary and corrected total images further confirmed the efficacy of the proposed method. The equivalent comparison of corrected total and primary spectral images revealed an error of around 3.5%.

Noise suppression for energy-resolved CT using similarity-based non-local filtration

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In energy-resolved CT, images are reconstructed independently at different energy levels, resulting in images with different qualities but the same object structures. We propose a similarity-based non-local filtration method to extract structural information from these images for noise suppression. This method can be implemented on low-energy CT images to improve the image contrast-to-noise ratio (CNR) or on decomposed material images to suppress noise standard deviation without spatial resolution loss. For each pixel, we calculate similarity to other pixels across the field based on CT numbers using an empirical exponential model. The calculation is repeated on each CT image at different energy levels. The averaged similarity values are used to generate a similarity matrix. Noise suppression is achieved by multiplying the image vector by the similarity matrix, which calculates the noise-reduced value of each pixel by averaging other similar pixels. Simulation studies on 19-channel energy-resolved CT ranging from 37-65 keV show that the proposed method improves CNR of iodine on the 37-keV CT image by a factor of 2.5. Compared with averaging all CT images for noise suppression, our method not only achieves 199% higher CNR but also reduces the error of iodine CT number from 50% to <1%. Phantom studies show that our method reduces the noise of decomposed material images by a factor of 5.3 while maintaining spatial resolution of 7 lp/cm. The noise suppression achieved by the similarity-based method is clinically attractive, especially for high CNR of iodine in contrast-enhanced CT and improved material decomposition in energy-selective CT.

Dual energy x-ray imaging and scoring of coronary calcium: physics-based digital phantom and clinical studies

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Coronary artery calcification (CAC) as assessed with CT calcium score is the best biomarker of coronary artery disease. Dual energy x-ray provides an inexpensive, low radiation-dose alternative. A two shot system (GE Revolution-XRd) is used, raw images are processed with a custom algorithm, and a coronary calcium image (CCI) is created, similar to the bone image, but optimized for CAC visualization, not lung visualization. In this report, we developed a physics-based, digital-phantom containing heart, lung, CAC, spine, ribs, pulmonary artery (PA), and adipose elements, examined effects on CCI, suggested physics-inspired algorithms to improve CAC contrast, and evaluated the correlation between CT calcium scores and a proposed DE calcium score. In simulated CCI, even a small mass of iodine (5mg) gives rise to a contrast Cg (delta-gray) divided by the background of 6%. Beam hardening from increasing adipose thickness (2cm to 8cm) reduced Cg by 18.5% and 24.8% in 120kVp and 60kVp images, but only reduced Cg by <10% in CCI. If a pulmonary artery (PA) moves or pulsates with blood filling between exposures, it can give rise to a significantly confounding PA signal in CCI similar in amplitude to CAC. Observations suggest modifications to CCI processing, which can further improve CAC contrast by a factor of 2 in clinical exams. The DE score had the best correlation with "CT mass score" among three commonly used CT scores. Results suggest that DE x-ray is a promising tool for imaging and scoring CAC, and there still remains opportunity for further CCI processing improvements.
Enhanced diagnostic value for CT angiography of calcified coronary arteries using dual energy and a novel high-Z contrast material: a phantom study

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Dual-energy CT (DECT) imaging has gained a lot of attention because of its capability to discriminate materials.

We propose a flexible DECT scan strategy which can be realized on a system with general X-ray sources and detectors. In order to lower dose and scanning time, our DECT acquires two projection data sets on two views covered by itself (projections collected in scanning) and by the other system with general X-ray sources and detectors. In order to lower dose and scanning time, our DECT acquires two projection data sets on two views covered by itself (projections collected in scanning) and by the other.

Reconstruction of limited angle dual-energy CT using mutual learning and cross-estimation

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Dual-energy CT (DECT) imaging has gained a lot of attention because of its capability to discriminate materials.

A constrained method for stabilized quantitative projection-based dual-energy material decomposition

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Dual-energy imaging has demonstrated the ability to improve the diagnostic potential of x-ray images in many areas of clinical practice.

This work aimed to quantify and compare the potential impact of gender difference on coronary artery calcium scoring with dual-energy CT. Four synthetic heart vessels with calcifications were inserted into an anthropomorphic thorax phantom. The vessels consisted of large/small vessels to represent men and women sizes respectively, and had sizes similar to average left main artery/left circumflex artery. The phantom was scanned with and without female breast plates to better represent gender differences in scans of a similar sized man and woman. Ten repeat scans were acquired in both single- and dual-energy mode and were reconstructed at 3 mm and 0.6 mm slices and using three reconstruction algorithms (FBP, IR-3, IR-5). Agatston and calcium volume scores were estimated from the reconstructed data using a segmentation-based approach. Total calcium score (summation of four vessels), and male/female calcium scores were calculated accordingly.

Both Agatston and calcium volume scores were found to be consistent between single- and dual-energy scans. The total calcium scores from 0.6 mm slice thickness were significantly higher than from the 3mm scans. Among different reconstruction algorithms, FBP yielded the highest and IR-5 yielded the lowest scores. The total calcium scores from the male phantom were significantly larger and the coefficients of variation for calcium scores were generally smaller than those from the female phantom. Both gender-based anatomical differences and vessel size were significant factors that impacted the calcium scores based on ANOVA. The calcium volume scores tended to be underestimated when the vessels were smaller. These findings are valuable for standardizing imaging protocols toward improved gender-specific calcium scoring.
Dual-energy computed tomography of the head: a phantom study assessing axial dose distribution, eye lens dose, and image noise level

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Purpose: The aim of this study was to compare the axial dose distribution, eye lens dose, and image noise level between dual-energy (DE) and a standard, single-energy (SE) head CT. Materials and Methods: Three DE (100/Sn140, 80/Sn140, and 140/80 kVp) and one SE (120 kVp) head CT acquisitions were performed using a second-generation dual-source CT device and a female head phantom at a volumetric CT dose index of 41 mGy. The axial absorbed dose distribution at the orbital level and the absorbed doses for the eye lens were acquired using glass dosemeters. CT attenuation numbers in Hounsfield units (HU) were obtained in the DE composite images and SE images of the phantom at the orbital level. Results: The absorbed doses at the orbital level were 32.6 ± 5.0, 29.5 ± 2.7, 30.5 ± 3.6, and 36.3 ± 3.4 mGy with 100/01 kVp, 80/Sn140, 140/80, and 120 kVp acquisitions, respectively (p < 0.001, Friedman’s test). The anterior surface dose was higher in the SE acquisitions than in the DE acquisitions. The doses absorbed in the eye lens were 33.9 ± 2.8, 30.6 ± 2.5, 34.9 ± 1.9, and 37.9 ± 1.0 mGy, respectively (p = 0.025). Standard deviations for the CT attenuation numbers were 12.2, 12.4, 13.9, and 11.7 HU, respectively (p < 0.001). Conclusion: DE head CT can be performed with a radiation dose lower than that of a standard SE head CT, with a slight increase in the image noise level. The 100/Sn140-kVp acquisition revealed the most balanced axial dose distribution.

Multi-energy method of digital radiography for imaging of biological objects

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This work has been dedicated to the search for a new possibility to use multi-energy digital radiography (MER) for medical applications. Our work has included both theoretical and experimental investigations of 3-energy MER for imaging the structure of biological objects. Using special software simulation methods and digital analysis based on the X-ray interaction energy dependence for each element of importance to medical applications in the X-ray range of energy up to 150 keV, we have implemented a quasi-linear approximation for the energy dependence of X-ray linear absorption coefficient \( \mu(E) \) that permits us to determine the intrinsic structure of biological objects. Our measurements utilize multiple X-ray tube voltages (i.e., 50, 100, and 150 kV) with Al and Cu filters of different thicknesses (6 mm Al, 2 mm Al + 0.2 mm Ta, and 5 mm Cu + 2 mm Al) to achieve 3-energy X-ray illumination of objects. The scintillator-photodiode detectors (scintillator ZnSe) are designed to optimize response for each corresponding energy range. During our experiments, the inspection object is illuminated in different time steps while switching between X-ray beams with different X-ray tube voltages. Following the multi-energy illumination, the outputs are software-processed to yield final images. To reconstruct and visualize the final images, we use both two-dimensional (2D) and three-dimensional (3D) palettes of identification. The result is a 2D and 3D representation of the object with color coding of each pixel according to the to data outputs. Following the experimental measurements and post-processing, we produce a 3D image of the biological object – in the case of our trials, fragments or parts of a hen and turkey. These results demonstrate that MER with our proposed methods of image processing represent an important new possibility for radiographic visualization and imaging. This research is supported in part by NATO’s Emerging Security Challenges Division in the framework of the Science for Peace and Security Programme (Project SfP-984605).

Iterative image reconstruction for multienergy computed tomography via structure tensor total variation regularization

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Multienergy computed tomography (MECT) has the potential to simultaneously o cerco multiple sets of energy-selective data belonging to specific energy windows. However, because sufficient photon counts are not available in the specific energy windows compared with that in the whole energy window, the MECT images reconstructed by the analytical approach often suffer from poor signal-to-noise (SNR) and strong streak artifacts. To eliminate this drawback, in this work we present a penalized weighted least-squares (PWLS) scheme by incorporating the new concept of structure tensor total variation (STV) regularization to improve the MECT images quality from low-milliampereseconds (low-mAs) data acquisitions. Henceforth the present scheme is referred to as PWLS-STV for simplicity. Spectrally, the STV regularization is derived by penalizing the eigenvalues of the structure tensor of every point in the MECT images. Thus it can provide more robust measures of image variation, which can eliminate the patchy artifacts often observed in total variation regularization. Subsequently, an alternating optimization algorithm was adopted to minimize the objective function. Experiments with a digital XCAT phantom clearly demonstrate that the present PWLS-STV algorithm can achieve more gains than the existing TV-based algorithms and the conventional “iterative backprojection (FBP) algorithm in terms of noise-induced artifacts suppression, resolution preservation, and material decomposition assessment.

Iterative CT reconstruction using coordinate descent with ordered subsets of data

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Image reconstruction based on minimization of a penalized weighted least-square criteria has become an important topic of research in X-ray computed tomography. This topic is motivated by increasing evidence that such a formalism may enable a significant reduction in dose imparted to the patient while maintaining or improving image quality. One important issue associated with this iterative image reconstruction concept is slow convergence and the associated computation cost. For this reason, there is interest in finding methods that produce approximate versions of the target image with a small number of iterations and an acceptable level of discrepancy. We introduce here a novel method to produce such approximations: ordered subsets in combination with iterative coordinate descent. Preliminary results demonstrate that this method can produce, within 10 iterations, attractive reconstructions that retain the noise properties of the targeted image.
Optimization-based reconstruction for reduction of CBCT artifact reduction in IGRT

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Kilo-voltage cone-beam computed tomography (CBCT) plays an important role in image guided radiation therapy (IGRT) by providing 3D spatial information of tumor potentially useful for optimizing treatment planning. In current IGRT CBCT system, reconstructed images obtained with analytic algorithms, such as FDK algorithm and its variants, may contain artifacts. In an attempt to compensate for the artifacts, we investigate optimization-based reconstruction algorithms such as the ASD-POCS algorithm for potentially reducing artifacts in IGRT CBCT images. In this study, using data acquired with a physical phantom and a patient subject, we demonstrate that the ASD-POCS reconstruction can significantly reduce artifacts observed in clinical reconstructions. Moreover, patient images reconstructed by use of the ASD-POCS indicate a contrast level of soft-tissue improved over that of the clinical reconstruction. We have also performed reconstructions from sparse-view data, and observe that, for current clinical imaging conditions, ASD-POCS reconstructions from data collected at one half of the current clinical projection views appear to show image quality, in terms of spatial and soft-tissue-contrast resolution, higher than that of the corresponding clinical reconstructions.

Resolution-enhancing hybrid, spectral CT reconstruction

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Spectral x-ray imaging based on photon-counting x-ray detectors (PCXD) is an area of growing interest. By measuring the energy of x-ray photons, a spectral CT System can better differentiate elements using a single scan. However, the spatial resolution achievable with most PCXDs limits their application particularly in preclinical CT imaging. Consequently, our group is developing a hybrid micro-CT scanner based on both a high-resolution energy-integrating (EID) and a lower-resolution, PCXD. To complement this system, here, we propose and demonstrate a spectral deblurring algorithm for hybrid image reconstruction, which iteratively combines the spectral contrast of the PCXD with the spatial resolution of the EID. In essence, the high resolution, spectrally resolved data (X) is recovered as the sum of two matrices: one with low column rank (XL) determined from the EID-based high-resolution CT data and one with sparse columns (XS) corresponding to the upsampled spectral contrast obtained from PCXD data. Spectral deblurring was tested in realistic cone beam CT simulations with the digital MOBY mouse phantom in a feasibility study focused on molecular imaging of the atherosclerotic plaque using activatable iodine and gold nanoparticles. The results show a good estimation of material concentrations at increased spatial resolution resolution when the pixel size ratio between the PCXD and EID is 5:1. The concentration accuracy was improved via spectral deblurring by 55% for iodine, 85% for gold, and 56% for calcium compared with interpolated reconstructions of the PCXD data. For the final manuscript, we will validate the algorithm’s performance using in vivo data.

Axial 3D region of interest reconstruction using 3D weighted cone beam BFP/DBPF algorithm cascaded with adequately oriented orthogonal butterfly filtering

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Axial cone beam (CB) computed tomography (CT) reconstruction is still the most desirable in clinical applications. As the potential candidates with analytic form for the task, the backprojection-filteration (BPF) algorithm and the derivative backprojection filtered (DBPF) algorithm, in which Hilbert filtering is the common algorithmic feature, are originally derived for exact helical and axial reconstruction from CB and fan beam projection data, respectively. These two algorithms have been heuristically extended for axial CB reconstruction via adoption of virtual PI-line segment. Unfortunately, however, streak artifacts are induced along the Hilbert filtering direction, since these algorithms are no longer accurate on the virtual PI-line segments. We have proposed to cascade the extended BPF/DBPF algorithm with orthogonal butterfly filtering for image reconstruction (namely axial CB-BPF/DBPF cascaded with orthogonal butterfly filtering), in which the orientation-specific artifacts caused by post-BP Hilbert transform can be eliminated, at a possible expense of losing the BPF/DBPF’s capability of dealing with projection data truncation. Our preliminary results have shown that this is not the case in practice. Hence, in this work, we carry out an algorithmic analysis and experimental study to thoroughly investigate the performance of the axial CB-BPF/DBPF cascaded with adequately oriented orthogonal butterfly filtering for 3D ROI reconstruction.
9783-158, Session PS7

Regularized CT reconstruction on unstructured grid

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Tomography reconstruction on an unstructured grid has been studied for years. Reconstruction on unstructured grid reduces the computational cost and alleviates the ill-posedness of the problem by decreasing the dimension of the solution space. However, there was no systematically study on edge-preserving regularization methods for CT reconstruction on unstructured grid. In this study, we propose a novel regularized CT reconstruction method on unstructured grid such as triangular or tetrahedral mesh. The idea of traditional total variation regularization method on structured grid is transplanted to unstructured grid via high-order discretization of the solution space. However, there was no systematically study on edge-preserving regularization method on unstructured grid, which bring difficulty to the development of the fast solver. A fixed-point proximity algorithm is developed for solving the related optimization problem. The extrapolation technique is applied to accelerate the convergence, which can efficiently reduce iteration numbers by over 50%. Finally, we compare the regularized CT reconstruction method to SART with no regularization on unstructured grid, SART with Tikhonov regularization on unstructured grid, and SART with total variation regularization in pixel domain, using three numerical phantoms with different noise levels. Numerical experiments demonstrated that the proposed regularization method on unstructured grid is effective to suppress noise and preserve edge features. Compared to the reconstruction in pixel domain, the proposed regularized CT reconstruction method is effective to reduce the computational cost and noise.

9783-159, Session PS7

Texture-preserving Bayesian image reconstruction of low-dose x-ray CT

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Markov random field (MRF) model has been widely used in Bayesian image reconstruction methods to reconstruct piece-wise smooth images in the presence of noise, such as in low-dose X-ray computed tomography (LDCT). While it can preserve edge sharpness via edge-preserving potential function, its regional smoothing may sacrifice tissue image textures, which have been recognized as useful imaging biomarkers, and thus it compromises clinical tasks, such as differentiating malignant vs. benign lesions, e.g., lung nodules or colon polyps. This study aims to shift the edge-preserving regional noise smoothing paradigm to texture-preserving framework for LDCT image reconstruction while retaining the advantage of MRF's neighborhood system on edge preservation. Specifically, we adapted the MRF model to incorporate the image textures of muscle, fat, lung, bone, etc. from previous full-dose CT scan as a priori knowledge for texture-preserving Bayesian reconstruction of current LDCT images. To show the feasibility of proposed reconstruction framework, experiments using clinical patient scans (with lung nodule or colon polyp) were conducted. The experimental outcome showed noticeable gain by the a priori knowledge for LDCT image reconstruction with the well-known Haralick texture measures. Thus, it is conjectured that texture-preserving LDCT reconstruction has advantages over edge-preserving regional smoothing paradigm for texture-specific clinical applications.
Fast conjugate gradient algorithm extension for analyzer-based imaging reconstruction

Oriol Cau데vevilla, Jovan G. Brankov, Illinois Institute of Technology (United States)

This paper presents an extension of the classic Conjugate Gradient Algorithm. Motivated by the Analyzer-Based Imaging inverse problem, the novel method maximizes the Poisson regularized log-likelihood with a non-linear transformation of parameter faster than other solutions. The new approach takes advantage of the special properties of the Poisson log-likelihood to conjugate each descend direction with respect all the previous directions taken by the algorithm. Our solution is compared with the general solution for non-quadratic unconstrained problems: the Polak-Ribiere formula. Both methods are applied to the ABI reconstruction problem.

Efficient iterative image reconstruction algorithm for dedicated breast CT

Natalia Antropova, Adrian Sanchez, Ingrid Reiser, Emil Y. Sidky, The Univ. of Chicago (United States); John M. Boone, Univ. of California, Davis (United States); Xiaochuan Pan, The Univ. of Chicago (United States)

Dedicated breast CT is currently being studied as a potential screening method for breast cancer. The scan protocol calls for low X-ray exposure, comparable to that of mammography and yields projection data that contains high levels of noise. Iterative image reconstruction (IIR) algorithms may be well-suited for the system since they potentially reduce the noise in the reconstructed images. However, IIR outcomes can be difficult to control since the algorithm parameters do not directly correspond to the image properties. Also, IIR algorithms are computationally demanding and have optimal parameter settings that depend on the size and shape of the breast and positioning of the patient. In this work, we design an efficient IIR algorithm with meaningful parameter specifications and that can be used on a large, diverse sample of breast CT cases. The flexibility and efficiency of this method comes from having the final image produced by a linear combination of two separately reconstructed images - one containing gray level information and the other with enhanced higher frequency components. Both of the images result from few iterations of separate IIR algorithms. The proposed algorithm depends on two parameters, both of which have a well-defined impact on image quality. The algorithm is applied to numerous breast CT cases from a UC Davis prototype system.

Direct reconstruction of enhanced signal in computed tomography perfusion

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High imaging dose has been a concern in computed tomography perfusion (CTP) as repeated scans are performed at the same location of a patient. On the other hand, signal changes only occur at limited regions of perfusion (CTP) as repeated scans are performed at the same location of a patient. In this work, we propose a new reconstruction strategy by effectively initializing the final phase high-quality CT to reconstruct the later phase CT acquired with a low-dose protocol. In the proposed strategy, initial high-quality CT is considered as a base image and enhanced signal (ES) is reconstructed directly by minimizing the penalized weighted least-square (PWLS) criterion. The proposed PWLS-ES strategy converts the conventional CT reconstruction into a sparse signal reconstruction problem. Digital and anthropomorphic phantom studies were performed to evaluate the performance of the proposed PWLS-ES strategy. Both phantom studies show that the proposed PWLS-ES method outperforms the standard iterative CT reconstruction algorithm based on the same PWLS criterion according to various quantitative metrics including: peak signal-to-noise ratio (PSNR), normalized mean square error (NMSE), root mean squared error (RMSE) and the universal quality index (UQI).
in the scaled domain, the relative difference between the two patches becomes smaller than the intensity difference measured in the standard method, which has an effect of lowering the penalties accordingly. Our numerical experiments using a software phantom, which contains several small features with different activities, demonstrate that, compared to the standard method, our method not only improves overall reconstruction accuracy in terms of the percentage error, but also reveals better recovery of fine details in terms of the contrast recovery coefficient.

9783-166, Session PS7

High-resolution and large-volume tomography reconstruction for x-ray microscopy

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A noticeable application of X-ray microscopy is to construct a high-resolution tomography of an object without physically slicing the object. For large objects, because of the limited field-of-view, a projection image of an object should be taken by several shots from different locations, and using an image stitching method to combine these image blocks together. All stitching algorithms require that any two adjacent image blocks have a large area of common overlap which contains many significant information. In this study, the overlap of image blocks should be small because our light source is the synchrotron radiation and the X-ray dosage should be minimized as possible. According the properties of synchrotron radiation, we simplify several steps of image alignment to enable the stitching success. First, the projection model of the synchrotron microscopy is regarded as the parallel beam that means we can ignore the scaling factor. Object tilting during the acquisition also can be ignored if the object is fixed in a container. Thus, we only consider the vertical and horizontal displacements. In addition, the neighbors of each image block are determinate because the arrangement of all image blocks is a uniform gird. During the reconstruction, the mechanical stability should be considered because it leads the misalignment problem in tomography. We adopt the feature-based alignment method to solve this problem. Finally, we apply the proposed method for a kidney of mouse for verification.

9783-167, Session PS7

An adaptive method for weighted median priors in transmission tomography reconstruction

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We present an adaptive method of selecting the center weight in the weighted-median prior for penalized-likelihood (PL) transmission tomography reconstruction. While the well-known median filter, which is closely related to the median prior, preserves edges, it is known to have an unfortunate effect of removing fine details because it tends to eliminate any structure that occupies less than half of the window elements. On the other hand, center-weighted median filters can preserve fine details by using relatively large center weights. But the large center weights can degrade monotonic regions due to insufficient noise suppression. In this work, to adaptively select the center weight, we first calculate pixel-wise standard deviation over neighbors of each pixel at every PL iteration and measure its cumulative histogram, which is a monotonically non-decreasing 1-D function.

We then normalize the resulting function to maintain its range over [1,9]. In this case the domain of the normalized function represents the standard deviation at each pixel, and the range can be used for the center weight of a median window. We implemented the median prior within the PL framework and used an alternating joint minimization algorithm based on a separable paraboloidal surrogates algorithm. The experimental results demonstrate that our proposed method not only compromises the two extreme cases (the highest and lowest center weights) yielding a good reconstruction over the entire image in terms of the percentage error, but also reveals better recovery of fine details in terms of the contrast recovery coefficient.

9783-168, Session PS7

Continuous analog of multiplicative algebraic reconstruction technique for computed tomography

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Iterative reconstruction is a well-known method of reconstructing images for computed tomography, and it has advantages over the filtered back-projection procedure, which is a transform method enabling fast reconstruction by a hardware implementation, in reducing artifacts even for fewer projections and noisy data.

We propose a hybrid dynamical system as a continuous analog to the block-iterative multiplicative algebraic reconstruction technique (BI-MART), which is a well-known iterative image reconstruction algorithm. The hybrid system is described by a switched nonlinear system with a piecewise smooth vector field or differential equation and, for consistent inverse problems, the convergence of non-negatively constrained solutions to a globally stable equilibrium is guaranteed by the Lyapunov theorem. Namely, we can prove theoretically that a weighted Kullback-Leibler divergence measure can be a common Lyapunov function for the switched system. We show that discretizing the differential equation by using the first-order approximation (Euler's method) based on the geometric multiplicative calculus leads to the same iterative formula of the BI-MART with the scaling parameter as a time-step of numerical discretization. The present paper is the first to reveal that a kind of iterative image reconstruction algorithm is constructed by the discretization of a continuous-time dynamical system for solving tomographic inverse problems. Iterative algorithms with not only the Euler method but also the Runge-Kutta methods of higher-orders applied for discretizing the continuous-time system can be used for image reconstruction. A numerical example showing the characteristics of the discretized iterative methods is presented.

9783-169, Session PS7

Texture enhanced optimization-based image reconstruction (TxE-OBIR) from sparse projection views

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The optimization based image reconstruction (OBIR) is proposed and investigated in order to reduce the radiation dose in X-ray computed tomography (CT) through acquiring sparse projection views. However, the OBIR usually generates images with a quite different noise texture compared to the clinical widely used reconstruction method (i.e. filtered back-projection – FBP). This may make radiologists and/or other physicians less confident while they are making clinical decisions. Recognizing the
Acceleration of iterative tomographic image reconstruction by reference-based back projection

Chang-Chieh Cheng, Ping-Hui Li, Yu-Tai Ching, National Chiao Tung Univ., (Taiwan)

The reconstruction methods of computational tomography (CT) can be classified into two major categories: analytical reconstruction and iterative reconstruction. A widely used algorithm of analytical reconstruction is the filtered backprojection (FBP) that has fast performance but could have artifacts and may poorly converge for inverse problems. Iterative reconstruction can be implemented by the algebraic reconstruction technique (ART), an algebraic scheme based on the Kaczmarz’s method, which requires a large number of iterations to estimate better results than the analytical reconstruction. However, the ART take much longer time than FBP even for parallel computer implementation is applied. In this study, we accelerate the reconstruction speed of ART by using the result of FBP to be an initial guess and the reference for the first iteration and each back projection stage respectively. Both two improvements can reduce the error between the forward projection of each iteration and the measurements. We use three methods of quantitative analysis: root-mean-square error (RMSE), peak signal to noise ratio (PSNR), and structural content (SC), to show that our method can reduce the number of iterations by more than half and the quality of the result is better than the original ART.

Noise reduction in computed tomography using a multiplicative continuous-time image reconstruction method

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In clinical X-ray computed tomography (CT), filtered back-projection (FBP) and iterative reconstruction (IR) are known methods to reconstruct images. The FBP procedure is widely used because of its high speed. In contrast to the transform method, IR methods can produce high quality reconstructed images with fewer artifacts even for projection data of low SNR. Based on the idea of continuous methods for solving inverse problems in CT, we have presented a continuous-time image reconstruction (CIR) system described by a nonlinear dynamical system with a smooth vector field. Recently, we have also proposed a multiplicative CIR method described by differential equations based on the minimization of a weighted Kullback-Leibler divergence. We prove theoretically that the divergence measure decreases along the solution to the CIR system, for consistent inverse problems. Considering the noisy nature of measured projection data in clinical X-ray CT, the inverse problem belongs to the category of ill-posed problems. Because it is difficult to analyze theoretically the convergence of the continuous-time as well as iterative image reconstruction systems in inconsistent cases, we perform numerical experiments. The purpose of this paper is to investigate the performance of noise reduction for our new CIR method through numerical experiments. The method is compared to the conventional CIR method and the maximum-likelihood expectation-maximization (ML-EM) method. We found that the proposed CIR has an advantage on noisy projection with lower SNR in terms of the distance to the actual solution under the same measure observed via the projection data, resulting in low patient dose. The results lead us to the conclusion that the multiplicative CIR method is effective and robust for noise reduction in CT compared to the conventional CIR and the ML-EM method.

Assessment of tomographic reconstruction performance using the Mojette transform

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The Mojette transform is a discrete and exact Radon transform, based on the discrete geometry of the projection and reconstruction lattice. This transform is only defined on discrete angles and the sampling step over each projection varies with the associated direction. This specific sampling scheme results in theoretical exact image reconstruction. However, the latter differs from the sampling provided by tomographic acquisition devices such as CT, that have constant acquisition bins for every gantry rotation angle. Hence, the application of the Mojette transform to reconstruct actual tomographic acquisition data requires either a Mojette compatible acquisition or an adaptation of the classical sampling to fit the structure of Mojette projections.

In this paper, we consider the latter option and use interpolation schemes to remap the original data in a pre-processing step, before using reconstruction algorithms based on the Mojette transform. Our goal is to compare the reconstructions obtained with the Mojette transform to the ones obtained with several usual projection/backprojection digitized Radon transform. We conducted a series of experiments to evaluate the performance of the Mojette reconstructions after data resampling, using simulated CT acquisition of a computerized phantom. By plotting the PSNR for the reconstruction against the initial projection number, we show that our method compares favorably to the classical methods, even after imperfect data resampling.

These experiments validate and demonstrate the performance of the Mojette transform sampling over classical implementations based on continuous space.

A wide-acceptance Compton spectrometer for spectral characterization of a medical x-ray source

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Accurate knowledge of the x-ray spectra used in medical treatment and radiography is important for dose calculations and material decomposition analysis. Indirect measurements via transmission through materials are possible. However, such spectra are challenging to measure directly due to the high photon fluxes. One method of direct measurement is via a Compton spectrometer (CS) method. In this approach the x-rays are converted to a much lower flux of electrons via Compton scattering on a converter foil (typically beryllium or aluminum). The electrons are then momentum selected by bending in a magnetic field. With tight angular acceptance of electrons into the magnet of ~ 1 deg, there is a simple linear correlation between incident photon energy and electron position recorded
on an image plate. Here we present measurements of Bremsstrahlung spectrum from a medical therapy machine, Scanditronix M22. Spectra with energy endpoints from 6 to 20 MeV are directly measured, using a wide acceptance CS. The CS has an energy range from 0.5 to 20 MeV. We discuss the sensitivity of the device and the effects of converter material and collimation on the accuracy of the reconstructed spectra. Approaches toward improving the sensitivity, including the use of coded apertures, and potential future applications to characterization of spectra are also discussed.

9783-174, Session PS8
X-ray spectrum estimation from transmission measurements by an exponential of a polynomial model
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There has been much recent research effort directed toward spectral computed tomography (CT). An important step in realizing spectral CT is determining the spectral response of the scanning system so that the relation between material thicknesses and X-ray transmission intensity is known. We propose a few parameter spectrum model that can accurately model the X-ray transmission curves and has a form which is amenable to simultaneous spectral CT image reconstruction and CT system spectrum calibration. While the goal is to eventually realize the simultaneous image reconstruction/spectrum estimation algorithm, in this work we investigate the effectiveness of the model on spectrum estimation from simulated transmission measurements through known thicknesses of known materials. The simulated transmission measurements employ a typical X-ray spectrum used for CT and contain noise due to the randomness in detecting finite numbers of photons. The proposed model writes the X-ray spectrum as the exponential of a polynomial (EP) expansion. The model parameters are obtained by use of a standard software implementation of the Nelder-Mead simplex algorithm. The performance of the model is measured by the relative error between the predicted and simulated transmission curves. The estimated spectrum is also compared with the model X-ray spectrum. For reference, we also employ a polynomial (P) spectrum model and show performance relative to the proposed EP model.

9783-175, Session PS8
A dual-energy medical instrument for measurement of x-ray source voltage and dose rate
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An original dual-energy detector and medical instrument have been developed to measure the output voltages and dose rates of X-ray sources. Theoretical and experimental studies were carried out to characterize the parameters of a new scintillator-photodiode sandwich-detector based on specially-prepared zinc selenide crystals in which the low-energy detector (LED) works both as the detector of the low-energy radiation and as an absorption filter allowing the high-energy fraction of the radiation to pass through to the high-energy detector (HED). The use of the LED as a low-energy filter in combination with a separate HED opens broad possibilities for such sandwich structures. In particular, it becomes possible to analyze and process the sum, difference and ratio of signals coming from these detectors, ensuring a broad (up to 106) measurement range of X-ray intensity from the source and a leveling of the energy dependence. We have chosen an optimum design of the detector and the geometry of the component LED and HED parts that allow energy-dependence leveling to within specified limits. The deviation in energy dependence of the detector does not exceed about 5% in the energy range from 30 to 120 keV. The developed detector and instrument allow contactless measurement of the anode voltage of an X-ray emitter from 40 to 140 kV with an error no greater than 3%. The dose rate measurement range is from 1 to 200 R/min. An original medical instrument has passed clinical testing and was recommended for use in medical institutions for X-ray diagnostics. This research is supported in part by NATO's Emerging Security Challenges Division in the framework of the Science for Peace and Security Programme (Project SfP-984605).

9783-176, Session PS9
Neutron spectroscopic imaging for precision medical diagnostics
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We have previously described a new method called Neutron Stimulated Emission Computed Tomography (NSECT) for precise and accurate imaging of biological elements in the human body. Using our experimental prototype, which utilizes a Van-de-Graaff accelerator to produce the desired neutrons, we have demonstrated NSECT’s performance in diagnosing hemochromatosis and cancer based on the element levels measured directly within the diseased tissue. We are now developing a clinical prototype scanner that will provide the same performance as our Van-de-Graaff-based experimental device but in a compact form that can be safely deployed in a clinic. The clinical prototype uses a compact DDN neutron generator measuring 12 inches in length that produces neutrons at 2.5 MeV. In this work, we evaluate the performance of the clinical NSECT system and present the first results (simulated) of precision medical diagnostics using the clinical prototype.

A simulation of the DDN generator-based NSECT system was developed in GEANT4 to model the clinical NSECT prototype. A high-efficiency collimator was used to collimate the neutron beam to 1 cm full-width-half-max. The design of the collimator was optimized to permit: a) Maximum flux of primary neutrons, and b) Minimum flux of scattered neutrons and secondary gammas. HPGe and LaBr detectors were used to complete the imaging system. Simulated scans were then run for cancer and other diseases in the brain, breast, liver and lung. The performance of the prototype clinical system was found to be at par with our previous experimental system, demonstrating its strong promise in translating NSECT into a clinic for precision medical diagnostics.

9783-177, Session PS9
In vivo small animal lung speckle imaging with a benchtop in-line XPC system
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For the first time, X-ray phase-contrast (XPC) images of mouse lungs have been acquired in vivo with a benchtop XPC system employing a conventional microfocus source. A strong speckled intensity pattern is present in lung regions of the XPC radiographs, previously only observed in synchrotron experiments and in situ benchtop studies. We show how the texture characteristics of the speckle is influenced by imaging system parameters and the amount of air present in the lungs at different points in the breathing cycle. These results represent a substantial milestone for pre-clinical lung imaging and the field of XPC imaging as a whole.
New CT system architectures for high-temporal resolution with applications to improved geometric dose efficiency and cardiac imaging, part II: x-ray source sub-system

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A new dual-drum CT system architecture has been recently introduced with the potential to achieve significantly higher temporal resolution than is currently possible in medical imaging CT. The concept relies only on known technologies; in particular rotation speeds several times higher than what is possible today could be achieved leveraging typical x-ray tube designs and capabilities. However, the architecture lends itself to the development of a new arrangement of x-ray sources in a toroidal vacuum envelope containing a rotating cathode ring and a (optionally rotating) shared anode ring to potentially obtain increased individual beam power as well as increase total exposure per rotation. The new x-ray source sub-system design builds on previously described concepts and could make the provision of multiple conventional high-power cathodes in a CT system practical by distributing the anode target between the cathodes. In particular, relying on known magnetic-levitation technologies, it is in principle possible to more than double the relative speed of the electron-beam with respect to the target, thus potentially leading to significant individual beam power increases as compared to today’s state-of-the-art. In one embodiment, the proposed design can be naturally leveraged by the dual-drum CT concept previously described to alleviate the problem of arranging a number of conventional rotating anode-stem x-ray tubes and power conditioners on the limited space of a CT gantry. In another embodiment, a system with three cathodes is suggested leveraging the architecture previously proposed by Franke.

A glass-sealed field emission x-ray tube based on cone shaped carbon nanotube emitter for medical imaging

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In this paper, we obtained the x-ray image from glass-sealed x-ray tube. The x-ray images show micrometer scale resolution with stable and repeatable measurements. The demonstrated CNT x-ray tube and their imaging processing are discussed.

A CNT based glass-sealed field emission x-ray tube with four electrode including anode, focusing, gate, cathode has been demonstrated. The high-performance CNT emitters were grown using the resist assisted patterning (RAP) process appear to be excellent candidates as electron sources for x-ray generation. The CNT-bundles emitters of elliptical shape were fabricated by using RAP with lithography process. The cone shape emitters could produce an enhanced and stable electron emission. This enhanced electron emission combined with the ability to control emitter pitch produces an enhancement in x-ray image. With these emitters, we obtained x-ray images of mouse for medical imaging.

Organ radiation exposure with EOS: GATE simulations versus TLD measurements

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The aim of this study was to compute the organs radiation exposure using the innovative EOS® system, in biplane mode, for a patient in Antero-Posterior (AP) or Posterior-Anterior (PA) positioning. EOS® is an imaging device allowing the simultaneous acquisition of two orthogonal, full-body images, during a vertical scan of the patient in standing position. To achieve our goal, we have developed a Monte-Carlo simulation based on a GATE environment, adapted to the particular configuration of the EOS® machine; we have also produced a virtual, voxelized anthropomorphic phantom based on CT-scan data of a CIRS female ATOM dosimetry phantom, which was placed at the system’s isocenter. The GATE numerical simulations provided us with several organs dose estimations, which we have compared to dose measurements acquired with Thermo Luminescent Detectors (TLDs) placed at specific positions on the same phantom. To our knowledge, this study presents the first organ dose estimations resulting from a simulation environment adapted to the specific geometry and physics of the EOS® device. Our results show a very good agreement between the simulated and measured organ doses, for both AP and PA positions; they also confirm a reduction in radiation exposure for some organs when the phantom is placed in the PA position.

Hartmann-Shack wavefront sensor for adaptive optics confocal scanning laser ophthalmoscopy

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Due to the usage of large dynamic range deformable mirrors in adaptive optical system of in vivo image of the retina in human eyes, Hartmann-Shack wavefront sensor with wide dynamic range should be designed for the new adaptive optical system. Generally, the dynamic range of the new Hartmann-Shack wavefront sensor should reach PV±10? and the measurement accuracy should reach RMS ?/50.

A Hartmann-Shack wavefront sensor (HWSFS) is designed for adaptive optics system of Confocal Scanning Laser Ophthalmoscopy in this article. The Hartmann-Shack wavefront sensor designed consists of a lenslet array with square configuration sub-apertures x sub-aperture size 0.2mmx0.2mm, focal length 5mm and a CCD camera with pixel size 3.75?mx3.75?. HWSFS designed are simulated through the software MATLAB. The result of simulation indicates that focus dynamic range PV±14?. Wavefront measurement accuracy in relative mode RMS ?/150, all these indicators reached the requirements of the system.

A method for absolute calibration of Hartmann-Shack wave-front sensor (HWSFS), in which the wavefronts differences of several spherical wavefronts is used to determine the focus dynamic range and the measurement accuracy of HWSFS, is proposed. Experiments based on the method is also setup. The results indicate that the the focus dynamic range reach PV±14? and the uncertainty of the Hartmann-Shack wave-front sensor calibrated by the proposed method is improved to less than RMS ?/100 (?=635nm) with modal reconstruction method.
Scattering-compensated cone beam x-ray luminescence computed tomography
Peng Gao, Fourth Military Medical Univ. (China)

Cone-beam x-ray luminescence computed tomography opens new possibilities to perform molecular imaging with x-ray. The x-ray scattering effect is a great issue in both cone beam CT and XLCT. It has been shown that if the scattering effect compensated, the reconstruction average relative error can be reduced form 40% to 12% in the in the pencil beam XLCT. However, the scattering effect in the cone beam XLCT has not been proved. To verify and reduce the scattering effect, we proposed scattering-compensated x-ray luminescence computed tomography using an added leading to prevent the spare x-ray outside the irradiated phantom in order to decrease the scattering effect. Phantom experiments of two tubes filled with Y2O3:Eu+ indicated the proposed method could reduce the scattering by an degree of 30% and can reduce the location error from 1.8mm to 1.2mm. Hence, the proposed method was feasible to the general case and actual experiments and it is easy to implement.

Microstructure analysis of the pulmonary acinus by a synchrotron radiation CT
Kohichi Minami, The Univ. of Tokushima (??)

Conversion of images at micro level of the normal lung and those with very early stage lung disease, and the quantitative analysis of morphology on the images can contribute to the thoracic image diagnosis of the next generation. The collection of every minute CT images is necessary in using high luminance synchrotron radiation CT for converting the images. The purpose of this study is to analyze the structure of secondary pulmonary lobules. We also show the structure of the secondary pulmonary lobe by means of extending our vision to a wider field through the image reconfiguration from the projection image of the synchrotron radiation CT.

Ultrasound waveform tomography with a total-generalized-variation regularization scheme
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Ultrasound sound-speed tomography may improve breast cancer characterization. We develop a new ultrasound waveform tomography method for accurate sound-speed reconstruction of breast tumors. We employ a total-generalized-variation regularization term as an extra penalty term in addition to the original data misfit term. The new objective function includes both the data misfit term and the total-generalized-variation regularization term. We solve the optimization problem by the alternating-direction minimization method. We use both numerical and real phantom data to validate the capability of our new ultrasound waveform tomography method for sound-speed reconstruction. The numerical phantom contains a spiculated tumor in a random background medium. The diameter of the spiculated tumor is 8.0 mm. The real phantom includes two pieces of chicken breast in a tissue-mimicking gelatin phantom. The phantom is scanned using our breast ultrasound tomography system with two parallel transducer arrays. Our new ultrasound waveform tomography method yields accurate sound-speed reconstructions for both the numerical and real phantoms without noticeable image artifacts.

Event-by-event PET image reconstruction using list-mode origin ensembles algorithm
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There is a great demand for real time or event-by-event (EBE) image reconstruction in emission tomography. Ideally, as soon as event has been detected by the acquisition electronics, it needs to be used in the image reconstruction software. This would greatly speed up the image reconstruction since most of the data will be processed and reconstructed while the patient is still undergoing the scan. Unfortunately, the current industry standard is that the reconstruction of the image would not start until all the data for the current image frame would be acquired. Implementing an EBE reconstruction for MLEM family of algorithms is possible, but not straightforward as multiple (computationally expensive) updates to the image estimate are required.

In this work an alternative Origin Ensembles (OE) image reconstruction algorithm for PET imaging is converted to EBE mode and is investigated whether it is viable alternative for real-time image reconstruction. In OE algorithm all acquired events are seen as points that are located somewhere along the corresponding line-of-responses (LORs), together forming a point cloud. Iteratively, with a multitude of quasi-random shifts following the likelihood function the point cloud converges to a reflection of an actual radionuclide distribution with the degree of accuracy that is similar to MLEM. New data can be naturally added into the point cloud. Preliminary results with simulated data show little difference between regular reconstruction and EBE mode, proving the feasibility of the proposed approach.

Quantitative analysis of L-SPECT system for small animal brain imaging
Tasneem Rahman, Murat Tahtali, Mark R. Pickering, UNSW Canberra (Australia)

This paper aims to investigate the performance of a newly proposed L-SPECT system for small animal brain imaging. The L-SPECT system consists of an array of 100 µm diameter pinholes. The proposed detector module has a 48mm by 48mm active area and the system is based on a pixelated array of NaI crystals (10x10x10 mm elements) coupled with an array of position sensitive photomultiplier tubes (PSPMTs). The performance of this system was evaluated with pinhole radius of 50µm, 60µm and 100µm. Monte Carlo simulation studies using the Geant4 Application for Tomographic Emission (GATE) software package were conducted to estimate the performance of this novel dual head L-SPECT where a geometric mouse phantom is used. All SPECT data were obtained using 120 views projection from 0° to 360° with a 3° step. Slices were reconstructed using the conventional filtered back projection (FBP) algorithm. We have evaluated the quality of the images in terms of spatial resolution (FWHM), sensitivity, signal-to-noise ratio (SNR) and volume sensitivity. The spatial resolution of our newly proposed L-SPECT was about 0.42 mm full width at half-maximum (FWHM) at a radius of rotation of 6 cm using 50 µm pinhole aperture where the sensitivity at 6 cm was 4500 cps/μCi. The analysis results show the combination of excellent spatial resolution and high detection efficiency over an energy range between 20-160 keV. The results demonstrate that SPECT imaging using a pixelated L-SPECT detector module is applicable in the quantitative study of the mouse brain imaging.
A depth-encoding PET detector inserting horizontal stripes glass between crystal layers

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This study introduces a depth-encoding PET detector inserting a horizontal stripes glass between the pixilated scintillation crystal layers. This design allows the light spreading that scintillation photons can travel only through the X direction and the alteration in the light distribution can generate a unique pattern diagram of the 2D flood histogram that identifies depth position as well as X-Y position of γ-ray interaction. A Monte Carlo simulation was conducted for the assessment of the DOI-PET detector. Two layer crystal blocks and the horizontal stripes glasses were modeled. The 11 different glass thicknesses range from 0 to 10 mm with 1 mm step were inserted between the crystal layers. The traced light distribution for each event was converted into the 2D flood histogram. Light loss caused by inserting the horizontal stripes glass between the crystal layers was estimated. Applicable weighting factors examined for each DOI-PET detector. The simulation results showed that the flood histogram without overlapping of each crystal position can be generated for the detectors by inserting the horizontal stripes glass of > 1 mm. It was proper to add the weighting factors of 0 into the resistors of Rx at the modified resistive charge division (RCD) networks. It was estimated that an average light loss dependency on the horizontal stripes glass thickness was approximately 35 photons/mm (~0.5%/mm).

This study demonstrated that the proposed DOI-PET detector can extract the 3D γ-ray interaction position without considerable performance degradations of PET detector from the 2D flood histogram.

In vitro flow assessment: from PC-MRI to computational fluid dynamics including fluid-structure interaction

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Initiation and development of cardiovascular diseases can be highly correlated to specific biomechanical parameters. To examine and assess biomechanical parameters, numerical simulation of cardiovascular dynamics has the potential to complement and enhance medical measurement and imaging techniques. As such, computational fluid dynamics (CFD) have shown to be suitable to evaluate blood velocity and pressure in scenarios, where vessel wall deformation plays a minor role. However, their is a need for further validation studies and the inclusion of vessel wall elasticity for morphologies being subject to large displacement.

In this work we consider a fluid-structure interaction (FSI) model including the full elasticity equation to capture the deformability of aortic wall soft tissue. We present a framework, in which either a CFD study can be performed on less deformable aortic segments or an FSI simulation for regions of large displacement such as the aortic root and arch. Both methods are validated by means of an aortic phantom experiment. The computational results are in good agreement with 2D phase-contrast magnetic resonance imaging (PC-MRI) velocity measurements as well as catheter-based pressure measurements. The FSI simulation shows longitudinal flow wave propagation enabled by the elastic model of the vessel wall, which the CFD model is not capable of. Reliable FSI simulation frameworks can enable the computation of further biomechanical parameters such as the stiffness or the stress distribution within the vessel wall.

Characterization of various tissue mimicking materials for medical ultrasound imaging

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Tissue mimicking materials are physical constructs exhibiting certain desired properties, used in machine calibration, medical imaging research, surgical planning, training, and simulation. For medical ultrasound, those specific properties include propagation speed and proportionality of attenuation coefficient over the diagnostic frequency range. We investigated the acoustic characteristics of polyvinyl chloride, polydimethylsiloxane and isopropanol using a time of flight technique, where a pulse was passed through a sample of known thickness contained in a water bath. The propagation speed in PVC is approximately 1400m/s depending on the exact chemical composition, and the attenuation coefficient ranges from 0.352dB/cm at 1MHz to 10.568dB/cm at 9MHz. The propagation speed in PMDS is in the range of 1100m/s, with an attenuation coefficient of 1.280dB/cm at 1MHz to 0.352dB/cm at 9MHz. At room temperature (22 °C), a mixture of water-isopropanol (7.25% isopropanol by volume) exhibits a propagation speed of 1540m/s, making it an excellent and inexpensive tissue-mimicking liquid for medical ultrasound imaging.

Quantitative evaluation of susceptibility effects caused by dental materials in head magnetic resonance imaging

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This work quantitatively evaluates the effects induced by susceptibility characteristics of materials commonly used in dental practice on the quality of head MR images in a clinical 1.5T device. The proposed evaluation procedure measures the image artifacts induced by susceptibility in MR images by providing an index consistent with the global degradation as perceived by the experts. Susceptibility artifacts were evaluated in a near-clinical setup, using a phantom with susceptibility and geometric characteristics similar to that of a human head. We tested different dentist materials, called PAL Keramit, Ti6Al4V-ELI, Keramit NP, ILOR F, Zirconia and used different clinical MR acquisition sequences, such as “classical” SE and fast, gradient, and diffusion sequences.

The evaluation is designed as a matching process between reference and artifacts affected images recording the same scene. The extent of the degradation induced by susceptibility is then measured in terms of similarity with the corresponding reference image. The matching process involves a multimodal registration task and the use an adequate similarity index psychophysically validated, based on correlation coefficient. The proposed analyses are integrated within a computer-supported procedure that interactively guides the users in the different phases of the evaluation method.
2-Dimensional and 3-dimensional indexes are used for each material and each acquisition sequence. From these, we drew a ranking of the materials, averaging the results obtained.

Zirconia and ILOR F appear to be the best choice from the susceptibility artefacts point of view, followed, in order, by PAL Keramit, Ti6AI4V-ELI and Keramit NP.

9783-193, Session PS10
Effects of tissue heterogeneity on single-coil, scanning MIT imaging
Joseph R. Feldkamp, Stephen Quirk, Kimberly-Clark Corp. (United States)

We recently reported on the use of a single induction coil to accomplish imaging of the electrical conductivity in human tissues via magnetic induction tomography (MIT). A key to the method was the development of a mapping equation that quantitatively relates an arbitrary electrical conductivity distribution to ohmic loss in a coil consisting of concentric circular loops in a plane. By making multiple coil loss measurements at a number of locations in the vicinity of the target, this mapping equation can be used to build an algorithm for 3D image construction of electrical conductivity. Important assumptions behind the mathematical formula included uniform dielectric constant throughout all space and continuous variation in conductivity. These two assumptions were tested in a series of experiments involving the use of human tissue phantoms created from agarose, doped with sufficient sodium chloride to yield physiological conductivities. Inclusions of doped agarose were scanned both while isolated and also while embedded in a matrix of agarose gel having lowered conductivity ~ to simulate effects of abrupt permittivity change. Furthermore, a single inclusion of doped agarose was scanned both with and without the placement of a very thin plastic barrier through its center to simulate the effect of “discontinuous” conductivity change. In either case, we will show that these effects are minimal on resultant images.

9783-195, Session PS10
Quantitative evaluation of PET image using event information bootstrap
Han Kyeol Kyeol, Shin Hye Kwak, Kyeong Min Kim, Joo Hyun Kang, Korea Institute of Radiological & Medical Sciences (Korea, Republic of); Yong Hyun Chung, Yonsei Univ. (Korea, Republic of); Sang-Keun Woo, Korea Institute of Radiological & Medical Sciences (Korea, Republic of)

We recently reported on the use of a single induction coil to accomplish imaging of the electrical conductivity in human tissues via magnetic induction tomography (MIT). A key to the method was the development of a mapping equation that quantitatively relates an arbitrary electrical conductivity distribution to ohmic loss in a coil consisting of concentric circular loops in a plane. By making multiple coil loss measurements at a number of locations in the vicinity of the target, this mapping equation can be used to build an algorithm for 3D image construction of electrical conductivity. Important assumptions behind the mathematical formula included uniform dielectric constant throughout all space and continuous variation in conductivity. These two assumptions were tested in a series of experiments involving the use of human tissue phantoms created from agarose, doped with sufficient sodium chloride to yield physiological conductivities. Inclusions of doped agarose were scanned both while isolated and also while embedded in a matrix of agarose gel having lowered conductivity ~ to simulate effects of abrupt permittivity change. Furthermore, a single inclusion of doped agarose was scanned both with and without the placement of a very thin plastic barrier through its center to simulate the effect of “discontinuous” conductivity change. In either case, we will show that these effects are minimal on resultant images.

9783-196, Session PS11
Design of a high-energy grating-based x-ray phase-contrast imaging setup

Interferometric X-ray imaging becomes more and more attractive for applications such as medical imaging or non-destructive testing, because it provides the opportunity to obtain additional information on the internal structure of radiographed objects. Therefore, three types of images are acquired: An attenuation-image like in conventional X-ray imaging, a image of the differential phase-shift generated by the object and the so called dark-field image, which contains information about the object’s granularity even on sub-pixel scale.

However, most experiments addressing grating-based X-ray phase-contrast imaging with polychromatic sources are restricted to energies up to 40 keV. However, for the application of this imaging method to thicker objects like human specimens or dense components are higher tube voltages required. This is why we designed and constructed a laboratory setup for high energies, which is able to image larger objects.

Furthermore, the mean visibility of the field of view was measured for several tube voltages to evaluate the performance of the setup. The result shows that the mean visibility has a peak value of 23% at a tube voltage of 60 kV. Moreover the standard deviation of the field of view’s visibility distribution is nearly constant 1.6% over the whole tube voltage range from 50 kV to 120 kV. This proofs a homogenous visibility within the field of view.

In addition a mean visibility of 16% can still be acquired at a tube voltage of 120 kV. Thus, good image quality is even for high energies provided.

9783-197, Session PS11
Feasibility of using energy-resolving detectors in differential phase-contrast imaging
Pavlo Baturin, Carestream Health, Inc. (United States)

Feasibility of using energy-resolving detectors in differential phase-contrast imaging was tested at high energies (up to 120 kV). A commercially available x-ray tube was modified for differential phase-contrast imaging (DPCI) by applying a single-exposure detector (SPECD) method. The SPECD method is based on the analysis of object contrast at different characteristic energies of the x-ray spectrum. The use of energy-resolving detectors allows the determination of object absorption and phase contrast at different characteristic energies. This is important for applications such as medical imaging, where the analysis of material properties and the differentiation of objects are required. In this paper, we present the results of the feasibility study and discuss the potential of energy-resolving detectors in differential phase-contrast imaging at high energies.
Joint reconstruction of refractive and absorption properties in propagation-based x-ray phase contrast tomography via nonlinear image reconstruction

Yujia Chen, Kun Wang, Washington Univ. in St. Louis (United States); Doga Gursoy, Carmen S. Hoyuelos, Francesco De Carlo, Argonne National Lab. (United States); Mark A. Anastasio, Washington Univ. in St. Louis (United States)

Propagation-based X-ray phase-contrast tomography (XPCT) provides the opportunity to image weakly absorbing objects and is being explored actively for a variety of important pre-clinical applications. Quantitative XPCT image reconstruction methods typically involve a phase retrieval step followed by application of an image reconstruction algorithm. Most approaches to phase retrieval have required acquiring multiple images at different object-to-detector distances and the introduction of simplifying assumptions, such as a single-material assumption, to linearize the imaging model. In order to overcome these limitations, a non-linear image reconstruction method has been proposed previously that jointly estimates the absorption and refractive properties of an object from XPCT projection data acquired at a single propagation distance without the need to linearize the imaging model. However, the numerical properties of this non-convex reconstruction problem remain largely unexplored. In this study, computer-simulation and experimental studies are conducted to investigate the feasibility of the joint reconstruction problem in practice. We demonstrate that the joint reconstruction problem is ill-conditioned and sensitive to system inconsistencies. Particularly, the method can generate inaccurate refractive index images only if the object is thin and has little phase wrapping in the data. However, we also observed that, for weakly absorbing objects, the refractive index images reconstructed by use of the joint reconstruction method are, in general, more accurate than those reconstructed using methods that simply ignore the object absorption.

Improvement of the visibility for x-ray phase contrast imaging using photon counting detector

Satoshi Sano, Shimadzu Corp. (Japan)

In the case of employing Talbot interferometer to the medical imaging, practical x-ray tubes radiate continuous X-rays and the interference intensity (so-called visibility) becomes worse because of the wide spectra of continuous X-rays. In order to achieve the high visibility, we have estimated the visibility improvement effect using the photon counting detector (PCD). The detected spectra using the 2D imaging PCD are distorted due to charge sharing and pileup, which would make visibility worse. First, we have made a model for Monte-Carlo calculation to calculate the distorted spectra and point spread function (PSF) for the charge sharing. The calculation model is based on the summation of the monochromatic response function which is the detected charge on the interested pixel for one photon injection. Distortion of spectra could be calculated under the change of pixel size, dead-time and dose rate.

Then we have obtained a result for the estimation of the visibility improvement effect using the PCD of CdTe. The visibilities of the energy integrating detector (EID) and the PCD are calculated and compared, where Talbot interferometer type is self-image direct detection. Visibilities of EID and PCD are 7% and 13%, respectively, where this result doesn’t include the pileup effect. The results including the pileup effect will be presented.

Quantification of signal detection performance degradation induced by phase-retrieval in propagation-based x-ray phase-contrast imaging

Cheng-Ying Chou, National Taiwan Univ. (Taiwan); Mark A. Anastasio, Washington Univ. in St. Louis (United States)

In propagation-based X-ray phase-contrast (PB XPC) imaging, the measured image contains a mixture of absorption- and phase-contrast. To obtain separate images of the projected absorption and phase (i.e., refractive) properties of a sample, phase retrieval methods can be employed. It has been suggested that phase-retrieval can improve image quality in PB XPC imaging. However, when objective (task-based) measures of image quality are employed, this is not necessarily true and phase retrieval can be detrimental. In this work, signal detection theory is utilized to quantify the performance of a Hotelling observer (HO) for detecting a known signal in a known background. Two cases are considered. In the first case, the HO acts directly on the measured intensity data. In the second case, the HO acts on either the retrieved phase or absorption image. We demonstrate that the performance of the HO is superior when acting on the measured intensity data. The loss of task-specific information induced by phase-retrieval is quantified by computing the efficiency of the HO as the ratio of the test statistic signal-to-noise ratio (SNR) for the two cases. The effect of the system geometry on this efficiency is systematically investigated. These studies are repeated for the case where a non-preshrinking matched filter is employed as the observer, which reveals the the impact of noise correlations on the detection efficiency. Our findings confirm that phase-retrieval can impair signal detection performance in XPC imaging.

Low dose phase contrast computed tomography for brain tumor follow-up

Marie Ruat, Christian Nemoz, ESRF - The European Synchrotron (France); Jean Francois Adam, Raphael Serduc, Inserm U836 (France); Cyril Ponchut, Helene Elleaume, ESRF - The European Synchrotron (France); Emmanuel Brun, Inserm U836 (France)

Studying the concentration of contrast agent in brain is of particular interest for the diagnosis, the understanding and the management of pathologies such as tumors. For instance, in the case of malignant glioma radiotherapy, dose enhancement occurs when the tumor is loaded with a high Z contrast agent. During the past two decades X-ray Phase Contrast Imaging (PCI) has shown a remarkable enhancement of image contrast and sensitivity for soft tissue. In this study, we compare results of PCI with the gold standard Synchrotron Radiation Computed Tomography (SRCT). PCI measurements were performed using the Maxipix-CdTe detector under development at ESRF. This detector features a monolithic 1 mm thick single crystal CdTe sensor (99% efficient at energies up to 60 keV) hybridised to a matrix of 3x1 Timexip chips, giving a total area of 768x256 pixels at 55 µm pitch (45 x 15 mm2). Its tomographic spatial resolution is of 0.06x0.06x0.06 mm3. The high efficiency of the detector enabled low dose imaging. Propagation based set-up was used with a single sample-to-detector distance of 11m. Monochromatic X-rays at 35 and 51 keV were used. Refractive and absorption indices maps were reconstructed using an iterative method implemented in the PyHST software. Both PCI and SRCT results were compared to H&E staining histology. We have successfully retrieved iodine contrast agent quantification for both steady-state protocol and dynamic contrast-enhanced perfusion imaging, with phantoms. In vivo SRCT imaging in rats bearing brain tumors also proved successful, following up the iodine uptake for 25 minutes.
Quantitative characterization of the microbubbles concentration by using a high-energy in-line phase contrast tomosynthesis prototype: a preliminary phantom study

Di Wu, Muhammad U. Ghani, Molly D. Wong, Yuhua Li, The Univ. of Oklahoma (United States); Kai Yang, Massachusetts General Hospital (United States); Wei R. Chen, Univ. of Central Oklahoma (United States); Bin Zheng, Hong Liu, The Univ. of Oklahoma (United States)

The purpose of this study is to demonstrate the feasibility of using a high-energy in-line phase contrast tomosynthesis system to quantitatively imaging microbubbles in a tissue simulating phantom under a limited radiation dose. The imaging prototype used in the investigation was an in-line phase contrast tomosynthesis system operated under 120 kVp tube voltage and 0.5 mA tube current. A combo filter made of 2.3 mm Cu, 0.8 mm Pb and 1.0 mm Al was employed to obtain as large as possible portion of x-ray photon energy higher than 60 keV. The tissue simulating phantom was built by three acrylic slabs and a wax slab to mimic a 40 mm thick compressed breast. There were two tiny-sized structures with 1 mm depth engraved on the two different layers. The microbubble suspensions with different concentrations were injected into those tiny structures. The in-line phase contrast angular projections acquired were used to reconstruct the in-plane slices of the tiny structures on different layers. The CNRs vs microbubble concentrations were investigated. As the result, the microbubble suspensions were clearly visible, showing higher CNR when compared with the areas with no microbubble. Furthermore, a monotonously increasing relation between CNRs and microbubble concentrations was observed after calculating the area CNR of the phase contrast tomosynthesis slices.

Low-dose performance of a whole-body research photon-counting CT scanner

Zhicong Yu, Shuai Leng, Mayo Clinic (United States); Steffen G. Kappler, Katharina Hahn, Siemens Healthcare GmbH (Germany); Zhoubo Li, Mayo Clinic (United States); Ahmed Halaweish, Siemens Healthcare (United States); Andre Henning, Siemens Healthcare GmbH (Germany); Erik L. Ritman, Cynthis H. McCollough, Mayo Clinic (United States)

Photon-counting CT (PCCT) is an emerging technique that may bring new possibilities to clinical practice. Compared to conventional CT, PCCT is able to exclude electronic noise that may severely impair image quality at low photon counts. This work focused on assessing the low-dose performance of a whole-body research PCCT scanner consisting of two subsystems, one equipped with an energy-integrating detector (EID), and the other with a photon-counting detector (PCD). Evaluation of the low dose performance of the research PCCT scanner was achieved by comparing the performance of the two subsystems, with an emphasis on examining the impact of electronic noise on image quality in low-dose situations.
Spectral CT using photon-counting x-ray detector (PCXD) can potentially increase accuracy of measuring tissue composition using energy-dependence of x-ray attenuation in different materials. Spectral CT is especially suited for imaging with K-edge contrast agents to address limited soft tissue contrast. However, PCXD spectral measurements suffer from distortion due to charge sharing, pulse pileup, and K-edge escape energy loss. To address distortion, we propose a novel distortion correction mechanism using artificial neural network (ANN) that learns from a training set composed of distorted input spectra and corresponding distortion-free true spectra obtained via X-ray simulation to find a correction. By simulation, we tested if K-edge and material contrast can be recovered in distortion-corrected spectra. We decomposed corrected and uncorrected spectral CT images into 3 materials: Compton scattering, photoelectric, and iodine. The material decomposition accuracy was vastly improved with distortion correction—79% reduced material concentration error and up to 44% enhancement in contrast-to-noise-ratio (CNR) vs. uncorrected images. We recently implemented a spectral micro-CT system with PCXD, where two 3D-printed phantoms containing iodine solutions were imaged in full spectrum mode with projection data acquired every 1 keV. Scanned phantoms were reconstructed and spatially registered to 3D models. Simulation-based x-ray projections were matched to acquired projections, allowing the ANN training phase. Post-training, ANN-based corrections were applied to correct other phantom data improving decomposed images CNR by 6 times and accuracy by 55% relative to direct decomposition from distorted data. Overall, results demonstrate experimental feasibility and potential advantages of ANN to correct distortion in spectral-CT using PCXD.

9783-208, Session PS13
Spot scanning proton therapy plan assessment: design and development of a dose verification application for use in routine clinical practice
Kurt E. Augustine, Timothy Walsh, Chris Beltran, Joshua Stoker, Daniel Mundy, Mark Parry, Martin Bues, Mirek Fatyga, Mayo Clinic (United States)

The use of radiation therapy for the treatment of cancer has been carried out clinically since the late 1800’s. Early on however, it was discovered that radiation dose which is sufficient to destroy cancer cells can also cause severe injury to surrounding healthy tissue. For the next century, advances in radiation physics and computer technology have made it possible to more accurately aim the high energy X-rays, making it more effective in destroying tumors while reducing the radiation dose to healthy tissue, but risk of severe complications remain significant. Radiation oncologists continually strive to find the perfect balance between a dose high enough to destroy the cancer and one that avoids damage to healthy organs. Spot scanning or “pencil beam” proton radiotherapy offers another option to improve the effectiveness vs. safety tradeoff. Unlike traditional photon therapy, proton beams stop in the target tissue, thus better sparing all organs beyond the targeted tumor. In addition, the beams are far narrower and thus can be more precisely “painted” onto the tumor, avoiding exposure to surrounding healthy tissue. Treatments are designed within commercial software applications called Treatment Planning Systems (TPS) which combine tissue visualization with radiation transport calculations. It is a general requirement in the practice of radiation therapy that radiation transport calculations should be verified by a software algorithm which is independent of the TPS. Proton beam radiotherapy facilities are small in number (presently only 12 in the US), so acceptable dose verification systems are currently not commercially available. For this reason, the Department of Radiation Oncology at the Mayo Clinic developed its own dose verification application for its newly opened proton beam radiotherapy treatment center. The architecture of the application, called 2nd Check, presented several unique challenges. Proton beam dose verification is based upon complicated, computationally intensive algorithms and therefore must be both efficient and flexible. To that end, the 2nd Check application offers two distinct methods for dose verification. One is a Monte Carlo, GPU-based simulation, and the other is based on an analytical, CPU technique, both of which were written in C++ and developed specifically to be run on Linux servers. To be able to provide consistent support, applications used in clinical settings typically need to be developed within institutionally standardized frameworks on common platforms using common programming languages and databases, which in this case is Window, .NET/C# and Microsoft SQL. The application also needs to work with other outside applications, like the Treatment Planning System. The best way to achieve interoperability is via international standards, in this case DICOM. Finally, to be useful in the routine clinical setting, the user interface needs to be highly intuitive, simple to use with minimal user interaction, and be runnable anywhere, i.e. desktop, laptop, tablet or phone. 2nd Check was architected to accommodate all these requirements. The two major components of the system include Varian Medical System’s Eclipse TPS, the Windows scheduler and web-based user interface, and the Linux based dose verification simulation engines. Based on a carefully-designed, flexible architecture integrating multiple applications, libraries, platforms, languages, and communication protocols, 2nd Check was developed and successfully deployed by the time the first proton beam therapy patient was treated at the clinic and is currently used routinely on every proton patient. Having an easy to use, efficient application for dose verification like 2nd Check greatly reduces the dosimetrist and physicist time and effort required for preparing each proton therapy plan, and more importantly, provides additional quality assurance and ultimately, improved safety for the patient.

9783-207, Session PS12
Feasibility study of sparse-angular sampling and sinogram interpolation in material decomposition with a photon-counting detector
Dohyeon Kim, Byungdu Jo, Su-Jin Park, Hyemi Kim, Hee-Joung Kim, Yonsei Univ. (Korea, Republic of)

Spectral computed tomography (CT) is a promising technique for obtaining enhanced image with contrast agent and distinguishing different materials. We focused on developing material decomposition technique with lower radiation exposure and shorter acquisition time. Sparse-angular views can reduce patient dose and scanning time for obtaining the reconstruction images. In this study, the sinogram interpolation method was used to improve the quality of material decomposed images in sparse angular sampling views. A prototype of spectral CT system with 64 pixels CZT-based photon counting detector was used. The source-to-detector distance and the source-to-center of rotation distance were 1200 and 1015 mm, respectively. The x-ray spectrum at 90 kVp with a tube current of 110 μA was used. Two energy bins (23-33 keV and 34-44 keV) were set to obtain the two images for decomposed iodine and calcification. We used PMMA phantom and its height and radius were 50 mm and 17.5 mm, respectively. The phantom contained 4 materials including iodine, gadolinium, calcification, and liquid state lipid. We evaluated the signal to noise ratio (SNR) of materials to examine the significance of sinogram interpolation method. The decomposed iodine and calcification images were obtained by projection based subtraction method using two energy bins with 36 projections. The SNR in decomposed images were improved by using sinogram interpolation method by increasing the signal of decomposed material and reducing the noise of decomposed material. In conclusion, the sinogram interpolation method can be used in sparse angular material decomposition method.
9783-209, Session PS13

**Estimation of the influence of radical effect in the proton beams using a combined approach with physical data and gel data**

Kiyofumi Haneda, Hiroshima International Univ. (Japan)

The purpose of this study was to estimate an impact on radical effect in the proton beams using a combined approach with physical data and gel data. This study used a polymer gel dosimeter. Polymer gel dosimeters have specific advantages when compared to other dosimeters. They can measure chemical reaction and they are at the same time a phantom that can map in three dimensions continuously and easily.

First, a depth-dose curve for the 210 MeV proton beam measured using a gel dosimeter and an ionization chamber. Second, the spatial distribution of the physical dose was calculated by Monte Carlo code system PhITS. To verify the accuracy of Monte Carlo calculation, the calculation results were compared with experimental data of an ionization chamber. Last, to evaluate of the rate of the radical effect against physical dose.

The simulation results were compared with measured the depth-dose distribution and good agreement was found, and the spatial distribution of a gel dose with threshold LET value of proton beam was calculated by the same code. Then, the relative distribution of the radical effect was calculated from the physical dose and gel dose. The relative distribution of the radical effect was calculated at each depth as the quotient of relative dose obtained using physical and gel dose. The agreement between the relative distributions of the gel dosimeter and Radical effect was good at the proton beams.

9783-210, Session PS14

**A generational approach to snapshot coded aperture x-ray diffraction imaging for medical applications**

Joel A. Greenberg, Manu N. Lakshmanan, Duke Univ. (United States); Scott Wolter, Elon Univ. (United States); David J. Brady, Anuj J. Kapadia, Duke Univ. (United States)

Coded aperture x-ray diffraction (XRD) imaging is a new method for measuring the molecular signature of the material or tissue present at different locations within a sample. Initial proof-of-concept studies have demonstrated the efficacy and potential of this method in practical medical imaging systems, such as for in-vivo cancer diagnosis [1,2]. As with all medical imaging systems, there is potential for improved performance though advances in hardware and software coupled with modifications to the core architecture. In this presentation, we describe different generations of snapshot coded aperture XRD imaging systems, demonstrate their effectiveness in providing clinically-relevant results, and discuss the considerations associated with choosing a particular configuration for a specific imaging task.

9783-211, Session PS14

**Validation of coded aperture coherent scatter spectral imaging for normal and neoplastic breast tissues via surgical pathology**

Robert E. Morris, Katie Albanese, Manu N. Lakshmanan, Shannon McCall, Joel A. Greenberg, Anuj J. Kapadia, Duke Univ. Medical Ctr. (United States)

This study intends to validate the sensitivity and specificity of coded aperture coherent scatter spectral imaging (CACSSI) by comparison to standard histological preparation and pathologic analysis methods. Breast abnormalities such as ductal carcinoma in situ (DCIS) as well as infiltrating ductal carcinoma were examined in this study. Chronology of validation is as follows; formalin fixed breast tumor samples were raster scanned via pencil beam coded aperture coherent scatter spectral imaging device. The collimated pencil beam is supplied by a diagnostic radiology X-ray tube operating at an accelerating voltage of 125kVp and 200mA per scan. A voxel-based image is rendered from each pencil beams’ reconstruction classification through comparison to know x-ray diffraction spectral form factors. Tissue samples were then sent for histological analysis. Samples were dehydrated, cleared, infiltrated, and embedded in paraffin wax, sectioned via rotary microtome, then stained and interpreted by a pathologist. To scrutinize differences a composite overlay of the CACSSI rendered image and pathologist interpreted stained sections validates the feasibility of CACSSI to differentiate normal and neoplastic breast structures such as ductal carcinoma in-situ and microcalcifications ex-vivo. CACSSI has demonstrated its feasibility in differentiating normal and neoplastic breast tissues through volumetric, non-rotational x-ray diffraction imaging. In the absence of tissue fixation and processing, accompanied by an automated classification algorithm implemented in the reconstruction, CACSSI is conceivably a viable modality in evaluating breast tissue. Through a comparison to pathologist annotated slides, the CACSSI system may be further optimized to maximize sensitivity and specificity for differentiation of breast carcinomas.

9783-212, Session PS15

**Development of a Hausdorff distance based 3D quantification technique to evaluate the CT imaging system impact on depiction of lesion morphology**

Pooyan Sahbaee, Marthony Robins, Justin B. Solomon, Ehsan Samei, Duke Univ. Medical Ctr. (United States)

The purpose of this study was to develop a 3D quantification technique to assess the impact of imaging system on depiction of lesion morphology. Regional Hausdorff Distance (RHD) was computed from two 3D volumes: virtual mesh models of synthetic nodules or “virtual nodules” and CT images of physical nodules or “physical nodules”. The method can be described in following steps. First, the synthetic nodule was inserted into anthropomorphic Kyoto thorax phantom and scanned in a Siemens scanner (Flash). Then, nodule was segmented from the image. Second, in order to match the orientation of the nodule, the digital models of the “virtual” and “physical” nodules were both geometrically translated to the origin. Third, the Hausdorff Distance was calculated from each pair of “virtual” and “physical” nodules. The minimum HD value represented the most matching pair.

Finally, the 3D RHD map and the distribution of RHD were computed for the matched pair. The technique was scalarized using the FWHM of the RHD distribution. The analysis was conducted for various shapes (spherical, lobular, elliptical, and speculated) and sizes of nodules. The calculated FWHM values of RHD distribution for the 8-mm spherical and speculated “virtual” and “physical” nodules were 0.33 and 0.92, respectively.

9783-213, Session PS15

**Synthesis of realistic lung nodule texture using a clustered lumpy background**

Yuese Zheng, Duke Univ. (United States) and Carl E. Ravin Advanced Imaging Institute (United States); Justin B. Solomon, Duke Univ. (United States) and Carl E. Ravin Advanced Imaging Labs. (United States); Daniele Marin M.D., Duke Univ. School of Medicine (United States) and Ehsan Samei, Carl E. Ravin Advanced Imaging Labs. (United States)
Realistic virtual lesion models are valuable in medical imaging applications including phantom design and observer studies. Internal tumor heterogeneity in nodules can be predictive of lesion malignancy but is not well understood and virtual lesion models will facilitate research in this area. The purpose of this study was to generate realistic virtual lung nodules with different internal heterogeneity characteristics. We propose a texture synthesis method that accounts for the effects of the imaging system to mimic the appearance of texture in real nodules. Using a public online database of chest CT images (Lung Image Database Consortium), 190 nodules were identified from 103 patients based on size (in-plane dimension>3 mm), malignancy score (>3 of 5), and CT scanner model (GE LightSpeed series). The nodules were further categorized by two radiologists according to heterogeneity level (1-homogeneous to 3-heterogeneous). For each nodule, twenty-one texture features were extracted based on the gray-level co-occurrence matrix and the gray-level run-length matrix. A three-dimensional Clustered Lumpy Background (3D-CLB) was used to simulate the nodule texture. Noise was added to the nodule using the noise power spectrum measured from the Mercury phantom on the GE LightSpeedVCT. The best fitting parameters of the 3D-CLB to represent the texture seen in the images were found using a genetic algorithm and the Mahalanobis distance between the texture features of simulated and real nodules. The resultant texture was objectively and visually similar to real nodules of the same heterogeneity category.

Second generation anthropomorphic physical phantom for mammography and DBT: Incorporating voxelized 3D printing and inkjet printing of iodinated lesion inserts

Dhiraj Sikaria, Stephanie Musinsky, Duke Univ. (United States); Gregory M. Sturgeon, Justin B. Solomon, Duke Univ. School of Medicine (United States); Andrew Dao, Duke Univ. School of Medicine (United States) and Duke Univ. (United States); Michael E. Gehm, Duke Univ. (United States); Ehsan Samei, Duke Univ. School of Medicine (United States); Stephen J. Glick, U.S. Food and Drug Administration (United States); Joseph Y. Lo, Duke Univ. School of Medicine (United States)

Physical phantoms are needed for the evaluation and optimization of clinical breast imaging systems, especially for new digital breast tomosynthesis (DBT) systems. Previously, we developed an anthropomorphic phantom based on human subject breast CT data and fabricated using commercial 3D printing. We now present three key advancements: voxelized 3D printing, photopolymer material doping, and 2D inkjet printing of lesion inserts. First, we bypassed the printer’s control software in order to print in voxelized form instead of conventional STL surfaces, thus improving resolution and allowing dithering to mix the two photopolymer materials into arbitrary proportions. We fabricated a test sample to demonstrate ability to print details ≤150 µm, and dithering to combine VeroWhitePlus and TangoPlus in 10% increments. Second, to address the limited attenuation difference among commercial photopolymer materials, we evaluated a beta sample from Stratasys Inc., in which the doping concentration of TiO₂ varied from 1.5 to 3%, which yielded increased attenuation corresponding to 98% breast density. By spanning 36% to 98% breast density, this can more than double our previous contrast. Third, using inkjet printers modified to print with iopamidol, we created 2D lesion patterns on paper that can be sandwiched into the phantom. Inkjet printing has advantages of being inexpensive and easy, and more contrast can be delivered by overprinting multiple times. FWHH for the printing technique was constant at 210 µm in the horizontal direction, but increased in the vertical direction to 330 µm after 10 overprints. Contrast increased linearly with overprinting at 0.7% per overprint. Together, these three new features provide the basis for creating a new anthropomorphic physical breast phantom with improved resolution and contrast, as well as the ability to insert 2D lesions for task-based assessment of performance.

Synthesized interstitial lung texture for use in anthropomorphic computational phantoms

Marc Becchetti, Justin B. Solomon, W. Paul Segars, Ehsan Samei, Duke Univ. (United States)

A realistic model of the anatomical texture from the pulmonary interstitium was developed with the goal of extending the capability of anthropomorphic computational phantoms (e.g., XCAT, Duke University), allowing for more accurate image quality assessment. Contrast-enhanced, high dose, thorax images for a healthy patient from a clinical CT system (Discovery CT750HD, GE healthcare) with thin (0.625 mm) slices and filtered back-projection (FBP) were used to inform the model. The interstitium which gives rise to the texture was defined using 24 volumes of interest (VOIs). These VOIs were selected manually to avoid vasculature, bronchi, and bronchioles. A small scale Hessian-based line filter was applied to minimize the amount of partial-volume superimposed vessels and bronchioles within the VOIs. The texture in the VOIs was characterized using 8 Haralick and 13 gray-level run length features. A clustered lumpy background (CLB) model with added noise and blurring to match CT system was optimized to resemble the texture in the VOIs using a genetic algorithm with the Mahalanobis distance as a similarity metric between the texture features. The most similar CLB model was then used to generate the interstitial texture to fill the lung. The optimization improved the similarity by 45%. This will substantially enhance the capabilities of anthropomorphic computational phantoms, allowing for more realistic CT simulations.
Development and comparison of projection and image space 3D nodule insertion techniques

Marthony Robins, Justin B. Solomon, Duke Univ. Medical Ctr. (United States); Jayashree Kalpathy-Cramer, Harvard Medical School (United States); Pooyan Sahbaee, Ehsan Samei, Duke Univ. Medical Ctr. (United States)

This study aimed to develop and compare two methods of inserting computerized virtual lesions into CT datasets. 24 physical synthetic nodules of three sizes and four morphologies were inserted into an anthropomorphic chest phantom (LÜNGMAN, KYOTO KAGAKU). The phantom was scanned (Somatom Definition Flash, Siemens Healthcare) with and without nodules present, and images were reconstructed with filtered back projection and iterative reconstruction (SAFIRE) at 0.6 mm slice thickness using a standard thoracic CT protocol at multiple dose settings. Virtual 3D CAD models based on the physical nodules were virtually inserted (accounting for the system MTF) into the nodule-free CT data using two techniques: projection-based and image-based. Nodule volumes were estimated using multiple commercial segmentation tools including (Ntution, TeraRecon, Inc.). Paired t-tests along with R2 goodness of fit between the virtually and physically inserted nodules were conducted. Both insertion techniques resulted in nodule volumes very similar to the real nodules (<5% difference) and in most cases the differences were not statistically significant. Also, R2 values were all >0.97 for both insertion techniques. These data imply that these techniques can confidently be used as a means of inserting virtual nodules in CT datasets. These techniques can be instrumental in building hybrid CT datasets composed of patient images with virtually inserted nodules.

kV x-ray dual digital tomosynthesis for image guided lung SBRT

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Two simulated sets of digital tomosynthesis images of the lungs, each set acquired at a 90 degree angle from the other, with 19 projection images used for each set and SART iterative reconstructed, gives dual tomosynthesis slice image quality approaching that of diagnostic spiral CT, with a data acquisition time that is less than 2% of that of cone beam CT. This fast kV acquisition, should allow real-time tracking of lung tumors in patients receiving SBRT, based on a novel TumoTrak(TM) multi-source X-ray tube design. Until this TumoTrak(TM) prototype is completed over the next year, its reconstructed performance was simulated from the DRR images created from a diagnostic spiral CT data set from a lung cancer patient. The resulting dual digital tomosynthesis reconstructed images of the lung tumor were exceptional and approached that of standard Feldkamp CT reconstruction of diagnostic spiral CT. The estimated dose was 46 mAs per dual digital tomosynthesis image or less than 10% of the 472 mAs of the diagnostic CT, for a 0.77 fps imaging rate sufficient to resolve respiratory motion in many free breathing patients during SBRT.

Design, optimization and evaluation of a smart pixel sensor array for low-dose digital radiography

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Amorphous silicon (a-Si:H) thin-film transistors (TFTs) are being widely used to build flat-panel X-ray detectors for digital radiography (DR). As the demand for low-dose X-ray imaging grows, a pixel with high signal to noise ratio (SNR) emerges. “Smart” pixel architecture is to use a dual-gate photosensitive thin-film transistor (TFT) for sensing, storage, and switch. It differs from a conventional passive pixel sensor (PPS) or active pixel sensor (APS) in that all these three functions are achieved by one device instead of three separate units. Thus, it is expected to have high fill factor and high resolution. In addition, it utilizes amplification of the dual-gate photosensitive TFT to form a one-transistor APS that leads to high SNR potentially. This paper addresses the design, optimization and evaluation of the smart pixel sensor array for low-dose X-ray DR. We will design and optimize the smart pixel from the scintillator to TFL levels and validate it through optical and electrical simulation and experimental results of a 2 by 2-pixel sensor array.

Modeling acquisition geometries with improved super-resolution in digital breast tomosynthesis

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In digital breast tomosynthesis (DBT), a reconstruction is created from multiple x-ray projection images. Our previous work demonstrated that the reconstruction is capable of super-resolution (i.e., subpixel resolution) relative to the detector. In order for super-resolution to yield a reliable improvement in image quality, it should be achievable at all positions in the reconstruction. This paper demonstrates that super-resolution is not achievable at all depths, or at all heights above the breast support. For this purpose, a bar pattern phantom was imaged using a commercial DBT system. A goniometry stand was used to orient the long axis of the parallel bars along an oblique plane relative to the breast support. This setup allowed a single test frequency to be visualized over a continuous range of depths. The orientation of the test frequency was parallel to the direction of the x-ray tube motion. An oblique reconstruction in the plane of the bar pattern phantom showed that the existence of super-resolution is depth-dependent. To identify design strategies for optimizing super-resolution, a theoretical model was then developed in which a test frequency higher than the alias frequency of the detector was simulated. Two design modifications that improve super-resolution are identified. In particular, it is shown that reducing the spacing between the x-ray source positions minimizes the number of depths lacking super-resolution. Additionally, introducing detector motion along the direction perpendicular to the breast support allows for more uniform super-resolution throughout the image volume. In conclusion, this work presents strategies for optimizing super-resolution in DBT.

Scatter estimation and removal of anti-scatter grid-line artifacts from anthropomorphic head phantom images taken with high-resolution image detectors

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In radiography, one of the best methods to eliminate image-degrading scatter radiation is the use of anti-scatter grids. However, with high-resolution dynamic imaging detectors, stationary anti-scatter grids can
leave grid-line shadows and moiré patterns on the image, depending upon the line density of the grid and the sampling frequency of the x-ray detector. Such artifacts degrade the image quality and may mask small but important details such as small vessels and interventional device features. Appearance of these artifacts becomes increasingly severe as the detector spatial resolution is improved. We have previously demonstrated that, to remove these artifacts by dividing out a reference grid image, one must first subtract the residual scatter that penetrates the grid; however, for objects with anatomic structure, scatter varies throughout the FOV and a spatially differing amount of scatter must be subtracted.

In this study, a standard stationary Smit-Rontgen X-ray grid (line density - 70 lines/cm, grid ratio - 13:1) was used with a high-resolution CMOS detector, the Dexasla 1207 (pixel size - 75 micron) to image anthropomorphic head phantoms. For a 15 x 15cm FOV, scatter profiles of the anthropomorphic head phantoms were estimated then iteratively modified to minimize the structured noise due to the varying grid-line artifacts across the FOV.

Images of the anthropomorphic head phantoms taken with the grid, before and after the corrections, were compared demonstrating almost total elimination of the artifact over the full FOV. Hence, with proper computational tools, anti-scatter grid artifacts can be corrected, even during dynamic sequences.

9783-222, Session PS16

Optical geometry calibration method for free-form digital tomosynthesis

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Digital tomosynthesis is a type of limited angle tomography that allows for 3D information reconstructed from a set of x-ray projection images taken at various angles using an x-ray tube, a mechanical arm to rotate the tube, and a digital detector. Tomosynthesis reconstruction requires the knowledge of the precise location of the detector with respect to each x-ray source. Current clinical tomosynthesis methods use a physically coupled source and detector so the geometry is always known and is always the same. This makes it impractical for mobile or field operations. We demonstrated a free form tomosynthesis with a decoupled source and detector setup that uses a novel optical method for accurate and real-time geometry calibration. We accomplish this by using a camera to track the motion of the source relative to the detector. A checkerboard pattern is positioned on or next to the detector using an extension arm in such a way that the pattern will not move relative to the detector. A camera is mounted on the source in a way that the pattern is visible during imaging and will not move relative to the source. The image of the pattern captured by the camera is then used to determine the relative camera/pattern position and orientation by analyzing the pattern distortion. This allows for accurate, real time geometry calibration of the x-ray source relative to the detector. Here we report the first demonstration of free form digital tomosynthesis systems using the method.

9783-223, Session PS16

Initial clinical evaluation of stationary digital chest tomosynthesis

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Computed Tomography (CT) is the gold standard for evaluating lung disease, including cystic fibrosis and lung nodules. CT effectively detects the lung disease symptoms and lung nodules as small as ~3mm but at a high cost and relatively high dose of radiation. Digital chest tomosynthesis (DCT) is an imaging modality that produces 3D images by collecting x-ray projection images over a limited angle. DCT is less expensive than CT and is about 1/10 the dose of radiation. The lower dose of radiation is important because regular scanning is an integral part of lung disease treatment.

We recently demonstrated the feasibility of stationary digital chest tomosynthesis (s-DCT) using a carbon nanotube (CNT) x-ray source with no mechanical motion. The electrically controlled switching allows for fast image acquisition and the possibility of prospective gated imaging. The short scan time reduces patient motion blur which is the largest source of image degradation for long scan time modalities.

Due to the electronic programmability of the CNT x-ray, s-DCT could be used in prospective gated imaging. Gated imaging can help with pediatric imaging by eliminating the need for a long breath hold.

The objective of this study is to evaluate the feasibility of using s-DCT as a faster, lower cost, and lower dose means for diagnosis and monitoring of lung disease patients. Under UNC’s institutional review board regulations we have successfully imaged 17 patients.

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Anatomical decomposition in dual energy chest digital tomosynthesis

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Lung cancer is the leading cause of cancer death worldwide and the early diagnosis of lung cancer has recently become more important. For early screening lung cancer, computed tomography (CT) has been used as a gold standard for lung cancer early diagnosis of lung cancer [1]. The major advantage of CT is that it is not susceptible to the problem of misdiagnosis caused by anatomical overlapping while CT has extremely high radiation dose and cost compared to chest radiography. Chest digital tomosynthesis (CDT) is a recently introduced new modality for lung cancer screening with relatively low radiation dose compared to CT [2] and also showing high sensitivity and specificity to prevent anatomical overlapping occurred in chest radiography. Dual energy material decomposition method has been proposed for better detection of pulmonary nodules as means of reducing the anatomical noise. In this study, possibility of materials decomposition in CDT was tested by simulation study and actual experiment using prototype CDT. The Gate v6 (Geant4 application for tomographic emission) and TASMIP code were used for simulation study and simulated cylinder shape phantom consisted of 4 inner beads which were filled with spine, rib, muscle and lung equivalent materials. The tomosynthesis scan was performed with a linear movement and 21 projection images were obtained over 30 degree of angular range with 1.5° degree of angular interval. The prototype CNT system has same geometry with simulation study and composed of E7869X (Toshiba, Japan) x-ray tube and FDX3543RPW (Toshiba, Japan) detector.

The result images showed that reconstructed with dual energy could clearly visualize lung field efficiency by removing unnecessary bone structure. Furthermore, dual energy CDT could enhance spine bone hidden by heart effectively. Dual energy tomosynthesis is a new technique; therefore, there is little guidance for its integration into the clinical practice and this study can be used to improve diagnosis efficiency of lung field screening using CDT.
Optimization of exposure parameters in digital tomosynthesis considering effective dose and image quality

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Digital tomosynthesis system (DTS), which scans an object in a limited angle, has been considered as an innovative imaging modality which can present lower patient dose than computed tomography and solve the problem of poor depth resolution in conventional digital radiography. Although it has many powerful advantages, only breast tomosynthesis system has been adopted in many hospitals. In order to reduce the patient dose while maintaining image quality, the acquisition conditions need to be studied. In this study, we analyzed effective dose and image qualities of chest phantom using commercialized universal chest digital tomosynthesis (CDT) R/F system to study the optimized exposure parameter. We set 9 different acquisition conditions including the default acquisition condition by user manual of Shimadzu (100 kVp with 0.5 mAs). The effective dose was calculated from PCXMC software version 1.51 by utilizing the total X-ray exposure measured by ion chamber. The image quality was evaluated by signal difference to noise ratio (SDNR) and figure of merit (FOM) in the regions of interest (ROIs) of coronary artery, rib, and pulmonary artery. The result indicated that the most suitable acquisition parameters among 9 conditions were condition 2 (90 kVp with 0.5 mAs), which indicated lower effective dose while maintaining reasonable SDNRs and FOMs for three specified regions. Further studies are needed to be conducted for detailed outcomes in CDT acquisition conditions.

Optimal kVp in chest computed radiography using visual grading scores: a comparison between visual grading characteristics and ordinal regression analysis

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Purposes: To determine the optimal peak voltage for chest computed radiography (CR) using visual grading scores and to compare the ordinal regression with the visual grading characteristics in visual grading analysis.

Methods: An Afga CR system was used to acquire images of an anthropomorphic chest phantom. Paraffin wax, green beans and folded aluminium foil were used to simulate lesions of pulmonary nodules, lines and micronodular opacities. The images were acquired under various voltages from 80 to 120 kVp and exposures from 0.5 to 12.5 mAs. The image qualities were evaluated by 5 experienced radiologists/radiographers based on the modified European image criteria using 1-5 visual grading scale. Both VGC and ordinal regression were employed for the visual grading analysis.

Results: The areas under the VGC were 0.5046, 0.5915, 0.4687 and 0.5351 for 80-90, 90-100, 100-110, 110-120 kVp comparisons, respectively. The location values from the ordinal regression were -0.583, -0.558, -0.037, and -0.242 for 80, 90, 100, 110 kVp respectively, taking the 120 kVp as the reference zero. Both VGC and ordinal regression produced the same results. The best image quality was produced under the 120 kVp, however, the 100 kVp was very close to the 120 kVp and performed better than the rest kVps.

Conclusions: The dependence of image quality on the applied kVp in chest CR imaging is not a monotonic function. Multiple kVps can be employed to produce the optimal quality images. The ordinal regression is a powerful tool in analysing the VGS quality data whilst the VGC can be considered as a special case of the ordinal regression.

Digital breast tomosynthesis reconstruction using spatially weighted non-convex regularization

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Subtle microcalcification clusters (MC) and spiculated masses are signs of early breast cancer. Detection of MC is challenging in digital breast tomosynthesis (DBT) due to the noisy background and large search volume. To alleviate this problem, we propose a new regularization method, referred to as the spatially weighted non-convex (SWNC) regularization method, and develop an efficient algorithm for DBT. This new technique is designed to enhance the MCs while preserving the appearance of the mass margins and breast parenchyma.

The SWNC regularization is inspired by the multi-scale bilateral filtering (MSBF) method that our group developed previously. It utilizes both the spatial and intensity differences between pixels within a small neighborhood centered at each pixel on each slice to estimate the presence of signal or noise. With a non-convex cost function, the SWNC method can suppress noise without blurring MCs and spiculations of masses. To solve the non-convex reconstruction problem, we apply the majorize-minimize separable quadratic surrogate algorithm (MM-SQS), which is further accelerated by ordered subset (OS), namely we use projection views sequentially to update the DBT image (MM-OS-SQS algorithm). The parameters of the SWNC method and the neighborhood size can be chosen based on the characteristics of the images.

We applied the new method to both heterogeneous breast phantom and human subject DBTs, and observed improved image quality. Quantitatively, the new method enhances the mean contrast-to-noise ratio (CNR) of the very subtle MCs in the phantom by 92.5% compared with the MSBF method and by 121.8% compared with the non-regularized simultaneous algebraic reconstruction technique (SART).

On the properties of artificial neural network filters for bone-suppressed digital radiography

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Single-shot bone-suppressed imaging using post-imaging processing can improve lesion conspicuity. Single-shot bone-suppressed imaging using post-imaging processing can improve lesion conspicuity. A nonlinear filter to extract bone structures from a radiograph can be designed using the artificial neural network (ANN) with the known bone features. In this study, we investigate the general properties of ANN filters for bone-suppressed digital radiography. The ANN filter properties are characterized in terms of various parameters such as the size and the number of teaching images, the number of neuron units, the learning rate, and so on. In addition, the filter performance is investigated with respect to the number of patients'
radiographs from which teaching images are sampled. For quantitative evaluation of the quality of single-shot bone-suppressed images, we calculate the mutual information (MI) between the single-shot bone-suppressed images and the bone-enhanced images obtained from a commercial dual-energy imaging modality. The preliminary result shows that the bone-suppressed image obtained from the ANN filter, which is designed with 5,000 teaching images from a single radiograph, results in MI of 0.6 compared with a commercial bone-enhanced image. The properties of ANN filters in terms of various parameters are discussed with numerical and experimental models. A nonlinear filter to extract bone structures from a radiograph can be designed using the artificial neural network (ANN) with the known bone features. In this study, we investigate the general properties of ANN filters for bone-suppressed digital radiography. The ANN filter properties are characterized in terms of various parameters such as the size and the number of teaching images, the number of neuron units, the learning rate, and so on. In addition, the filter performance is investigated with respect to the number of patients’ radiographs from which teaching images are sampled. For quantitative evaluation of the quality of single-shot bone-suppressed images, we calculate the mutual information (MI) between the single-shot bone-suppressed images and the bone-enhanced images obtained from a commercial dual-energy imaging modality. The preliminary result shows that the bone-suppressed image obtained from the ANN filter, which is designed with 5,000 teaching images from a single radiograph, results in MI of 0.6 compared with a commercial bone-enhanced image. The properties of ANN filters in terms of various parameters are discussed with numerical and experimental models.

9783-229, Session PS16

Effects of angular range on image quality of chest digital tomosynthesis

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Chest digital tomosynthesis (CDT) is a new 3D imaging technique that promises to have the potential as a screening and diagnostic tool. We investigated the effect of the angular range on the image quality using newly developed CDT system. The four different acquisition sets were generated using ±15°, ±20°, ±30°, and ±35° angular ranges with 21 projection views (PVs). The contrast-to-noise ratio (CNR) and artifact spread function (ASF) were used to evaluate the image quality. The results indicated that the CNRs for heart tissue increased with increasing angular range, whereas the CNRs for spine bone decreased. The vertical resolution measured by ASF was better in wide angle range. The results showed that appropriate angular range can improve the image quality, thereby diagnostic accuracy for the patient.

9783-230, Session PS16

Quantitative comparison of spatial resolution in step-and-shoot and continuous motion digital breast tomosynthesis

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This study compares the spatial resolution in step-and-shoot and continuous motion acquisition modes of Digital Breast Tomosynthesis (DBT) using an ex vivo prototype system. The prototype system employs flat panel detector with a 50μm pixel pitch, a micro focus x-ray tube and a motorized stage. A sharp knife edge with a thickness of 0.2mm was used to measure the modulation transfer function (MTF) in both modes for comparison purposes. The edge was rotated from 7.5° to 75° in 15° increments to acquire 11 angular projections using 40kVp, 300μA and 5.55s per projection. In continuous motion mode, the motorized stage moved the test object for the entire exposure time at a speed of 0.377 mm/s. The impact of acquisition speed in continuous DBT was also investigated, and a high speed of 0.753 mm/s was used for comparison. In step-and-shoot mode, the cutoff frequencies in projection view (0°) and reconstructed DBT slices were 6.55 lp/mm and 5.23 lp/mm. In continuous acquisition mode, the cutoff frequencies reduced approximately 45% to 3.5 lp/mm and 2.87 lp/mm in projection view and reconstructed DBT slices. At a high acquisition speed in continuous motion mode, the cutoff frequencies in the projection view and DBT slices dropped about 17-19% to 2.91 lp/mm and 2.38 lp/mm, respectively. The results of this study showed that the spatial resolution dropped significantly in the continuous motion mode of the DBT due to the blur caused by the rotation of the stage. Moreover, acquisition speed of the rotation stage also impacts the spatial resolution. Future studies will focus on methods for removal of the blur in an effort to improve the spatial resolution in the continuous acquisition mode.

9783-231, Session PS16

Tomosynthesis reconstruction algorithms using distance driven method

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Distance driven method represents a state of art method that can be used in reconstruction algorithms for x-ray techniques. C-arm tomosynthesis is an x-ray imaging technique that provides three dimensional information of the object by moving the C-shaped gantry around the patient. With limited angular view, C-arm system was investigated in this paper to generate volumetric data of the object with low radiation dosage and examination time. This paper is our new computer simulation study that demonstrates two reconstruction methods based on distance driven method including: simultaneous algebraic reconstruction technique (SART) and maximum likelihood expectation maximization (MLEM). Distance driven method is an efficient method that has low computational cost and free artifacts compared with other methods such as ray driven, pixel driven methods. Tomosynthesis projection images of simulated spherical object were simulated with a virtual C-arm tomosynthesis with a total view angle of 40 degrees. This study demonstrated the sharpness of in-plane reconstructed structure and effectiveness of removing out-of-plane blur for each reconstruction algorithm. Results showed the ability of C-arm tomosynthesis to generate three dimensional tomosynthesis images with respective reconstruction algorithms.

9783-232, Session PS16

Image quality of ray tracing reconstruction algorithms for C-arm tomosynthesis

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C-arm system is three dimensional imaging techniques. Both x-ray source and the detector are mounted on C-arm wheeled structure to provide wide variety of movement around the patient. In this paper, C-arm system was investigated to provide three dimensional information over a limited angular view to reduce radiation exposure and examination time. Reconstruction algorithms based on ray tracing method such as ray tracing back projection (ray tracing BP), simultaneous algebraic reconstruction technique (SART) and maximum likelihood expectation maximization (MLEM) were developed as reconstruction algorithms for C-arm tomosynthesis. Tomosynthesis projection images of simulated spherical object were simulated with a virtual C-arm tomosynthesis with a total view angle of 40 degrees. This study demonstrated the sharpness of in-plane reconstructed structure and effectiveness of removing out-of-plane blur for each reconstruction algorithms. The results showed the ability of ray tracing based reconstruction algorithms to provide three dimensional images from limited angle C-arm tomosynthesis.
Integration of kerma-area product and cumulative air kerma determination into a skin dose tracking system for fluoroscopic imaging procedures

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The skin dose tracking system (DTS) that we developed provides a color-coded mapping of the cumulative skin dose distribution on a 3D graphic of the patient during fluoroscopic procedures in real time. The DTS has now been modified to also calculate the kerma area product (KAP) and cumulative air kerma (CAK) for fluoroscopic interventions using data obtained in real-time from the digital bus on a Toshiba Infinix system. KAP is the integral of air kerma over the beam area and is typically measured with a large-area transmission ionization chamber incorporated into the collimator assembly. In this software, KAP is automatically determined for each x-ray pulse as the product of the air kerma/mAs from a calibration file for the given kVp and beam filtration times the mAs per pulse times the length and width of the beam times a field nonuniformity correction factor. Field nonuniformity is primarily the result of the heel effect and the correction factor was determined from the beam profile measured using radio-chromatic film. Dividing the KAP by the beam area at the intervention reference point provides the area-averaged CAK. The KAP and CAK per x-ray pulse are summed after each pulse to obtain the total procedure values in real-time. The calculated KAP and CAK were compared to the values displayed by the fluoroscopy machine with excellent agreement. The DTS now is able to automatically calculate both KAP and CAK without the need for measurement by an add-on transmission ionization chamber.

Improving detector spatial resolution using pixelated scintillators with a barrier rib structure

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Indirect conversion flat panel detectors (FPDs) based on amorphous silicon (a-Si) technology are widely used in digital x-ray imaging. In such FPDs a scintillator layer is used for converting x-rays into visible light photons. However, the lateral spread of these photons inside the scintillator layer reduces spatial resolution of the FPD. In this study, FPDs incorporating pixelated scintillators with a barrier rib structure were developed to limit lateral spread of light photons thereby improving spatial resolution. For the pixelated scintillator, a two-dimensional barrier rib structure was first manufactured on a substrate layer, coated with reflective materials, and filled to the rim with the scintillating material of gadolinium oxysulfide (GOS). Several scintillator samples were fabricated, with pitch size varying from 160 to 280 μm and rib height from 200 to 280 μm. The samples were directly coupled to an a-Si flat panel photodiode array with a pitch of 200 μm to convert optical photons to electronic signals. With the pixelated scintillator, the detector modulation transfer function was shown to improve significantly (by 94% at 2 lp/mm) compared to a detector using an unstructured GOS layer. However, the prototype does show lower sensitivity due to the decrease in scintillator fill factor. The preliminary results demonstrated the feasibility of using the barrier-rib structure to improve the spatial resolution of FPDs. Such an improvement would greatly benefit nondestructive testing applications where the spatial resolution is the most important parameter. Further investigation will focus on improving the detector sensitivity and exploring its medical applications.

Solid-state flat panel imager with avalanche amorphous selenium

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A flat panel imager with avalanche gain is being developed to achieve quantum noise limited x-ray imaging at low doses. To overcome the electronic noise of the thin film transistor (TFT) readout, the signal must be amplified prior to storage in the pixel’s capacitor. This can be accomplished using a thin layer of avalanche amorphous selenium (a-Se) referred to as High Gain Avalanche Rushing Photocathode (HARP). We have previously fabricated a multi-layer solid-state HARP structure capable of producing a reliable avalanche gain of 80 and suitable for deposition onto a TFT array. In this work, we present the first solid-state HARP prototype detector with continuous HARP deposited over the entire active area of a TFT array with 87 μm pixel pitch and 24 cm x 30 cm in size. To mitigate the risk of breakdown in this prototype, we divided the high voltage electrode into several smaller area detectors ranging from 1 x 1 to 9 x 7 cm. An electric field Ese of up to 100 V/μm was applied across the a-Se layer without breakdown. Under direct x-ray exposure with a 28 kVp W/Rh spectrum, reliable x-ray avalanche gain of 7 was achieved, which corresponds to an avalanche gain of 30 under optical exposure. Images at low exposure levels without avalanche gain are dominated by the electronic noise. Quantum noise limited images are obtained as the electric field is increased above the avalanche threshold. Reliable and uniform avalanche gain was achieved from all sensors.

The new generation of x-ray detectors: higher DQE and less aliasing with lower exposures

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The ability to improve visualization of structural information in digital radiography, without increasing radiation exposures, requires improved image quality at high spatial frequencies. Image quality in radiology is quantified by the detective quantum efficiency (DQE) of the detector as a function of spatial frequency. We present a method of increasing DQE at high spatial frequencies by improving the modulation transfer function (MTF) and reducing spatial aliasing. The Apodized Aperture Pixel (AAP) design uses a detector with micro-elements to synthesize desired pixels. A cascaded system analysis (CSA) that incorporates x-ray interactions is used for comparison of the theoretical MTF, noise power spectrum (NPS), and DQE. Using a clinical system to demonstrate AAP and conventional images, we show experimental comparisons of the MTF, NPS, and DQE. The MTF was improved by 50% and the DQE by nearly 100% at the sampling cutoff frequency, compared to conventional pixels, resulting in improved image contrast and signal-to-noise ratio at high frequencies for a given pixel size.

DQE simulation of a-Se x-ray detectors using ARTEMIS

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Detective Quantum Efficiency (DQE) is one of the most important image quality metrics for evaluating the performance of flat-panel x-ray detectors.
In this work, we simulate the DQE of amorphous selenium (a-Se) x-ray detectors with a detailed Monte Carlo transport code (ARTEMIS) for modeling semiconductor-based direct x-ray detectors. The transport of electron-hole pairs is achieved with a spatiotemporal model that accounts for recombination and trapping of carriers and Coulombic effects of space charge and external applied electric field. A range of incident x-ray energies have been simulated from 10 to 100 keV. The DQE results can be used to study the spatial resolution characteristics of detectors at different energies.

9783-43, Session 8
High-dynamic range CMOS-based mammography detector for FFDM and DBT
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Digital Breast Tomosynthesis (DBT) requires excellent image quality at very low dose levels while Full Field Digital Mammography (FFDM) requires high saturation dose levels. These opposing requirements can only be met by a detector with a high dynamic range. This paper will discuss a wafer-scale CMOS-based mammography detector with 49.5µm pixels and a CsI scintillator. Excellent image quality is obtained for FFDM as well as DBT applications, comparing favorably with a-Se detectors that dominate the X-ray mammography market today.

The typical dynamic range of a mammography detector is not high enough to accommodate both the low noise and the high saturation dose requirements for DBT and FFDM applications, respectively. An approach based on gain switching does not provide the signal-to-noise benefits in the low-dose DBT conditions. The solution to this is to add frame summing functionality to the detector. In one X-ray pulse several image frames will be acquired and summed. The requirements to implement this into a detector are low noise levels, high frame rates and low lag performance, all of which are unique characteristics of CMOS detectors. Results are presented to prove that excellent image quality is achieved and not compromised by frame summing.

This method of frame summing gave the opportunity to optimize the detector noise and saturation level for DBT application, so that high DQE performance at low dose levels is achieved, without compromising the FFDM performance. Another advantage of the CMOS-based X-ray detectors using a CsI scintillator is the superior lag and ghosting performance.

9783-44, Session 9
An open library of CT patient projection data
Baiyu Chen, Shuai Leng, Lifeng Yu, David R. Holmes III, Joel G. Fletcher, Cynthia H. McCollough, Mayo Clinic (United States)

Lack of access to projection data from patient CT scans is a major limitation for development and validation of new reconstruction algorithms. To meet this critical need, we are building a library of CT patient projection data in an open and vendor-neutral format, DICOM-CT-RD, which is an expanded DICOM format that contains sinogram data, acquisition geometry, patient information, and pathology identification. The library consists of scans of various types (head scans, chest scans, abdomen scans, ECG-gated scans, and dual-energy scans). For each scan, three types of data are provided, including DICOM-CT-RD projection data at various dose levels, reconstructed CT images, and a free-form text file. Several instructional documents are provided to help the users extract information from DICOM-CT-RD files, including a dictionary file for the DICOM-CT-RD format, a DICOM-CT-RD reader, and a user manual. Radiologist detection performance based on the reconstructed CT images is also provided. So far 328 head cases, 228 chest cases, and 228 abdomen cases have been collected for potential inclusion. The final library will include a selection of 50 head, chest, and abdomen scans each from at least two different manufacturers, and a few ECG-gated scans and dual-source, dual-energy scans. It will be freely available to academic researchers, and is expected to greatly facilitate the development and validation of CT reconstruction algorithms.

9783-45, Session 9
A generalized Fourier penalty in prior-image-based reconstruction for cross-platform imaging
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Sequential CT studies present an excellent opportunity to apply prior-image-based reconstruction (PIBR) methods that leverage high-fidelity prior imaging studies to improve image quality and/or reduce x-ray exposure in subsequent studies. One major obstacle in applying PIBR is that the initial and subsequent studies are often performed on different scanners (e.g. diagnostic CT followed by CBCT for interventional guidance); this results in mismatch in attenuation values due to hardware and software differences. While improved artifact correction techniques can potentially mitigate such differences, the correction is often incomplete. Here, we present an alternate strategy where the PIBR itself is used to mitigate these differences. We define a new penalty for the previously introduced PIBR called Reconstruction of Difference (RoD). RoD differs from many other PIBRs in that it reconstructs only changes in the anatomy (vs. reconstructing the current anatomy). Direct regularization of the difference image in RoD provides an opportunity to selectively penalize spatial frequencies of the difference image (e.g. low frequency differences associated with attenuation offsets and shading artifacts) without interfering with the variations in unchanged background image. We leverage this flexibility and introduce a novel regularization strategy using a generalized Fourier penalty within the RoD framework and develop the modified reconstruction algorithm. We evaluate the performance of the new approach in both simulation studies and in physical CBCT test-bench data. We find that generalized Fourier penalty can be highly effective in reducing low-frequency x-ray artifacts through selective suppression of spatial frequencies in the reconstructed difference image.

9783-46, Session 9
Limits to dose reduction from iterative reconstruction and the effect of through-slice blurring
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Iterative reconstruction methods have become very popular and show the potential to reduce dose. We present a limit to the maximum dose reduction possible with new reconstruction algorithms obtained by analyzing the information content of the raw data, assuming the reconstruction algorithm does not have a priori knowledge about the object or correlations between pixels. This limit applies to the task of estimating the density of a lesion embedded in a known background object, where the shape of the lesion is known but its density is not. Under these conditions, the density of the lesion can be estimated directly from the raw data in an optimal manner. This optimal estimate will meet or outperform the performance of any reconstruction method operating on the raw data, under the condition that the reconstruction method does not introduce additional prior information. The raw data bound can be compared to the lesion density estimate from FBP in order to produce a limit on the dose reduction possible from new reconstruction algorithms. The possible dose reduction from iterative
reconstruction varies on the object, but for a lesion embedded in the center of a water cylinder, it is less than 40%. Additionally, comparisons between iterative reconstruction and filtered backprojection are sometimes confounded by the effect of through-slice blurring in the iterative reconstruction. We analyzed the magnitude of the variance reduction brought about by through-slice blurring on scanners from two different vendors and found it to range between 11% and 48%.

9783-47, Session 9
Compensation of skull motion and breathing motion in CT using data-based and image-based metrics, respectively
Herbert K. Bruder, Christopher Rohkohl, Karl Stierstorfer, Thomas G. Flohr, Siemens AG (Germany)

We present a novel reconstruction for motion compensation (MC) of non-cardiac organs. With non-cooperative patients or in emergency cases, breathing motion or motion of the skull may compromise image quality. Our algorithm is based on the optimization of image based, or data based motion metrics, respectively. A similar approach was successfully applied in cardiac CTA [1]. While motion correction of the coronary vessels requires a local motion model, global motion models are sufficient for organs like the lung or the skull. The parameter vector for global affine motion is estimated iteratively, using commercially available optimization algorithms or, alternatively, using the steepest descent method. In each of the iterations, the image is updated using motion compensated reconstruction [2] or the data are updated using motion-sensitive forward projection. Evaluation of the metric value, e.g. the image entropy, provides information for the next iteration loop. We demonstrate the efficiency of the method in thoracic imaging by evaluating PET-CT data from free-breathing patients. In neuroimaging, data from stroke patients showing skull tremor were analyzed. It will be shown that motion artifacts can be largely reduced and spatial resolution was restored.

9783-48, Session 9
Reduction of truncation artifacts in CT images via a discriminative dictionary representation method
Yang Chen, Univ. of Wisconsin-Madison (United States) and Southeast Univ. (China); Ke Li, Yinfeng Li, Univ. of Wisconsin-Madison (United States); Jiang Hsieh, GE Healthcare (United States); Guang-Hong Chen, Univ. of Wisconsin-Madison (United States)

When the scanning field of view (FOV) is not sufficiently large to enclose the entire cross-section of the patient, or a patient needs to be internationally positioned to be partially outside the scanning FOV for some clinical purposes, truncation artifacts inevitably appear in the reconstructed CT images. Conventional wisdom to reduce truncation artifacts is to complete the truncated data by data extrapolation methods with different a priori assumptions. In this paper, we present a novel method to directly work in image domain to reduce truncation artifacts. Specifically, a discriminative dictionary include both a sub-dictionary of normal tissue structures and a sub-dictionary with truncation artifacts has been used to separate a truncation artifact contaminated image into two sub-images: one is the truncation artifacts reduced image and the other one is the truncation artifacts. Both physical phantom experimental results and in vivo human subject studies have been performed to validate the proposed novel method and to characterize the performance of the proposed method.

9783-49, Session 9
Reduction of motion artifacts in cardiac CT based on partial angle reconstructions from short scan data
Juliane Hahn, Deutsches Krebsforschungszentrum (Germany); Herbert K. Bruder, Thomas Allmendinger, Karl Stierstorfer, Thomas Flohr, Siemens Healthcare GmbH (Germany); Marc Kachelriess, Deutsches Krebsforschungszentrum (Germany)

Until today, several software-based approaches to increase the temporal resolution in cardiac computed tomography by estimating (MVFs) have been developed. Thereunder, the majority are motion compensation algorithms, which estimate the MVFs employing a three-dimensional registration routine working on reconstructions of multiple cardiac phases. We present an algorithm that requires nothing more than the data needed for a short scan reconstruction for motion estimation and motion-compensated reconstruction, which both are based on the reconstruction of volumes from a limited angular range. Those partial angle reconstructions are centered at different time points during the short scan and have a temporal resolution of about 10ms each. The MVFs are estimated by a constrained cost function optimization routine employing a motion artifact measuring cost function. During optimization, the MVFs are applied directly by warping the partial angle reconstructions, and the motion compensation is established by simply adding the shifted images. In order to enforce smooth vector fields and keep the number of parameters low, the motion is modeled by a low degree polynomial. Furthermore, to find a good estimation of the MVFs even in phases with rapid cardiac motion, the constrained optimization is re-initialized multiple times. The algorithm is validated with the help of a simulation study and applied to patient data, where motion-compensated reconstructions are performed in various cardiac phases. We show that the image quality can be improved, also in more rapid cardiac phases due to re-initialization of the optimization routine.

9783-50, Session 10
Estimation of signal and noise for a whole-body research photon counting CT system
Zhoubo Li, Shuai Leng, Zhicong Yu, Mayo Clinic (United States); Steffen G. Kappler, Siemens AG (Germany); Cynthia H. McCollough, Mayo Clinic (United States)

Photon-counting CT (PCCT) may yield potential value for many clinical applications due to its relative immunity to electronic noise, increased geometric efficiency relative to current scintillating detectors, and the ability to resolve energy information about the detected photons. However, there are a large number of parameters that require optimization, particularly the energy thresholds configurations. Fast and accurate estimation of signal and noise in PCCT can benefit the optimization of acquisition parameters for specific diagnostic tasks. Based on the acquisition parameters and detector response of our research PCCT system, we derived mathematical models for both signal and noise. The signal model took the tube spectrum, beam filtration, object attenuation, water beam hardening, and detector response into account. The noise model considered the relationship between noise and radiation dose, as well as the propagation of noise as threshold data are subtracted to yield energy bin data. To determine the absolute noise value, a noise look-up table (LUT) was acquired using a limited number of calibration scans. The noise estimation algorithm then used the noise LUT to estimate noise for scans with a variety of combination of energy thresholds, dose levels, and object attenuation. Validation of the estimation algorithms was performed on our whole-body research PCCT system using semi-anthropomorphic water phantoms and solutions of calcium and iodine. The algorithms achieved accurate estimation of signal and noise for a variety of scanning parameter combinations. The proposed method can be used to optimize energy thresholds configuration for many clinical applications of PCCT.
Material decomposition and virtual non-contrast imaging in photon counting computed tomography: an animal study

Ralf Gutjahr, Technische Univ. München (Germany) and Siemens Healthcare (Germany); Christoph Polster, Institut für Klinische Radiologie, Ludwig-Maximilians-Univ. Hospital München (Germany) and Siemens Healthcare (Germany); Steffen G. Kappler, Siemens Healthcare GmbH (Germany); Hubertus Pietsch, Gregor Jost, Bayer Schering Pharma AG (Germany); Katharina Hahn, Friederike Schöck, Martin Sedlmair, Thomas Allmendinger, Bernhard Schmidt, Bernhard Krauss, Thomas G. Flohr, Siemens Healthcare GmbH (Germany)

The energy resolving capabilities of Photon Counting Detectors (PCD) in Computed Tomography (CT) facilitate energy-sensitive measurements. The provided image-information can be processed with Dual Energy (DE) and Multi Energy (ME) algorithms. A novel PCD-CT prototype firstly allows acquiring images with a close to clinical configuration of both the X-ray tube and the CT-detector. In this study two algorithms (Material Decomposition and Virtual Non-Contrast (VNC)) are applied on a data set obtained from the PCD-CT prototype system. A living rabbit is measured. Two contrast agents (CA) are applied: A gadolinium based CA used to enhance contrasts for vascular imaging, and xenon, used to evaluate local ventilation impairments of the animal’s lung. Four different images are generated: a) a mixed image as a linear combination of the two input images, b) a VNC image, suppressing any traces of CAs imitating a native CT scan, c) a VNC image with a gadolinium image as an overlay, where contrast enhancements in the coronary vascular system are highlighted using colored labels, and d) a VNC image with a xenon image as an overlay, indicating local ventilation characteristics. All images are generated from two images based on energy bin information. It is shown that a modified version of the commercially available software framework is capable of providing images with full diagnostic value obtained from the PCD-CT prototype system.

Lossless compression of projection data from photon counting detectors

Picha Shunhavanich, Norbert J. Pelc, Stanford Univ. (United States)

With many attractive attributes, photon counting detectors with many energy bins are being considered for clinical CT systems. In practice, a large amount of projection data acquired for multiple energy bins must be transferred in real time through slip rings and data storage subsystems, causing a bandwidth bottleneck problem. The higher resolution of these detectors and the need for faster acquisition additionally contribute to this issue. In this work, we introduce a new approach to lossless compression, specifically for projection data from photon counting detectors, by utilizing the dependencies in the multi-energy data. The proposed predictor estimates the value of a projection data sample as a weighted average of its neighboring samples and an approximation from another energy bin, and the prediction residuals are then encoded. Context modeling using three or four quantized local gradients is also employed to detect edge characteristics of the data. Using three simulated phantoms including a head phantom, compression of 2.4:1-2.5:1 is achieved. The proposed predictor, using zero, three and four gradient contexts is compared to JPEG-LS and the ideal predictor (noiseless projection data). Among our proposed predictors, three-gradient context is preferred with a compression ratio from Golomb coding 6.3% higher than JPEG-LS and only 3.8% lower than the ideal predictor. In encoder efficiency, the Golomb code with the proposed three-gradient contexts has higher compression than block floating point. From the initial simulation results, the proposed predictor provides good control over the bits needed to represent multi-energy projection data.

A high-resolution imaging technique using a whole-body research photon counting detector CT system

Shuai Leng, Zhicong Yu, Mayo Clinic (United States); Ahmed Halaweish, Siemens Healthcare (United States); Steffen G. Kappler, Katharina Hahn, Andre Henning, Siemens Healthcare GmbH (Germany); Zhubo Li, John I. Lane, David L. Levin, Steven M. Jorgensen, Erik L. Ritman, Cynthia H. McCollough, Mayo Clinic (United States)

A high-resolution (HR) data collection mode has been introduced to the whole-body, research photon-counting-detector CT system installed in our laboratory. In this mode, 64 rows of 0.45 mm x 0.45 mm detectors pixels were used, which corresponded to a pixel size of 0.225 mm x 0.225 mm at the iso-center. Spatial resolution of this HR mode was quantified by measuring the MTF from a scan of a 50 micron wire phantom. An anthropomorphic lung phantom, cadaveric swine lung, temporal bone and heart specimens were scanned using the HR mode, and image quality was subjectively assessed by two experienced radiologists. Comparison of the HR mode images against their energy integrating system (EID) equivalents using comb filters was also performed. High spatial resolution of the HR mode was evidenced by the MTF measurement, with 15 lp/cm and 20 lp/cm using zero, three and four gradient contexts is compared to JPEG-LS and the ideal predictor (noiseless projection data). Among our proposed predictors, three-gradient context is preferred with a compression ratio from Golomb coding 6.3% higher than JPEG-LS and only 3.8% lower than the ideal predictor. In encoder efficiency, the Golomb code with the proposed three-gradient contexts has higher compression than block floating point. From the initial simulation results, the proposed predictor provides good control over the bits needed to represent multi-energy projection data.

On the analogy between pulse-pile-up in energy-sensitive, photon-counting detectors, and level-crossing of shot noise

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Shot noise processes are omnipresent in physics and many of their properties have been extensively studied in the past, including the particular problem of level crossing of shot noise. Energy-sensitive, photon-counting detectors using comparators to discriminate pulse-heights are currently heavily investigated for medical applications, e.g. for x-ray computed tomography and x-ray mammography. Surprisingly, no mention of the close relation between the two topics can be found in the literature on photon-counting detectors. In this paper, we point out the close analogy between level crossing of shot noise and the problem of determining count rates of photon-counting detectors subject to pulse pile-up. The latter is very relevant for obtaining precise forward models for photon-counting detectors operated under conditions of very high x-ray flux employed, e.g. in future clinical x-ray computed tomography. Although several attempts have been made to provide reasonably accurate, approximative models for the registered number of counts in x-ray detectors under conditions of high flux and arbitrary x-ray spectra, see, no exact, analytic solution is given in the literature. In this paper we present such a solution for arbitrary response functions, continuous spectra and continuous pulse shapes based on a result from the theory of level crossing. We briefly outline the theory of level crossing including the famous Rice theorem and translate from the language of level crossing to the language of photon-counting detection.
Short term reproducibility of a high contrast 3-D isotropic optic nerve imaging sequence in healthy controls

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The optic nerve (ON) plays a crucial role in human vision transporting all visual information from the retina to the brain for higher order processing. There are many diseases that affect the ON structure such as optic neuritis, anterior ischemic optic neuropathy and multiple sclerosis. Because the ON is the sole pathway for visual information from the retina to areas of higher level processing measures of ON damage have been shown to correlate well with visual deficits. Increased intracranial pressure has been shown to correlate with the size of the cerebrospinal fluid (CSF) surrounding the ON. These measures are generally taken at an arbitrary point along the nerve and do not account for changes along the length of the ON. We propose a high contrast and high-resolution 3-D acquired isotropic imaging sequence optimized for ON imaging. We have acquired scan-rescan data using the optimized sequence and a current standard of care protocol for 10 subjects. We show that this sequence has superior contrast-to-noise ratio to the current standard of care while achieving a factor of 11 higher resolution. We apply a previously published automatic pipeline to segment the ON and CSF sheath and measure the size of each individually. We show that these measures of ON size have lower short-term reproducibility than the population variance and the variability along the length of the nerve. We find that the proposed imaging protocol is (1) useful in detecting population differences and local changes and (2) a promising tool for investigating biomarkers related to structural changes of the ON.

Crystal timing offset calibration method for time of flight PET scanners

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In time of flight (TOF) positron emission tomography (PET), precise calibration of the timing offset of each crystal of a PET scanner is essential. Conventionally this calibration requires a specially designed tool just for this purpose. In this study a method that uses a planar source to measure the crystal timing offsets (CTO) is developed. The method uses list mode acquisitions of a planar source placed at multiple orientations inside the PET scanner field-of-view (FOV). The placement of the planar source in each acquisition is figured out from the measured data, so that a fixture for exactly placing the source is not required. The expected coincidence time difference for each detected list mode event can be found from the planar source placement and the detector geometry. A deviation of the measured time difference from the expected one is due to CTO of the two crystals. The least squared solution of the CTO is found iteratively using the list mode events. The effectiveness of the crystal timing calibration method is evidenced by placing back each list mode event into the imaging space with the timing offset applied to each event. The zigzagged outlines of the phantoms in the images become smooth after the crystal timing calibration is applied. In conclusion, a crystal timing calibration method is developed. The method uses multiple list mode acquisitions of a planar source to find the least squared solution of crystal timing.

Solving outside-axial-field-of-view scatter correction problem in PET via digital experimentation

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Unaccounted scatter impact from unknown outside-axial-field-of-view (AFOV) activity in PET is an important degrading factor for image quality and quantitation. Resource consuming and unpopular way to account for the outside-AFOV activity is to perform an additional PET/CT scan of the adjacent regions. In this work we investigate a solution to the outside-AFOV scatter problem without performing a PET/CT scan of the adjacent regions. The main motivation for the proposed method is that the measured random corrected prompt (RCP) sinogram in the background region surrounding the measured object contains only scattered events, originating from both inside- and outside-AFOV activity. In this method, the scatter correction simulation iterates through many randomly-chosen outside-AFOV activity estimates along with known inside-AFOV activity, generating a plethora of scatter distribution sinograms. The iterations stop when a decent match is found between a simulated scatter sinogram (that include supposed outside-AFOV activity) and the measured RCP sinogram in the background region. The combined scatter impact from inside- and outside-AFOV activity can then be used for scatter correction during final image reconstruction phase. Preliminary results using measured phantom data indicate successful phantom length estimate with the method, and, therefore, accurate outside-AFOV scatter estimate.
An x-ray photon interacts with photon counting detectors (PCDs) and generates an electron charge cloud or multiple clouds. The clouds (thus, the photon energy) may be split between two adjacent PCD pixels when the interaction occurs near pixel boundaries, producing a count at both of the two pixels. This is called double-counting with charge sharing. The output of individual PCD pixel is integer counts and Poisson distributed; however, the outputs of adjacent pixels are correlated due to double-counting. Major problems are the lack of detector noise model for the spatio-energetic cross-talk and the lack of an efficient simulation tool. Monte Carlo simulation can accurately simulate these phenomena and produce noisy data; however, it is not computationally efficient.

In this study, we developed a detector model which takes the following effects into account and efficient software simulator which uses Poisson random number generator to produce correlated noisy integer counts. The effects include (1) detection efficiency and incomplete charge collection; (2) photoelectric effect with total absorption; (3) photoelectric effect with fluorescence x-ray emission and re-absorption; (4) photoelectric effect with fluorescence x-ray emission which leaves PCD completely; and (5) electric noise.

The model produced total detector spectrum similar to previous MC simulation data. The model can be used to predict spectrum and correlation with various different settings. The simulated noisy data demonstrated the expected performance: (a) data were integers; (b) the mean and covariance matrix was close to the target values; (c) noisy data generation was very efficient.

Comparison of quantitative k-edge empirical estimators using an energy-resolved photon-counting detector
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Using an energy-resolving photon counting detector, the amount of k-edge material in the x-ray path can be estimated using a process known as material decomposition. However, non-ideal effects within the detector make it difficult to accurately perform this decomposition. This work evaluated the k-edge material decomposition accuracy of two empirical estimators. A neural network estimator and a linearized maximum likelihood estimator with error look-up tables (A-table method) were evaluated through simulations and experiments. Each estimator was trained on system-specific calibration data rather than specific modeling of non-ideal effects into account and efficient software simulator which uses Poisson random number generator to produce correlated noisy integer counts. The effects include (1) detection efficiency and incomplete charge collection; (2) photoelectric effect with total absorption; (3) photoelectric effect with fluorescence x-ray emission and re-absorption; (4) photoelectric effect with fluorescence x-ray emission which leaves PCD completely; and (5) electric noise.

The model produced total detector spectrum similar to previous MC simulation data. The model can be used to predict spectrum and correlation with various different settings. The simulated noisy data demonstrated the expected performance: (a) data were integers; (b) the mean and covariance matrix was close to the target values; (c) noisy data generation was very efficient.

Improving material decomposition by spectral optimization of photon counting computed tomography
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Photon counting detectors in Computed Tomography (CT) facilitate measurements of spectral distributions of detected X-ray quanta in discrete energy bins. Along with the dependency on wavelength and atomic number (Z) of the mass attenuation coefficient, this information allows for reconstructing CT images of the different material bases. Decomposition of two materials is considered standard in today’s dual-energy techniques. With photon-counting detectors the decomposition of more than two materials becomes achievable. Efficient detection of CT-typical X-ray spectra is a hard requirement in a clinical environment. This is fulfilled by only a few sensor materials such as CdTe or CdZnTe. In contrast to energy integrating CT-detectors, the pixel dimensions must be reduced to avoid pulse pile-up problems at clinically relevant count rates. Reducing pixel sizes leads to increased K-escape and charge sharing effects. As a consequence, the correlation between incident and detected X-ray energy is reduced. This degradation is quantified by the detector response function. The goal of this study is to improve the achievable material decomposition by adapting the incident X-ray spectrum with respect to the properties (i.e. the detector response function) of a photon-counting detector. A significant improvement of the material decomposition equivalent metric is achievable when using specific materials as X-ray pre-filtration (K-edge-filtering) while maintaining the applied patient dose and image quality.

Optimal selection of thresholds for photon counting CT
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Recent advances in Photon Counting CT (PCCT) have facilitated the...
multispectral acquisition of multiple image volumes with differing energy thresholds. This presents the user with several choices for energy threshold combinations. As compared to standard clinical Dual kVp CT, where the user typically has only three choices of kVp pairings (e.g., 80/150Sn, 90/150Sn, 100/150Sn), a “quad” PCCT system with 14 threshold settings has Choose(14,4) = 1001 possible threshold combinations (assuming no restrictions). In this paper we describe the means of determining the optimal selection of thresholds for: (1) the discrimination of pure materials and (2) the decomposition of material mixtures into their components. We observe that for more than three materials, the ordering of the threshold combinations from best to worst for these tasks may not be identical. We demonstrate our approach on phantom data.

9783-64, Session 13
Method for dose-reduced 3D catheter tracking on a scanning-beam digital x-ray system using dynamic electronic collimation

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Scanning-beam digital x-ray (SBDX) is an inverse geometry x-ray fluoroscopy system capable of tomosynthesis-based 3D catheter tracking. This work proposes a method of dose-reduced 3D tracking using dynamic electronic collimation (DEC) of the SBDX x-ray tube. Positions in the 2D focal spot array are selectively activated to create a region-of-interest (ROI) x-ray field around the tracked catheter. The ROI position is updated for each frame based on a motion vector calculated from the two most recent 3D tracking results. The technique was evaluated with SBDX data acquired as a catheter tip inside a chest phantom was pulled along a 3D trajectory. DEC scans were retrospectively generated from the detector images stored for each focal spot position. The kera-area-product and integral kerma for DEC versus full field-of-view (FOV) scanning were calculated using an SBDX Monte Carlo simulation code. DEC imaging of a catheter tip in a volume measuring 11.4 cm across at isocenter required 340 active focal spots per frame, versus 4473 spots in full-FOV mode. Comparison of DEC versus full-FOV 3D tracking coordinates found that the root-mean-squared differences were less than 0.1 mm in the X,Y, and Z directions. Using DEC the kerma-area product was reduced to 0.3% of the full-FOV value, and integral kerma was reduced to 8.1% of the full-FOV value. Dynamic electronic collimation can reduce dose with minimal change in tracking performance.

9783-65, Session 13
Multi-gamma-source CT imaging system: a feasibility study with the Poisson noise

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This study was performed to test a feasibility of multi-gamma-source CT imaging system. Gamma-source CT employs radioisotopes that emit monochromatic energy gamma-rays. The advantages of gamma-source CT include its immunity to beam hardening artifacts, its capacity of quantitative CT imaging, and its higher performance in low contrast imaging compared to the conventional x-ray CT. Radioisotope should be shielded by use of a pin-hole collimator so as to make a fine focal spot. Due to its low gamma-ray flux in general, the reconstructed image from a single gamma-source CT would suffer from high noise in data. To address this problem, we proposed a multi-gamma source CT imaging system and developed an iterative image reconstruction algorithm accordingly in this work. Conventional imaging model assumes a single linear imaging system typically represented by $Mf=g$. In a multi-gamma-source CT system however, the inversion process is not any more based on a single linear system since one cannot separate a detector pixel value into multiple ones that are corresponding to each rays from the sources. Instead, the imaging model can be constructed by a set of linear system models each of which assumes an estimated measurement $g_2$. Based on this model, the proposed algorithm has a weighting step which distributes each projection data into multiple estimated measurements. We used two gamma sources at various positions and with varying intensities in this numerical study to demonstrate its feasibility. Therefore, the measured projection data(g) is separated into each estimated projection data($g_1$) - ($g_2$) in this study. The proposed imaging protocol is believed to contribute to both medical and industrial applications.

9783-66, Session 13
Investigation of noise and contrast sensitivity of an electron multiplying charge couple device (EMCCD) based cone beam micro-CT system

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A small-animal Micro-CT system was built using an Electron-Multiplying CCD (EMCCD) having pre-digitization amplification technology, high-resolution, high-sensitivity and low-noise. Noise and signal sensitivity in the CBCT-reconstructed images when using this special pre-digitization amplification technology were investigated.

Noise analysis was performed by scanning a water phantom with the micro-focal-spot x-ray parameters set to the minimum allowable (20 kVp and 0.5 mA) and with the EMCCD gain varied. Contrast sensitivity was evaluated by using a phantom with five tubes containing iodine contrast with concentrations ranging from 30% to 70%. First, the phantom was scanned using various x-ray exposures at 40 kVp and constant gain. Next, we took a set of data for the same set of x-ray exposure values where we adjusted the gain such that the air-value signal of a projection was the same as that of the highest exposure and lowest gain. A standard FDK algorithm was used to reconstruct the data.

NPS plots show that noise power level increases as the gain increases. Contrast sensitivity was analyzed by calculating the ratio of signal-to-noise ratio (SNR) for increased gain with that for low-constant gain at each exposure. The SNR value for low-constant gain was always lower than the SNR for high detector gain at all x-ray settings and iodine contrast levels. The largest increase of SNR approached 2 for the low contrast feature with 30% iodine concentration. Despite an increase in noise level as the gain is increased, SNR improvement demonstrates the advantage of the unique on-chip detector gain.

9783-67, Session 13
High-spatial-resolution nanoparticle x-ray fluorescence tomography

Jakob C. Larsson, William Vågberg, Carmen Vogt, Ulf Lundström, Daniel H. Larsson, Hans M. Hertz, KTH Royal Institute of Technology (Sweden)

X-ray fluorescence tomography (XFCT) has potential for high-resolution 3D molecular x-ray bio-imaging. In this technique the fluorescence signal from targeted nanoparticles (NPs) is measured, providing information about the spatial distribution and concentration of the NPs inside the object. However, present laboratory XFCT systems typically have limited spatial resolution (~1 mm) and suffer from long scan times and high radiation dose even at high
NP concentrations, mainly due to low efficiency and poor signal-to-noise ratio. We have developed a laboratory XFCT system with high spatial resolution (sub-100 μm), low NP concentration and vastly decreased scan times and dose, opening up the possibilities for in vivo small-animal imaging research. The system consists of a high-brightness liquid-metal-jet microfocus x-ray source, x-ray focusing optics and two photon counting detectors. By using the source’s characteristic 24 keV line-emission together with carefully matched molybdenum nanoparticles the Compton background is greatly reduced, increasing the SNR. Each measurement provides information about the spatial distribution and concentration of the Mo nanoparticles, as well as the absorption and Compton scattering of the object. An iterative reconstruction method is used to produce the final XFCT image.

In addition, we present new strategies to visualize fast micrometer-scale movements in small animals. To eliminate the motion artifacts we developed several strategies successfully applied to various biological systems. For periodic motions such as breathing, heart beat or wing beat the optical flow guided retrospective gating of tomographic projections is a promising new method. In more complex biological systems with multiple motion patterns, such as time gating of tomographic projections is a promising new method. In more complex biological systems with multiple motion patterns, such as periodic motions such as breathing, heart beat or wing beat the optical flow guided retrospective gating of tomographic projections is a promising new method in the future.

9783-68, Session 13

**Time resolved in vivo x-ray imaging at the micrometer scale in 3D opens new avenues in functional anatomy**

Rajmund Mokso, Goran Lovric, Paul Scherrer Institut (Switzerland); Martin Nyvlt, Marek Skeren, Czech Technical Univ. in Prague (Czech Republic); Johannes Schittny, Univ. Bern (Switzerland); Matthias Roth-Kleiner, Ctr. Hospitalier Univ. Vaudois (Switzerland); Marco F. M. Stampanoni, ETH Zürich (Switzerland) and Paul Scherrer Institut (Switzerland)

In-vivo X-ray imaging of small animals is routinely performed down to a spatial resolution of several tens of micrometers. Breaking the 10 μm barrier is very difficult due to the high radiation dose deposited in the tissue and the motion of the sample during tomographic acquisition. To tackle these challenges we propose new strategies to visualize fast micrometer-scale internal movements in small animals. We optimize the radiation dose by retrieving the information encoded in the refraction of X-rays by the tissue. To eliminate the motion artifacts we developed several strategies successfully applied to various biological systems. For periodic motions such as breathing, heart beat or wing beat the optical flow guided retrospective gating of tomographic projections is a promising new method. In more complex biological systems with multiple motion patterns, such as time gating of tomographic projections is a promising new method. In more complex biological systems with multiple motion patterns, such as time gating of tomographic projections is a promising new method. In more complex biological systems with multiple motion patterns, such as time gating of tomographic projections is a promising new method.

### 9783-69, Session 13

**800-MeV magnetic-focused flash proton radiography for high-contrast imaging of low-density biologically relevant targets using an inverse-scatter collimator**

Matthew Freeman, Frank E. Merrill, Dale Tupa, Los Alamos National Lab. (United States)

Proton radiography shows great promise as a tool to aid proton beam therapy (PBT) guidance in real time. Here, we demonstrate two ways in which the technology may progress to meet that goal. Firstly, through the utilization of a proton beam that is 800 MeV in energy, target tissue receives a dose of radiation with very tight lateral constraint. This could present a benefit over the traditional treatment energies of ~200-300 MeV, where up to 1 cm of lateral tissue can receive scattered radiation at the target. At 800 MeV, the beam travels completely through the object with minimal deflection, thus constraining lateral dose to a smaller area. The second novelty of this system is the utilization of magnetic quadrupole refocusing lenses that mitigate the chromatic blur caused by multiple Coulomb scattering (MCS) within an object, enabling high resolution imaging of thick objects, such as the human body. We demonstrate this system on ex vivo salamander and mouse specimens, as well as a shockwave through xenon, to demonstrate the available contrast. The resulting images provide contrast sufficient to visualize thin tissue, as well as fine detail within the target volumes, and the ability to measure the slightest changes in density. Such a system, combined with PBT, would enable the delivery of a highly specific dose of radiation that is monitored and guided in real time.

### 9783-70, Session 14

**Method to study sample size limit of small-angle x-ray scattering computed tomography**

Mina Choi, U.S. Food and Drug Administration (United States) and Univ. of Maryland, College Park (United States); Bahaa Ghammaoui, Andreu Badal, Aldo Badano, U.S. Food and Drug Administration (United States)

Small-angle x-ray scattering (SAXS) imaging is an emerging medical tool that can be used for in vivo detailed tissue characterization and has the potential to provide added contrast to conventional x-ray projection and CT imaging. We used a publicly available MC-GPU code to simulate x-ray trajectories in a SAXS-CT geometry for a target material embedded in a background material with varying sample sizes (3, 5, and 10 mm). Our target material was a water solution of gold nanoparticle (GNP) spheres with a radius of 6.75 nm due to its well-characterized scatter profile at small angles and highly scattering properties. The background material was water. Our objective is to study how the scatter profile degrades at larger target imaging depths and increasing sample sizes. We have found that scatter profiles of the GNPs can still be reconstructed at depths up to 5 mm embedded at the center of a 10 mm cylinder. We are performing further studies to quantify sample size limits with other scattering targets and background materials.

### 9783-71, Session 14

**Onmidirectional scattering x-ray imaging with gratings**

Matias E. Kagias, Zhentian Wang, Paul Scherrer Institut (Switzerland) and ETH Zürich (Switzerland); Pablo Villanueva, Konstantins Jefimovs, Paul Scherrer Institut (Switzerland); Marco F. M. Stampanoni, Paul Scherrer Institut (Switzerland) and ETH Zürich (Switzerland)

X-ray dark-field imaging can provide complementary information about the unresolved microstructures of the sample. The dark-field signal can be accessed with various methods based on coherent illumination, spanning from self-imaging to speckle scanning. The directional sensitivity of the existing methods is limited to a few directions, specifically with conventional interferometers only one direction is accessible and with 2D interferometers up to four. More directions can be sensed however, rotation of the sample or the optical components is required, resulting in mechanically complicated setups that are difficult to be realized in industrial or medical settings. Additionally, dose and scan time limitations come into play when multiple scans have to be performed. Nonetheless, conventional methods require an absorption grating, which exhibits manufacturing difficulties. The authors propose a new method that allows the simultaneous acquisition of dark-field images in all possible directions in a single shot. This is achieved by a specialized phase grating and means of recording the generated interference fringe with sufficient spatial resolution. The grating...
Coded aperture x-ray diffraction imaging for lung cancer detection

Anuj J. Kapadia, Robert E. Morris, Manu N. Lakshmanan, Katie Albanese, Ehsan Samei, Joel A. Greenberg, Duke Univ. (United States)

Coded-aperture X-ray diffraction imaging has shown promise in identifying cancer based on its molecular scatter signature. Malignant cells exhibit distinctive diffraction features arising from their chemical and bio molecular structure, which are significantly different from those of benign and other indolent abnormalities. We have developed a scatter-imaging prototype scanner that can measure these signatures and identify malignant tumors. Here, we describe the development, testing and performance of our coded aperture X-ray diffraction imaging system for detection of lung and breast cancer. A prototype bench-top diffraction imaging setup was built to test the feasibility of the proposed technology for lung imaging. The prototype was used to measure the diffraction patterns associated with malignant tumors in excised specimens of the breast, colon, and finally lung tumors obtained through surgery. Each tumor was irradiated at a range of X-ray energies and tube currents (50-100 kVp and 100-500 mAs). Scattered X-ray signal was captured using an array of energy-sensitive CZT detectors (Multix, France) with approximately 3-5 keV energy resolution; and the primary X-ray transmitted signal was captured using a Varian 2D flat-panel energy-integrating detector. A simultaneous transmission / scatter image corresponding to the tumor specimen. A series of calibration phantoms was scanned for two reasons: a) to provide a baseline estimate of system-related noise, and b) to evaluate the imaging resolution associated with the scanner. Results: The imaging resolution of the system was determined to be 5 mm (in X, Y and Z directions). The scan time ranged from 1-10 sec per specimen. The measured scatter signatures were found to agree remarkably well with the corresponding tissue signature reported in literature. The results demonstrate strong potential for Coded-aperture X-ray imaging in identifying lung tumors based on their molecular scatter signatures. The simultaneous transmission-and-scatter imaging system could potentially provide a way to determine tissue identity simultaneously with a CT scan when performed in patients in the future.

Coded aperture x-ray diffraction imaging with transmission computed tomography side-information

Ikenna Odinaka, Joel A. Greenberg, Yan Kaganovsky, Andrew D. Holmgren, Mehadi Hassan, Duke Univ. (United States); David G. Pollitte, Joseph A. O’Sullivan, Washington Univ. in St. Louis (United States); Lawrence Carin, David J. Brady, Duke Univ. (United States)

Coded aperture X-ray diffraction (coherent scatter spectral) imaging provides fast and dose-efficient measurements of the molecular structure of an object. The information provided is spatially-dependent and material-specific, and can be utilized in medical applications requiring material discrimination, such as tumor imaging. However, current coded aperture coherent scatter spectral imaging system assume a uniformly attenuating object, and are plagued by image degradation due to non-uniform self-attenuation. We propose accounting for such non-uniformities in the self-attenuation by utilizing an X-ray computed tomography (CT) image (reconstructed attenuation map). In particular, we present an iterative algorithm for coherent scatter spectral image reconstruction, which incorporates the attenuation map, at different stages, resulting in more accurate coherent scatter spectral images in comparison to their uncorrected counterpart.

Task-driven tube current modulation and regularization design in computed tomography with penalized-likelihood reconstruction

Grace J. Gang, Jeffrey H. Siewerdsen, Joseph W. Stayman, Johns Hopkins Univ. (United States)

Purpose: This work applies task-driven optimization to design CT tube current modulation and directional regularization in penalized-likelihood (PL) reconstruction. The relative performance of modulation schemes commonly adopted for filtered-backprojection (FBP) reconstruction were also evaluated for PL in comparison.

Methods: We adopt a task-driven imaging framework that utilizes a patient-specific anatomical model and information of the imaging task to optimize imaging performance in terms of detectability index (d’). This framework leverages a theoretical model based on implicit function theorem and Fourier approximations to predict local spatial resolution and noise...
characteristics of PL reconstruction as a function of the imaging parameters to be optimized. Tube current modulation was parameterized as a linear combination of Gaussian basis functions, and regularization was based on the design of (directional) pairwise penalty weights for the 8 in-plane neighboring voxels. Detectability was optimized using a covariance matrix adaptation evolutionary strategy algorithm. Task-driven designs were compared to conventional tube current modulation strategies for a Gaussian detection task in a pelvis phantom.

Results: The task-driven design yielded the best performance, improving d' by -16% over an unmodulated acquisition. Contrary to FBP, PL reconstruction using automatic exposure control and modulation based on minimum variance (in FBP) performed worse than the unmodulated case, decreasing d' by 35% and 20%, respectively.

Conclusions: This work shows that conventional tube current modulation schemes suitable for FBP can be suboptimal for PL reconstruction. Thus, the proposed task-driven optimization provides additional opportunities for improved imaging performance and dose reduction beyond that achievable with conventional acquisition and reconstruction.

9783-76, Session 15

Design, fabrication, and implementation of voxel-based 3D printed textured phantoms for task-based image quality assessment in CT

Justin B. Solomon, Duke Univ. School of Medicine (United States); Alexandre H. Ba, Institut Univ. de Radiophysique Appliquée (Switzerland); Andrew Diao, Duke Univ. (United States); Joseph Y. Lo, Eianni Bier, Duke Univ. School of Medicine (United States); François O. Bochud, Institut Univ. de Radiophysique Appliquée (Switzerland); Michael E. Gehm, Duke Univ. (United States); Ehsan Samei, Duke Univ. School of Medicine (United States)

In CT, task-based image quality studies are typically performed using uniform background phantoms with low-contrast signals. Such studies may have limited clinically relevancy for modern non-linear CT systems due to possible influence of background texture on image quality. The purpose of this study was to design anatomically informed textured phantoms for task-based assessment of low-contrast detection. Liver volumes were segmented from 23 abdominal CT cases. The volumes were characterized in terms of texture features from gray-level co-occurrence and run-length matrices. Using a 3D clustered lumpy background (CLB) model, a synthesis technique based on a genetic optimization algorithm was used to find the CLB parameters that were most reflective of the liver textures, accounting for CT system factors of spatial blurring and noise. With the modeled background texture as a guide, a cylinder phantom (165 mm in diameter and 30 mm height) was designed, containing 20 low-contrast spherical signals (6 mm in diameter at targeted contrast levels of -5, 9, 12, 15, and 20HU, 4 repeats per signal). The phantom was voxelized and input into a commercial multi-material 3D printer (Object Connex 350), with custom software for voxel-based printing. Using principles of digital halftoning and dithering, the 3D printer was programmed to distribute two base materials (VeroWhite and TangoPlus, nominal voxel size of 42x84x30 microns) to achieve the targeted spatial distribution of x-ray attenuation properties. The phantom was used for task-based image quality assessment of a newly released commercial iterative reconstruction algorithm (ADMIRE) using a channelized Hotelling observer paradigm. The results were compared to those from a complementary uniform background phantom. The comparison showed demonstrable differences, proportional to the complexity of the background being present.

9783-77, Session 15

Detectable change of lung nodule volume with CT in a phantom study with high- and low-contrast tasks

Marios A. Gavrielides, Qin Li, Rongping Zeng, Qi Gong, Kyle J. Myers, Berkman Sahiner, Nicholas A. Petrick, U.S. Food and Drug Administration (United States)

In previous work we developed a method for predicting the minimum detectable change (MDC) in nodule volume based on volumetric CT measurements. MDC was defined as the minimum increase in a nodule volume distinguishable from the baseline measurement at a specified level of detection performance, assessed using the area under the ROC curve (AUC). In this work we derived volume estimates of a set of synthetic nodules and calculated the detection performance for distinguishing them from baseline measurements. Eight spherical nodules of 100HU radiodensity ranging in diameter from 5.0mm to 5.75mm and 8.0mm to 8.75mm with 0.25mm increments were placed in an anthropomorphic phantom with either no background (high-contrast task) or gelatin background (low-contrast task). The phantom was scanned using varying exposures, and reconstructed with slice thickness of 0.75, 1.5, and 3.0mm and various reconstruction kernels. Volume measurements were derived using a previously developed matched filter approach. Results showed that nodule size, slice thickness, and nodule-to-background contrast affected detectable change in nodule volume when using our volume estimator and the acquisition settings from our study. We also found that experimental data for the 8mm baseline nodules matched very well with our predicted values of MDC (even for the low-contrast task, agreement was within <5% of percent change for a given AUC). These results support more effort into examining the use of this metric toward standardizing imaging protocols for lung nodule size change assessment.

9783-78, Session 15

Investigation of optimal parameters for penalized maximum-likelihood reconstruction applied to iodinated contrast-enhanced breast CT

Andrey V. Makeev, Lynda C. Ikejimba, U.S. Food and Drug Administration (United States); Joseph Y. Lo, Duke Univ. (United States); Stephen J. Glick, U.S. Food and Drug Administration (United States)

Although digital mammography has reduced breast cancer mortality by approximately 30%, sensitivity and specificity are still far from perfect. In particular, the performance of mammography is especially limited for women with dense breast tissue. Two out of every three biopsies performed in the US are unnecessary thereby resulting in increased patient anxiety, pain, and possible complications. One promising tomographic breast imaging method that has recently been approved by the FDA is dedicated breast CT (BCT). However, visualizing lesions with BCT can still be challenging for women with dense breast tissue due to the minimal contrast for lesions surrounded by fibroglandular tissue. In recent years, there has been renewed interest in improving lesion conspicuity in x-ray breast imaging by administration of an iodinated contrast agent. Due to the fully 3D imaging nature of BCT, as well as sub-optimal contrast enhancement while the breast is under compression with mammography and breast tomosynthesis, dedicated BCT of the uncompressed breast is likely to offer the best solution for injected contrast-enhanced x-ray breast imaging. It is well known that use of statistically based iterative reconstruction in CT results in improved image quality and lower radiation dose. We have previously explored use of the penalized maximum likelihood (PML) algorithm for BCT, and through simulation studies have investigated the optimal free parameters in the algorithm for maximizing detection of microcalcifications.
One of the challenges when characterizing performance of reconstruction algorithms using a numerical model observer is having sufficient number of signal realizations to estimate an unbiased signal template. An obvious way to address this is to perform multiple acquisitions of a phantom with a single inserted signal. But for low-dose, weak signal detection tasks, this would require hundreds of acquisitions and image reconstructions.

In this study, we have used a novel phantom with iodine enhanced signals imaged on a recently FDA approved breast CT system (Koning Inc., Rochester, NY) to optimize free parameters of the PML algorithm for the application of iodinated contrast-enhanced BCT. To objectively assess task performance, a Fourier domain ideal observer is used.

9783-80, Session 15

Comparison of model and human observer performance in FFDM, DBT, and synthetic mammography

Lynda C. Ikejimba, Duke Univ. Medical Ctr. (United States); Stephen J. Glick, U.S. Food and Drug Administration (United States); Ehsan Samei, Joseph Y. Lo, Duke Univ. Medical Ctr. (United States)

Purpose: Physical phantoms play an important role in image assessment of breast imaging systems. Using uniform and anthropomorphic physical phantoms, detectability was compared for small, low contrast signals in three imaging modes: full field digital mammography (FFDM), digital breast tomosynthesis (DBT), and synthetic mammography (SM). The purpose of this work was to assess task performance of the three imaging modes using different phantom types.

Methods: Images of the phantoms were acquired using a Hologic Selenia Dimensions system. Images were taken at 1.4 mGy average glandular dose. A contrast detail insert of small, low-contrast disks was created using an inkjet printer with iodine-doped ink. The disks varied in diameter from 210 to 630 µm, and in contrast from 1.1% contrast to 2.8% in regular increments. Human and model observers performed a 4 AFC experiment. Two observer models were used; a non-prewhitening matched filter with eye model (NPWE) and a channelized Hotelling observer with Gabor channels (Gabor-CHO).

Results: Overall, detectability was higher for FFDM and DBT than for SM. Generally, observer performance was lower for the anthropomorphic phantom than the uniform one, confirming the detection challenge posed by anatomy. The structure in the phantom background had a bigger impact on outcome for DBT than for FFDM or SM. The NPWE showed excellent agreement with humans for the uniform phantom, but in the presence of background structure the Gabor-CHO was superior.

Conclusion: Because results of any analysis may be dependent in part on the type of phantom used, it is crucial that any conclusions of modality performance be taken in the context of the phantom itself. Anthropomorphic phantoms may provide more clinically relevant measures of performance than conventional, uniform phantoms.
Conference 9784: Image Processing
Tuesday - Thursday 1 – 3 March 2016
Part of Proceedings of SPIE Vol. 9784 Medical Imaging 2016: Image Processing

9784-1, Session 1

Multi-voxel algorithm for quantitative bi-exponential MRI T1 estimation
Piet Bladt, Gwendolyne Van Steenkiste, Gabriel Ramos-Llordén, Arjan den Dekker, Jan Sijbers, Univ. Antwerpen (Belgium)

Purpose: Quantification of the spin-lattice relaxation time, T1, of tissues is important for characterization of tissues in clinical magnetic resonance imaging (MRI). In T1 mapping, T1 values are estimated from a set of T1-weighted MRI images. Due to the limited spatial resolution of the T1-weighted images, one voxel might consist of two tissues, causing partial volume effects (PVE). In conventional mono-exponential T1 estimation, these PVE result in systematic errors in the T1 map. To account for PVE, single-voxel bi-exponential estimators (SBEs) have been suggested. Unfortunately, SBEs suffer from low accuracy and precision. In this work, we propose a joint multi-voxel bi-exponential estimator (JMBE) and compare its performance to the SBE.

Methods and experiments: First, the proposed JMBE is constructed based on a maximum likelihood estimation framework. Next, the accuracy of the JMBE was evaluated against that of the SBE using sets of simulated voxels from a numerical brain phantom containing two different tissues. For both imaging settings, the minimal signal-to-noise ratio (SNR) needed to estimate both T1 values with sufficient accuracy was investigated.

Results: To produce accurate results, the SBE requires single-voxel SNRs that are unattainable in a clinical setup. In contrast to the SBE, and for clinically achievable single-voxel SNRs, the JMBE is accurate and efficient if four or more neighboring voxels are used in the joint estimation framework.

Conclusion: Considering clinically realistic SNRs, accurate results for quantitative bi-exponential T1 estimation are only achievable when information of neighboring voxels is incorporated by means of the JMBE algorithm.

9784-2, Session 1

Automatic coronary lumen segmentation with partial volume modeling improves lesions’ hemodynamic significance assessment
Moti Freiman, Yechiel Lamash, Philips Medical Systems Technologies Ltd. (Israel); Guy Gilboa, Technion-Israel Institute of Technology (Israel); Hannes Nickisch, Sven Prevrhal, Holger Schmitt, Philips Research (Germany); Mani Vembar, Philips Healthcare (United States); Liran Goshen, Philips Medical Systems Technologies Ltd (Israel)

The determination of hemodynamic significance of coronary artery lesions from cardiac computed tomography angiography (CCTA) based on flow simulations has the potential to improve current CCTA’s specificity, thus resulting in improved clinical decision making. Accurate coronary lumen segmentation required for flow simulation is challenging due to several factors. Specifically partial-volume effect in small-diameter lumen may result in overestimation of the lumen diameter that can lead to an erroneous assessment. In this work, we present a coronary artery segmentation algorithm tailored specifically for flow simulations by accounting for partial volume effect. Our algorithm detects lumen regions that may be subject to partial volume effect by analyzing the coronary centerline intensity profile and integrating this information into a machine-learning based graph min-cut segmentation framework to obtain accurate coronary lumen segmentations. We demonstrate the improvement in hemodynamic significance assessment achieved by accounting for partial volume effect in the automatic segmentation of 91 coronary artery lesions from 85 patients. We compared hemodynamic significance assessments by means of fractional flow reserve (FFR) resulted from simulations on 3D models generated by our segmentation algorithm with and without accounting for partial volume effect. By accounting for partial volume effect we improved the area under the curve for detecting hemodynamically significant CAD by 29% (N=91, 0.66 vs. 0.85, p<0.05, Delong’s test) with invasive FFR threshold of 0.8 as the reference standard. Our algorithm has the potential to facilitate non-invasive hemodynamic significance assessment of coronary lesions.

9784-3, Session 1

Contour tracking and probabilistic segmentation of tissue phase mapping MRI
Teodora Chitiboi, Fraunhofer MEVIS (Germany) and Jacobs Univ. Bremen (Germany); Anja B. Hennemuth, Fraunhofer MEVIS (Germany); Susanne Schnell, Varun Chowdhary, Amir Honarmand, Michael Markl, Northwestern Univ. (United States); Lars Linsen, Jacobs Univ. Bremen gGmbH (Germany); Horst K. Hahn, Fraunhofer MEVIS (Germany) and Jacobs Univ. Bremen (Germany)

Many cardiovascular diseases manifest as an abnormal motion pattern of the heart muscle (myocardium). Local cardiac motion can be non-invasively quantified with magnetic resonance imaging (MRI), using methods such as tissue phase mapping (TPM), which directly measures the local myocardial velocities over time with high temporal and spatial resolution. The challenges to routine clinical use of TPM for the diagnosis and monitoring of cardiac fitness lie in providing a fast and accurate myocardium segmentation and a robust quantitative analysis of the velocity field. Both of these tasks are difficult to automate on routine clinical data because of the high levels of noise and low contrast.

In this work, we propose to address these challenges with a segmentation approach that combines smooth, iterative contour displacement and probabilistic segmentation using particle tracing based on the underlying velocity field. The proposed solution enabled the efficient and reproducible segmentation of TPM datasets from 27 patients and 14 volunteers, showing good potential for routine use in clinical studies. Our method allows for a more reliable quantitative analysis of local myocardial velocities, by giving a higher weight to velocity vectors corresponding to pixels more likely to belong to the myocardium. The accuracy of the contour propagation was evaluated on nine subjects, showing an average error smaller than the spatial resolution of the image data. Statistical analysis concluded that the difference between the segmented contours and the ground truths was not significantly higher than the variability between the manual ground truths.

9784-4, Session 1

Automatic detection of cardiovascular risk in CT attenuation correction maps in Rb-82 PET/CTs
Ivana Isgum, Bob D. de Vos, Jelmer M. Wolterink, Univ. Medical Ctr. Utrecht (Netherlands); Damini Dey, Daniel S. Berman, Mathieu Rubeaux, Cedars-Sinai Medical Ctr. (United States); Tim Leiner, Univ. Medical Ctr. Utrecht (Netherlands); Piotr J. Slomka, Cedars-Sinai Medical Ctr. (United States)

CT attenuation correction (CTAC) images acquired with PET/CT visualize coronary artery calcium (CAC) and enable their quantification. CAC scores
acquired with CTAC have been suggested as a marker of cardiovascular disease (CVD). In this work, an algorithm previously developed for automatic CAC scoring in dedicated cardiac CT was applied for automatic CAC detection in CTAC. The study included 134 consecutive patients undergoing 82-Rb PET/CT. Low-dose rest CTAC scans were acquired (100 kV, 3 mm slice thickness). A reference standard was defined by an experienced observer using a standard 130 HU threshold. Five scans were removed from analysis due to artifacts.

The algorithm extracted potential CAC by intensity-based thresholding and 3D connected component labeling. Each candidate was described by location, size, shape and intensity features. An ensemble of randomized decision trees was used to identify CAC. The data set was randomly divided into training and test set. Automatically identified CAC was quantified using volume and Agatston scores.

In 33 test scans, the system detected on average 469 mm$^3$/730 mm$^3$ (64%) of CAC with 36 mm$^3$ false positives per scan. The intraclass correlation coefficient for volume scores was 0.84. Each patient was assigned to one of four CVD risk categories based on the Agatston scores (0-10, 10-100, 100-400, >400). 85% of patients were assigned to the correct category (linearly weighted $R^2$.82).

Automatic detection of CVD risk based on CAC scoring in rest CTAC images is feasible. This may enable large scale studies evaluating clinical value of CAC scoring in CTAC data.

9784-5, Session 1

**Combining the boundary shift integral and tensor-based morphometry for brain atrophy estimation**

Mateusz Michalkiewicz, Akshay Pai, Datalogisk Institut (Denmark); Kelvin Leung, Univ. College London (United Kingdom); Stefan Sommer, Sune Darkner, Lauge Sørensen, Jon Sporring, Datalogisk Institut (Denmark); Mads Nielsen, Datalogisk Institut (Denmark) and Biomediq (Denmark)

Brain atrophy from structural magnetic resonance images (MRIs) is widely used as an imaging surrogate marker for Alzheimer’s disease. Their utility has been limited due to the large degree of variance and subsequently high sample size estimates. The only consistent and reasonably powerful atrophy estimation methods has been the boundary shift integral (BSI). In this paper, we first propose a tensor-based morphometry (TBM) method to measure voxel-wise atrophy that we combine with BSI. The combined model decreases the sample size estimates significantly when compared to BSI and TBM alone.

9784-6, Session 2

**Image processing pipelines: applications in magnetic resonance histology** *(Keynote Presentation)*

G. Allan Johnson, Robert Anderson, Evan Calabrese, James Cook, Christopher Long, Alexandra Badea, Ctr. for In Vivo Microscopy (United States)

No Abstract Available

9784-7, Session 2

**Auto tract: automatic cleaning and tracking of fibers**

Juan Prieto, Francois Budin, Jean Y. Yang, Martin A. Styner, The Univ. of North Carolina at Chapel Hill (United States)

We propose a new tool named Autotrack to automate fiber tracking in diffusion tensor imaging (DTI).

Autotrack uses prior knowledge from a source DTI and a set of corresponding fiber bundles to extract new fibers for a target DTI.

Autotrack starts by aligning both DTIs and uses the source fibers as seed points to initialize a tractography algorithm.

We enforce similarity between the source and traced fibers by computing metrics such as fiber length and fiber distance between the models.

By analyzing these metrics, individual fiber tracts can be pruned in the target model.

We show that both source and target fibers have similar characteristics. This work is motivated by medical applications in which known bundles of fiber tracts in the human brain need to be analyzed for multiple datasets.

9784-8, Session 2

**Supervised hub-detection for brain connectivity**

Niklas Kasenburg, Univ. of Copenhagen (Denmark); Matthew G. Liptrot, Univ. of Copenhagen (Denmark) and Technical Univ. of Denmark (Denmark); Nina L. Reislev, Ellen Garde, Copenhagen Univ. Hospital Hvidovre (Denmark); Mads Nielsen, Aasa Feragen, Univ. of Copenhagen (Denmark)

A structural brain network consists of connections between physically defined brain regions. Brain network analysis aims to find features associated with a parameter of interest through supervised prediction models such as regression. Unsupervised preprocessing steps like clustering are often applied, but can smooth discriminative signals in the population, degrading predictive performance. We present a novel hub-detection optimized for supervised learning that both clusters network nodes based on population level variation in connectivity and also takes the learning problem into account. The found hubs are a low-dimensional representation of the network and are chosen based on predictive performance as features for a linear regression.

We apply our method to the problem of finding age-related changes in structural connectivity. We compare our supervised hub-detection (SHD) to an unsupervised hub-detection and a linear regression using the original network connections as features. The results show that the SHD is able to retain regression performance, while still finding hubs that represent the underlying variation in the population well. Although here we applied the SHD to brain networks, it can be applied to any network regression problem. Further development of the presented algorithm will be the extension to other predictive models such as classification or non-linear regression.

9784-9, Session 2

**Coresets versus clustering: comparison of methods for redundancy reduction in very large white matter fiber sets**

Guy Alexandroni, Gali Zimmerman Moreno, Nir Sochen, Hayit Greenspan, Tel Aviv Univ. (Israel)

Recent advances in Diffusion Weighted Magnetic Resonance Imaging (DW-MRI) have shown that diffusion imaging provides a non-invasive method to explore brain microstructure at a fine spatial scale. The huge amount of data collected from diffusion MRI makes the segmentation and analysis of the data computationally challenging. One approach to this issue is to reduce the number of fiber bundles to a smaller set that is representative of the original data. In this work, we compare two different methods to select a small representation of the complete set of fiber bundles. One method uses coreset selection and the other uses unsupervised clustering. We evaluate and compare the performance of these methods for a task related to automatic CVD risk assessment using CAC.
MRI) of white matter in conjunction with improved tractography algorithms produce impressive reconstructions of White Matter (WM) pathways in the brain. These sets, termed fiber sets, often contain hundreds of thousands of fibers, or more. In order to make fiber based analysis more practical, the fiber set needs to be preprocessed to eliminate redundancies and to keep only essential representative fibers. In this paper we demonstrate and compare two distinctive frameworks for selecting this reduced set of fibers. The first framework comprises pre-clustering the fibers into sub-groups using K-means, followed by further decomposition using Hierarchical Clustering. For the second clustering stage seven distance metrics, suitable for measuring fibers similarity were evaluated. The reduced set was achieved by replacing each cluster with one representative fiber. The second framework is based on an efficient geometric approximation algorithm named Coreset. Coresets present a new approach to optimization and have huge success especially in tasks requiring prohibitively large computation time and/or memory space. Here it is used for extracting the main fibers from dense WM fiber datasets, leaving a small set that well represents the main structures and connectivity of the brain. We use a novel approach, based on 3D indicator structure, for comparing the frameworks and estimating the anatomical information loss as a function of the reduction rate. The proposed comparison was applied to High Angular Resolution Diffusion-Weighted Imaging (HARDI) scans of 4 healthy individuals. The best performance was received for Coreset framework.

9784-10, Session 3

Enhanced cortical thickness measurements for rodent brains via Lagrangian-based RK4 streamline computation

Joohwi Lee, Sun Hyung Kim, Ilwoo Lyu, The Univ. of North Carolina at Chapel Hill (United States); Ipek Oguz, The Univ. of Iowa (United States); Martin A. Styner, The Univ. of Iowa (United States) and The Univ. of North Carolina at Chapel Hill (United States)

The cortical thickness of the mammalian brain is an important morphological characteristic that can be used to investigate and observe the brain’s developmental changes that might be caused by biologically toxic substances such as ethanol or cocaine. Although various cortical thickness analysis methods have been proposed that are applicable for human brain and have developed into well-validated open-source software packages, cortical thickness analysis methods for rodent brains have not yet become as robust and accurate as those designed for human brains. Based on a previously proposed cortical thickness measurement pipeline for rodent brain analysis, we present an enhanced cortical thickness pipeline in terms of accuracy and anatomical consistency. First, we propose a Lagrangian-based computational approach in the thickness measurement step in order to minimize local truncation error using the fourth-order Runge-Kutta method. Second, by constructing a line object for each streamline of the thickness measurement, we can visualize the way the thickness is measured and achieve sub-voxel accuracy by performing geometric post-processing. Last, with emphasis on the importance of an anatomically consistent partial differential equation (PDE) boundary map, we propose an automatic PDE boundary map generation algorithm that is specific to rodent brain anatomy, which does not require manual labeling. The results show that the proposed cortical thickness pipeline can produce statistically significant regions that are not observed in the the previous cortical thickness analysis pipeline.

9784-11, Session 3

Anatomy-aware measurement of segmentation accuracy

Hamid R. Tizhoosh, Univ. of Waterloo (Canada); Ahmed A. Othman, Suez Canal Univ. (Egypt)

Quantifying the accuracy of segmentation and manual delineation of organs, tissue types and tumours in medical images is a necessary measurement that suffers from multiple problems. One major shortcoming of all accuracy measures is that they neglect the anatomical significance or relevance of different zones within a given segment, hence, they measure the overlap of a given segment with a ground-truth without any anatomical discrimination. For instance, if we understand the rectal wall or urethral sphincter as anatomical zones, then current accuracy measure ignores their significance when they are applied to contour the boundary of the prostate gland. In this paper we propose an anatomy-aware measurement scheme for segmentation accuracy of medical images. The idea is to create a master gold based on a consensus shape containing not just the outline of the segment but also the outlines of the internal zones if existent or relevant. To apply this new approach to accuracy measurement we also introduce extensions of both Dice coefficient and Jaccard index and investigate their effect using 50 synthetic prostate ultrasound images with 10 different segments for each image. We show that through anatomy-sensitive calculation of segmentation accuracy, namely by considering relevant anatomical zones, not only the measurement of individual users can change but also the inter-observer variability may shift.

9784-12, Session 3

Automatic segmentation and statistical shape modeling of the paranasal sinuses to estimate natural variations

Ayushi Sinha, Simon Leonard, Austin Reiter, Johns Hopkins Univ. (United States); Masaru Ishii M.D., Johns Hopkins Bayview Medical Ctr. (United States); Russell H. Taylor, Gregory D. Hager, Johns Hopkins Univ. (United States)

We present an automatic segmentation and statistical shape modeling system for the paranasal sinuses which allows us to locate structures in and around the sinuses, as well as to observe the natural variations that occur in these structures. This system involves deformably registering a given patient image to a manually segmented template image, and using the resulting deformation field to transfer labels from template to patient. We use 3D snake splines to correct errors in the deformable registration. Once we have several accurately segmented images, we build statistical shape models for each structure in the sinus allowing us to observe the mean shape of the population, as well as the variations observed in the population. These shape models are useful in several ways. First, regular video-CT registration methods are insufficient to accurately register pre-operative computed tomography (CT) images with intra-operative endoscopy video because of deformations that occur in structures containing high amounts of erectile tissue. Our aim is to estimate these deformations using our shape models, as well as to distinguish normal variations in anatomy from abnormal variations, and automatically detect and stage pathology. We can also compare the mean shape and variances of different populations, such as different genders or ethnicities, and observe the differences and similarities, as well as of different age groups, and observe the developmental changes that occur in the sinuses.

9784-13, Session 3

Combining multi-atlas segmentation with brain surface estimation

Yuankai Huo, Vanderbilt Univ. (United States); Aaron Carass, Johns Hopkins Univ. (United States); Susan M. Resnick, National Institute on Aging (United States); Dzung L. Pham, Henry M. Jackson Foundation (United States); Jerry L. Prince, Johns Hopkins Univ. (United States); Bennett A. Landman, Vanderbilt Univ. (United States)

Whole brain segmentation (with comprehensive cortical and subcortical labels) and cortical surface reconstruction are two essential techniques
for investigating the human brain. The two tasks are typically conducted independently, however, which leads to spatial inconsistencies and hinders further integrated cortical analyses. To obtain self-consistent whole brain segmentations and surfaces, FreeSurfer segregates the subcortical and cortical segmentations before and after the cortical surface reconstruction. However, this “segmentation to surface to parcellation” strategy has shown limitation in various situations. In this work, we propose a novel “multi-atlas segmentation to surface” method called Multi-atlas CRUISE (MaCRUISE), which achieves self-consistent whole brain segmentations and cortical surfaces by combining multi-atlas segmentation with the cortical reconstruction method CRUISE. To our knowledge, this is the first work that achieves the reliability of state-of-the-art multi-atlas segmentation and labeling methods together with accurate and consistent cortical surface reconstruction. Compared with previous methods, MaCRUISE has three features: (1) MaCRUISE obtains 132 cortical/subcortical labels simultaneously from a single multi-atlas segmentation before reconstructing volume consistent surfaces; (2) Fuzzy tissue memberships are combined with multi-atlas segmentations to address partial volume effects; (3) MaCRUISE reconstructs topologically consistent cortical surfaces by using the sulci locations from multi-atlas segmentation. Two data sets, one consisting of five subjects with expertly traced landmarks and the other consisting of 100 volumes from elderly subjects are used for validation. Compared with CRUISE, MaCRUISE achieves self-consistent whole brain segmentation and cortical reconstruction without compromising on surface accuracy. MaCRUISE is comparably accurate to FreeSurfer while achieving greater robustness across an elderly population.

9784-14, Session 3
Automated segmentation of upper digestive tract from abdominal contrast-enhanced CT data using hierarchical statistical modeling of organ inter-relations
Shunta Hirayama, Yoshito Otake, Nara Institute of Science and Technology (Japan); Toshiyuki Okada, Univ. of Tsukuba (Japan); Masatoshi Hori M.D., Noriyuki Tomiyama M.D., Osaka Univ. (Japan); Yoshinobu Sato, Nara Institute of Science and Technology (Japan)

We have studied the automatic segmentation of multi-organ region from abdominal CT images ever. In previous work, we have proposed the automatic segmentation of multiple organ region by performing a hierarchical statistical modeling using a relationship between organs. In this paper, we have proposed automatically segmentation of the upper digestive tract from abdominal contrast-enhanced CT using segmented multi organs so far. Segment and compare the esophagus, stomach and duodenum using hierarchical statistical modeling which is our proposed method, and conventional statistical atlas method. In addition, preliminary experiment is performed which is adding gas region to the candidate area at segmentation step. They were evaluated quantitatively by Dice coefficient, Jaccard index and the average symmetric surface distance of the segmented region and correct region data.

9784-15, Session 4
Segmentation and labeling of the ventricular system in normal pressure hydrocephalus using patch-based tissue classification and multi-atlas labeling
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Normal pressure hydrocephalus (NPH) affects older adults and is thought to be caused by obstruction of the normal flow of cerebrospinal fluid (CSF). NPH typically presents with cognitive impairment, gait dysfunction, and urinary incontinence, and may account for more than five percent of all cases of dementia. Unlike most other causes of dementia, NPH can potentially be treated and the neurological dysfunction reversed by shunt surgery or endoscopic third ventriculostomy (ETV), which drain excess CSF. However, a major diagnostic challenge remains to robustly identify shunt-responsive NPH patients from patients with enlarged ventricles due to other neurodegenerative diseases. Currently, radiologists grade the severity of NPH by detailed examination and measurement of the ventricles based on stacks of 2D magnetic resonance images (MRIs). Here we propose a new method to automatically segment and label different compartments of the ventricles in NPH patients from MRIs. While this task has been achieved in healthy subjects, the ventricles in NPH are both enlarged and deformed, causing current algorithms to fail. Here we combine a patch-based tissue classification method with a registration-based multi-atlas labeling method to generate a novel algorithm that labels the lateral, third, and fourth ventricles in subjects with ventriculotomy. The method is also applicable to other neurodegenerative diseases such as Alzheimer’s disease; a condition considered in the differential diagnosis of NPH. Comparison with state of the art segmentation techniques demonstrate substantial improvements in labeling the enlarged ventricles, indicating that this strategy may be a viable option for the diagnosis and characterization of NPH.
The bumps on the hippocampus

Yi Gao, Stony Brook Univ. (United States); Lawrence Ver Hoef, The Univ. of Alabama at Birmingham (United States)

The hippocampus has been the focus of more imaging research than any other subcortical structure in the human brain. However a feature that has been almost universally overlooked are the bumpy ridges on the inferior aspect of the hippocampus, which we refer to as hippocampal dentation. These bumps arise from folds in the CA1 layer of Ammon’s horn. Similar to the folding of the cerebral cortex, hippocampal dentation allows for greater surface area in a confined space. However, while quantitative studies of radiologic brain images have been advancing for decades, examining numerous approaches to hippocampal segmentation and morphology analysis, virtually all published 3D renderings of the hippocampus show the under surface to be quite smooth or mildly irregular; we have rarely seen the characteristic bumpy structure in the reconstructed 3D scene, one exception being the 9.4T postmortem study. This is presumably due to the fact that, based on our experience with high resolution images, there is a dramatic degree of variability in hippocampal dentation between individuals from very smooth to highly dentated. An apparent question is, does this indicate that this specific morphological signature can only be captured using expensive ultra-high field techniques? Or, is such information buried in the data we commonly acquire, awaiting a computation technique that can extract and render it clearly? In this study, we propose a super-resolution technique that captures the fine scale morphometric features of the hippocampus based on common T1-weighted 3T MR images.

Unsupervised fetal cortical surface parcellation

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At the core of many neuro-imaging studies, atlas-based brain parcellation is used for example to study normal brain evolution across the lifespan. It relies on the assumption that the same anatomical features can be found on all subjects to be studied and that these features are stable enough to allow correspondence between the different brain surfaces. These methods, however, often fail when applied to fetal MRI data, due to the lack of consistent anatomical features across gestation. This paper presents a novel surface-based fetal cortical parcellation framework which attempts to circumvent the lack of consistent anatomical features by proposing a parcellation of the brain based on only learned geometrical features.

A mesh signature incorporating both extrinsic and intrinsic geometrical features is proposed and used in a clustering scheme to define a parcellation of the fetal brain. This parcellation is then learned using a Random Forest (RF) based learning approach and then further refined in an alpha-expansion graph-cut scheme. Based on the votes obtained by the RF inference procedure, a probability map is computed and used as a data term in the graph-cut procedure. The smoothness term is defined by learning a transition matrix based on the dihedral angles of the faces. Qualitative and quantitative results on a cohort of both healthy and high-risk fetuses are presented.

Both visual and quantitative assessments show good results demonstrating a reliable method for fetal brain data and the possibility of obtaining a parcellation of the fetal cortical surfaces using only geometrical features.

Geodesic denoising for optical coherence tomography images

Ehsan Shahriari Varnousfaderani, Hamilton Glaucoma Ctr. (United States); Wolf-Dieter Vogl, Jing Wu, Bianca S. Gerendas, Christian Simader, Georg Langs, Sebastian M. Waldstein M.D., Ursula Schmidt-Erfurth, Christian Doppler Lab. for Ophthalmic Image Analysis (Austria)

Optical coherence tomography (OCT) is an optical signal acquisition method capturing micrometer resolution, cross sectional three-dimensional images. OCT images are used widely in ophthalmology to diagnose and monitor retinal diseases such as age-related macular degeneration (AMD) and Glaucoma. While OCT allows the visualization of retinal structures such as vessels and retinal layers, image quality and contrast is reduced by speckle noise, obfuscating small, low intensity structures and structural boundaries. Existing denoising methods for OCT images may remove clinically significant image features such as texture and boundaries of anomalies. In this paper, we propose a novel patch based denoising method, called as Geodesic Denoising. The method reduces noise in OCT images while preserving clinically significant, although small, pathological structures, such as fluid-filled cysts in diseased retinas. Our method selects optimal image patch distribution representations based on geodesic patch similarity to noisy samples. Patch distributions are then randomly sampled to build a set of best matching candidates for every noisy sample, and the denoised value is computed based on a geodesic weighted average of the best candidate samples. Our method is evaluated qualitatively on real pathological OCT scans and quantitatively on a set of ground truth, noise free synthetic OCT scans with artificially added noise and pathologies. Experimental results show that performance of our method is comparable with state of the art denoising methods while outperforming them in preserving the critical clinically relevant structures.

Combined self-learning based single-image super-resolution and dual-tree complex wavelet transform denoising for medical images

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In this paper, we propose a novel self-learning based single-image super-resolution (SR) method, which is coupled with dual-tree complex wavelet transform (DTCWT) based denoising to better recover high-resolution (HR) medical images. Unlike previous methods, this self-learning based SR approach enables us to reconstruct HR medical images from a single low-resolution (LR) image without extra training on HR image datasets in advance. The relationships between the given image and its scaled down versions are modeled using support vector regression with sparse coding and dictionary learning, without explicitly assuming reoccurrence or self-similarity across image scales. In addition, we perform DTCWT based denoising to initialize the HR images at each scale instead of simple bicubic interpolation. We evaluate our method on a variety of medical images. Both quantitative and qualitative results show that the proposed approach outperforms bicubic interpolation and state-of-the-art single-image SR methods while effectively removing noise.
Sinogram smoothing and interpolation via alternating projections onto the slope and curvature constraints
Davood Karimi, Rabab Kreidieh Ward, The Univ. of British Columbia (Canada)

Reduction in the radiation dose in computed tomography (CT) requires reducing the number of the energy of the photons that enter the patient’s body. The images reconstructed from such noisy or undersampled measurements will contain much noise and artifacts that can significantly reduce the diagnostic value of the image. Effective sinogram denoising or interpolation can reduce these noise and artifacts. In this paper, we present a novel approach to sinogram smoothing and interpolation. The proposed method iteratively estimates the local slope and curvature of the sinogram and forces the sinogram to follow the estimated slope and curvature. This is performed by projection onto the set of constraints that define the slope and the curvature. Projection onto these constraints have simple analytical solutions that admit accurate and fast processing. Moreover, these operations are highly parallelizable because the equations defining the slope and curvature constraints for all the points in a sinogram can be summarized as five convex sets, regardless of the size of the sinogram. We apply the proposed method on simulated and real data and examine its effect on the quality of the reconstructed image. Our results show that the proposed method is highly effective and can lead to a substantial improvement in the quality of the images reconstructed from noisy or undersampled sinogram measurements, outperforming the bilateral filtering algorithm. Therefore, the proposed method can be a very useful tool for low-dose CT.

A novel structured dictionary for fast processing of 3D medical images, with application to computed tomography restoration and denoising
Davood Karimi, Rabab Kreidieh Ward, The Univ. of British Columbia (Canada)

Sparse representation of signals in learned overcomplete dictionaries has proven to be a powerful tool with applications in denoising, restoration, compression, reconstruction, and more. However, a major challenge remains. Finding the sparse representation of a signal in these dictionaries requires solving an optimization problem that leads to very long computational times, especially in 3D image processing. Moreover, the sparse representation found by greedy algorithms is usually sub-optimal. In this paper, we propose a novel two-level dictionary structure that improves the performance and the speed of standard greedy sparse coding methods. The first (i.e., the top) level in our dictionary is a fixed orthonormal basis, whereas the second level includes the atoms that are learned from the training data. We explain how such a dictionary can be learned from the training data and how the sparse representation of a new signal in this dictionary can be computed. As an application, we use the proposed dictionary structure for removing the noise and artifacts in 3D computed tomography (CT) images. Our experiments with real CT images show that the proposed method achieves better results than standard dictionary-based methods while substantially reducing the computational time.

Enhanced intravascular near-infrared spectroscopy (NIRS) imaging system for detection of lipid core plaques in coronary arteries
Zhihua He, Stephen T. Sum, InfraReDx, Inc. (United States)

An FDA-cleared catheter-based near-infrared spectroscopy (NIRS) system detects lipid core plaques (LCP) in patients undergoing percutaneous coronary intervention. The detection results are summarized as a 2D probability map presented in pseudo-color (denoted as a Chemogram map). Within a Chemogram map, the regions with high probability of LCP are displayed as yellow, the regions with noise and model uncertainties are displayed as outlier (black). Due to the mixture of outlier regions and diffused yellow regions, physicians are sometimes challenged in interpreting the Chemogram map in a clinical setting. This paper describes an image processing based method to enhance the Chemogram map readability by displaying only the LCP of interest.

The proposed four-step Chemogram map enhancement algorithm is developed based on the prior knowledge of LCP and composition of different types of outliers. The features of interest are detected through the first three steps using both the Chemogram map and the outlier map. In the fourth step, the corresponding detection results are used to compose a clean Chemogram map showing only significant yellow regions that correspond to LCP and no outlier overlay. The LCP detection performance of the corresponding enhanced Chemogram map was evaluated by testing on data from 212 vessel segments of 84 autopsy hearts. The performance was evaluated based on ROC analysis of 2mm Chemogram blocks against histology. The ROC analysis of the enhanced Chemogram map yielded an area under the curve of 0.80 (95% CI [0.78-0.85]) which is comparable to the LCP detection performance of the original Chemogram map cleared by the FDA.

In summary, a method to enhance the Chemogram map is described. The enhanced Chemogram map offers physicians a clean display which is easier to interpret, while still maintaining good LCP detection performance.

The proposed four-step Chemogram map enhancement algorithm is developed based on the prior knowledge of LCP and composition of different types of outliers. The features of interest are detected through the first three steps using both the Chemogram map and the outlier map. In the fourth step, the corresponding detection results are used to compose a clean Chemogram map with only significant yellow regions which correspond to LCP region, without introduction of outlier overlay. The LCP detection performance of the corresponding enhanced crispy Chemogram map is evaluated by testing on data from 212 vessel segments of 84 autopsy hearts. The performance is evaluated based on ROC analysis of 2mm block Chemogram against histology. The ROC analysis of the crispy Chemogram map yields AUC Of 0.803 (95% CI [0.78-0.85]) which is comparable to the LCP detection performance of the original Chemogram map cleared by the FDA.

In summary, a method to enhance Chemogram map is described. The enhanced crispy Chemogram map offers physicians a clean display which is easier to interpret, while still maintaining good LCP detection performance.

Landmark based shape analysis for cerebellar ataxia classification and cerebellar atrophy pattern visualization
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Cerebellar dysfunction can lead to a wide range of movement disorders. Studying the cerebellar atrophy pattern associated with different cerebellar disease types can potentially help the diagnosis, prognosis and treatment planning. In this paper, we present a landmark based shape analysis pipeline to classify healthy control and different ataxia types, and to visualize the characteristic cerebellar atrophy patterns associated with different types. A highly informative feature representation of the cerebellar structure is constructed by extracting dense homologous landmarks on the boundary surfaces of cerebellar sub-structures. A diagnosis group classifier based on this representation is built using partial least square dimension reduction and regularized linear discriminant analysis. Characteristic atrophy pattern for an ataxia type is visualized by sampling along the discriminant direction between healthy controls and the ataxia type. Experimental results show that the proposed method can successfully classify healthy controls and different ataxia types. The visualized cerebellar atrophy patterns were consistent with the regional volume decreases observed in previous studies, but the proposed method provides intuitive and detailed understanding about changes of overall size and shape of the cerebellum, as well as that of individual lobules.

9784-25, Session 6

**Multi-object, model-based, multi-atlas, segmentation for rodent brains using dense discrete correspondences**

Joowhi Lee, Ilwoo Lyu, Martin A. Styner, The Univ. of North Carolina at Chapel Hill (United States)

The delineation of rodent brain structures is challenging due to low contrast multiple cortical and subcortical organs that are closely interfacing to each other. Atlas-based segmentation has been widely employed due to its capability to delineate multiple organs at the same time via image registration. The use of multiple atlases and subsequent label fusion techniques has further improved robustness and accuracy of atlas-based segmentation. However, the accuracy of atlas-based segmentation is still prone to registration errors; for example, the segmentation of in vivo MR images can be less accurate and robust against image artifacts than the segmentation of post mortem images. In order to improve the accuracy and robustness of atlas-based segmentation, we propose a multi-object model-based multi-atlas segmentation method. We first establish spatial correspondences across atlases using a set of dense pseudo-landmark particles. We build a multi-object point distribution model using those particles in order to capture inter- and intra-subject variation among brain structures. The segmentation is obtained by fitting the model into a subject image, followed by label fusion process. Our result shows that the proposed method resulted better accuracy than compared segmentation methods including a widely used ANTs registration tool.

9784-26, Session 6

**Fast correspondences for statistical shape models of brain structures**

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Statistical shape models based on point distribution models (PDMs) are powerful tools for image segmentation or shape analysis. The most challenging part of the generation of the PDM is the identification of corresponding landmarks among all shapes. Since in general the true correspondences are unknown, correspondences are frequently established under the hypothesis that correct correspondences lead to a compact model, which is mostly tackled by continuous optimisation methods. In favour of the prospect of an efficient optimisation, we present a simplified view of the correspondence problem for SSMs that is based on point-set registration with a flavour of the population-based methods. First, regularised deformable point-set registration is performed for obtaining correspondences between shapes on a global scale, i.e. establishing rough correspondences that may still not be accurate on a local scale. Then, by using a mesh fairing procedure that is invariant to mesh parametrisation, consensus of the correspondences on a global and local scale among the entire set of shapes is achieved. Since both, point-set registration and mesh fairing, can be implemented in an efficient way, the evaluation of multiple putative groupwise correspondences comes into reach, which adds a hint of population-basedness to our method. We demonstrate that for the generation of SSMs of deep brain structures the proposed approach is preferable over existing population-based methods due to the significantly shorter runtime whilst at the same time improving the quality of the PDM with respect to specificity and generalisation.

9784-27, Session 6

**Robust group-wise rigid registration of point sets using t-mixture model**

Nishant Ravikumar, Ali Gooya, Alejandro F. Frangi, Zeike A. Taylor, The Univ. of Sheffield (United Kingdom)

A probabilistic framework for robust, group-wise rigid alignment of point-sets using a mixture of Student’s t-distributions is proposed. Rigid registration is challenging for groups of complex 3D shapes, especially when the point sets are of varying lengths, are corrupted by an unknown degree of outliers or in the presence of missing data. Medical images (in particular magnetic resonance (MR) images), their segmentations and consequently point-sets generated from these are highly susceptible to corruption by outliers. This poses a problem for robust correspondence estimation and accurate alignment of shapes, necessary for training statistical shape models (SSMs). To address these issues, this study proposes to use a t-mixture model (TMM), to approximate the underlying joint probability density of a group of similar shapes and align them to a common reference frame. The heavy-tailed nature of t-distributions provides a more robust registration framework in comparison to state of the art algorithms. Significant reduction in alignment errors is achieved in the presence of outliers, using the proposed TMM-based group-wise rigid registration method, in comparison to its Gaussian mixture model (GMM) counterparts. The proposed TMM-framework is compared with a group-wise variant of the well known Coherent Point Drift (CPD) algorithm and two other group-wise methods using GMMs, for both synthetic and real image-derived point sets. Rigid alignment errors for groups of shapes are quantified using the Hausdorff distance (HD) and mean absolute surface distance (MASD) metrics.

9784-28, Session 6

**Multi-region statistical shape model for cochlear implantation**

Jordi Romero Romero, Univ. Pompeu Fabra (Spain); Hans M. Kjer, Technical Univ. of Denmark (Denmark); Gemma Piella, Mario Ceresa, Miguel Angel González Ballester, Univ. Pompeu Fabra (Spain)
Statistical shape models are commonly used to analyze the variability between similar anatomical structures and their use is successfully established as a tool for the analysis or segmentation of medical images. However, just using a simple model to capture the global variability of complex structures is not enough to achieve the best results. Typically, the anatomical variability between structures is associated to the variability of their physiological regional. In this paper, a complete pipeline is proposed for building a statistical shape model to study the local variability of physiological regions of the inner ear. The proposed model, which is based on an extension of the Point Distribution Model (PDM), is built for a training set of 17 high-resolution images (24.5 μm) of the inner ear. The model is evaluated according to its generalization ability. The results are compared with the results of a global model (without regions) built directly using a PDM. The evaluation results suggest that better accuracy can be achieved using a regional modeling of the inner ear.

**9784-29, Session 6**

**Whole abdominal wall segmentation using Augmented Active Shape Models (AASM) with multi-atlas label fusion and level set**

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The abdominal wall is an important structure differentiating subcutaneous and visceral compartments and intimately involved with maintaining abdominal structure. Segmentation of the whole abdominal wall on routinely acquired computed tomography (CT) scans remains challenging due to variations and complexities of the wall and surrounding tissues. In this study, we propose a slice-wise augmented active shape model (AASM) approach to robustly segment both the outer and inner surfaces of the abdominal wall. Multi-atlas label fusion (MALF) and level set (LS) techniques are integrated into the traditional ASM framework. The AASM approach globally optimizes the landmark updates in the presence of complicated underlying local anatomical contexts. The proposed approach was validated on 184 axial slices of 20 CT scans. The Hausdorff distance against the manual segmentation was significantly reduced using the proposed approach compared to that using ASM, MALF, and LS individually. Our segmentation of the whole abdominal wall enables subcutaneous and visceral fat measurement, with high correlation to the measurement derived from manual segmentation (p > 0.93). This study presents the first generic segmentation of the whole abdominal wall with high correlation to visceral and subcutaneous fat volumes.

**9784-30, Session 7**

**Image-based navigation for functional endoscopic sinus surgery using structure from motion**

Simon Leonard, Austin Reiter, Ayushi Sinha, Masaru Ishii M.D., Russell H. Taylor, Gregory D. Hager, Johns Hopkins Univ. (United States)

Functional endoscopic endonasal surgeries (FEES) are minimally invasive procedures routinely used in otolaryngology. During these procedures, surgeons must navigate through the narrow sinus cavities to reach the source of the problem and they frequently remove cartilages or tissues that are adjacent, and often occlude, critical arteries, nerves or organs. In this paper, we present a method to facilitate this task by 1) registering endoscopic images to CT data and 2) overlaying areas of interests on endoscope images to improve the safety of the procedure. First, our system uses structure from motion (SfM) to generate a small cloud of 3D points from a short video sequence. Then, it uses iterative closest point (ICP) algorithm to register the points to a 3D mesh that represents a section of a patient’s sinuses. The scale of the point cloud is approximated by measuring the magnitude of the endoscope’s motion during the sequence. We have recorded several video sequences from five patients and, given a reasonable initial registration estimate, our results demonstrate an average registration error of 1.21 ± mm when the endoscope is viewing non-erectile tissues and an average registration error of 0.91 ± mm when the endoscope is viewing non-erectile tissues. Our implementation SfM + ICP can execute in less than 7 seconds and can use as few as 15 frames (0.5 second of video). Future work will involve clinical validation of our results and strengthening the robustness to initial guesses and erectile tissues.

**9784-31, Session 7**

**Coronary calcium visualization using dual energy chest radiography with sliding organ registration**

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Coronary artery calcification (CAC) is the lead biomarker for atherosclerotic heart disease. We are developing a new technique to image CAC using a regionally ordered, low cost, low radiation dual energy (DE) chest radiography (using the two-shot GE Revolution XRd system). In this paper, we proposed a novel imaging processing method (CorCalDx) based on sliding organ registration to create a bone-image-like, coronary calcium image (CCI) that significantly reduces motion artifacts and improves CAC conspicuity. Experiments on images of a physical dynamic cardiac phantom showed that CorCalDx reduced 73% of the motion artifact area as compared to standard DE over a range of heart rates up to 90 bpm and x-ray exposures. Residual motion artifact in the phantom CCI is greatly suppressed in gray level and area (0.88% of the heart area). In a Functional Measurement Test (FMT) with 20 clinical exams, image quality improvement of CorCalDx against standard DE (measured from -10 to +10) was significantly suggested (p < 0.0001) by three radiologists for cardiac motion artifacts (7.2 ± 2.1) and cardiac anatomy visibility (6.1 ± 3.5). CorCalDx was always chosen best in every image tested. In preliminary assessments of 12 patients with 18 calcifications, 90% of motion artifact regions in standard DE results were removed in CorCalDx results, with 100% sensitivity of calcium detection, showing great potential of CorCalDx to improve CAC detection and grading in DE chest radiography.

**9784-32, Session 7**

**Combined registration and motion correction of longitudinal retinal OCT data**

Andrew Lang, Aaron Carass, Omar Al-Louzi, Pavan Bhargava, Sharon D. Solomon, Peter A. Calabresi, Jerry L. Prince, Johns Hopkins Univ. (United States)

Optical coherence tomography (OCT) has become an important modality for examination of the eye. To measure layer thicknesses in the retina, automated segmentation algorithms are often used, producing accurate and reliable measurements. However, subtle changes are difficult to detect since the magnitude of the change can be very small. Thus, tracking disease progression over short periods of time is difficult. Additionally, unstable eye position and motion alter the consistency of these measurements, even in healthy eyes. Thus, both registration and motion correction are important for processing longitudinal data of a specific patient. In this work, we propose a method to jointly do registration and motion correction. Given the registration errors predicted by the system, we show how to deblur OCT images and correct motion artifacts to achieve more reliable measurements.
two scans of the same patient, we initially extract blood vessel points from a fundus projection image generated on the OCT data and estimate point correspondences. Due to saccadic eye movements during the scan, motion is often very abrupt, producing a sparse set of large displacements between successive B-scan images. Thus, we use lasso regression to estimate the movement of each image. By iterating between this regression and a rigid point-based registration, we are able to simultaneously align and correct the data. With longitudinal data from 39 healthy control subjects, our method improves the registration accuracy by 43% compared to simple alignment to the fovea and 8% when using point-based registration only. We also show improved consistency of repeated total retina thickness measurements.

9784-33, Session 7
Effects of spatial resolution on image registration
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This paper presents a theoretical analysis of the effect of spatial resolution on image registration. Based on the assumption of additive Gaussian noise on the images, the mean and variance of the distribution of of the sum of squared differences (SSD) were estimated. Using these estimates, we evaluate a distance between the SSD distributions of aligned images and non-aligned images. The experimental results show that by matching the resolutions of the moving and fixed images in the registration one can get a better image registration result. The results agree with our theoretical analysis of SSD, but also reveals it may be valid for mutual information as well.

9784-34, Session 7
Non-rigid contour-to-pixel registration of photographic and quantitative light-induced fluorescence imaging of decalcified teeth
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Quantitative light-induced fluorescence (QLF) is widely used to assess the damage of a tooth due to decalcification. In digital photographs, calcification appears as white spot lesions, i.e. white spots on the tooth surface.

We propose a novel multimodal registration approach for the matching of digital photographs and QLF images of decalcified teeth. The registration is based on the idea of contour-to-pixel matching. Here, the curve, which represents the shape of the tooth, is extracted from the QLF image using a contour segmentation by binarization and morphological processing. This curve is aligned to the photo with a non-rigid variational registration approach. Thus, the registration problem is formulated as minimization problem with an objective function that consists of a data term and a regularizer for the deformation.

To construct the data term, the photo is pointwise classified into tooth and non-tooth regions. Then, the signed distance function of the tooth region allows to measure the mismatch between curve and photo.

As regularizer a higher order, linear elastic prior is used. The resulting minimization problem is solved numerically using bilinear Finite Elements for the spatial discretization and the Gauss-Newton algorithm. The evaluation is based on 150 image pairs, where an average of 5 teeth have been captured from 32 subjects. All registrations have been confirmed correctly by a dental expert. The contour-to-pixel methods can directly be used in 3D for surface-to-voxel tasks.

9784-35, Session 8
Slide specific models for segmentation of differently stained digital histopathology whole slide images
Nicolas Brieu, Olivier Pauly, Johannes Zimmermann, Gerd Binnig, Günter Schmidt, Nathalie Harder, Definiens AG (Germany)

The automatic analysis of whole slide images (WSIs) of stained histopathology tissue sections plays a crucial role in the development of new biomarkers in oncology. Such analysis relies on the accurate detection of cells and nuclei. This task is however challenged by the low visual differentiation of high pleomorphic objects and by the diversity of tissue appearance between different slides. The key idea of this work is to take advantage of the well-differentiated objects in each slide to learn about the appearance of the tissue and in particular about the appearance of the low-differentiated objects. We detect well-differentiated objects, learn slide-specific visual context models, and finally use the resulting posterior maps to perform the final detection steps. The accuracy of the method is demonstrated against ground truth segmentation data on a set of differently stained images.

9784-36, Session 8
Relative value of diverse brain MRI and blood-based biomarkers for predicting cognitive decline in the elderly
Sarah Madsen, Greg Ver Steeg, The Univ. of Southern California (United States); Madelaine Daianu, Univ. of California, Los Angeles (United States); Adam Mezher, Neda Jahanshad, Talia M. Nir, Xue Hua, Boris A. Gutman, Aram Galstyan, Paul M. Thompson, The Univ. of Southern California (United States)

Cognitive decline accompanies many debilitating illnesses, including Alzheimer’s disease (AD). In old age, brain tissue loss also occurs along with cognitive decline. Although blood tests are easier to perform than brain MRI, few studies have compared brain scans to standard blood tests to see which kinds of information best predict future decline. In 504 older adults from the Alzheimer’s Disease Neuroimaging Initiative (ADNI), we used linear regression to assess the relative value of different types of data to predict cognitive decline, including 196 blood panel biomarkers, 249 MRI biomarkers obtained from the FreeSurfer software, demographics, and the AD-risk gene APOE. A subset of MRI biomarkers was the strongest predictor. There was no specific blood marker that increased predictive accuracy on its own, we found that a novel unsupervised learning method, CorEx, captured weak correlations among blood markers, and the resulting clusters offered unique predictive power.

9784-37, Session 8
Measuring glomerular number from kidney MRI images
Jayaraman J. Thiagarajan, Lawrence Livermore National Lab. (United States); Karthikeyan Natesan Ramamurthy, IBM Thomas J. Watson Research Ctr. (United States); Berkay Kanberoglu, David H. Frakes, Kevin M. Bennett, Andreas S. Spanias, Arizona State Univ. (United States)
Measuring the glomerular number in the entire, intact kidney using non-destructive techniques is of immense importance in studying several renal and systemic diseases. Commonly used approaches either require destruction of the entire kidney or perform extrapolation from measurements obtained from a few isolated sections. A recent magnetic resonance imaging (MRI) method, based on the injection of a contrast agent (cationic ferritin), has been used to effectively identify glomerular regions in the kidney. In this work, we propose a robust, accurate, and low-complexity method for estimating the number of glomeruli from such kidney MRI images. The proposed technique has a training phase and a low-complexity testing phase. In the training phase, organ segmentation is performed on a few expert-marked training images, and glomerular and non-glomerular image patches are extracted. Using non-local sparse coding to compute similarity and dissimilarity graph between the patches, the subspace in which the glomerular regions can be discriminated from the rest are estimated. For novel test images, the image patches extracted after preprocessing are embedded using the discriminative subspace projections. The glomerular and non-glomerular region candidates are identified in this space using region identification methods, and counted using object counting approaches after reconstructing the three-dimensional image from the slices. The testing phase is of low computational complexity since it involves only matrix multiplications, clustering, and simple morphological operations. Preliminary results with MRI data obtained from five kidneys of rats show that the proposed non-invasive, low-complexity approach performs comparably to conventional approaches such as acid maceration and stereology.

9784-38, Session 8
Response monitoring using quantitative ultrasound methods and supervised dictionary learning in locally advanced breast cancer

Mehrdad J. Gangeh, Univ. of Toronto (Canada); Brandon Fung, Sunnybrook Research Institute (Canada); Hadi Tadayyon, Univ. of Toronto (Canada); William T. Tran, Sunnybrook Research Institute (Canada); Gregory J. Czarnota, Sunnybrook Health Sciences Ctr. (Canada)

A non-invasive computer-aided-theraagnosis (CAT) system was developed for the early assessment of responses to neoadjuvant chemotherapy in patients with locally advanced breast cancer. The CAT system was based on quantitative ultrasound spectroscopy methods comprising several modules including feature extraction, a metric to measure the dissimilarity between “pre-” and “mid-treatment” scans, and a supervised learning algorithm for the classification of patients to responders/non-responders. One major requirement for the successful design of a high-performance CAT system is to accurately measure the changes in parametric maps before treatment onset and during the course of treatment. To this end, a unified framework based on Hilbert-Schmidt independence criterion (HSIC) was used for the design of feature extraction from parametric maps and the dissimilarity measure between the “pre-” and “mid-treatment” scans. For the feature extraction, HSIC was used to design a supervised dictionary learning (SDL) method by maximizing the dependency between the scans taken from “pre-” and “mid-treatment” with “dummy labels” given to the scans. For the dissimilarity measure, an HSIC-based metric was employed to effectively measure the changes in parametric maps as an indication of treatment effectiveness. The HSIC-based feature extraction and dissimilarity measure used a kernel function to nonlinearly transform input vectors into a higher dimensional feature space and computed the population means in the new space, where enhanced group separability was ideally obtained. The results of the classification using the developed CAT system indicated an improvement of performance compared to a CAT system with basic features using histogram of intensity.

9784-39, Session 8
Deeply learnt hashing forests for content based image retrieval in prostate MR images

Amit Shah, Sailesh Conjeti, Nassir Navab, Amin Katouzian, Technische Univ. München (Germany)

Deluge in the size and heterogeneity of medical image databases necessitates the need for content based retrieval systems for their efficient organization. In this paper, we propose such a system to retrieve prostate MR images which share similarities in appearance and content with a query image. We introduce deeply learnt hashing forests (DL-HF) for this image retrieval task. DL-HF effectively leverages the semantic descriptiveness of deep learnt Convolutional Neural Networks. This is used in conjunction with hashing forests which are unsupervised random forests. DL-HF hierarchically parses the deep-learned feature space to encode subspaces with compact binary codewords. We propose a similarity preserving feature descriptor called Parts Histogram which is derived from DL-HF. Correlation defined on this descriptor is used as a similarity metric for retrieval from the database. Validations on publicly available multi-center prostate MR image database established the validity of the proposed approach. The proposed method is fully-automated without any user-interaction and is not dependent on any external image standardization like image normalization and registration. This image retrieval method is generalizable and is well-suited for retrieval in heterogeneous databases other imaging modalities and anatomies.

9784-40, Session 8
A high-throughput mouse phenotyping framework using robust principal component analysis

Zhongliu Xie, Imperial College London (United Kingdom); Asanobu Kitamoto, National Institute of Informatics (Japan); Masaru Tamura, RIKEN (Japan); Toshihiko Shiroishi, National Institute of Genetics (Japan); Duncan F. Gillies, Imperial College London (United Kingdom)

Intensive international efforts are underway towards phenotyping the entire mouse genome within the next decade, by modifying its 25,000 genes one-by-one for comparative study. With vast amounts of data to analyze, the traditional means via time-consuming histological examination is clearly impractical, leading to an overwhelming demand for some high-throughput phenotyping framework, especially with the use of biomedical image informatics to automatically identify phenotypes concerning morphological abnormality. Existing work has either excessively relied on volumetric contrast which is insensitive to phenotypes involving no severe volume variations, or tailored for specific defects thus fails to serve a general phenotyping purpose. Furthermore, the prevailing requirement of an atlas for image segmentation in contrast to its limited availability further complicate the issue in practice. In this paper we propose a high-throughput general-purpose phenotyping framework that is able to efficiently perform batch-wise anomaly detection without prior knowledge of the phenotype and the need for atlas-based segmentation. Anomaly identification is centered at group-wise feature extraction and decomposition using robust principal component analysis (R-PCA), and is sensitive to defects involving both volumetric and non-volumetric variations.

9784-63, Session PS1
Mutual information criterion for feature selection with application to classification of breast microcalcifications

Idit Diamant, Tel Aviv Univ. (Israel); Jacob Goldberger, Bar-
9784-64, Session PS1

Single trial classification for the categories of perceived emotional facial expressions: an event-related fMRI study

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Recently, several studies have successfully applied multivariate pattern analysis methods to predict the categories of emotions. However, these studies are mainly focused on self-experienced emotions, such as the emotional states elicited by music or movie. In this study, we aimed to determine the discriminability of perceived emotional facial expressions. In a rapid event-related fMRI design, subjects were instructed to classify four categories of facial expressions (happy, disgust, angry, and neutral) by pressing different buttons, and each facial expression stimulus lasted for 2s. All participants performed 5 fMRI runs. One multivariate pattern analysis method, support vector machine was trained to predict the categories of facial expressions. For feature selection, ninety masks of anatomical automatic labeling (AAL) defined anatomical areas were firstly generated and each were treated as the input of the classifier; then, the most stable AAL areas were selected according to prediction accuracies, and comprised the final feature set. The leave-one-run-out cross validation result showed that: for the 6 pair-wise classification conditions, the accuracy, sensitivity and specificity were all above chance prediction, among which, happy vs. neutral and angry vs. disgust achieved the lowest results. The results suggested specific and identifiable neural signatures of perceived emotional facial expressions may exist.

9784-65, Session PS1

Template-based automatic extraction of the joint space of foot bones from CT scan

Eunbi Park, Taeho Kim, Jinah Park, KAIST (Korea, Republic of)

Clean bone segmentation is critical in studying the joint anatomy for measuring the spacing between the bones. However, separation of the coupled bones in CT images is sometimes difficult due to ambiguous gray values coming from the noise and the heterogeneity of bone materials as well as narrowing of the joint space. For the applications required to have fine reconstruction of the individual local boundaries, therefore, manual operation is a common practice where the segmentation remains to be a bottleneck.

In this paper, we present an automatic method for extracting the joint space by applying graph-cut on Markov random field (MRF) model to the ROI identified by a template of 3D bone structures. The template has the articular surface encoded which directs for identifying the joint region of the high-intensity bone boundaries together with the fuzzy joint area of interest. The localized information including the shape from the template model within the ROI effectively separates the bones nearby. By specifying the ROI composing of two types of tissue, the object extraction problem was reduced to binary segmentation and solved via graph-cut to minimize an energy function. Based on the shape of a joint space marked by the template, the hard constraint was set by the initial seeds which were automatically generated from thresholding and morphological operations. The performance and the robustness of the proposed method are evaluated on 12 volumes of ankle CT data, where each volume includes a set of 4 tarsal bones (calcaneus, talus, navicular and cuboid).

9784-66, Session PS1

Tissue classification of large-scale multi-site MR data using fuzzy k-nearest neighbor method

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This paper describes enhancements to automate classification of brain tissues for multi-site degenerative magnetic resonance imaging (MRI) data analysis. Processing of large collections of MR images is a key research technique to advance our understanding of the human brain. Previous studies have developed a robust multi-modal tool for automated tissue classification of large-scale data based on expectation maximization (EM) method initialized by group-wise prior probability distributions. This work aims to augment the EM-based classification using a non-parametric fuzzy k-Nearest Neighbor (k-NN) classifier that can model the unique anatomical states of each subject in the study of degenerative diseases. The presented method is applicable to multi-center heterogeneous data analysis and is validated on a set of 12 simulated multi-modal MR datasets having six different levels of noise and two degrees of bias-field provided with known ground truth. Dice index and average Hausdorff distance are used to compare the accuracy and robustness of the proposed method to a state-of-the-art classification method implemented based on EM algorithm. Both evaluation measurements show that presented enhancements produce superior results as compared to the EM only classification.

9784-67, Session PS1

Texture analysis for survival prediction of pancreatic ductal adenocarcinoma patients with neoadjuvant chemotherapy

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Pancreatic ductal adenocarcinoma (PDAC) is the fourth leading cause of cancer related death in the United States. The five-year survival rate for all stages is around 6%, and around 2% when presenting with distant disease. Only 10-20% of all patients present with resectable disease, but recurrence rates are high with only 5 to 15% remaining free of disease at 5 years. At this time, we are unable to distinguish between resectable PDAC patients with occult metastatic disease from those with potentially curable disease. Early classification of these tumor types may eventually lead to changes in initial management including the use of neoadjuvant chemotherapy or radiation, or in the choice of postoperative adjuvant treatments. Texture analysis is an emerging methodology in oncoligic imaging for quantitatively assessing tumor heterogeneity that could potentially aid in the stratification of these patients. The present study derives several texture-based features from CT images of PDAC patients, acquired prior to neoadjuvant chemotherapy,
and analyzes their performance, individually as well as in combination, as biomarkers of prognosis. A fuzzy minimum redundancy maximum relevance method with leave-one-image-out technique is included to select discriminating features from the set of extracted features. With a Naïve Bayes classifier, the proposed method predicts the 5-year overall survival of PDAC patients prior to neoadjuvant therapy and achieves the best results in terms of the area under the receiver operating characteristic curve of 0.858 and accuracy of 83.0% for four-fold cross-validation technique.

9784-68, Session PS1

Learning-based landmarks detection for osteoporosis analysis

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Osteoporosis is the common cause for a broken bone among senior citizens. Early diagnosis of osteoporosis requires routine examination which may be costly for patients. A potential low cost diagnosis is to identify a senior citizen at high risk of osteoporosis by pre-screening during routine dental examination. Therefore, osteoporosis analysis using dental radiographs serves as a key step in routine dental examination. The aim of this study is to localize landmarks in dental radiographs which are helpful to assess the evidence of osteoporosis. We collect eight landmarks which are critical in osteoporosis analysis. To address the challenges such as large variations of appearances in subjects, in this paper, we formulate the task into a multi-class classification problem. A hybrid feature tool is used to represent these landmarks. In the experiments, we also evaluate the performances of individual feature component and the hybrid fused feature. Our proposed method achieves average detection error of 2.9mm.

9784-69, Session PS1

2D image classification for 3D anatomy localization: employing deep convolutional neural networks

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Localization of anatomical regions of interest (ROIs) is a preprocessing step in many medical image analysis tasks. While trivial for humans, it is complex for automatic methods. Classic machine learning approaches require the challenge of hand crafting features to describe differences between ROIs and background. Deep convolutional neural networks (CNNs) alleviate this by automatically finding hierarchical feature representations from raw images. We employ this trait to detect anatomical ROIs in 2D image slices in order to localize them in 3D.

In 100 low-dose non-contrast enhanced non-ECG synchronized screening chest CT scans, a reference standard was defined by manually delineating rectangular bounding boxes around three anatomical ROIs (heart, aortic arch, and descending aorta). The scans were evenly divided into training and test sets. Every anatomical ROI was automatically identified using a combination of three CNNs, each analyzing one orthogonal image plane. While single CNNs predicted presence or absence of a specific ROI in the given plane, the combination of their results provided a 3D bounding box around it.

Classification performance of all CNNs, expressed in area under the receiver operating characteristic curve, was >>0.988. Additionally, the performance of localization was evaluated. Median Dice scores for automatically determined bounding boxes around the heart, aortic arch, and descending aorta were 0.89, 0.70, and 0.85 respectively. The results demonstrate that accurate automatic 3D localization of anatomical structures by CNN-based 2D image classification is feasible.

9784-70, Session PS1

Neural network-based visual body weight estimation for drug dosage finding

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Body weight adapted drug dosages are important for emergency treatments.

This paper describes an improved body weight estimation approach for emergency patients in a trauma room, based on images from a RGBD sensor and a thermal camera. The improvements are archived by several extensions: The sensor fusion of RGBD and thermal camera eases filtering and segmentation of the patient’s body from the background. Robustness and accuracy is gained by an artificial neural network (ANN), which considers features from the sensors as input to calculate the patient’s body weight, e.g. the patient’s volume, surface and shape parameters. The ANN is trained offline with 30 percent of the patients data. Preliminary experiments with 69 real patients show an accuracy close to 90 percent for a threshold of ten percent real body weight. Results are compared to the patient’s self estimation, a physician’s guess and an anthropometric method: If the patient is knowledgeable it is the best possibility for body weight adapted drug dosages, with 97 percent accuracy. The treating physician and the anthropometric estimation achieve an accuracy of approximately 70 percent. The here presented approach gets an accuracy of nearly 90 percent and would be the best solution if a patient can not provide his own body weight or can not be weighted on a scale. These preliminary results demonstrate a sufficient approach for an upcoming clinical trial with 1,000 patients for body weight estimation.

9784-71, Session PS1

Localization of skeletal and aortic landmarks in trauma CT data based on the discriminative generalized Hough transform

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Computed tomography is the modality of choice for poly-trauma patients to assess rapidly skeletal and vascular integrity of the whole body. Often several scans with and without contrast medium or with different spatial resolution are acquired. Efficient reading of the resulting extensive set of image data is vital, since it is often time critical to initiate the necessary therapeutic actions. A set of automatically found landmarks can facilitate navigation in the data and enables anatomy oriented viewing.

Following this intention, we selected a comprehensive set of 17 skeletal and 5 aortic landmarks. Landmark localization models for the Discriminative Generalized Hough Transform (DGHT) were automatically created based on a set of about 20 training images with ground truth landmark positions. A hierarchical setup with 4 resolution levels was used. Localization results were evaluated on a separate test set, consisting of 50 to 128 images (depending on the landmark) with available ground truth landmark locations. The image data covers a large amount of variability cause by differences of field-of-view, resolution, contrast agent, patient gender and pathologies. The median localization error for the set of aortic landmarks was 14.4 mm and for the set of skeleton landmarks 5.5 mm. Median localization errors for individual landmarks ranged from 3.0 mm to 31.0
We explore the prediction power of the image features versus the clinical parameters and converted into risk likelihood scores using Bayes modeling. Handling this type of data. Using multi-atlas segmentation, 154 image-based risk outcomes in available TBI datasets. Herein, we propose a Bayesian framework for early risk prediction in traumatic brain injury (TBI). Computed tomography (CT) acquired at admission showed some latent prognostic value in prior studies; however, no robust clinical risk predictions have been achieved based on the imaging data in large-scale TBI analysis. The major challenge lies in the lack of predictive outcomes than the clinical data (including Marshall CT classification) for discharge disposition with an area under the curve of 0.81 vs. 0.67, but less predictive than clinical data for discharge Glasgow Coma Scale (GCS) score with an area under the curve of 0.65 vs. 0.85. However, in both cases, combining imaging and clinical data increased the combined area under the curve with 0.86 for discharge disposition and 0.88 for discharge GCS score. In conclusion, CT data have meaningful prognostic value for TBI patients beyond what is captured in clinical measures and the Marshall CT classification.

9784-74, Session PS1

HT-BONE: A graphical user interface for the identification of bone profiles in CT images via extended Hough transform

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It has been recently proved that the computational analysis of X-ray Computed Tomography (CT) images allows assessing the alteration of compact bone asset due to hematological diseases. HT-BONE implements a new method, based on an extension of the Hough transform (HT) to a wide class of algebraic curves, able to accurately measure global and regional geometric properties of trabecular and compact bone districts. In the case of CT/PET analysis, the segmentation of the CT images provides masks that can be applied to Positron Emission Tomography (PET) data for extracting the metabolic activity in the region surrounded by compact bone tissue. HT-BONE offers an intuitive, user-friendly, Matlab-based Graphical User Interface (GUI) for all input/output procedures and the automatic managing of the segmentation process also from non-expert users: the CT/PET data can be loaded and browsed easily and the only pre-processing required is the drawing of Regions Of Interest (ROIs) around the bone districts under consideration. For each bone district specific families of curves, whose reliability has been tested in previous works, is automatically selected for the recognition task via HT. As output, the software returns masks of the segmented compact bone regions, images of the Standard Uptake Values (SUV) in the masked region of PET slices, together with the values of the parameters in the curve equations utilized in the HT procedure. This information can be used for all those pathologies and clinical conditions for which the alteration of the compact bone asset or bone marrow distribution play a crucial role.

9784-73, Session PS1

A bayesian framework for early risk prediction in traumatic brain injury

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Early detection of risk is critical in determining the course of treatment in traumatic brain injury (TBI). Computed tomography (CT) acquired at admission showed some latent prognostic value in prior studies; however, no robust clinical risk predictions have been achieved based on the imaging data in large-scale TBI analysis. The major challenge lies in the lack of consistent and complete medical records for patients, and an inherent bias associated with the limited number of patients samples with high-risk outcomes in available TBI datasets. Herein, we propose a Bayesian framework with mutual information-based forward feature selection to handle this type of data. Using multi-atlas segmentation, 154 image-based features (capturing intensity, volume and texture) were computed over 22 ROIs in 1791 CT scans. These features were combined with 14 clinical parameters and converted into risk likelihood scores using Bayes modeling. We explore the prediction power of the image features versus the clinical measures for various risk outcomes. The imaging data alone were more predictive of outcomes than the clinical data (including Marshall CT classification) for discharge disposition with an area under the curve of 0.81 vs. 0.67, but less predictive than clinical data for discharge Glasgow Coma Scale (GCS) score with an area under the curve of 0.65 vs. 0.85. However, in both cases, combining imaging and clinical data increased the combined area under the curve with 0.86 for discharge disposition and 0.88 for discharge GCS score. In conclusion, CT data have meaningful prognostic value for TBI patients beyond what is captured in clinical measures and the Marshall CT classification.

9784-75, Session PS1

GBM heterogeneity characterization by radiomic analysis of phenotype anatomical planes

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Glioblastoma multiforme (GBM) is the most common malignant primary tumor of the central nervous system, and can spread into other parts of the brain quickly. GBM has three phenotypes namely, necrosis (N), contrast enhancement (CE), and edema/invasion (E), which are characterized by a different texture heterogeneity in magnetic resonance imaging (MRI). To assess this heterogeneity, first order statistics provide a limited characterization because they do not integrate spatial information. Consequently, such features are rarely used for sub-classifying GBM. In this study, we propose a novel model to characterize GBM phenotype using gray level co-occurrence matrices (GLCM) in three anatomical planes.
Feature extraction based on the 2D GLCM was applied on the data of 42 GBM patients, obtained from the cancer genome atlas (TCGA). Intensity-based automatic image registration was applied to align fixed T1-weighted (T1?WI) post-contrast images and its corresponding fluid attenuated inversion recovery (FLAIR) images. We then segmented GBM phenotypes using a 3D Slicer tool. Texture features were computed for each GBM phenotype by applying 12 quantifier functions to each anatomical plane, and then averaging the values obtained in the three planes. Various classifier models were used to evaluate the effectiveness of the features for discriminating between GBM phenotypes.

Results showed a phenotype classification accuracy of over 89%, a sensitivity of 97% and a specificity of 96%, using a linear discriminant analysis (LDA) classifier. This model has the potential to provide important characteristics of tumors, which can be used for the sub-classification of GBM phenotypes.

9784-76, Session PS1

A framework for classification and segmentation of branch retinal artery occlusion in SD-OCT

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Branch retinal artery occlusion (BRAO) is an ocular emergency which could lead to blindness. Quantitative analysis of BRAO region in the retina is very needed to assessment of the severity of retinal ischemia. In this paper, a fully automatic framework was proposed to classify and segment BRAO based on 3D spectral-domain optical coherence tomography (SD-OCT) images. To the best of our knowledge, this is the first automatic 3D BRAO segmentation framework. First, a support vector machine (SVM) based classifier is designed to differentiate BRAO into acute phase and chronic phase, and the two types are segmented separately. To segment BRAO in chronic phase, a threshold-based method is proposed based on the thickness of inner retina. While for segmenting BRAO in acute phase, a two-step segmentation is performed, which includes the bayesian posterior probability based initialization and the graph-search-graph-cut based segmentation. The proposed method was tested on SD-OCT images of 23 patients (12 of acute and 11 of chronic phase) using leave-one-out strategy. The experimental results validate the feasibility of the proposed method.

9784-77, Session PS1

Segmentation techniques evaluation based on a single compact breast mass classification scheme

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In this work some segmentation techniques are evaluated by using a simple centroid-based classification system regarding breast mass delineation in digital mammography images. The aim is to determine the best one for future CADx developments. Six techniques were tested: Otsu, SOM, EiCAMM, Fuzzy C-Means, K-Means and Level-Set. All of them were applied to segment 317 mammography images from DDSM database. A single compact set of attributes was extracted and two centroids were defined, one for malignant and another for benign cases. The final classification was based on proximity with a given centroid and the best results were presented by the Level-Set technique with a 68.1% of Accuracy, which indicates this method as the most promising for breast masses segmentation aiming a more precise interpretation in schemes CADx.

9784-78, Session PS1

Capturing population based patient-specific characters for prostate segmentation on 3D CT images

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Prostate segmentation on CT images is a challenging task. In this paper, we explore the population based patient-specific characteristics for the segmentation of the prostate on CT images. Because pure population learning does not consider the inter-patient variations and because pure patient-specific learning may not perform well because of the limited patient-specific information, we are combining the population and patient-specific information to improve the segmentation performance. Specifically, we train a population model based on the population data and train a patient-specific model based on the manual segmentation on three slice of the new patient. We compute the similarity between the two models to explore the influence of applicable population knowledge on the target patient. By combining the patient-specific knowledge with the influence, we can capture the population based patient-specific characteristics to calculate the probability of a pixel belonging to the prostate. Finally, we smooth the prostate surface according to the prostate-density value of the pixels in the distance transform image. We conducted the leave-one-out validation experiments on a set of 15 patient volumes. Manual segmentation results from a radiologist serve as the gold standard for the evaluation. Experimental results show that our method achieved an average DSC of 85.15% as compared to the manual segmentation. The hybrid method outperformed the pure population model based method or the pure patient-specific learning approach. The CT segmentation method can have various applications in prostate cancer diagnosis and therapy.

9784-79, Session PS1

Patch Forest: when random forest meets patch-based segmentation

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The development of an accurate, robust and fast segmentation algorithm has long been a research focus in medical computer vision. State-of-the-art methods often involve non-linearly registering a target image with a set of training atlases to enable label propagation over the target space to perform segmentation (a.k.a. multi-atlas label propagation), or employing a patch-based segmentation which relaxes voxel-to-voxel correspondence to a series of patch similarity comparisons in a semantic context. Despite a high accuracy being reported in many scenarios, computational efficiency has been a major obstacle. Inspired by recent work on random forests, we propose a patch forest framework, which can significantly improve the efficiency of patch-based segmentation at runtime by equipping it with a fast patch search engine, while retaining an equal level of accuracy. Furthermore, an efficient forest training scheme has been developed using a dynamic grid mechanism. An empirical validation study has been carried out on the segmentation of hippocampus in the human brain.
9784-80, Session PS1

**Automated detection of retinal landmarks for the identification of clinically relevant regions in fundus photography**

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Automatic, quick and reliable identification of retinal landmarks from fundus photography is key for measurements used in research, diagnosis, screening and treating of common diseases affecting the eyes. This study presents a fast method for the detection of the centre of mass of the vascular arcades, optic nerve head (ONH) and fovea, used in the definition of five clinically relevant areas in use for screening programmes for diabetic retinopathy (DR).

Thirty-eight fundus photographs showing 7203 DR lesions were analysed to find the landmarks manually by two retina-experts and automatically by the proposed method. The automatic identification of the ONH and fovea were performed using template matching based on normalised cross correlation. The centre of mass of the arcades was obtained by fitting an ellipse on sample coordinates of the main vessels. The coordinates were obtained by processing the image with hessian filtering followed by shape analyses and finally sampling the results. The regions obtained manually and automatically were used to count the retinal lesions falling within, and to evaluate the method.

92.7% of the lesions were falling within the same regions based on the landmarks selected by the two experts. 91.7% and 89.0% were counted in the same areas identified by the method and the first and second expert respectively.

The inter-repeatability of the proposed method and the experts is comparable, while the 100% intra-repeatability makes the algorithm a valuable tool in tasks like analyses in real-time, of large datasets and of intra-patient variability.

9784-81, Session PS1

**Automatic basal slice detection for cardiac analysis**

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Identification of the basal slice in cardiac imaging is a key step to measuring the ejection fraction (EF) of the left ventricle (LV). Despite research on cardiac segmentation, basal slice identification is routinely performed manually. Manual identification, however, has been shown to have high inter-observer variability, with a variation of the EF by up to 8%. Therefore, an automatic way of identifying the basal slice is still required.

Prior published methods operate by automatically tracking the mitral valve points from the long-axis view of the LV. These approaches assumed that the basal slice is the first short-axis slice below the mitral valve. However, guidelines published in 2013 by the society for cardiovascular magnetic resonance indicate that the basal slice is the uppermost short-axis slice with more than 50% myocardium surrounding the blood cavity. Consequently, these existing methods are at times identifying the incorrect short-axis slice. Correct identification of the basal slice under these guidelines is challenging due to the poor image quality and blood movement during image acquisition. This paper proposes an automatic tool that focuses on the two-chamber slice to find the basal slice. To this end, an active shape model is trained to automatically segment the two-chamber view for 51 samples using the leave-one-out strategy. The basal slice was detected using temporal binary profiles created for each short-axis slice from the segmented two-chamber slice. From the 51 successfully tested samples, 92% and 84% of detection results were accurate at the end-systolic and the end-diastolic phases of the cardiac cycle, respectively.

9784-82, Session PS2

**Guidewire path tracking and segmentation in 2D fluoroscopic time series using device paths from previous frames**

Martin G. Wagner, Charles M. Strother, Charles A. Mistretta, Univ. of Wisconsin-Madison (United States)

The 3D reconstruction of interventional devices such as guidewires from monoplane and biplane fluoroscopic images requires their segmentation in the 2D projection images. In many cases segments of the guidewire overlap which makes resolving the correct device path a complex task. The purpose of this work is to present a novel guidewire tracking and segmentation algorithm, which uses the device curvature as well the similarity to device paths, segmented from previous frames, to determine the current shape of the device. The image is binarized using a ridgeless parameter as well as gray level thresholding. A topology preserving thinning algorithm is then used to reduce the segmented area to centerline segments. In order to find the most likely device path a dynamic programming approach is used that minimizes a cost function based on spatial and directional difference between adjacent segments as well as the device path of the previous frame. The quantitative evaluation was performed using 7 data sets acquired from a canine study. Device shapes with different complexities are compared to semi-automatic segmentations. An average segmentation accuracy of 0.50 ± 0.41 mm was achieved where each point along the device was compared to the point on the reference device centerline with the same distance to the device tip. In all cases the device path could be resolved correctly. This would allow a more accurate and reliable reconstruction of the 3D structure of the device.

9784-83, Session PS2

**Diseased pancreas segmentation**

Konstantin Dmitriev, Ievgenia Gutenko, Saad Nadeem, Arie Kaufman, Stony Brook Univ. (United States)

Accurate segmentation of abdominal organs from medical images is an essential part of surgical planning and computer-aided disease diagnosis. Many existing algorithms are specialized to the segmentation of healthy organs. Diseased pancreas segmentation is especially challenging due to its low contrast boundaries, variability in shape, location and the stage of the pancreatic cancer. We present a semi-automatic segmentation algorithm for pancreata with cysts. In contrast to the automatic segmentation approaches for healthy pancreas segmentation which are amenable to atlas/statistical shape approaches, a pancreas with cysts can have even higher variability with respect to the shape of the pancreas due to the size and shape of the cyst(s) and hence, can show fine results with only semi-automatic steerable approaches. We use a novel combination of random walker and region growing approaches to delineate the boundaries of the pancreas and cysts with respective best dice coefficients of 85.10% and 86.65%, and respective best volumetric overlap errors of 26.04% and 23.54%. Results show that the proposed algorithm for diseased pancreas segmentation is accurate and stable.

9784-84, Session PS2

**Fast global interactive volume segmentation with regional supervoxel descriptors**

Imanol Luengo, The Univ. of Nottingham (United
We propose a novel approach towards fast multi-class volume segmentation that exploits supervoxels in order to reduce complexity, time and memory requirements. Current methods for biomedical image segmentation typically require either complex mathematical models with slow convergence, or expensive-to-calculate image features, which makes them non-feasible for large volumes with many objects (tens to hundreds) of different classes, as is typical in modern medical and biological datasets.

Recently, graphical models such as Markov Random Fields (MRF) or Conditional Random Fields (CRF) are having a huge impact in different computer vision areas (i.e. image parsing) as they provide global regularization for multiclass problems over a energy minimization framework. These models have yet to find impact in biomedical imaging due to complexities in training and slow inference in 3D images due to the very large number of voxels.

Here, we define an interactive segmentation approach over a supervoxel space by defining novel, robust and fast regional descriptors for supervoxels. These then allow us to train an Extremely Random Forest regressor, learned from user-drawn scribbles on a 2D slice, which is then used to estimate class-probabilities of supervoxels. These likelihoods are finally refined by a MRF model for 3D segmentation. Results demonstrate the effectiveness on a cryo-soft X-ray tomography dataset by segmenting cell areas with just a couple of user scribbles as the only input for our algorithm. Further results demonstrate the effectiveness of our method to fully extract different organelles from the volume with another few seconds of user interaction.

We propose a novel approach towards fast multi-class volume segmentation based on optimal feature learning framework.

Xiaofeng Yang, Peter J. Rossi, Ashesh B. Jani, Hui Mao, Tomi Ogunleye, Walter J. Curran, Tian Liu, Emory Univ. (United States)

We propose a 3D segmentation method for transrectal ultrasound (TRUS) images, which is based on patch-based feature learning framework. Patient-specific anatomical features are extracted from aligned training images and adopted as signatures for each voxel. The most robust and informative features are identified by the feature selection process to train the kernel support vector machine (K SVM). The well-trained SVM was used to localize the prostate of the new patient. Our segmentation technique was validated with a clinical study of 10 patients. The accuracy of our approach was assessed using the manual segmentations (gold standard). The mean volume Dice Overlap Coefficient was 89.7%. We have developed a new prostate segmentation approach based on the optimal feature learning framework, demonstrated its clinical feasibility, and validated its accuracy with manual segmentations.

Accurate airway segmentation based on intensity structure analysis and graph-cut

Qier Meng, Takayuki Kitsaka, Yukitaka Nimura, Masahiro Oda, Kensaku Mori, Nagoya Univ. (Japan)

This paper presents a novel airway segmentation method based on intensity structure analysis and graph-cut. Airway segmentation is an important step in analyzing chest CT volumes for computerized lung cancer detection, emphysema diagnosis, asthma diagnosis, and pre- and intra-operative bronchoscope navigation. However, obtaining a complete 3-D airway tree structure from a CT volume is quite challenging. Several researchers have proposed automated algorithms basically based on region growing and machine learning techniques. However these methods failed to detect the peripheral bronchi branches. They caused a large amount of leakage. This paper presents a novel approach that permits more accurate extraction of complex bronchial airway region.

Ours method are composed of three steps. First, the Hessian analysis is utilized for enhancing the line-like structure in CT volumes, then a multiscale cavity-enhancement filter is employed to detect the cavity-like structure from the previous enhanced result. In the second step, we utilize the support vector machine to construct a classifier for removing the FP regions generated. Finally, the graph-cut algorithm is utilized to connect all of the candidate voxels to form an integrated airway tree. We applied this method to eight cases of 3D chest CT volumes. The results showed that the branch detection rate of this method can reach about 70% without leaking into the lung parenchyma areas.

Random-forest-classification of large volume structures for visuo-haptic rendering in CT images

André Mastmeyer, Dirk Fortmeier, Heinz Handsel, Univ. zu Lübeck (Germany)

For voxel-based visuo-haptic rendering in CT scans of the liver area, the fully
automatic segmentation of large volume structure such as skin, soft-tissue, lungs and intestine (risk structures) is important. Using a machine learning-based approach, several existing segmentations from 10 segmented gold-standard patients are learned by random decision forests individually and collectively. The core of this paper is feature selection and the application of the learned classifiers to a new patient data set. In a leave-one-out fashion, the obtained full volume segmentations are compared to the gold-standard segmentations of the unseen patient. The proposed classifiers use a multi-dimensional feature space to estimate the hidden truth, instead of relying on state of the art threshold and connectivity based segmentation. The result of our efficient whole-body section classification is a multi-label map with the considered tissues. For actual visuo-haptic simulation, other smaller volume structures would have to be segmented additionally. We also take a look at including some of these structures (e.g. liver) into the classifier to distinguish tissues valuable to be included in our classifier. For a small experimental leave-one-out set-up consisting of 10 patients, the proposed method performs more efficiently compared to the standard semi-automatic segmentation methods. In a first leave-one-out experiment we obtain mean DICE ratios of 0.76 0.98, 0.93 and 0.75 for skin, soft-tissue, risk structures and hard bone.

9784-89, Session PS2

Active appearance model and deep learning for more accurate prostate segmentation on MRI

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Prostate segmentation on 3D MR images is a challenging task due to image artifacts, large inter-patient prostate shape and texture variability, and lack of a clear prostate boundary specifically at apex and base levels. We propose a supervised machine learning model that combines atlas based Active Appearance Model (AAM) with Deep Learning model to segment the prostate on MR images. The performance of the segmentation method is evaluated on 20 unseen MR images datasets. The proposed method combining AAM and Deep Learning achieves a mean Dice Similarity Coefficient (DSC) of 0.925 for whole 3D MR images of the prostate using axial cross-sections. The proposed model utilizes the adaptive atlas based AAM model and deep learning to achieve significant segmentation accuracy.

9784-90, Session PS2

Automated segmentation of MS lesions in FLAIR, DIR and T2-w MR images via an information theoretic approach

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Magnetic Resonance Imaging (MRI) is a vital tool in the diagnosis and characterization of multiple sclerosis (MS). MS lesions can be imaged with relatively high contrast using either Fluid Attenuated Inversion Recovery (FLAIR) or Double Inversion Recovery (DIR). Automated segmentation and accurate tracking of MS lesions from MRI remains a challenging problem. In this work, we present an information theoretic approach to cluster the voxels in colorized MR data (FLAIR, DIR, T2-weighted) to automatically segment MS lesions of various sizes and noise levels. Clustering using the Improved Jump Method (IJM), assisted by edge suppression, provides the segmentation of white matter (WM), gray matter (GM), cerebrospinal fluid CSF and potential MS lesions that are selected as a subset of slices determined to be the best MS lesion candidates via Otsu’s method. From this preliminary clustering, the modal data values for the tissues can be determined. A Euclidean distance is then used to estimate the fuzzy memberships of each brain voxel for all tissue types and their 50/50 partial volumes. From these, binary discrete and fuzzy MS lesion masks are constructed. Validation is provided by using three synthetic MS lesions brains (mild, moderate and severe) with labeled ground truths. The MS lesions of mild, moderate and severe designations were detected with a sensitivity of 83.2%, and 88.5%, and 94.5%, with the corresponding Dice similarity coefficients (DSC) of 0.7098, 0.8739 and 0.8266 respectively. The effect of MRI noise is also examined by simulated noise and application of a bilateral filter in preprocessing.

9784-91, Session PS2

Lung vessel segmentation in CT images using graph cuts

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Accurate lung vessel segmentation is an important operation for lung CT analysis. Hessian-based filters are popular for pulmonary vessel enhancement. However, due to their low response at vessel bifurcations and vessel boundaries, extracting lung vessels by thresholding the vesselness is inaccurate. Some literature turns to graph cuts for more accurate segmentation, as it incorporates neighbourhood information. In this work, we propose a new graph cuts cost function combining appearance and shape, where CT intensity represents appearance and vesselness from a Hessian-based filter represents shape. In order to make the graph representation computationally tractable, voxels that are considered clearly background are removed using a low threshold on the vesselness map. The graph structure is then established based on the neighbourhood relation of the remaining voxels. Vessels are segmented by minimizing the energy cost function with the graph cuts optimization framework. We optimized the parameters and evaluated the proposed method with two manually labeled sub-volumes. For independent evaluation, we used the 20 CT scans of the VESSEL12 challenge. The evaluation results of the sub-volumes dataset show that the proposed method produced a more accurate vessels segmentation. For the VESSEL12 dataset, our method obtained a competitive performance with an area under the ROC of 0.975, especially among the binary submissions.

9784-92, Session PS2

Enhancing a diffusion algorithm for 4D image segmentation using local information

Philipp Lössel, Vincent Heuveline, Ruprecht-Karls-Univ. Heidelberg (Germany)

Inspired by the diffusion of a particle, we present a novel approach for performing a semiautomatic segmentation of tomographic images in 3D, 4D or higher dimensions to meet the requirements of high-throughput measurements in a synchrotron X-ray microtomograph. Given a small number of 2D-slices with at least two manually labeled segments, one can either analytically determine the probability that an intelligently weighted random walk starting at one labeled pixel will be at a certain time at a specific position in the dataset or determine the probability approximately by performing several random walks. While the weights of a random walk take into account local information at the starting point, the random walk itself can be in any dimension. Starting a great number of random walks in each labeled pixel, a voxel in the dataset will be hit by several random walks over time. Hence, the image can be segmented by assigning each voxel to the label where the random walks most likely started from. Due to the high scalability of random walks, this approach is suitable for high-throughput measurements.

Additionally, we describe an interactively adjusted active contours slice by slice method considering local information, where we start with one manually labeled slice and move forward in any direction. This approach is superior with respect to accuracy towards the diffusion algorithm but
inferior in the amount of tedious manual processing steps. The methods were applied on 3D and 4D datasets and evaluated by means of manually labeled images obtained in a realistic scenario with biologists.

9784-93, Session PS2

Precise renal artery segmentation for estimation of renal vascular dominant regions

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This paper presents a renal artery segmentation method combining graph-cut and template-based tracking methods and its application to estimation of renal vascular dominant region. For the purpose of giving a computer assisted diagnose for kidney surgery planning, it is important to obtain the correct topological structures of renal artery for estimation of renal vascular dominant areas. Renal artery has a low contrast and its precise extraction is a difficult task. Previous method utilizing vesselness measure based on Hessian analysis, still cannot extract the tiny blood vessels especially in low-contrast area. Although model-based methods including superellipsoid model or cylindrical intensity model are low-contrast sensitive to the tiny blood, problems including over-segmentation and poor bifurcations detection still remain. In this paper, we propose a novel blood vessel segmentation method combining graph-cut and template modeling tracking method. First, graph-cut algorithm is utilized to obtain the rough segmentation. Then template model tracking method is used to increase the performance of tiny blood vessel extraction. Rough segmentation using graph-cut can solve the bifurcations detection problem effectively. Precise segmentation using template model tracking can focus on the tiny blood vessels. By combining these two approaches, our proposed method can segment 70% of the renal artery of 1mm in diameter or larger. In addition, we demonstrate such precise segmentation can contribute to divide renal regions into a set of blood vessel dominant regions.

9784-94, Session PS2

An SPM12 extension for multiple sclerosis lesion segmentation

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Purpose: Magnetic resonance imaging is nowadays the hallmark to diagnose multiple sclerosis (MS), characterized by white matter lesions. Several approaches have been recently presented to tackle the lesion segmentation problem, but none of them have been accepted as a standard tool in the daily clinical practice. In this work we present yet another tool able to automatically segment white matter lesions.

Methods: This work is an extension of Roura et al. [1], where external and platform dependent pre-processing libraries (brain extraction, noise reduction and intensity normalization) were required to achieve an optimal performance. Here we have updated and included all these required pre-processing steps into a single framework (SPM software). Therefore, there is no need of external tools to achieve the desired segmentation results. Besides, we have changed the working space from T1w to FLAIR, reducing interpolation errors produced in the registration process from FLAIR to T1w space. Finally a post-processing constraint based on shape and location has been added to reduce false positive detections.

Results: The evaluation of the tool has been done on 24 MS patients. Qualitative and quantitative results are shown with both approaches in terms of lesion detection and segmentation.

Conclusion: We have simplified both installation and implementation of the approach, providing a multiplatform tool integrated into the SPM software, which relies only on using T1w and FLAIR images. We have reduced with this new version the computation time of the previous approach while maintaining the performance.

9784-95, Session PS2

A neural network approach to lung nodule segmentation

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Computed tomography (CT) imaging is a sensitive and specific lung cancer screening tool for the high-risk population and shown to be promising for detection of lung cancer. This study proposes an automatic methodology for detecting and segmenting lung nodules from CT images. The proposed methods begin with thorax segmentation, lung extraction and reconstruction of the original shape of the parenchyma using morphology operations. Next, a multi-scale hessian-based vesselness filter is applied to extract lung vasculature in lung. The lung vasculature mask is subtracted from the lung region segmentation mask to extract 3D regions representing candidate pulmonary nodules. Finally, the remaining structures are classified as nodules through shape and intensity features which are together used to train an artificial neural network. Up to 75% sensitivity and 98% specificity was achieved for detection of lung nodules in our testing dataset, with an overall accuracy of 97.62±0.72% using 11 selected features as input to the neural network classifier, based on 4-fold cross-validation studies. Overall area under curve (AUC) from receiver operator characteristics for identifying nodules was 0.9476.

9784-96, Session PS2

Loosely coupled level sets for retinal layers and drusen segmentation in subjects with dry age-related macular degeneration

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Optical coherence tomography (OCT) is used to produce high-resolution three-dimensional images of the retina, which permit the investigation of retinal irregularities. In dry age-related macular degeneration (AMD), a chronic eye disease that causes central vision loss, disruptions such as drusen and changes in retinal layer thicknesses occur which could be used as biomarkers for disease monitoring and diagnosis. Due to the topology disrupting pathology, existing segmentation methods often fail. Here, we present a solution for the segmentation of retinal layers in dry AMD subjects by extending our previously presented loosely coupled level set framework which operates on attenuation coefficients. In eyes affected by AMD, Bruch’s membrane becomes visible only below the drusen and our segmentation framework is adapted to handle such a partially discernible interface. Furthermore, the initialization stage, which tentatively segments
Improving cerebellar segmentation with statistical fusion

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The cerebellum is a somatotopically organized central component of the central nervous system well known to be involved with motor coordination and increasingly recognized roles in cognition and planning. Recent work in multi-atlas labeling has created methods that offer the potential for fully automated 3-D parcellation of the cerebellar lobules and vermis (which are organizationally equivalent to cortical gray matter areas). This work explores the trade-offs of using different statistical fusion techniques and post hoc optimizations in two datasets with distinct imaging protocols. We offer a novel fusion technique by extending the ideas of the Selective and Iterative Method for Performance Level Estimation (SIMPLE) to a patch-based performance model. We demonstrate the effectiveness of our algorithm, Non-Local SIMPLE, for segmentation of a mixed population of healthy subjects and patients with severe cerebellar anatomy. Under the first imaging protocol, we show that Non-Local SIMPLE outperforms previous gold-standard segmentation techniques. In the second imaging protocol, we show that Non-Local SIMPLE outperforms previous gold standard techniques but is outperformed by a non-locally weighted vote with the deeper population of atlases available. This work advances the state of the art in open source cerebellar segmentation algorithms and offers the opportunity for routinely including cerebellar segmentation in magnetic resonance imaging studies that acquire whole brain T1-weighted volumes with approximately 1 mm isotropic resolution.

Automatic brain tumor segmentation with a fast Mumford-Shah algorithm

Sabine Müller, Joachim Weickert, Univ. des Saarlandes (Germany); Norbert Graf, Universitätsklinikum des Saarlandes (Germany)

Brain tumors account only for a very small fraction of all types of cancer but belong to the most fatal forms. Therefore, research to develop methods for automatic brain tumor segmentation is of crucial importance.

We enrich this toolbox by proposing a fully-automatic but intuitive method for brain tumor segmentation that does not require any training phase. Our approach is based on a sequence of segmentations using the Mumford-Shah cartoon model with varying boundary penalization. While the Mumford-Shah cartoon model is classical and powerful, its algorithmic realization has been traditionally very slow. Recently, Strelaiovsky et al. proposed a primal-dual based 2D real-time minimization for this kind of methods. In order to make it applicable to the segmentation of brain tumors, we extend their algorithm to the medically relevant 3D setting, as we consider 3D MRI data with four acquisition modalities.

Moreover, we suggest a new confidence refinement and show that it can improve the precision of our segmentation substantially. Additionally, we propose a simple and intuitive algorithm to divide a brain tumor in sub-components, i.e. edema, necrosis and core, and demonstrate that it gives a proper sub-segmentation.

Our method is evaluated on 198 data sets with high-grade brain tumors and 25 with low-grade brain tumors from the MICCAI brain tumor segmentation challenge. We achieve Dice scores comparable to state-of-the-art methods, but within a computation time of only three minutes.

Cellular image segmentation using n-agent cooperative game theory

Ian Dimock, Justin W. L. Wan, Univ. of Waterloo (Canada)

Image segmentation is an important problem in computer vision and has significant applications in the segmentation of cellular images. Many different imaging techniques exist and produce a variety of image properties which pose difficulties to image segmentation routines. Bright-field images are particularly challenging because of the non-uniform shape of the cells, the low contrast between cells and background, and imaging artifacts such as halos and broken edges. Classical segmentation techniques often produce poor results on these challenging images. Previous attempts at bright-field imaging are often limited in scope to the images that they segment. In this paper, we introduce a new algorithm for automatically segmenting cellular images. The algorithm incorporates two game theoretic models which allow each pixel to act as an independent agent with the goal of selecting their best labelling strategy. In the non-cooperative model, the pixels choose strategies greedily based only on local information. In the cooperative model, the pixels can form coalitions, which select labelling strategies that benefit the entire group. Combining these two models produces a method which allows the pixels to balance both local and global information when selecting their label. With the addition of k-means and active contour techniques for initialization and post-processing purposes, we achieve a robust segmentation routine. The algorithm is applied to several cell image datasets including bright-field images, fluorescent images and simulated images. Experiments show that the algorithm produces good segmentation results across the variety of datasets which differ in cell density, cell shape, contrast, and noise levels.
9784-101, Session PS2

Cochlea segmentation using iterated random walks with shape prior

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Cochlear implants can restore hearing to deaf or partially deaf patients. In order to plan the intervention, a model from high resolution images is built from accurate cochlea segmentations and then, adapted to a patient-specific model. Thus, a precise segmentation is required. We propose a new framework for segmentation of micro-CIT cochlear images using random walks where a distance shape prior is combined with a region term. Then, the region term can take advantage of the high contrast between the background and foreground and the distance prior guides the segmentation to the exterior of the cochlea as well as to less contrasted regions inside the cochlea. A confidence map is used to reduce the influence of the prior in high gradient areas as the region term is reliable in these areas. Finally, a refinement is performed preserving the topology. To preserve topology, we compute the orientation of the outward normal vector of the contour points and vectors with opposite directions in a patch are considered a possible topology violation. In addition, to avoid leakage, a voting map is created using the non-rigid registration of the training data into the target image and adding all the resulting binary images to obtain the votes. This map will be used to avoid the contour evolving in certain regions. We tested the proposed approach with 10 data sets and compared it with the latest techniques with random walks and priors. The experiments suggest that this method gives promising results for the shape cochlea segmentation.

9784-102, Session PS2

A novel 3D graph cut based co-segmentation of lung tumor on PET-CT images with gaussian mixture models

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Positron Emission Tomography (PET) and Computed Tomography (CT) have been widely used in clinical practice for radiation therapy. Most existing methods only use one image modality, either PET or CT, which suffer from the low spatial resolution in PET or low contrast in CT. On the basis of Ju’s works [1], in this paper, a novel 3D graph cut method is proposed, which integrates Gaussian Mixture Models (GMMs) into the graph cut method. We also employed the random walk method as an initialization tool to provide object seeds for the improved graph cut segmentation on PET and CT images. The constructed graph consists of two sub-graphs and a special link between the sub-graphs which penalizes the difference segmentation between the two modalities. Finally, the segmentation problem is solved by the max-flow/min-cut method. The proposed method was tested on 20 patients’ PET-CT images, and the experimental results demonstrated the accuracy and efficiency of the proposed algorithm.

9784-103, Session PS2

Automatic co-segmentation of lung tumor based on random forest in PET-CT images

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In this paper, a fully automatic method is proposed to segment the lung tumor in clinical 3D PET-CT images. The proposed method effectively combines PET and CT information to make full use of the high contrast of PET images and superior spatial resolution of CT images. Our approach consists of three main parts: (1) initial segmentation, which includes thresholding based segmentation and exclusion of isolated points in PET images; (2) coarse segmentation, in which monotonic downhill function is applied to rule out structures which have similar standardized uptake values (SUV) to the lung tumour but do not satisfy a monotonic property in PET images; (3) fine segmentation, random forest method is applied to accurately segment the lung tumour by extracting effective features from PET and CT images simultaneously. We validated our algorithm on a dataset which consists of 24 3D PET-CT images from different patients with non-small cell lung cancer (NSCLC). The average TPVF, FPVF and accuracy rate (ACC) were 86.83%, 0.03% and 99.93%, respectively. The correlation analysis show our segmented lung tumor volumes has strong correlation (0.973) with the ground truth labeled by a clinical expert.

9784-104, Session PS2

A framework for probabilistic atlas-based organ segmentation

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Probabilistic atlas based on human anatomical structure has been widely used for organ segmentation. The challenge is how to register the probabilistic atlas to the patient volume. Additionally, there is the disadvantage that the conventional probabilistic atlas may cause a bias toward the specific patient study because of the single reference. Hence, we propose a template matching framework based on an iterative probabilistic atlas for organ segmentation. Firstly, we find a bounding box for the organ based on human anatomical localization. Then, the probabilistic atlas is used as a template to find the organ in this bounding box by using template matching technology. The algorithm is robust in segmenting normal and pathological spleens and livers, such as the presence of tumors and large morphological changes. Comparing our method with conventional and recently developed atlas-based methods, our results show an improvement in the segmentation accuracy for multiple organs (p<0.00001).

9784-105, Session PS2

Joint detection and segmentation of vertebral bodies in CT images by sparse representation error minimization

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Automated detection and segmentation of vertebral bodies from spinal computed tomography (CT) images is usually a prerequisite step for numerous spine-related medical applications, such as diagnosis, surgical planning and follow-up assessment of spinal pathologies. However, automated detection and segmentation are challenging tasks due to a relatively high degree of anatomical complexity, presence of unclear boundaries and articulation of vertebrae with each other. In this paper, we describe a sparse representation error minimization (SEM) framework for joint detection and segmentation of vertebral bodies in CT images. By minimizing the sparse representation error of sampled intensity values, we are able to recover the oriented bounding box (OBB) and the corresponding
binary mask for each vertebral body in the CT image. The performance of the proposed SEM framework was evaluated on five CT images of the thoracolumbar spine. The resulting Euclidean distance of $1.75 \pm 1.02$ mm, computed between the center points of detected and corresponding reference vertebral body OBBs, and Dice coefficient of $92.3 \pm 2.7\%$, computed between the resulting and corresponding reference vertebral body segmentations, indicate that the proposed framework can successfully detect and segment vertebral bodies in CT images of the thoracolumbar spine.

9784-106, Session PS3

A method for mapping tissue volume model onto target volume using volumetric self-organizing deformable model

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This paper proposes a new method for mapping volume models of human tissues onto a target volume with simple shapes. The proposed method is based on our modified self-organizing deformable model (mSDM) which finds the one-to-one mapping with no foldovers between arbitrary surface model and a target surface. By extending mSDM to apply to volume models, the proposed method, called volumetric SDM (VSDM), establishes the one-to-one correspondence between the tissue volume model and its target volume. At the same time, VSDM can preserve geometrical properties of the original model before and after mapping. This characteristic of VSDM makes it easy to find the correspondence between tissue models.

9784-107, Session PS3

Shape-based multifeature brain parcellation from Stony Brook University

Saad Nadeem, Arie Kaufman, Stony Brook Univ. (United States)

We present a 3D multifeature cortical brain parcellation (delineation of different areas on the cortex) approach, as opposed to the traditional 2D approaches, based on 3D shape measures (area, mean curvature, geodesic depth, etc.). Our approach is based on a novel insight regarding shape-based delineation of brain feature (folds, gyri or sulci) boundaries. We use angle-and-area preserving mapping to map the 3D cortical brain surface to a planar domain (such as a disc or a rectangle). Then we overlay the shape measures to parcellate the different brain features: folds, gyri and sulci. We use Mindboggle 101 manually segmented cortical brain datasets to evaluate our results. We were able to achieve the following accuracies: 72.4% for gyri, 78.5% for major sulci and 98.4% for folds.

9784-108, Session PS3

A multi-GPU optical flow algorithm for real-time cloud-based 3D deformable image registration

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Deformable image registration (DIR) algorithms for lung anatomy aim to provide an accurate estimation of non-rigid volumetric deformations between a given pair of 3D images. One of the key limitations of the DIR algorithms is its computational time. In this paper, we present a cloud-based framework for 3D deformable image registration. The framework enables clinics to instantiate, manage and perform all DIR calculations in the cloud. The cloud framework consisted of a set of 14 Nvidia GPUs distributed over a set of 4 server nodes in the cloud. For each DIR process, a single server in the cloud, is allocated as the control server. The control server estimates the amount of computation based on the data size and then distributes the optical flow registration process among the multiple GPUs based on the GPU’s current workload. A site-specific division of the optical flow registration was investigated. The process continues until the leaf server node in the multi-GPU cloud setup is reached. Each of the servers compute the DIR and writes the DVF for its allocated image section into the cloud file system. Our analysis showed that a computational speed-up of ~650X and ~150x was observed for 4D-CT lung registration and head and neck CT datasets, respectively. The data transfer of the results from the cloud to the client formed the critical limitation in the process.

9784-109, Session PS3

Estimation of aortic valve leaflets from 3D CT images using local shape dictionaries and linear coding

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Aortic valve (AV) disease is a significant cause of morbidity and mortality. The preferred treatment modality for severe AV disease is surgical resection and replacement of the native valve with either a mechanical or tissue prosthesis. In order to develop effective and long-lasting treatment methods, it is important to have an understanding of the AV mechanical environment which is dependent on the blood flow-induced loading, the aortic tissue material properties, and the precise anatomical geometry. Computational analyses, e.g. finite element (FE) based dynamic simulations, have been very effective methods for studying valve biomechanics, which requires accurate 3D geometry of aortic valve for model initialization. Currently, the shape of an aortic valve is usually constructed from 3D CT images though many hours of manual annotation, tedious and painful. Therefore, there is a pressing need for robust automatic methods for creating 3D patient-specific AV models.

In this paper, we present a method for estimating the diastolic aortic valve shape from 3D cardiac CT images, which is represented by triangle meshes of three leaflets. We propose a pipeline for aortic valve shape estimation, and propose novel algorithms for building local shape dictionaries and for building landmark detectors and curve detectors using local shape dictionaries. We also propose novel algorithms for aortic valve mesh construction and shape model fitting. The method is evaluated on patient image dataset using a leave-one-out approach and achieves an accuracy of 0.69 mm.

9784-110, Session PS3

Multi-level approach for statistical appearance models with probabilistic correspondences

Julia Krüger, Jan Ehrhardt, Heinz Handels, Univ. zu Lübeck (Germany)

Statistical shape and appearance models are often based on the accurate identification of one-to-one correspondences in a training data set. At the same time, the determination of these corresponding landmarks is the most challenging part of such methods. Hufnagel et al. developed an alternative method using correspondence probabilities for a statistical shape model. In Ehrhardt et al. [SPIE 2014] we propose the use of probabilistic correspondences for statistical appearance models by incorporating appearance information into the framework. We employ a point-based representation of image data combining position and appearance.
information. The model is optimized and adapted by a maximum a-posteriori (MAP) approach deriving a single global optimization criterion with respect to model parameters and observation dependent parameters, that directly affects shape and appearance information of the considered structures. Because initially unknown correspondence probabilities are used and a higher number of degrees of freedom is introduced to the model (by adapting sampling point positions as well as appearance features of a sampling point) a regularization of the model generation process is advantageous. For this purpose we extent the derived global criterion by a regularization term which penalizes implausible topological changes. Furthermore, we propose a multi-level approach for the optimization, which increases the robustness of the model generation process.

9784-111, Session PS3

Shape complexes in continuous max-flow segmentation

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Optimization-based segmentation approaches deriving from discrete graph-cuts and continuous max-flow have become increasingly nuanced, allowing for topological and geometric constraints on the resulting segmentation while retaining global optimality. However, these two considerations, topological and geometric, have yet to be combined in a unified manner. This paper presents the concept of textit(shape complexes), which combine geodesic star convexity with extendable continuous max-flow solvers. These shape complexes allow more complicated shapes to be created through the use of multiple labels and super-labels, with geodesic star convexity governed by a topological ordering. These problems can be optimized using extendable continuous max-flow solvers. Previous work required computationally expensive co-ordinate system warping which are ill-defined and ambiguous in the general case. These shape complexes are validated in a set of synthetic images as well as atrial wall segmentation from contrast-enhanced CT. Shape complexes represent a new, extendable tool alongside other continuous max-flow methods that may be suitable for a wide range of medical image segmentation problems.

9784-112, Session PS3

Automatic segmentation of 4D cardiac MR images for extraction of ventricular chambers using a spatio-temporal approach

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An accurate ventricular function quantification is important to support the evaluation, diagnosis and prognosis of several cardiac pathologies. However, expert heart delineation, specifically in the right ventricle, is a time consuming task with high inter-and-intra observer variability. A fully automatic 3D+time heart segmentation framework is herein proposed for short-axis-cardiac MRI sequences. This approach estimates the heart using exclusively information from the sequence itself without setting any parameters. The proposed framework consists in segmenting each heart volume by using a coarse-to-fine approach, which starts by localizing the heart using a spatio-temporal analysis, followed by a segmentation of the basal heart that is then propagated to the apex by using a non-rigid-registration strategy, and finally this volume is refined. The proposed framework was performed over 48 patients datasets supplied by the organizers of the MICCAI 2012 RV segmentation challenge. Results show the robustness, efficiency and competitiveness of the proposed method both in terms of accuracy and computational load.

9784-113, Session PS3

Interactive and scale invariant segmentation of the rectum/sigmoid via user-undefined templates

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Among all types of cancer, gynecological malignancies belong to the 4th most frequent type of cancer among women. Besides chemotherapy and external beam radiation, brachytherapy is the standard procedure for the treatment of these malignancies. In the progress of treatment planning, localization of the tumor as the target volume and adjacent organs of risks by segmentation is crucial to accomplish an optimal radiation distribution to the tumor while simultaneously preserving healthy tissue. Segmentation is performed manually and represents a time-consuming task in clinical daily routine. This study focuses on the segmentation of the rectum/sigmoid colon as an Organ-At-Risk in gynecological brachytherapy. The proposed segmentation method uses an interactive, graph-based segmentation scheme with a user-defined template. The scheme creates a directed two dimensional graph, followed by the minimal cost closed set computation on the graph, resulting in an outlining of the rectum. The graphs outline is dynamically adapted to the last calculated cut. Evaluation was performed by comparing manual segmentations of the rectum/sigmoid colon to results achieved with the proposed method. The comparison of the algorithmic to manual results yielded to a Dice Similarity Coefficient value of 83.85±4.08%, in comparison to 83.97±8.08% for the comparison of two manual segmentations of the same physician. Utilizing the proposed methodology resulted in a median time of 128 seconds per dataset, compared to 300 seconds needed for pure manual segmentation.

9784-114, Session PS3

Automatic segmentation of mammogram and tomosynthesis images

Dustin Sargent, Sun Young Park, Merge Healthcare (United States); Jin Ho Jung, Doowon Technical College (Korea, Republic of)

Breast abnormalities are detected primarily by looking for irregularities in the skin and areas of calcification. These abnormalities can be most readily identified as asymmetries when viewing the breasts side-by-side. Since the breasts are imaged separately during mammography, the accuracy and efficiency of mammogram reading can be improved with a preprocessing algorithm that aligns the breasts for comparison. Likewise, the same preprocessing can improve the results of automatic tissue classification algorithms for mammography. To address this problem, we present an automated segmentation algorithm for mammogram and tomosynthesis multi-frame images. Our algorithm employs region-growing and contour analysis along with k-means clustering. The algorithm retains only the anatomy while removing irrelevant image regions, allowing the images to be aligned for easy side-by-side comparison. Further, our algorithm can be applied to mammograms, tomosynthesis images, and scanned images. Scanned images are particularly difficult, as they are noisy and contain artifacts. Our method has been tested on approximately 750 images, including all three of the aforementioned image types, and has correctly segmented the diagnostically relevant image region in 97% of cases.

9784-115, Session PS3

Automated separation of merged Langerhans islets

Jan Švihlík, Univ. of Chemistry and Technology Prague (Czech Republic) and Czech Technical Univ. in Prague (Czech Republic); Jan Kybic, Czech Technical Univ. in Prague (Czech Republic); Dustin Sargent, Sun Young Park, Merge Healthcare (United States); Jin Ho Jung, Doowon Technical College (Korea, Republic of)
Quantitative comparison between the straight-forward and anatomical insertion technique for pedicle screw placement

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Spinal deformity correction with vertebral fixation is nowadays the preferred surgical treatment, where pedicle screws are inserted through pedicles into corresponding vertebral bodies and afterwards connected with rods. In clinical practice, the straight-forward and anatomical insertion technique are currently being used for pedicle screw placement. However, it is difficult to quantitatively compare both techniques and determine which technique is more adequate for each planned pedicle screw before surgery (i.e. preoperatively). In this paper, we therefore describe a framework for quantitative comparison between the straight-forward and anatomical insertion technique for pedicle screw placement by evaluating the screw fastening strength. Quantitative comparisons were performed on computed tomography images of 11 patients with 74 manually planned pedicle screws, who underwent the vertebral fixation procedure. The first quantitative comparison was performed between the straight-forward and anatomical pedicle screw insertion technique, which resulted in a relatively high agreement with mean absolute difference of 0.0 mm in screw diameter, 2.9 mm in screw length, 1.2 mm in pedicle crossing point and 6.5 degrees in screw inclinations. The second quantitative comparison was performed between the best resulting pedicle screw insertion technique and manually obtained pedicle screw plans, which again resulted in a relatively high agreement with mean absolute difference of 0.5 mm in screw diameter, 4.7 mm in screw length, 2.4 mm in pedicle crossing point and 6.0 degrees in screw inclinations. Both the straight-forward and anatomical insertion technique proved approximately equal in terms of the screw fastening strength.

A fast myocardium blood flow estimation method based on super-pixel and deconvolution

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In this paper we propose an efficient approach for myocardial blood flow (MBF) computation which combines super-pixel assignment and deconvolution using singular value decomposition (SVD). The pixels on myocardium region are grouped by simple linear iterative clustering (SLIC). SLIC is an adaptation of k-means for super-pixel generation. The number of distance calculations in the optimization is dramatically reduced by limiting the search space to a region proportional to the super-pixel size. This reduces the complexity to be linear in the number of pixels N and independent of the number of super-pixels k. We then compute MBF on those super-pixel regions from SLIC to speed up the processing. We compared the performance (including A. average MBF computation time for one slice, B. flow contrast-to-noise ratio between ischemic and normal LV myocardium tissue. C. flow signal-to-noise on normal LV myocardium tissue) between the conventional SVD (CSVD) algorithm, fixed pixel region SVD (FSVD) and the SLIC super-pixel SVD (SSSVD) algorithm. Unlike FSVD which computes MBF on pixel regions with the same size, SSSVD computes MBF on irregular super-pixel regions and each region contains pixels with feature similarity. This allows SSSVD grouping pixels with a small super-pixels number and generating a more homogeneous MBF map. Our initial results suggest that MBF maps produced from SSSVD have higher flow-CNR and flow-SNR across hemodynamic conditions. The SPSVD algorithm is also faster than the CSVD algorithm for computing MBF and the super-pixel clustering technique can be applied to speed iterative parameter estimation analysis models.

Reconstruction of coronary artery centrelines from x-ray rotational angiography using a probabilistic mixture model

Serkan Cimen, Ali Gooya, Alejandro F. Frangi, The Univ. of Sheffield (United Kingdom)

Three-dimensional reconstruction of coronary arterial trees from X-ray rotational angiography (RA) images have the potential to compensate the limitations of RA due to projective imaging. Most of the existing bottom-up model based reconstruction algorithms are either based on matching of coronary centreline points from 2D X-ray images or back-projection of 2D vessel response maps onto 3D space for further processing. All of these methods have their shortcomings such as dependency on accurate 2D centreline segmentations or inability to handle motion. In this paper, the reconstruction is approached from a novel perspective, and is formulated as a probabilistic reconstruction method based on mixture model (MM) representation of point sets describing the coronary arteries. Specifically, it is assumed that the coronary arteries could be represented by a set of 3D points, whose spatial locations denote the Gaussian components in the MM. Additionally, an extra uniform distribution is incorporated in the mixture model to accommodate outliers (noise, over-segmentation etc.) in the 2D centreline segmentations. Treating the given 2D centreline segmentations as data points generated from MM, the 3D means, isotropic variance, and mixture weights of the Gaussian components are estimated by maximizing a likelihood function. Initial results from a phantom study show that the proposed method is able to handle outliers in 2D centreline segmentations, which indicates the potential of our formulation. Preliminary reconstruction results in the clinical data is also presented.

Rotationally invariant clustering of diffusion MRI data using spherical harmonics

Matthew G. Liptrot, Francois B. Lauze, Univ. of Copenhagen (Denmark)

We present a simple approach to the voxelwise classification of brain tissue acquired with diffusion weighted MRI (DWI). The approach leverages the
power of spherical harmonics (SH) to summarise the diffusion information that is sampled at many points over a sphere. We use simple rotationally invariant features of these SH summaries to directly classify voxels whose diffusion characteristics are similar yet whose primary diffusion orientations differ.

This therefore permits a model-free classification of DWI voxels according to their inferred underlying fibre properties, whilst ignoring the specifics of orientation.

In detail, we initially de-noise the individual gradients volumes with a gaussian scale-space approach. We then compute the SH transforms, thereby generating a composite set of spherical basis functions. From these, voxelwise rotationally invariant feature vectors are constructed for classification. Using a simple Gaussian mixture model, we examined the classification performance for a range of sub-classes (3-20). The results were compared against existing alternatives for tissue classification, specifically fractional anisotropy (FA) and the standard gaussianity model used by Camino.

The approach was tested on two publicly-available datasets: an ex-vivo pig brain and in-vivo human brain from the Human Connectome Project.

We show how a robust classification of DWI data can be performed directly, without model reconstruction, thereby avoiding any biases or potential confounds of model choice.

As such, the method could prove useful in subsequent model reconstructions where it could inform about individual voxel complexities and improve model parameter choice.

9784-120, Session PS4

Effects of EPI distortion correction pipelines on the connectome in Parkinson’s Disease

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Echo-planar imaging (EPI) is commonly used in diffusion weighted imaging (DWI) and is susceptible to nonlinear geometric distortions arising from inhomogeneities in the static magnetic field. These field inhomogeneities can be measured and corrected through a fieldmap image acquired during scanning. However, in studies where the fieldmap image is unavailable, these susceptibility artifacts can be corrected, to some extent, by nonlinear registration of the DWI to a corresponding structural image. We analyzed two nonlinear registration based EPI distortion correction pipelines that were optimized for the particular weighting of the structural image registration target. The first pipeline used a 3D nonlinear registration to a T1 weighted image target while the second pipeline used a 1D nonlinear registration to a T2 weighted image target. We studied the differences between both pipelines in their ability to characterize high-level measures of brain connectivity in Parkinson’s disease in 189 individuals (58 healthy controls, 131 people with Parkinson’s disease (PD)) as part of the Parkinson’s Progression Markers Initiative (PPMI) dataset. In each participant, we computed a structural connectome using regions of interest from a structural based cortical parcellation combined with DWI based whole-brain tractography to quantify connectivity strengths between those regions. We evaluated the test-retest reliability of the connectome in each EPI distortion correction pipeline using a second diffusion scan acquired for each participant. In addition, we used support vector machine (SVM) classification to assess how the correction pipelines influenced the accuracy of connectome based classification of PD and controls.

9784-121, Session PS4

Fitting parametric models of diffusion MRI in regions of partial volume

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People do regional analysis by fitting models per voxel and then averaging over a region, accounting for partial volume only to some degree. Instead, we propose to fit the models per region directly, enabling explicit PV modelling and thus fitting models in convoluted areas such as the cortex. In this work we provide a method for including the partial volume in the calculation of the model parameters for a region. We use a high-resolution segmentation from a T1 scan, downsampled into the space of the diffusion image, to assign each voxel a probabilistic membership to each tissue class. Diffusion model parameters are represented as the linearly-weighted sum of the parameters calculated for each tissue class, via optimisation of the whole region at once. This means that a region’s parameter estimates will utilise all of the available data.

We demonstrate this method improves parameter estimation in digital phantoms for the diffusion tensor (DT) and NODDI models. The method provides accurate parameter estimates even in regions where the normal approach fails completely for example, where partial volume is in every voxel. We also apply this model to brain data from preterm infants, where the thin, convoluted, maturing cortex necessitates such an approach.

9784-122, Session PS4

Motion correction for q-space imaging by multiple interleaved b0 images

Miyu Muto, Mizuki Iwabuchi, Weiwei Du, Masayuki Fukuzawa, Kyoto Institute of Technology (Japan); Koji Sakai, Jun Tazoe, Hiroyasu Ikeno, Kei Yamada, Kyoto Prefectural Univ. of Medicine (Japan)

Subject-motion in a large number of diffusion weighted images (DWIs) for q-space analysis was detected and corrected by using a simple protocol to add multiple interleaved b0 images between each DWI set and at the very end of data acquisition. The realignment matrix was detected from all the b0 images and the DWIs were realigned with the matrix detected from the nearest b0 image. Degree of improvement in q-space analysis was estimated by calculating total residual sum of squares (RSS) in bi-exponential curve fitting process and also on the fractional anisotropy (FA) of zero displacement (ZDP). The local increase of total RSS at the edges between cerebral gyri and sulci in the uncorrected slices were mostly diminished in the corrected ones, while the local RSS increases around basal ganglia and near the ventricles were somewhat present in the corrected ones. The volume average of RSS was reduced by 55% with the motion correction process while the reduction rate in slice average of RSS was varied from slice to slice. An abnormally large FA-ZDP region at a left cerebral sulcus in the uncorrected slice was diminished in the corrected ones, which strongly suggests the effect of motion correction process. The number of additional b0 images accounted for 3% of the total number of DWIs, which suggests its feasibility for future clinical application.
9784-123, Session PS4

Axonal diameter and density estimated with 7-Tesla hybrid diffusion imaging in transgenic Alzheimer rats

Madelaine Daianu, Univ. of California, Los Angeles (United States); Russell E. Jacobs, California Institute of Technology (United States); Terrence C. Town, The Univ. of Southern California (United States); Paul M. Thompson, Univ. of California, Los Angeles (United States)

Diffusion-weighted magnetic resonance imaging (DWI) is a powerful tool that enables the study of brain tissue microstructure. DWI is sensitive to subtle changes in the brain’s white matter (WM) and can provide insight into abnormal brain changes in conditions such as Alzheimer’s disease (AD). In this study, we used 7-Tesla hybrid diffusion imaging (HYDI) to scan 3 transgenic rats (line TgF344-AD) ex vivo at 10, 15 and 24 months, which correspond to different phases of the human disease. We acquired 300 DWI volumes across 5 q-sampling shells (b=1000, 3000, 4000, 8000, 12000 s/mm²). From the top three b-value shells with highest SNR, we reconstructed markers of WM disease, including indices of axon density and diameter in the corpus callosum (CC) – aiming to quantify processes that occur in AD. As expected, apparent anisotropy decreased across the disease time points, and there were decreases in the intra- and extra-axonal MR signal along the axons. In line with histologic data, axonal diameters were greater in the splenium and body of the CC than the genu, with changes over time that may reflect neuritic dystrophy – enlarged axons and dendrites seen previously on electron microscopy in the cortex and hippocampus of these rats. This was further supported by increases in the MR signal that may derive from glial cells, CSF and other small compartments in the WM structure. Tractography detected more fibers in the CC at 10 versus 24 months. These novel findings offer great potential to provide technical and scientific insight into the neurobiology of disease.

9784-124, Session PS4

Segmentation of thalamus from MR images via task-driven dictionary learning

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Thalamus segmentation is required to track changes in thalamic volume over time. In this work, we introduce a task-driven dictionary learning framework to find the optimal dictionary given a set of eleven features obtained from T1-weighted MRI and diffusion tensor imaging. A linear classifier is designed concurrently to classify voxels as belonging to the thalamus or non-thalamus class. Morphological post-processing is applied to produce the final thalamus segmentation. Due to the uneven size of the training data set between the non-thalamus and thalamus samples, a non-uniform sampling scheme is proposed to train the classifier to better discriminate between the two classes around the boundary of the thalamus. Experiments are conducted on data collected from 22 subjects with manually delineated ground truth. The experimental results are promising in terms of improvements in the Dice coefficient of the thalamus segmentation over state-of-art atlas-based thalamus segmentation algorithms.

9784-125, Session PS4

Finding significantly connected voxels based on histograms of connection strengths

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We explore a new approach for connectivity based segmentations of subcortical brain regions. Connectivity based segmentations are usually based on fibre connections from the seed region to predefined target regions. We present a method for finding significantly connected voxels based on the distribution of connection strengths. Paths from seed voxels to all voxels in a target region are obtained from a shortest-path tractography. For each seed voxel we approximate the distribution with a histogram of path scores. We hypothesise that the majority of estimated connections are false-positives and that their connection strength is distributed differently from true-positive connections. Therefore, an empirical null-distribution is defined for each target region as the accumulative normalized histogram over all voxels in the seed region. Single histograms are then tested against the corresponding null-distribution and significance is determined using the false discovery rate (FDR). Segmentations are based on significantly connected voxels and their FDR. In this work we focus on the thalamus and the target regions were chosen by dividing the cortex into a prefrontal/temporal zone, motor zone, somatosensory zone and a parieto-occipital zone. The obtained segmentations consistently show a sparse number of significantly connected voxels that are located near the surface of the anterior thalamus over a population of 40 subjects.

9784-126, Session PS4

Thalamus parcellation using multi-modal feature classification and thalamic nuclei priors

Jeffrey Glaister, Aaron Carass, Johns Hopkins Univ. (United States); Joshua V. Stough, George Mason Univ. (United States); Peter A. Calabresi, Jerry L. Prince, Johns Hopkins Univ. (United States)

Segmentation of the thalamus and thalamic nuclei is useful to quantify volumetric changes from neurodegenerative diseases. Most thalamus segmentation algorithms only use T1-weighted magnetic resonance images and current thalamic parcellation methods require manual interaction. Smaller nuclei, such as the lateral and medial geniculater, are challenging to locate due to their small size. We propose an automated segmentation algorithm using a set of features derived from diffusion tensor image (DTI) and thalamic nuclei location priors. After extracting features, a hierarchical random forest classifier is trained to locate the thalamus. A second random forest classifies thalamic voxels as belonging to one of six thalamic nuclei classes. The proposed algorithm was tested using a leave-one-out cross validation scheme and compared with the state-of-art algorithms. The proposed algorithm has a higher Dice score compared to other methods for the whole thalamus and several nuclei.

9784-127, Session PS4

A 3D high resolution ex vivo white matter atlas of the common squirrel monkey (Saimiri sciureus) based on diffusion tensor imaging

Yuru Gao, Prasanna Parvathaneni, Kurt G. Schilling, Zhourbing Xu, Ann S. Choe, Bennett A. Landman, Adam M. Anderson, Vanderbilt Univ. (United States)

Practically speaking, modern magnetic resonance imaging (MRI) brain atlases are high quality 3-D volumes with specific structures labeled for each position in the volume. Atlases are essential in providing a common space for interpretation of results across studies, for anatomical education, and providing quantitative image-based navigation. Extensive work has been devoted to atlas construction for humans, macaque, and several non-primate species (e.g., rat). One notable gap in the literature is the common squirrel monkey – for which the primary published atlases date from the 1960’s. The common squirrel monkey has been used extensively used as
surrogate for human in biomedical studies given its anatomical neuro-system similarities and practical consideration. This work is a continuation of development a multi-modal MRI atlas for the common squirrel monkey, for which a structural imaging space and gray matter parcels have been previously constructed. This study identifies 50 white matter (WM) tracts with diffusion tensor imaging (DTI) on three animals and combines these data to define the anatomical locations of these tracks in a standardized coordinate system compatible with previous development. An anatomist reviewed the resulting tracts and the inter-animal reproducibility (i.e., the dice index of each WM parcel across animals in common space) was assessed. The indices range from 0.05 to 0.7 due to the differences of local registration quality and the variation of WM position across individuals. However, the combined WM labels from the 3 animals still represents the general locations of WM parcels, delivering basic atlas function.

9784-128, Session PS4
Fast and accurate simulations of diffusion-weighted MRI signals for the evaluation of acquisition sequences
Gaetan Rensonnet, Damien Jacobs, Benoît M. Macq, Univ. Catholique de Louvain (Belgium); Maxime Taquet, Harvard Medical School (United States)
Diffusion-weighted magnetic resonance imaging (DW-MRI) is a powerful tool to probe the diffusion of water through tissues. Through the application of magnetic gradients of appropriate direction, intensity and duration constituting the acquisition parameters, information can be retrieved about the underlying microstructural organization of the brain. In this context, an important and open question is to determine an optimal sequence of such acquisition parameters for a specific purpose. The use of simulated DW-MRI data for a given microstructural configuration provides a convenient and efficient way to address this problem.

We first present a novel hybrid method for the synthetic simulation of DW-MRI signals that combines analytic expressions in simple geometries such as spheres and cylinders and Monte Carlo (MC) simulations elsewhere. Our hybrid method remains valid for any acquisition sequence and provides identical levels of accuracy with a computational time that is 80% shorter than that required by MC simulations for commonly-encountered microstructural configurations.

We apply our novel simulation technique to estimate the radius of axons under various noise levels with different acquisition protocols commonly used in the literature. The results of our comparison suggest that protocols favoring a large number of gradient intensities such as a Cube and Sphere (CUSP) imaging provide more accurate radius estimation than conventional single-shell HARDI acquisition for an identical acquisition time.

9784-129, Session PS4
BOLD delay times using group delay in sickle cell disease
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Sickle cell disease (SCD) is an inherited blood disorder that effects red blood cells, which can lead to vasoocclusion, ischemia and infarct. This disease often results in neurological damage and strokes, leading to morbidity and mortality. Functional Magnetic Resonance Imaging (fMRI) is a non-invasive technique for measuring and mapping the brain activity. Blood Oxygenation Level-Dependent (BOLD) signals contain also information about the neurovascular coupling, vascular reactivity, oxygenation and blood propagation. Temporal relationship between BOLD fluctuations in different parts of the brain provides also a mean to investigate the blood delay information cite{christen2015noncontrast}. We use the induced desaturation as a label to profile transit times through different brain areas, reflecting oxygen utilization of arteries, veins and tissue. Differences in different parts among the two groups were observed. These findings suggest that sickle cell disease causes blood propagation modifications, and these changes could be used as a biomarker of the malady.

9784-130, Session PS5
Luminosity and contrast normalization in color retinal images based on standard reference image
Ehsan Shahrian Varnousfaderani, Siamak Yousefi, Akram Belgith, Michael H. Goldbaum M.D., Hamilton Glaucoma Ctr. (United States)
Color retinal images are used manually or automatically for diagnosis and monitoring progression of a retinal diseases. Color retinal images have large luminosity and contrast variability within and across images due to the large natural variations in retinal pigmentation and complex imaging setups. The quality of retinal images may affect the performance of automatic screening tools therefore different normalization methods are developed to uniform data before applying any further analysis or processing. In this paper we propose a new reliable method to remove non-uniform illumination in retinal images and improve their contrast based on contrast of the reference image. The non-uniform illumination is removed by normalizing luminance image using local mean and standard deviation. Then the contrast is enhanced by shifting histograms of uniform illuminated retinal image toward histograms of the reference image to have similar histogram peaks. This process improve the contrast without changing inter correlation of pixels in different color channels. In compliance with the way humans perceive color, the uniform color space of LUV is used for normalization. The proposed method is widely tested on large dataset of retinal images with present of different pathologies such as Exudate, Lesion, Hemorrhage and Cotton-Wool and in different illumination conditions and imaging setups. Results shows that proposed method successfully equalize illumination and enhances contrast of retinal images without adding any extra artifacts.

9784-131, Session PS5
A Shearlet-based algorithm for quantum noise removal in low-dose CT images
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Low-dose CT (LDCT) scanning is a potential way to reduce the radiation exposure of X-ray in the population. It is necessary to improve the quality of low-dose CT images. In this paper, we propose an effective algorithm for quantum noise removal in LDCT images using shearlet transform. Because the quantum noise can be simulated by Poisson process, we first transform the quantum noise by using anscombe variance stabilizing transform (VST), producing an approximately Gaussian noise with unitary variance. Second, the non-noise shearlet coefficients are obtained by adaptive hard-threshold
processing in shearlet domain. Third, we reconstruct the de-noised image using the inverse shearlet transform. Finally, an aniscombe inverse transform is applied to the de-noised image, which can produce the improved image. The main contribution is to combine the aniscombe VST with the shearlet transform. By this way, the edge coefficients and the noise coefficients can be separated from high frequency sub-bands effectively. A number of experiments are performed over some LDCT images by using the proposed method. Experimental results show that this method can effectively reduce the quantum noise while enhancing the subtle details. The proposed algorithm has better image quality compare with many existing de-noising methods. The PSNR has increased by 9.27% and 6.17% respectively, and the MSSIM has increased by 2.62% and 1.77% respectively compared with literature methods [1-2].

9784-132, Session PS5

Glasses for 3D ultrasound computer tomography: phase compensation
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Ultrasound Computer Tomography (USCT) is a promising new imaging system for breast cancer diagnosis. We success-fully tested our 3D USCT system in a pilot study and are currently conducting a successive clinical study with 200 pa-tients. The 3D USCT consists of several hundreds of US transducers forming semi-ellipsoidal aperture. Spherical waves are sequentially emitted by individual and received in parallel by many transducers. Reflectivity image volumes are reconstructed by SAFT imaging. However, straight forward SAFT imaging leads to blurred images due to system imper-fections. described here is the extension of a previous proposed de-blurring approach applying aperture characteristics by including additional priori information, resulting now also in spatial phase compensation.

Building on a 2013 conference presented approach the system modeling approach was significantly extended to by more apriori knowledge. Included in the model was the transducer frequency and angular response as measured before as approx. at 2.6 MHz, 50 % relative bandwidth and a directivity of ± 23° at -6dB. The coded excitation and signal chain filtering was applied using a project typical a sample frequency of 10MHz and using chirp of approx. 1MHz bandwidth (3dB) around 2.5MHz. The SAFT reconstruction applied used standard parameters and project constraints like using 2/3 of the full data set filtered by the angular constraints: data under <60° receiver-emitter in-between angle got rejected. While the simulation was extended also by amplitude and jitter noise capabilities for the following analysis, this was deactivated to not disturb a representation of systematic influences by side lobe artifacts due to frequency phase shifts and amplitude changes.

The approach was evaluated with a simulation and a clinical data set. An increase in the SNR was observed with Simulation of system representing point scatterers as also the clinical data.

9784-133, Session PS5

Adaptive non-local means method for speckle reduction in ultrasound images
Ling Ai, Ming Yue Ding, Xuming Zhang, Huazhong Univ. of Science and Technology (China)

Noise removal is a crucial step to enhance the quality of ultrasound images. However, some existing despeckling methods cannot ensure satisfactory restoration performance. In this paper, an adaptive non-local means (ANLM) filter is proposed for speckle noise reduction in ultrasound images. The distinctive property of the proposed method lies in that the decay parameter will not take the fixed value for the whole image but adapt itself to the variation of the local features in the ultrasound images. In the proposed method, the pre-filtered image will be obtained using the traditional NLM method. Based on the pre-filtered result, the local gradient will be computed and it will be utilized to determine the decay parameter adaptively for each image pixel. The final restored image will be produced by the ANLM method using the obtained decay parameters. Simulations on the synthetic image show that the proposed method can deliver sufficient speckle reduction while preserving image details very well and it outperforms the state-of-the-art despeckling filters in terms of peak signal-to-noise ratio (PSNR) and structural similarity (SSIM). Experiments on the clinical ultrasound image further demonstrate the practicality and advantage of the proposed method over the compared filtering methods.

9784-134, Session PS5

Subject-specific patch-based denoising for contrast-enhanced cardiac MR images
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Many patch-based techniques in imaging, e.g., Non-local means denoising, require tuning parameters to yield optimal results. In real-world applications, e.g., denoising of MR images, ground truth is generally not available and the process of choosing an appropriate set of parameters is a challenge. Recently, Zhu et al. proposed a method to define an image quality measure, called Q, that does not require ground truth. In this manuscript, we evaluate the effect of various parameters of the NL-means denoising on this quality metric Q. Our experiments are based on the late-gadolinium enhancement (LGE) cardiac MR images that are inherently noisy. Our described exhaustive evaluation approach can be used in tuning parameters of patch-based schemes. Even in the case that an estimation of optimal parameters is provided using another existing approach, our described method can be used as a secondary validation step. Our preliminary results suggest that denoising parameters should be case-specific rather than generic.

9784-135, Session PS5

Calibration free beam hardening correction for cardiac CT perfusion imaging
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Mycocardial perfusion imaging using CT (MPI-CT) and coronary CTA have the potential to be non-invasive gate-keepers for coronary angiography. Beam hardening artifacts (BHA) prevent accurate blood flow calculation in MPI-CT. BHC methods require either, energy-sensitive CT scanner, not widely available or typically a calibration-based method. We developed a calibration-free BHC method suitable for MPI-CT. The algorithm works with any BHC method and iteratively determines model parameters using our proposed cost function. In this work, we use the polynomial BHC extended to three materials. The image is segmented into soft tissue, bone, and iodine images, based on mean HU and temporal enhancement. Forward projections of bone and iodine images are obtained, and in each iteration polynomial correction for cardiac CT perfusion imaging is applied. Corrections are then back projected and combined to obtain the current iteration’s BHC image. This process is iterated until cost is minimized. We evaluate the algorithm on simulated and physical phantom images and on preclinical MPI-CT. The scans were obtained on a prototype
To compensate for those disadvantages, this paper first introduces an alternate approach to wavelet-encoded MRI by itself is limited due to the SNR penalties. Encoding in conventional MRI data acquisition with wavelet encoding by this paper revisits wavelet-encoded MR imaging [2] which replaces phase encoding to exploit the sparsity of MR images showing great potential to reduce the scan time significantly, however, it poses its own unique problems. [1] to exploit the sparsity of MR images showing great potential to reduce the resolution of MRI, Compressed Sensing (CS) in MR imaging is proposed in [2]. Because there is still a great need to improve temporal resolution of MPI-CT images, BHA was reduced from 28±6 HU to less than 4±4 HU at peak enhancement. Results suggest that the algorithm can be used to reduce BHA in conventional CT and improve MPI-CT accuracy.

9784-136, Session PS5
Temporal enhancement of two-dimensional color doppler echocardiography
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Two-dimensional color Doppler echocardiography is widely used for assessing blood flow inside the heart and blood vessels. Currently, frame acquisition time for this method varies from tens to hundreds of milliseconds, depending on Doppler sector parameters. That leads to low frame rates of resulting video sequences equal to tens of Hz, which is insufficient for some diagnostic purposes, especially in pediatrics. In this paper, we present a new approach for reconstruction of 2D color Doppler cardiac images, which results in the frame rate increased to hundreds of Hz. This approach relies on a modified method of frame reordering originally applied to real-time 3D echocardiography. There are no previous publications describing application of this method to 2D Color Doppler data. The approach has been tested on several in-vivo cardiac 2D color Doppler datasets with approximate duration of 30 sec and native frame rate of 15 Hz. The resulting image sequences had equivalent frame rates at 500Hz.

9784-137, Session PS5
An adaptive undersampling scheme of wavelet-encoded parallel MR imaging for more efficient MR data acquisition
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Magnetic Resonance Imaging (MRI) offers noninvasive high resolution, high contrast cross-sectional anatomic images through the body. The data of the conventional MRI is collected in spatial frequency (Fourier) domain, which is called k-space. Because there is still a great need to improve temporal resolution of MRI, Compressed Sensing (CS) in MRI imaging is proposed in [1] to exploit the sparsity of MR images showing great potential to reduce the scan time significantly, however, it poses its own unique problems. This paper revisits wavelet-encoded MR imaging [2] which replaces phase encoding in conventional MRI data acquisition with wavelet encoding by applying wavelet-shaped spatially selective radiofrequency (RF) excitation, and keeps the readout direction as frequency encoding. The practicality of wavelet-encoded MRI by itself is limited due to the SNR penalties and poor time resolution compared to conventional Fourier-based MRI. To compensate for those disadvantages, this paper first introduces an undersampling scheme named significance map for sparse wavelet-encoded k-space to speed up data acquisition as well as allowing for various adaptive imaging strategies. The proposed adaptive wavelet-encoded undersampling scheme does not require prior knowledge of the subject to be scanned. Multiband (MB) parallel imaging is also incorporated with wavelet-encoded MRI by exciting multiple regions simultaneously for further reduction in scan time desirable for medical applications. The simulation and experimental results are presented showing the feasibility of the proposed approach in significant reduction of the redundancy of the wavelet k-space data while maintaining relatively high quality.

9784-139, Session PS5
 Improve synthetic retinal OCT images with present of pathologies and textural information
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The lack of noise free Optical Coherence Tomography (OCT) images makes it challenging to quantitatively evaluate performance of image processing methods such as denoising methods. The synthetic noise free OCT images are needed to evaluate performance of image processing methods. The current synthetic methods fail to generate synthetic images that represent real OCT images with present of pathologies. They cannot correctly imitate real OCT data due to a tendency to smooth the data, losing texture information and even, pathologies such as cysts are simply smoothed away by these methods. The first aim of this paper is to use mathematical models to generate a synthetic noise free image that represent real retinal OCT B-scan or volume with present of clinically important pathologies. The proposed method partitions a B-scan obtained from real OCT into three regions (vitreous, retina and choroid) by segmenting the inner limiting membrane (ILM) and retinal pigment epithelium (RPE) surfaces as well as cysts regions by medical experts. Then retina region is further divided into small blocks. Different smoothness functions are used to estimate OCT signals in vitreous, choroid and cyst regions and in blocks of retina region. Estimating signals in block resolution enables our proposed method to capture more temporal information by using a simple mathematical model (smoothness function) and using annotated cyst enables our method to model cyst pathology accurately. The qualitative evaluations show that proposed method generated more realistic B-scans with present of pathologies and textural information than other methods.

9784-140, Session PS6
Speeding up 3D speckle tracking using PatchMatch
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Echocardiography provides valuable information to diagnose heart dysfunction. A typical exam records several minutes of real-time cardiac images. To enable complete analysis of 3D cardiac strains, 4-D (3-D+T) echocardiography is used. This results in a HUGE dataset and requires effective automated analysis. US speckle tracking is an effective method for tissue motion analysis. It involves correlation of a 3D kernel (window) around a voxel with kernels in later frames. The search region is usually confined to a local neighborhood, due to biomechanical and computational constraints. For high strains and moderate frame rates, however, this search region will remain large, leading to a considerable computational burden. Moreover, speckle decorrelation (due to high strains) leads to errors in tracking. To solve this, spatial motion
coherency between adjacent voxels should be imposed, e.g., by averaging their correlation functions [Chen et al.]. This requires storing correlation functions for neighboring voxels, thus increasing memory demands.

In this work, we propose an EFFICIENT search using ‘PatchMatch’ [Barnes et al.], a powerful method to find correspondences between images. Here we adopt PatchMatch for 3D volumes and RF signals. As opposed to an exact search, PatchMatch performs random sampling of the search region and propagates successive matches among neighboring voxels. We show that:

1) Inherently smooth offset propagation in PatchMatch contributes to spatial motion coherence without any additional processing or memory demand. 2) For typical scenarios, PatchMatch is at least 20 times faster than the exact search, while maintaining comparable tracking accuracy.

9784-141, Session PS6
Respiration correction by clustering in ultrasound images
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Respiratory motion is a challenging factor for ultrasound image acquisition, image-guided procedures and perfusion quantification of angiogenesis in the abdominal and thoracic region. To reduce the influence of the respiratory motion, respiratory correction methods were investigated.

In this paper we propose a novel, cluster-based respiratory correction method. Unlike the traditional gating method, we don’t need to estimate the breathing cycle accurate. In the proposed method, we assign the image frames of the corresponding respiratory phase using spectral clustering and selecting correction images automatically by finding a cluster in which points are close to each other. The method is tested on simulation image sequence and real ultrasound image sequence. The experimental results show the effectiveness of our proposed method in quantitative and qualitative.

9784-142, Session PS6
Demons versus level-set motion registration for coronary 18F-sodium fluoride PET
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Ruptured coronary atherosclerotic plaques commonly cause acute myocardial infarction. It has been recently shown that active microcalcification, a characteristic of vulnerable plaques, can be imaged using 18F-sodium fluoride (18F-NaF) PET. However, cardiac motion degrades image quality. In this study, we aimed to compare demons and level-set registration techniques for coronary motion correction of 18F-NaF PET. To this end, fifteen patients underwent 18F-NaF PET and prospective coronary CT angiography (CCTA). PET data were reconstructed in 10 ECG gated bins that were registered using demons and level-set methods guided by the extracted coronary arteries from CCTA. Noise levels, target-to-background ratios (TBR) and global motion were compared to assess image quality.

Compared to the reference standard of using only diastolic PET images (1/4 of the counts) of PET data, cardiac motion registration using either level-set or demons techniques reduced image noise (~46%, p<0.0001) due to the use of counts from all gates and increased TBR difference between 18F-NaF positive and negative lesions. The motion with demons registration is in accordance with the ranges that have been reported in the literature, contrary to the results obtained with level-set registration.

Moreover, the demons method produces smoother deformation fields, exhibiting no singularities, unlike the level-set one, which presents between 4 and 8% of singularities, depending on the coronary artery considered. As a conclusion, demons registration produces more realistic deformations and offer smoother motion fields for the registration of 18F-NaF PET. Further investigations of the optimal registration technique of this novel coronary PET imaging technique is warranted.

9784-144, Session PS6
Deformable image registration for multimodal lung-cancer staging
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Positron emission tomography (PET) and X-ray computed tomography (CT) serve as major diagnostic imaging modalities in the lung-cancer staging process. Modern scanners provide co-registered whole-body PET/CT studies, collected while the patient breathes freely, and high-resolution chest CT scans, collected under a brief patient breath hold. Unfortunately, no method exists for registering a PET/CT study into the space of a high-resolution chest CT scan. If this could be done, vital diagnostic information offered by the PET/CT study could be brought seamlessly into the procedure plan used during live cancer-staging bronchoscopy. We propose a method for the deformable registration of whole-body PET/CT data into the space of a high-resolution chest CT study. We then demonstrate its potential for procedure planning and subsequent use in multimodal image-guided bronchoscopy.

9784-145, Session PS6
Improved B-spline image registration between exhale and inhale lung CT images based on intensity and gradient orientation information
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Registration of lung CT images acquired at different respiratory phases is clinically relevant in many applications, such as follow-up analysis, lung function analysis based on mechanical elasticity, or pulmonary airflow analysis, etc. In order to find accurate and reliable transformation for registration, a proper choice of dissimilarity measure is important. Even though various intensity-based measures have been introduced for precise registration, the registration performance may be limited since they mainly take intensity values into account without effectively considering useful spatial information. In this paper, we attempt to improve the non-rigid registration accuracy between exhale and inhale CT images of the lung, by proposing a new dissimilarity measure based on gradient orientation representing the spatial information in addition to vessel-weighted intensity and normalized intensity information. Since we need non-rigid registration due to the easy deformation of lung, the B-spline free-form deformation (FFD) is adopted as the transformation model. The experimental results for six clinical datasets show that the proposed method provides more accurate registration results than competitive registration methods.
Unified registration framework for cumulative dose assessment in cervical cancer across external beam radiotherapy and brachytherapy

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Dose accumulation across External Beam Radiotherapy (EBRT) and Brachytherapy (BT) treatment fractions in cervical cancer is extremely challenging due to structural dissimilarities and large inter-fractional anatomical deformations between the EBRT and BT images. The brachytherapy applicator and the bladder balloon, present only in the EBRT image, introduce missing structural correspondences for the underlying registration problem. Complex anatomical deformations caused by the applicator and the balloon, different rectum and bladder filling and tumour shrinkage compound the registration difficulties. Conventional free-form registration methods struggle to handle such topological differences. In this paper, we propose a registration pipeline that first transforms the original images to their distance maps based on segmentations of critical organs and then performs non-linear registration of the distance maps. The resulting dense deformation field is then used to transform the original anatomical image. The registration accuracy is evaluated on 27 image pairs from stage 2B-4A cervical cancer patients. The algorithm reaches a Hausdorff distance of less than 0.5mm for the uterus, 2.2mm for the bladder and 1.7mm for the rectum when applied to (EBRT,BT) pairs, taken at time points more than 3 months apart. This generalized model-free framework can be used to register any combination of EBRT and BT images as opposed to methods in the literature that are tuned for either only (BT,BT) pair, or only (EBRT,EBRT) pair or only (BT,EBRT) pair. A unified framework for 3D dose accumulation across multiple EBRT and BT fractions has been proposed to facilitate adaptive personalized radiation therapy.

Lung iodine mapping by subtraction with image registration allowing for tissue sliding

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As pulmonary embolism is a fairly common and serious entity, rapid diagnosis and treatment has a significant impact on morbidity and mortality rates. Iodine maps representing tissue perfusion are commonly generated by dual-energy CT acquisitions to provide additional information regarding the severity of an occlusion. Alternatively, the iodine map can be generated by subtracting pre- and post-contrast CT scans as previously reported. Although accurate image registration is essential, subtraction has the advantage of a higher signal-to-noise ratio and suppression of bone. This paper presents an improvement over the previously reported registration algorithm. Significantly, allowance for sliding motion at tissue boundaries is included in the regularisation. Pre- and post-contrast helical CT scans were acquired for thirty subjects using a Toshiba Aquilion ONE® scanner. Ten of these subjects were designated for algorithm development, while the remaining 20 were reserved for qualitative clinical evaluation. Quantitative evaluation is performed against the previously reported method and using publicly available data for comparison against other methods. Clinical evaluation on a sliding scale from 1 (excellent) to 5 (non-diagnostic) indicates a slight, but non-significant improvement in adequacy of mean score of lung segmentation (2.79 to 2.47) and registration (2.90 to 2.87). Comparison of 100 landmarks in seven datasets of the previous report shows no significant change in the mean Euclidean error of 0.6 mm. Evaluation in the publicly available DIR-Lab data with 300 annotations results in a mean Euclidean error of 5.2 mm in the 10 4D cases and 8.9 mm in the 10 inspiration/expiration cases.

Improved registration of DCE-MR images of the liver by adding prior information into autocorrelation of local image structure (ALOST)

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In Dynamic Contrast-Enhanced MRI (DCE-MRI) of the liver, a series of images is acquired over a period of 20 minutes. Due to the patient’s breathing, the liver is subject to quite a displacement between acquisitions. Furthermore, due to its location in the abdomen, the liver also undergoes marked deformation. As a result, accurate liver registration is challenging. We present a registration framework that incorporates a liver segmentation to improve the registration accuracy. The segmented liver acts as prior knowledge to our in-house developed registration method called ALOST. Autocorrelation of local image structure (ALOST) is a continuous optimization method, which uses local phase features to overcome space-variant intensity distortions. The proposed framework can restrain the solution field to the liver and allow for ALOST to obtain a more accurate solution. In the prior segmentation part, we semi-automatically identify the liver in a hepatic phase volume (20 min after the contrast agent was injected). Subsequently, we apply the segmentation as a mask to the other DCE-MRI volumes during registration. It is shown that the registration result becomes more accurate compared with the original ALOST approach. [In the full paper, a semi-automatic liver segmentation method is developed that takes liver shape and intensity characteristics over time into consideration to further improve the accuracy and efficiency of the registration.]

Precise anatomy localization in CT data by an improved probabilistic tissue type atlas

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Automated interpretation of CT scans is an important, clinically relevant area as the number of such scans is increasing rapidly and the interpretation time consuming. Anatomy localization is an important prerequisite for any such interpretation task. This can be done by image-to-atlas registration, where the atlas serves as a reference space for annotations such as organ probability maps. Tissue type based atlases allow fast and robust processing of arbitrary CT scans. Here we present two methods which significantly improve organ localization based on tissue types. A first problem is the definition of tissue types, which until now is done heuristically based on experience. We present a method to determine suitable tissue types from sample images automatically. A second problem is the restriction of the transformation space: all prior approaches
use global affine maps. We present a hierarchical strategy to refine this
global affine map. For each organ or region of interest a localized tissue
type atlas is computed and used for a subsequent local affine registration
step. A three-fold cross validation on 311 CT images with different fields-of-
view demonstrates a reduction of the organ localization error by 33%.

9784-150, Session PS6

A first step toward uncovering the truth about weight tuning in deformable image registration

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Deformable image registration is currently predominantly solved by
optimizing a weighted linear combination of objectives. Successfully tuning
the weights associated with these objectives is not trivial, leading to trial-
and-error approaches. Such an approach assumes an intuitive interplay
between weights, optimization objectives and target registration errors.
However, it is not known whether this always holds for existing registration
methods. To investigate the interplay between weights, optimization
objectives and registration errors, we employ multi-objective optimization.
Here, objectives of interest are optimized simultaneously, causing a set
of multiple optimal solutions to exist, called the optimal Pareto front. Our
medical application is in breast cancer and includes the very hard prone-
supine registration problem. In total, we study the interplay in three different
ways. First, we run many random linear combinations of objectives using
the well-known registration software elastix. Second, since the optimization
algorithms used in registration are typically of a local-search nature, final
solutions may not always form a Pareto front. We therefore employ a
multi-objective evolutionary algorithm that finds weights that correspond
solutions may not always form a Pareto front. We therefore employ a
multi-objective evolutionary algorithm that finds weights that correspond
of different objectives and registration errors, we employ multi-objective optimization.
Here, objectives of interest are optimized simultaneously, causing a set
of multiple optimal solutions to exist, called the optimal Pareto front. Our
medical application is in breast cancer and includes the very hard prone-
supine registration problem. In total, we study the interplay in three different
ways. First, we run many random linear combinations of objectives using
the well-known registration software elastix. Second, since the optimization
algorithms used in registration are typically of a local-search nature, final
solutions may not always form a Pareto front. We therefore employ a
multi-objective evolutionary algorithm that finds weights that correspond
solutions may not always form a Pareto front. We therefore employ a
multi-objective evolutionary algorithm that finds weights that correspond

9784-151, Session PS6

Multi-modal co-registration via multi-
scale textural and spectral embedding representations

Lin Li, Case Western Reserve Univ. (United States)

Intensity-based similarity measures assume that the original signal
intensity of different modality images can provide statistically consistent
information about the two modalities to be co-registered. However in
multi-modal registration problems, intensity-based similarity measures are
very often inadequate to identify an optimal transformation. Texture
features, e.g. Gabor wavelets, can improve the performance of the multi-
modal co-registration by providing a more similar appearance than intensity.
Furthermore, texture features extracted at different length scales (window
sizes) can provide different details of the underlying structural information.
In this paper we introduce a novel approach for multi-modal co-registration
using mutual information (MI). Our approach uses Independent Component
Analysis (ICA) to identify statistical independent components of Gabor
and Haralick features. Since ICA based schemes do not tend to rank the

9784-152, Session PS6

Smart grid initialization reduces the computational complexity of multi-
objective image registration based on a dual-dynamic transformation model to
account for large anatomical differences

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We recently demonstrated the strong potential of using dual-dynamic
transformation models when tackling deformable image registration
problems involving large anatomical differences. Dual-dynamic
transformation models employ two moving grids instead of the common
single moving grid for the target image (and single fixed grid for the source
image). We previously employed powerful optimization algorithms to make
use of the additional flexibility offered by a dual-dynamic transformation model with good results, directly obtaining insight into the trade-off
between important registration objectives as a result of taking a multi-
objective approach to optimization. However, optimization has so far been
initialized using two regular grids, which still leaves a great potential of
dual-dynamic transformation models untapped: a-priori grid alignment
with image structures/areas that are expected to deform more. This allows
(far) less grid points to be used, compared to using a sufficiently refined
regular grid, leading to (far) more efficient optimization, or, equivalently,
more accurate results using the same number of grid points. We study the
implications of exploiting this potential by experimenting with two new
smart grid initialization procedures: one manual expert-based and one
automated image-feature-based. We consider a CT test case with large
differences in bladder volume with and without a multi-resolution scheme
and find a substantial benefit of using smart grid initialization.

9784-153, Session PS6

Accurate quantification of local changes for carotid arteries in 3D ultrasound images using convex optimization-based
deformable registration

Jieyu Cheng, City Univ. of Hong Kong (Hong Kong, China);
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Kong (Hong Kong, China)

An accurate registration of carotid images greatly helps to monitor,
characterize, and quantify progression/regression of carotid atherosclerotic
burden in response to therapies. With this regard, we introduce a new
image-based non-rigid registration method, in this work, to align the input
baseline 3D carotid Ultrasound (US) image onto another image acquired at
an different time session, which essentially minimizes the sum of absolute
intensity differences (SAD) under a variational optical-flow perspective. In addition, a multi-scale optimization framework is implemented to capture locally large deformations.

The proposed 3D non-rigid registration approach was evaluated by measuring the overlap between the deformed manually segmented surfaces of both vessel-wall and lumen at baseline and the corresponding segmentation surfaces at follow-up time point with multiple metrics, e.g., Dice similarity coefficient (DSC) and mean absolute distance (MAD). It was tested over 5 subjects and, comparing to the initial rigid registration, yielded an outstanding improvement in accuracy: a mean DSC of textbf{79.3$pm$3.8%} (rigid: 73.9$pm$3.4%) for lumen and textbf{85.9$pm$4.0%} (rigid: 84.7$pm$3.2%) for outer-wall, and a mean MAD of textbf{0.46$pm$0.08 mm} (rigid: 0.55$pm$0.08 mm) for lumen and textbf{0.52$pm$0.13 mm} (rigid: 0.54$pm$0.11 mm) for outer-wall. This showed the promising potential of the proposed approach for accurately assessing local changes in atherosclerotic burden over time.

9784-154, Session PS6

FLIRT: an open-software suite for real-time 2D/3D image registration for image guided radiotherapy research

Hugo C. Furtado, Medizinische Univ. Wien (Austria) and Christian Doppler Lab. for Medical Radiation Research for Radiation Oncology (Austria); Christelle Gendrin, Jakob Spoer, Elisabeth Steiner, Medizinische Univ. Wien (Austria); Tracy Underwood, Institut Univ. du Cancer de Toulouse (France); Thomas Kuenzler, Institut für Medizinische Physik, Landeskrankenhaus Feldkirch (Austria); Dietmar Georg, Wolfgang Birkfellner, Medizinische Univ. Wien (Austria).

Radiotherapy treatments have changed at a tremendously rapid pace. Dose delivered to the tumor has escalated while organs at risk (OARs) are better spared. The impact of moving tumors during dose delivery has become higher due to very steep dose gradients. Intra-fractional tumor motion has to be managed adequately to reduce errors in dose delivery. For tumors with large motion such as tumors in the lung, tracking is an approach that can reduce position uncertainty. Tumor tracking approaches range from purely image intensity based techniques to motion estimation based on surrogate tracking.

Research efforts are often based on custom designed software platforms which take too much time and effort to develop. To address this challenge we have developed an open software platform especially focusing on tumor motion management.

FLIRT is a freely available open-source software platform. The core method for tumor tracking is purely intensity based 2D/3D registration. The platform is written in C++ using the Qt framework for the user interface. The performance critical methods are implemented on the graphics processor using the CUDA extension. One registration can be as fast as 90ms (1Hz).

This is suitable to track tumors moving due to respiration (~0.3Hz) or heartbeat (~1Hz). Apart from focusing on high performance, the platform is designed to be flexible and easy to use. Current use cases range from tracking feasibility studies, patient positioning and method validation. Such a framework has the potential of enabling the research community to rapidly perform patient studies or try new methods.

9784-156, Session PS6

Deformable image registration with a featurelet algorithm: implementation as a 3D-slicer extension and validation

Andreas Renner, Hugo C. Furtado, Yvette Seppenwoolde, Wolfgang Birkfellner, Dietmar Georg, Medizinische Univ. Wien (Austria).

A radiotherapy (RT) treatment can last for several weeks. In that time organ motion and shape changes introduce uncertainty in dose application. Monitoring and quantifying the change can yield a more precise irradiation margin definition and thereby reduce dose delivery to healthy tissue and adjust tumor targeting. Deformable image registration (DIR) has the potential to fulfill this task by calculating a deformation field (DF) between a planning CT and a repeated CT of the altered anatomy. Application of the DF on the original contours yields new contours that can be used for an adapted plan. DIR is a challenging method and therefore needs careful user interaction. Without a proper graphical user interface (GUI) a misregistration cannot be easily detected by visual inspection and the results cannot be fine-tuned by changing registration parameters. To provide a DIR algorithm with such a GUI available for everyone, we created the extension Featurelet-Registration for the open source software platform 3D Slicer. The registration logic is an upgrade of an in-house-developed DIR method, which is a featurelet-based piecewise rigid registration. The so called „featurelets“ are equally sized rectangular subvolumes of the moving image which are rigidly registered to rectangular search regions on the fixed image. The output is a deformed image and a deformation field. Both can be visualized directly in 3D Slicer facilitating the interpretation and quantification of the results. For validation of the registration accuracy two deformable phantoms were used. The performance was benchmarked against a demons algorithm with comparable results.

9784-155, Session PS6

In-vivo cell tracking to quantify endothelial cell migration during zebrafish angiogenesis

Prahlad G. Menon, Duquesne Univ. (United States) and Univ. of Pittsburgh (United States); Elizabeth R. Rochon, Beth L. Roman, Univ. of Pittsburgh (United States)

The mechanism of endothelial cell migration as individual cells or collectively while remaining an integral component of a functional blood vessel has not been well characterized. An understanding of such cell migration patterns will help biologists demystify the mechanisms of vascular remodeling. In addition, questions concerning how external factors such as blood flow and genetics interact and affect cellular processes are just beginning to be asked. Zebrafish are an ideal vertebrate model for imaging based in-vivo inspection of cellular migration owing to its innate transparency. As imaging techniques become more sensitive and the toolbox of transgenic zebrafish grows, data acquisition is no longer a limiting factor for vascular development studies; whereas the ability to accurately track endothelial cells as they migrate within a functional vessel wall, under a variety of conditions (i.e. blood flow, drug treatments, genetic manipulations), has been found wanting due to difficulty in extracting pertinent data from these cellular tracks. In this study, our overarching goal is to define an image processing workflow to facilitate quantification of endothelial cell movements within the first aortic arch at the onset of heartbeat and blood flow. Endothelial cell imaging was conducted at this developmental time-point i.e. 24-28 hours post fertilization (hpf) when flow first begins, using 3D+time two-photon confocal microscopy of a live, wild-type, transgenic, zebrafish expressing green fluorescent protein (GFP) in endothelial cell nuclei. An image processing pipeline comprised of image signal enhancement, median filtering for speckle noise reduction, automated identification of the nuclei positions, extraction of the relative movement of nuclei between consecutive time instances, and final tracking of nuclei, was designed for achieving the tracking of endothelial cell nuclei and the identification of their movement towards or away from the heart. Pilot results lead to a hypothesis that upon the onset of heart beat and blood flow, endothelial cells migrate collectively towards the heart (by 21.31±10.35 ?m) in opposition to blood flow (i.e. subtending 142.17±21.17 degrees with the flow direction).

In-vivo cell tracking to quantify endothelial cell migration during zebrafish angiogenesis

Prahlad G. Menon, Duquesne Univ. (United States) and
9784-41, Session 9

On the fallacy of quantitative segmentation for T1-weighted MRI

Andrew J. Plassard, Robert L. Harrigan, Allen T. Newton, Vanderbilt Univ. (United States); Swati Rane, Univ. of Washington (United States); Srivastava Pallavaram, Pierre F. D’Haese, Benoit M. Dawant, Daniel O. Claassen, Bennett A. Landman, Vanderbilt Univ. (United States)

T1-weighted magnetic resonance imaging (MRI) generates contrasts with primary sensitivity to local T1 properties (with lesser T2 and PD contributions). The observed signal intensity is determined by these local properties and the sequence parameters of the acquisition. In common practice, a range of acceptable parameters is used to ensure “similar” contrast across scanners used for any particular study (e.g., the ADNI standard MPRAPE). However, different studies may use different ranges of parameters and report the derived data as simply “T1-weighted”. Physics and imaging authors pay strong heed to the specifics of the imaging sequences, but image processing authors have historically been more lax. Herein, we consider three T1-weighted sequences acquired the same underlying protocol (MPRAPE) and vendor (Philips), but “normal study-to-study variation” in parameters. We show that the gray matter/white matter/cerebrospinal fluid contrast is subtly but systematically different between these images and yields systematically different measurements of brain volume. The problem derives from the visually apparent boundary shifts, which would also be seen by a human rater. We present and evaluate two solutions to produce consistent segmentation results across imaging protocols. First, we propose to acquire multiple sequences on a subset of the data and use the multi-modal imaging as atlases to segment target images any of the available sequences. Second (if additional imaging is not available), we propose to synthesize atlases of the target imaging sequence and use the synthesized atlases in place of atlas imaging data. Both approaches significantly improve consistency of target labeling.

9784-42, Session 9

Computed tomography synthesis from magnetic resonance images of the pelvic region by a combination of random classification and regression forests and auto-context features

Daniel Andreasen, Technical Univ. of Denmark (Denmark) and Gentofte and Herlev Hospital (Denmark); Jens M. Edmund, Gentofte and Herlev Hospital (Denmark); Vasileios Zografos, Bjoern H. Menze, Technische Univ. München (Germany); Koen Van Leemput, Technical Univ. of Denmark (Denmark) and A.A. Martinos Ctr. for Biomedical Imaging, Massachusetts General Hospital (United States)

In radiotherapy treatment planning that is only based on magnetic resonance imaging (MRI), the electron density information usually obtained from a computed tomography (CT) must be derived from the MRI by synthesizing a so-called pseudo CT (pCT). This is a non-trivial task since MRI intensities are neither uniquely nor quantitatively related to electron density. Typical approaches involve either a voxel-based classification or regression model or an atlas-based model, requiring either specialized MRI sequences to solve intensity ambiguities or multiple registrations between atlas and subject scans.

In this work, we explore a machine learning approach for creating a pCT of the pelvic region from conventional MRI sequences by using a random forest. Input to the algorithm is information about local texture, edges and spatial features derived from the MRI, that help to solve intensity ambiguities. Furthermore, we use the concept of auto-context by sequentially training a number of classification forests to create and improve context features that we ultimately use to train a regression forest for pCT prediction.

We evaluate the pCT quality in terms of the voxel-wise error and the radiologic accuracy as measured by water equivalent path lengths. We compare the performance of our method against baseline pCT strategies, which either set all MRI voxels in the subject equal to the CT value of water, or in addition transfers the bone volume from the real CT. We show an improved performance compared to both of these approaches suggesting that our method may be useful for MRI-only radiotherapy.

9784-43, Session 9

Endoscopic-CT: learning-based photometric reconstruction for endoscopic sinus surgery

Austin Reiter, Simon Leonard, Ayushi Sinha, Masaru Ishii, Russell H. Taylor, Gregory D. Hager, Johns Hopkins Univ. (United States)

In this work we present a method for dense reconstruction of anatomical structures using white light endoscopic imagery based on a learning process that estimates a mapping between light reflectance and surface geometry. Our method is unique in that few unrealistic assumptions are considered (i.e., we do not assume a Lambertian reflectance model nor do we assume a point light source) and we learn a model on a per-patient basis, thus increasing the accuracy and extensibility to different endoscopic sequences. The proposed method assumes accurate video-CT registration through a combination of Structure-from-Motion (SfM) and Trimmed-ICP, and then uses the registered 3D structure and motion to generate training data with which to learn a multivariate regression of observed pixel values to known 3D surface geometry. We demonstrate with a non-linear regression technique using a neural network towards estimating depth images and surface normal maps, resulting in high-resolution spatial 3D reconstructions to an average error of 0.53mm (on the low side, when anatomy matches the CT precisely) to 1.12mm (on the high side, when the presence of liquids causes scene geometry that is not present in the CT for evaluation). Our results are exhibited on patient data and validated with associated CT scans. In total, we processed 206 total endoscopic images from patient data, where each image yields approximately 1 million reconstructed 3D points per image.

9784-44, Session 9

Framework for quantitative evaluation of 3D vessel segmentation approaches using vascular phantoms in conjunction with 3D landmark localization and registration

Stefan Wörz, Deutsches Krebsforschungszentrum (Germany) and Ruprecht-Karls-Univ. Heidelberg (Germany); Philipp Hoegen, UniversitätsKlinikum Heidelberg (Germany); Wei Liao, Ruprecht-Karls-Univ. Heidelberg (Germany); Matthias Müller-Eschner, Hans-Ulrich Kauczor, UniversitätsKlinikum Heidelberg (Germany); Hendrik von Tengg-Kobligk, Inselspital Bern (Switzerland); Karl Rohr, Ruprecht-Karls-Univ. Heidelberg (Germany)

We introduce a framework for quantitative evaluation of 3D vessel segmentation approaches using vascular phantoms. Phantoms are designed using a CAD system and created with a 3D printer, and comprise realistic shapes including branches and pathways such as abdominal aortic aneurysms (AAA). To transfer ground truth information to the 3D
Optical coherence tomography (OCT) is a noninvasive imaging modality that has begun to find widespread use in retinal imaging for the detection of a variety of ocular diseases. In addition to structural changes in the form of altered retinal layer thicknesses, pathological conditions may also cause the formation of edema within the retina. In multiple sclerosis, for instance, the nerve fiber and ganglion cell layers are known to thin. Additionally, the formation of pseudocysts called microcystic macular edema (MME) have also been observed in about 5% of MS patients, and its presence has been shown to be correlated with disease severity. Separate algorithms have previously been developed to segment the retinal layers and MME, but since MME occur within specific regions of the retina, a simultaneous approach is advantageous. In this work, we propose an automated globally optimal graph-theoretic approach that simultaneously segments the retinal layers and the MME in volumetric OCT scans. SD-OCT scans from one eye of 12 MS patients and 8 healthy controls were acquired and the pseudocysts manually traced. The overall precision and recall of the pseudocyst detection was found to be 0.85 and 0.87, respectively.

Learning of anatomical views and measurements from redundant but inconsistent reference data for 3D sonographic fetal brain screening

Irina Waechter-Stehle, Tobias Klinder, Cristian Lorenz, Philips Research (Germany); Jean Michel Rouet, Philips France (France); David Roundhill, Gary Andrews, Philips Ultrasound, Inc. (United States); Angelo Cavallaro, Raffaele Napolitano, Malid Molloholli, Tess Norris, Univ. of Oxford (United Kingdom); Aris Papageorgiou, Univ. of Oxford (United Kingdom)

In a fetal brain screening examination, a standardized set of anatomical views is inspected and certain biometric measurements are taken in these views. Acquisition of recommended planes requires a certain level of operator expertise. 3D ultrasound has the potential to reduce the manual task to only capture a volume containing the head and to subsequently determine the standard 2D views and measurements automatically. For this purpose, a segmentation model of the fetal brain was created and trained with expert annotations. It was found that the annotations show a considerable intra- and inter-observer variability. To handle the variability, we propose a method to train the model with redundant but inconsistent reference data from many expert users. If the outlier-cleaned average of all reference annotations is considered as ground truth, errors of the automatic view detection are lower than the errors of all individual users and errors of the measurements are in the same range as user error. The resulting functionality allows the completely automated estimation of views and measurements in 3D fetal ultrasound images.

Breast segmentation in MRI using Poisson surface reconstruction initialized with random forest edge detection

Anne L. Martel, Sunnybrook Research Institute (Canada); Cristina Gallego-Ortiz, Univ. of Toronto (Canada); Yingli Lu, Sunnybrook Research Institute (Canada)

Brain tumor segmentation from multi-modal magnetic resonance (MR) images is of high value in radiotherapy planning, as well as when monitoring tumor growth and investigating treatment response. Automatic tumor segmentation is challenging since tumor location, shape and appearance vary greatly across patients. Moreover, brain tumor images often exhibit significant intensity inhomogeneity as well as large intensity variations between subjects, particularly when they are acquired with different scanners or at different imaging facilities.

Most current state-of-the-art methods in brain tumor segmentation exploit the specific intensity contrast information of annotated training images, which hinders their applicability to images acquired with different imaging protocols. In this paper we propose a fully automated generative model that achieves segmentation accuracy comparable to the current state of the art while being readily extendable to any number of input contrasts and not tied to any specific imaging protocol.

The method is based on the type of generative model often used for segmenting healthy brain tissues, where tissues are modeled by Gaussian mixture models combined with a spatial tissue prior. We extend this basic model with a tumor prior, which uses convolutional restricted Boltzmann machines (RBMs) to model the shape of complete tumor, including edema, and tumor core. The RBMs are trained on the annotations of annotated training images, without the use of the intensity information in the training images. Experiments on public benchmark data of patients suffering from low- and high-grade gliomas show that the method's performance is comparable to current state-of-the-art methods.

Simultaneous segmentation of retinal surfaces and microcystic macular edema in SD-OCT volumes

Bhavna J. Antony, Andrew Lang, Johns Hopkins Univ. (United States); Emily K. Swingle, The Ohio State Univ. (United States); Omar Al-Louzi, Aaron Carass, Sharon D. Solomon, Peter A. Calabresi, Shiv Saidha, Jerry L. Prince, Johns Hopkins Univ. (United States)

Optical coherence tomography (OCT) is a noninvasive imaging modality...
Pathologies of the optic nerve and orbit impact millions of Americans and
States). Bennett A. Landman, Vanderbilt Univ. (United States); Yifu Luo, Robert L. Harrigan, Stephen M. Bennett (United States); Kevin Mundy, Vanderbilt Univ. Medical Ctr. (United States); Shikha Chaganti, Katrina M. Nelson, Vanderbilt Univ. (United States).

Structural functional associations of the orbit in thyroid eye disease: Kalman filters to track extraocular rectal muscles
Shikha Chaganti, Katrina M. Nelson, Vanderbilt Univ. (United States); Kevin Mundy, Vanderbilt Univ. Medical Ctr. (United States); Yifu Luo, Robert L. Harrigan, Stephen M. Damon, Daniel Fabbri, Vanderbilt Univ. (United States); Louise A. Mawn, Vanderbilt Univ. Medical Ctr. (United States); Bennett A. Landman, Vanderbilt Univ. (United States)

Simultaneous macula detection and optic disc boundary segmentation in retinal fundus images
Fantin Girard, Ecole Polytechnique de Montreal (Canada); Conrad Kavalec, St. Mary’s Hospital Ctr. (Canada); Sébastien Grenier, Ecole Polytechnique de Montréal (Canada); Housssem Ben Tahar, DIAGNOS Inc. (Canada); Farida Cheriet, Ecole Polytechnique de Montréal (Canada)

Quality assurance using outlier detection on an automatic segmentation method for the cerebellar peduncles
Ke Li, Johns Hopkins Univ. (United States); Chuyang Ye, Brainnetome Ctr., Institute of Automation (China); Zhen Yang, Aaron Carass, Johns Hopkins Univ. (United States); Sarah H. Ying, The Johns Hopkins School of Medicine (United States); Jerry L. Prince, Johns Hopkins Univ. (United States)

The optic disc (OD) and the macula are important structures in automatic diagnosis of most retinal diseases inducing vision defects such as glaucoma, diabetic or hypertensive retinopathy and age-related macular degeneration. We propose a new method to detect simultaneously the macula and the OD boundary. First, the color fundus images are processed to compute several maps highlighting the different anatomical structures such as vessels, the macula and the OD. Then, macula candidates and OD candidates are found simultaneously and independently using seed detectors identified on the corresponding maps. After selecting a set of macula/OD pairs, the top candidates are sent to the OD segmentation method. The segmentation method is based on local K-means applied to color coordinates in polar space followed by a polynomial fitting regularization step. Pair scores are updated, resulting in the final best macula/OD pair. The method was evaluated on two public image databases: ONHSD and MESSIDOR. The results show an overlapping area of 0.84 on ONHSD and 0.90 on MESSIDOR, which is better than recent state of the art methods. Our segmentation method is robust to contrast and illumination problems and outputs the exact boundary of the OD, not just a circular or elliptical model.

The macula detection has an accuracy of 94%, which again outperforms other macula detection methods. This shows that combining the OD and macula detections improves the overall accuracy. The computation time for the whole process is 6.4 seconds, which is faster than other methods in the literature.

Cerebellar peduncles (CPs) are white matter tracts connecting the cerebellum to other brain regions. Automatic segmentation methods of the CPs have been proposed for studying their structure and function. Usually the performance of these methods is evaluated by comparing segmentation results with manual delineations (ground truth). However, when a segmentation method is run on new data (for which no ground truth exists) it is highly desirable to efficiently detect and assess algorithm failures so that these cases can be excluded from scientific analysis. In this work, two outlier detection methods aimed at assessing the performance of an automatic CP segmentation algorithm are presented. The first one is a univariate non-parametric method using a box-whisker plot. We first categorize automatic segmentation results of a database of diffusion tensor imaging (DTI) scans from 48 subjects as either a success or a failure. We then design three kinds of features from the image data of nine categorized failures for failure detection. Results show that most of these features can efficiently detect the true failures. The second method—supervised classification—was employed on a larger DTI dataset of 249 manually categorized subjects. Four classifiers—linear discriminant analysis (LDA), logistic regression (LR), support vector machine (SVM), and random forest classification (RFC)—were trained using the designed features and evaluated using a leave-one-out cross-validation. Results show that the LR performs worst among the four classifiers and the other three perform comparably, which demonstrates the feasibility to automatically detect segmentation failures using classification methods.

Quality assurance using outlier detection on an automatic segmentation method for the cerebellar peduncles
Ke Li, Johns Hopkins Univ. (United States); Chuyang Ye, Brainnetome Ctr., Institute of Automation (China); Zhen Yang, Aaron Carass, Johns Hopkins Univ. (United States); Sarah H. Ying, The Johns Hopkins School of Medicine (United States); Jerry L. Prince, Johns Hopkins Univ. (United States)

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The macula detection has an accuracy of 94%, which outperforms other methods in the literature.
9784-53, Session 11

**A learning-based, fully automatic liver tumor segmentation pipeline based on sparsely annotated training data**

Michael Goetz, Eric Heim, Keno Maerz, Tobias Norajitra, Deutsches Krebsforschungszentrum (Germany); Mohammadreza R. Hafezi, Nassim Fard, Arianeh Mehrabi, Ruprecht-Karls-Univ. Heidelberg (Germany); Max Knoll, Christian Weber, Deutsches Krebsforschungszentrum (Germany); Lena Maier-Hein, Klaus H. Maier-Hein, Deutsches Krebsforschungszentrum (Germany)

Current fully automatic liver tumor segmentation systems are designed to work on a single CT-image. This hinders these systems from the detection of more complex types of liver tumor. We therefore present a new algorithm for liver tumor segmentation that allows incorporating different CT scans and requires no manual interaction. We derive a liver segmentation with state-of-the-art shape models which are robust to initialization. The tumor segmentation is then achieved by classifying all voxels into healthy or tumorous tissue using Extremely Randomized Trees with an auto-context learning scheme. Using DALSA enables us to learn from only sparse annotations and allows a fast set-up for new image settings. We validate the quality of our algorithm with exemplary segmentation results.

9784-54, Session 11

**SVM-based failure detection of GHT localizations**

Thomas Blaffert, Cristian Lorenz, Hannes Nickisch, Jochen Peters, Jürgen Weese, Philips Research (Germany)

This paper addresses the localization of anatomical structures in medical images by a Generalized Hough Transform (GHT). As localization is often a pre-requisite for subsequent model-based segmentation, it is important to assess whether or not the GHT was able to locate the desired object. The GHT by its construction does not make this distinction. We present an approach to detect incorrect GHT localizations by deriving collective features of contributing GHT model points and by training a Support Vector Machine (SVM) classifier. On a training set of 204 cases, we demonstrate that for the detection of incorrect localizations classification errors of down to 3% are achievable. This is three times less than the observed intrinsic GHT localization error.

9784-55, Session 11

**Embedded sparse representation of fMRI data via group-wise dictionary optimization**

Dajiang Zhu, Univ. of Southern California (United States); Binbin Lin, Univ. of Michigan (United States); Joshua Faskowitz, Univ. of Southern California (United States); Jieping Ye, Univ. of Michigan (United States); Paul M. Thompson, Univ. of Southern California (United States)

Sparse learning enables dimension reduction and efficient modeling of high dimensional signals and images, but it may need to be tailored to best suit specific applications and datasets. Here we used sparse learning to efficiently represent functional magnetic resonance imaging (fMRI) data from the human brain. We propose a novel embedded sparse representation (ESR), to identify the most consistent dictionary atoms across different brain datasets via an iterative group-wise dictionary optimization procedure. In this framework, we introduced additional criteria to make the learned dictionary atoms more consistent across different subjects. We successfully identified four common dictionary atoms that follow the external task stimuli with very high accuracy. After projecting the corresponding coefficient vectors back into the 3-D brain volume space, the spatial patterns are also consistent with traditional fMRI analysis results. Our framework reveals common features of brain activation in a population, as a new, efficient fMRI analysis method.

9784-56, Session 11

**Genome-wide association study of coronary and aortic calcification in lung cancer screening CT**

Bob D. De Vos, Jessica Van Setten, Pim A. de Jong, Willem P. T. M. Mali, Univ. Medical Ctr. Utrecht (Netherlands); Matthijs Oudkerk, Univ. Medical Ctr. Groningen (Netherlands); Max A. Viergever, Ivana Isgum, Univ. Medical Ctr. Utrecht (Netherlands)

Articular calcification has been related to cardiovascular disease (CVD) and osteoporosis. However, little is known about the role of genetics and exact pathways leading to articular calcification and its relation to bone density changes indicating osteoporosis.

In this study, we conducted a genome-wide association study of articular calcification burden, followed by a look-up of known single nucleotide polymorphisms (SNPs) for coronary artery disease (CAD) and myocardial infarction (MI), and bone mineral density (BMD) to test for a shared genetic basis between the traits.

The study included a subcohort of Dutch-Belgian lung cancer screening trial comprised of 2,552 participants. The participants underwent baseline CT scanning in one of two hospitals participating in the trial. Low-dose chest CT images were acquired without contrast enhancement and without ECG-synchronization. In these images coronary and articular calcifications were identified automatically. Subsequently, the detected calcifications were quantified using Agatston and volume scores.

Genotype data was available for these participants. A genome-wide association study was conducted on 10,220,814 SNPs using a linear regression model to reduce multiple testing burden, known CAD/MI and BMD SNPs were specifically tested (45 SNPs from the CARDioGRAMplusC4D consortium and 60 SNPs from the GEFOS consortium). No novel significant SNPs were found. Significant enrichment for CAD/MI SNPs were observed in testing Agatston and coronary volume scores, and moreover a significant enrichment of BMD SNPs was shown in aorta volume scores. This may indicate genetic relation of BMD SNPs and articular calcification burden.

9784-57, Session 12

**Automatic localization of landmark sets in head CT images with regression forests for image registration initialization**

Dongqing Zhang, Yuan Liu, Jack H. Noble, Benoit M. Dawant, Vanderbilt Univ. (United States)

Cochlear Implants (CIs) are electrode arrays that are surgically inserted into the cochlea. Individual contacts stimulate frequency-mapped nerve endings thus replacing the natural electro-mechanical transduction mechanism. CIs are programmed post-operatively by audiologists but this is currently done using behavioral tests without imaging information that permits relating electrode position to inner ear anatomy. We have recently developed a series of image processing steps that permit the segmentation of the inner ear anatomy and the localization of individual contacts. We have proposed a new programming strategy that uses this information and we have shown in a study with more than 100 participants that hearing was improved in 72% of long term recipients when this strategy is used. A limiting factor to
Semi-automated registration of pre- and intra-operative liver CT for image-guided interventions

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Percutaneous radio frequency ablation (RFA) is a promising method for liver tumor resection when conventional surgery is not preferred. RFA is a minimally invasive treatment and performed under CT image guidance. For optimal guidance, registration of the high-quality pre-operative CT image to the low-quality intra-operative CT image is required. This is a highly challenging registration task due to large differences in pose and image quality. In this study, we introduce a semi-automated registration algorithm to address this problem. The method is based on a conventional nonrigid intensity-based registration framework, extended with a novel point-to-surface constraint. The point-to-surface constraint serves to improve the alignment of the liver boundary, while requiring minimal user interaction during the operation. The method assumes that for the pre-operative CT, a liver segmentation is available. During the intervention, the operator needs to click only a few points on the liver boundary in the intra-operative CT. These points in the intraoperative image are driven towards the surface boundary on the pre-operative image, using a penalty term that is added to the registration cost function. The algorithm is tested on five real datasets acquired during clinical interventions and it is shown to outperform conventional rigid and non-rigid registrations in all cases.

Evaluation of body-wise and organ-wise registrations for abdominal organs

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Identifying cross-sectional and longitudinal correspondence in the abdomen on computed tomography (CT) scans is necessary for quantitatively tracking change and understanding population characteristics, yet abdominal image registration is a challenging problem. The key difficulty in solving this problem is huge variations in organ dimensions and shapes across subjects. The current standard registration method uses the global or body-wise registration technique, which is based on the global topology for alignment. This method (although producing decent results) has substantial influence of outliers, thus leaving room for significant improvement. Here, we study a new image registration approach using local (organ-wise registration) by first creating organ-specific bounding boxes and then using these regions of interest (ROIs) for aligning references to target. Based on Dice Similarity Coefficient (DSC), Mean Surface Distance (MSD) and Hausdorff Distance (HD), the organ-wise approach is demonstrated to have significantly better results by minimizing the distorting effects of organ variations. This paper compares exclusively the two registration methods by providing novel quantitative and qualitative comparison data and is a subset of the more comprehensive problem of improving the multi-atlas segmentation by using organ normalization.

3D prostate MR-TRUS non-rigid registration using dual optimization with volume-preserving constraint

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We introduce an efficient and novel convex optimization-based approach to the challenging non-rigid registration of 3D prostate magnetic resonance (MR) and transrectal ultrasound (TRUS) images, which incorporates a new volume preserving constraint to essentially improve the accuracy of targeting suspicious regions during the 3D TRUS guided prostate biopsy. Especially, we propose a fast sequential convex optimization scheme to efficiently minimize the employed highly nonlinear image fidelity function using the robust multi-channel modality independent neighborhood descriptor (MIND) across the two modalities of MR and TRUS. The registration accuracy was evaluated using 10 patient images by calculating the target registration error (TRE) using manually identified corresponding intrinsic fiducials in the whole prostate gland. We also compared the MR and TRUS manually segmented prostate surfaces in the registered images in terms of the Dice similarity coefficient (DSC), mean absolute surface distance (MAD), and maximum absolute surface distance (MAXD). Experimental results showed that the proposed method with the introduced volume-preserving prior significantly improves the registration accuracy comparing to the method without the volume-preserving constraint, by yielding an overall mean TRE of 2.0±0.7 mm, and an average DSC of 86.5±3.5%, MAD of 1.4±0.6 mm and MAXD of 6.5±3.5 mm.

Robust endoscopic pose estimation for intraoperative organ-mosaicking

Daniel Reichard, Sebastian Bodenstedt, Stefan Suwelack, Karlsruher Institut für Technologie (Germany); Martin Wagner, Hannes Kenngott, Universität Klinikum Heidelberg (Germany); Beat Müller-Stich, Heidelberg School of Medicine (Germany); Rüdiger Dillmann, Stefanie Speidel, Karlsruher Institut für Technologie (Germany)

The number of minimally invasive procedures is growing every year. These procedures are highly complex and very demanding for the operating surgeons. It is therefore important to provide intraoperative assistance to alleviate these difficulties. For most computer-assistance systems, like augmented reality, a registration step is required to map preoperative data (e.g. CT images) to the ongoing intraoperative scene. Without additional hardware, the (stereo-) endoscope is the prime intraoperative data source and with it, stereo-reconstruction methods can be used to obtain 3D models from target structures. To link reconstructed parts from different frames (mosaicking), the endoscope movement has to be known. In this paper, we present a camera tracking method that uses dense depth and feature registration which are combined with a Kalman Filter scheme. It provides a robust position estimation that shows promising results in ex vivo and in silico experiments.
The heritability of the functional connectome is robust to common nonlinear registration methods

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Nonlinear registration algorithms are routinely used in brain imaging, to align data for inter-subject and group comparisons, and for voxelwise statistical analyses. To understand how the choice of registration method affects maps of functional brain connectivity in a sample of 611 twins, we evaluated three popular nonlinear registration methods: Advanced Normalization Tools (ANTS), Automatic Registration Toolbox (ART), and FMRIBs Nonlinear Image Registration Tool (FNIRT). Using both structural and functional MRI, we used each of the three methods to align the MNI152 brain template, and 80 regions of interest (ROIs), to each subject’s T1-weighted (T1w) anatomical image. We then transformed each subject’s ROIs onto the associated resting state functional MRI (rs-fMRI) scans and computed a connectivity network or functional connectome for each subject. Given the different degrees of genetic similarity between pairs of monozygotic (MZ) and dizygotic (DZ) twins, we used structural equation modeling to estimate the additive genetic influences on the elements of the function networks, or their heritability. The functional connectome and derived statistics were relatively robust to nonlinear registration effects.
9785-1, Session 1

**Inner and outer coronary vessel wall segmentation from CCTA using an active contour model with machine learning-based 3D voxel context-aware image force**

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In this paper, we present a fully automated approach to coronary vessel segmentation, which involves calcification or soft plaque delineation in addition to accurate lumen delineation, from 3D Cardiac Computed Tomography Angiography data. Adequately virtualizing the coronary lumen plays a crucial role for simulating blood flow by means of fluid dynamics while additionally identifying the outer vessel wall in the case of arteriosclerosis is a prerequisite for further plaque compartment analysis. Our method is a hybrid approach complementing Active Contour Model-based segmentation with an external image force that relies on a Random Forest Regression model generated offline. The regression model provides a strong estimate of the distance to the true vessel surface for every surface candidate point taking into account 3D wavelet-encoded contextual image features, which are aligned with the current surface hypothesis. The associated external image force is integrated in the objective function of the active contour model, such that the overall segmentation approach benefits from the advantages associated with snakes and from the ones associated with machine learning-based regression alike. This yields an integrated combined approach achieving competitive results on a publicly available benchmark data collection (Rotterdam segmentation challenge).

9785-2, Session 1

**Automated identification of best-quality coronary artery segments from multiple-phase coronary CT angiography (cCTA) for vessel analysis**

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We are developing an automated method to identify the best quality segment among the corresponding segments in the multiple-phase CTA. The coronary artery trees are automatically extracted from different cCTA phases using our multi-scale vessel segmentation and tracking method. An automated registration method is then used to align the multiple-phase artery trees. The corresponding coronary artery segments are identified in the registered vessel trees and are strengthened by curved planar reformation (CPR). Four features are extracted from each segment in each phase as quality indicators in the original CT volume and the straightened CPR volume. Each quality indicator is used as a voting classifier to vote the corresponding segments. A newly designed weighted voting ensemble (WVE) classifier is finally used to determine the best-quality coronary segment. An observer preference study is conducted with five readers to visually rate the quality of the vessels in 1 to 6 ratings. Six and 20 CTA cases are used as training and test set in this study. For the 20 test cases, the agreement between automatically identified best-quality (AI-BQ) segments and radiologist’s top 2 ratings is 78.3%, and between AI-BQ and the other four readers are 76.4%, 84.3%, 84.3% and 87.0%, respectively. The analysis of inter-observer variation shows that the agreement of the top 2 ratings between the radiologist and the other 4 readers are 81.4%, 82.6%, 81.8% and 75.3%, respectively. The results demonstrated that the performance of our automated method was comparable to those of experienced readers for identification of the best-quality coronary segments.

9785-3, Session 1

**3D assessment of the carotid artery vessel wall volume: an imaging biomarker for diagnosis of the Atherosclerotic Disease**

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This study investigates a novel method of 3D evaluation of the carotid vessel wall using two different Magnetic Resonance (MR) sequences. The method focuses on energy minimization by level-set boundary evolution. The level-set framework allows for the introduction of prior knowledge that is learnt from some images on the solution. The lumen is detected using a 3D TOF sequence. The lumen MRA segmentation (contours) was then transferred and registered to the corresponding images on the Magnetic Resonance Imaging plaque hemorrhage (MRIPH) sequence. The 3D registration algorithm was applied to align the sequences. The same technique used for lumen detection was then applied to extract the outer wall boundary. Our preliminary results show that the segmentations are well correlated with those obtained from a 2D reference sequence (2D-TIWI). The estimated Vessel Wall Volume (VWV) can be used as an imaging biomarker to help radiologists diagnose and monitor atherosclerotic disease. Furthermore, the 3D map of the Vessel Wall Thickness (WVT) and Vessel Wall Signal Intensity may be used as complementary information to monitor disease severity.

9785-4, Session 1

**A system for automatic aorta sections measurements on chest CT**

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A new method is proposed for caliber measurement of the ascending aorta (AA) and descending aorta (DA). A key component of the method is the automatic detection of the carina, as an anatomical landmark around which an axial volume of interest (VOI) can be defined to observe the aortic caliber. For each slice in the VOI, a linear profile line connecting the AA with the DA is found by pattern matching on the underlying intensity profile. Next, the aortic center position is found using Hough transform on the best linear segment candidate. Finally, region growing around the center provides an accurate segmentation and caliber measurement. We evaluated the algorithm on 113 sequential chest CT scans, slice width 0.75-3.75mm, 90 with contrast. The algorithm success rates were computed as the percentage of scans in which the center of the AA was found. Automated measurements of AA caliber were compared with independent measurements of two experienced chest radiologists, comparing the absolute difference between the two radiologists with the absolute difference between the algorithm and each of the radiologists. The measurement stability was demonstrated by computing the STD of the absolute difference between the radiologists, and between the algorithm and the radiologists.
Results: Success rates of 93% and 74% were achieved, for contrast injected cases and non-contrast cases, respectively. These results indicate that the algorithm can be robust in large variability of image quality, such as the cases in a real-world clinical setting. The average absolute difference between the algorithm and the radiologists was 1.85 mm, slightly lower than the average absolute difference between the radiologists, which was 2.1 mm. The STD of the absolute difference between the algorithm and the radiologists was 1.5 mm vs 1.6 mm between the two radiologists. These results demonstrate the clinical relevance of the algorithm measurements.

**9785-6, Session 2**

**Differentiation of fat, muscle, and edema in thigh MRIs using random forest classification**

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There are many diseases that affect the distribution of muscles, including Duchenne and fascioscapulohumeral dystrophy among other myopathies. In these disease cases, it is important to quantify both the muscle and fat volumes to track the disease progression. There has been evidence that edema or inflammation can be a good predictor for muscle deterioration.

We present a fully-automated method that examines magnetic resonance (MR) images of the thigh and identifies the fat, muscle, and edema using a random forest classifier. First the thigh regions are automatically segmented using the T1 sequence. Then, inhomogeneity artifacts were corrected using the N3 technique. The T1 and STIR (short tau inversion recovery) images are then aligned using landmark based registration with the bone marrow. The normalized T1 and STIR intensity values are used to train the random forest. Once trained, the random forest can accurately classify the aforementioned classes.

This method was evaluated on MR images of 9 patients. The precision values are 0.84±0.08, 0.98±0.01 and 0.51±0.27 for muscle, fat, and edema, respectively. The recall values are 0.95±0.02, 0.93±0.04 and 0.42±0.09 for muscle, fat, and edema, respectively. This demonstrates the feasibility of utilizing information from multiple MR sequences for the accurate quantification of fat, muscle and edema.

**9785-7, Session 2**

**Assessing vertebral fracture risk on volumetric quantitative computed tomography by geometric characterization of trabecular bone structure**

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The current clinical standard for measuring Bone Mineral Density (BMD) is dual X-ray absorptiometry, however more recently BMD derived from volumetric quantitative computed tomography has been shown to demonstrate a high association with spinal fracture susceptibility. In this study, we propose a method of fracture risk assessment using structural properties of trabecular bone in spinal vertebrae. Experimental data was acquired via axial multi-detector CT (MDCT) from 12 spinal vertebrae specimens using a whole-body 256-row CT scanner with a dedicated calibration phantom. Common image processing methods were used to annotate the trabecular compartment in the vertebral slices creating a circular region of interest (ROI) that excluded cortical bone for each slice. The pixels inside the ROI were converted to values indicative of BMD. High dimensional geometrical features were derived using the scaling index method (SIM) at different radii and scaling factors (SF). The mean BMD values within the ROI were then extracted and used in conjunction with a support vector machine to predict the failure load of the specimens. Prediction performance was measured using the root-mean-square error (RMSE) metric and determined that SIM combined with mean BMD features (RMSE = 0.82 + 0.37) outperformed MDCT-measured mean BMD (RMSE = 1.1 + 0.33) (p < 10^-4). These results demonstrate that biomechanical strength prediction in vertebrae can be significantly improved through the use of SIM-derived texture features from trabecular bone.
Classification of voting patterns to improve the generalized Hough transform for epiphyses localization

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This paper presents a general framework for object localization in medical (and non-medical) images. In particular, we focus on objects of regular shape, like epiphyseal regions, which are localized based on a voting framework using the Generalized Hough Transform (GHT). In this paper, we suggest to combine the GHT voting with a classifier which rates the voting characteristics of the GHT model at individual Hough cells. Specifically, a Random Forest classifier rates whether the model points voting for an object position constitute a regular shape or not, and we incorporate this measure into the GHT votes. Thereby, we achieve a success rate of 99.4% for localizing 12 epiphyseal regions of interest in 412 hand radiographs. The mean error was 6 pixels on images with a mean resolution of 1185x2006 pixels.

Medical Sieve: a cognitive assistant for radiologists and cardiologists

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Radiologists and cardiologists today have to view large amounts of imaging data relatively quickly leading to eye fatigue. Further, they have only limited access to clinical information relying mostly on their visual interpretation of imaging studies for their diagnostic decisions. In this paper, we present Medical Sieve, an automated cognitive assistant for radiologists and cardiologists to help in their clinical decision making. The sieve is a clinical informatics system that collects clinical, textual and imaging data of patients from electronic health records systems. It then analyzes multimodal content to detect anomalies if any, and summarizes the patient record collecting relevant information driven from the automatic detection of a chief complaint. The results of anomaly detection are then fed into a reasoning engine which uses both evidence both from patient-independent clinical knowledge and large-scale patient-driven similar patient statistics to arrive at potential differential diagnosis to help in clinical decision making. In compactly summarizing all relevant information to the clinician per chief complaint, the system still retains links to the raw data for detailed review providing holistic summaries of patient conditions and comparisons to similar patients to learn about diagnosis, treatments and outcomes that have worked for similar patients. Results of clinical studies in the domains of cardiology and breast radiology have already shown the promise of the system in differential diagnosis and imaging studies summarization.

Acne image analysis: lesion localization and classification

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Acne is a common skin condition present predominantly in adolescent population, but may continue into adulthood. Scarring occurs commonly as a sequel to severe inflammatory acne. The presence of acne and resultant scars are more than cosmetic, with a significant potential to alter quality of life and even job prospects. The psychosocial effects of acne and scars can be extremely devastating and may be a risk factor for serious psychological concerns. Treatment efficacy is generally determined based on an invalidated gestalt by the physician and patient. However, the validated assessment of acne can be challenging and time consuming. Acne can be classified into several morphologies including closed comedones (white head), open comedones (black head), papules, pustules, cyst (nodules) and scars. For a validated assessment, the different morphologies need to be counted independently, a method that is far too time consuming for the limited time for consultation. However, the application of image recording is practical, since dermatologists can validate the severity of acne within seconds after uploading an image. This paper covers the processes of region-of-interest extraction and acne lesion feature extraction. Feature extraction methods using discrete wavelet frames and grayscale co-occurrence matrix were presented and their effectiveness in separating the six major acne lesion classes were discussed. Several classifiers were used to test the extracted features. Correct classification accuracy as high as 85.5% was achieved using the binary classification tree with fourteen principle components used as descriptors. Further studies are underway to further improve the algorithm performance and validate it on a larger database.

Classification of melanoma lesions using sparse coded features and random forests

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Malignant melanoma is the most dangerous type of skin cancer, yet it is the most treatable kind of cancer, conditioned by its early diagnosis which is a challenging task for clinicians and dermatologists. In this regard, CAD systems based on machine learning and image processing techniques are developed to differentiate melanoma lesions from benign and dysplastic nevi using dermoscopic images. Generally, these frameworks are composed of sequential processes: pre-processing, segmentation, and classification. The pre-processing stage faces mainly two challenges: (i) each process is complex with the need to tune a set of parameters, and is specific to a given dataset; (ii) the performance of each process depends on the previous one, and the errors are accumulated throughout the framework. In this paper, we propose a framework for melanoma classification based on sparse coding which does not rely on any pre-processing or lesion segmentation. Our framework uses Random Forests classifier and sparse representation of three features: SIFT, Hue and Opponent angle histograms, and RGB intensities. The experiments are carried out on the public PH2 dataset using a 10-fold cross-validation. The results show that SIFT sparse-coded feature achieves the highest performance with sensitivity and specificity of 100% and 90.3% respectively, with a dictionary size of 800 atoms and a sparsity level of 2. Furthermore, the descriptor based on RGB intensities achieves similar results with sensitivity and specificity of 100% and 71.3%, respectively, for a smaller dictionary size of 100 atoms. In conclusion, dictionary learning techniques encode strong structures of dermoscopic images and provide discriminant descriptors.
In this work, we present a novel framework for automatic detection of abnormalities in chest radiographs. The representation model is based on the Fisher Vector encoding method. In the representation process, we encode each chest radiograph using a set of extracted local descriptors. These include localized texture features that address typical local texture abnormalities as well as spatial features. Using a Gaussian Mixture Model, a rich image descriptor is generated for each chest radiograph. An improved representation is obtained by selection of features that correspond to the relevant region of interest for each pathology. Categorization of the X-ray images is conducted using supervised learning and the SVM classifier. The proposed system was tested on a dataset of 636 chest radiographs taken from a real clinical environment. We measured the performance in terms of area (AUC) under the receiver operating characteristic (ROC) curve. Results show an AUC value of 0.878 for abnormal mediastinum detection, and AUC values of 0.827 and 0.817 for detection of right and left lung opacities, respectively. These results improve upon the state-of-the-art as compared with two alternative representation models.

9785-13, Session 3

Intensity targeted radial structure tensor analysis and its application for automated mediastinal lymph node detection from CT volumes

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This paper presents new blob-like enhancement filter based on Intensity Targeted Radial Structure Tensor (ITRST) analysis to improve mediastinal lymph node detection from chest CT volumes. Blob-like structure enhancement filter based on Radial Structure Tensor (RST) analysis can be utilized for initial detection of lymph node candidate regions. However, some of lymph nodes cannot be detected because RST analysis is influenced by neighboring regions whose intensity is very high or low, such as contrast-enhanced blood vessels and air. To overcome the problem, we propose ITRST analysis that integrate the prior knowledge on detection target intensity into RST analysis. Our lymph node detection method consists of two steps. First, candidate regions are obtained by ITRST analysis. Second, false positives (FPs) are removed by the Support Vector Machine (SVM) classifier. We applied the proposed method to 47 cases. 100 % of lymph nodes were detected with 365.0 FPs/case by ITRST analysis, while only 85.5 % were detected with 364.0 FPs/case by RST analysis. After false positive (FP) reduction by SVM, ITRST analysis outperformed RST analysis in lymph node detection performance.

9785-14, Session 3

Automatic aortic root segmentation in CT: a whole-body dataset

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The purpose of this study was to automatically segment the aortic root in computed tomography angiography (CTA) images to support trans-catheter aortic valve replacement (TAVR) procedures. TAVR is an evolving surgical technique for patients with severe aortic stenosis disease. Typically, in this application a CTA data set is obtained of the patient’s arterial system from the subclavian artery to the femoral arteries, to evaluate the quality of the vascular access route and analyze the aortic valve to determine if and which prosthesis should be used. In this paper, we concentrate on the automated segmentation of the aortic root.

In general terms, the method in this study included 4 major steps. First, the patient’s cardiac CTA image was resampled to reduce the computation time and create a mask for the second step. Next, the cardiac CTA image was segmented using an atlas based approach. The most similar atlas was selected from a total of 8 atlases based on its image similarity to the input CTA image. Third, the aortic root segmentation from the previous step was transferred to the patient’s whole-body CTA image by affine registration and refined in the fourth step using a deformable subdivision surface model fitting procedure based on image intensity.

The pipeline was applied to 9 patients. The ground truth was created by an analyst who semi-automatically corrected the contours of the automatic method, where necessary. The average Dice similarity index between the segmentations of the automatic method and the ground truth was found to be 0.974±0.024. In conclusion, the current results are very promising and will be further tested in additional patient data sets.

9785-15, Session 3

Effects of CT dose and nodule characteristics on CAD performance in a cohort of 90 National Lung Screening Trial patients

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Lung cancer screening CT is already performed at low dose. There are many techniques to reduce the dose further, but it is not clear how such techniques will affect nodule detectability. In this work, we used an in-house CAD algorithm to evaluate detectability. 90 scans and their raw CT data files were drawn from the National Lung Screening Trial (NLST) database. All scans were acquired at ~2 mGy CTDIvol with fixed tube current, 1 mm slice thickness, and B50 reconstruction kernel on a Sensation 64 scanner (Siemens Healthcare). We used the raw CT data to simulate two additional reduced-dose scans for each patient corresponding to 1 mGy and 0.5 mGy. Radiologists’ findings on the NLST reader forms indicated 29 nodules in the cohort, which we subdivided based on LungRADS criteria. For the category 4 (suspicious) nodules, CAD sensitivities were 100%, 75%, and 50% at screening dose, 1 mGy, and 0.5 mGy respectively. For small and non-solid nodules meeting the category 2 (benign) criteria, sensitivities were 0%, 5%, and 29%. Mean subject-level sensitivities were 29%, 29%, and 39%, with false-positive rates of 1.7, 2.8, and 13.5. Subject-level sensitivities were low at all doses due to the prevalence of category 2 nodules (21 out of 29), which the CAD algorithm was not designed to detect. The false-positive rate increased sharply between 1.0 and 0.5 mGy, indicating a substantial loss of CAD robustness. From the LungRADS analyses, we concluded that dose affects detectability differently depending on the nodule characteristics and CAD algorithm.

9785-16, Session 3

An automated lung nodule detection system for CT images using synthetic minority oversampling

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Pulmonary nodules are a potential manifestation of lung cancer, and their early detection can remarkably enhance the survival rate of patients. This paper presents an automated pulmonary nodule detection algorithm for lung CT images. The algorithm utilizes a two-stage approach comprising nodule candidate detection followed by reduction of false positives. The nodule candidate detection involves thresholding, followed by morphological opening. The geometrical features at this stage are selected from properties of nodule size and compactness, and lead to reduced number of false positives. An SVM classifier is used with a radial basis function kernel. The data imbalance, due to uneven distribution of nodules and non-nodules as a result of the candidate detection stage, is proposed to be addressed by oversampling of majority class using Synthetic Minority Over-sampling Technique (SMOTE), and over-implication of its misclassification penalty. Experiments were performed on 97 CT scans of a publically-available (LIDC-IDRI) database. Performance is evaluated in terms of sensitivity and false positives per scan (FP/scan). Results indicate noteworthy performance of the proposed approach (nodule detection sensitivity after 4-fold cross-validation is 92.91% with 3 FP/scan). Comparative analysis also reflects a comparable and often better performance of the proposed setup over some of the existing techniques.

9785-17, Session 4

Quantification of mammographic masking risk with volumetric breast density maps: how to select women for supplemental screening

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The sensitivity of mammograms is low for women with dense breasts, since cancers may be masked by dense tissue. In this study, we investigated methods to identify women with density patterns associated with high masking risk. Risk measures are derived from volumetric breast density maps.

We used the last negative screening mammograms of 93 women who subsequently presented with an interval cancer (IC), and, as controls, 930 randomly selected normal screening exams from women without cancer.

Volumetric breast density maps were computed from the mammograms, which provide the dense tissue thickness at each location. These were used to compute absolute and percentage glandular tissue volume.

We modeled the masking risk for each pixel location using the absolute and percentage dense tissue thickness and we investigated the effect of taking the cancer location probability distribution (CLPD) into account.

For each method, we selected cases with the highest masking measure (by thresholding) and computed the fraction of ICs as a function of the fraction of controls selected. The latter can be interpreted as the negative supplemental screening rate (NSSR).

Between the models, when incorporating CLPD, no significant differences were found. In general, the methods performed better when CLPD was included. At higher NSSRs some of the investigated masking measures had a significantly higher performance than volumetric breast density. These measures may therefore serve as an alternative to identify women with a high risk for a masked cancer.

9785-18, Session 4

Seamless lesion insertion in digital mammography: methodology and reader study

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Collection of large repositories of clinical images containing verified cancer locations is costly and time consuming due to difficulties associated with both the accumulation of data and establishment of the ground truth. This problem poses a significant challenge to the development of machine learning algorithms that require large amounts of data to properly train and avoid overfitting. In this paper we expand the methods in our previous publications by making several modifications that significantly increase the speed of our insertion algorithms, thereby allowing them to be used for inserting lesions that are much larger in size. These algorithms have been incorporated into an image composition tool that we have made publicly available. This tool allows users to modify or supplement existing datasets by seamlessly inserting a real breast mass or micro-calcification cluster extracted from a source digital mammogram into a different location on another mammogram. We demonstrate examples of the performance of this tool on clinical samples taken from the University of South Florida Digital Database for Screening Mammography (DDSM). Finally, we report the results of a reader study evaluating the realism of inserted lesions compared to clinical lesions. Analysis of the radiologist scores in the study using receiver operating characteristic (ROC) methodology indicates that inserted lesions cannot be reliably distinguished from clinical lesions.

9785-19, Session 4

Workflow improvements for digital breast tomosynthesis: computerized generation of enhanced synthetic images

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In a typical 2D mammography workflow scenario, a computer-aided detection (CAD) algorithm may be used as a second reader, serving as a spell checker for a radiologist. In the case of 3D digital breast tomosynthesis (DBT), CAD detections may be located at multiple reconstruction heights leading to increased image browsing and interpretation time. We propose an alternative approach in which the detection algorithm identifies suspicious regions of interest from 3D reconstructed DBT slices and then merges the findings with a 2D synthetic projection image. The resultant enhanced synthetic 2D image combines the benefits of familiar 2D breast view with superior appearance of suspicious locations from 3D slices. Moreover, clicking on 2D suspicious locations brings up the display of the corresponding 3D region in a DBT volume. We explored the use of the enhanced synthetic images in a concurrent read paradigm by conducting a 5 reader study on 30 patients. We observed that introduction of the enhanced synthetic view reduced radiologist’s average interpretation time by 5.4%, increased sensitivity by 6.7% and specificity by 15.6%.

9785-20, Session 4

A fully automated system for quantification of background parenchymal enhancement in breast DCE-MRI

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Background parenchymal enhancement (BPE) observed in breast dynamic contrast enhanced magnetic resonance imaging (DCE-MRI) has been
identified as an important biomarker associated with risk for developing breast cancer. In this study, we present a fully automated framework for quantification of BPE. We initially segmented fibroglandular tissue (FGT) of the breasts using an improved version of an existing method. Subsequently, we computed BPE_abs (volume of the enhancing tissue), BPE_rf (BPE_abs divided by FGT volume) and BPE_rb (BPE_abs divided by breast volume), using different relative enhancement threshold values between 1% and 100%. To evaluate and compare the previous and improved FGT segmentation methods, we used 20 breast DCE-MRI scans and computed dice similarity coefficient (DSC) values with respect to manual segmentations. For evaluation BPE quantification, we used a dataset of 95 breast DCE-MRI scans, for which two breast radiologists visually determined BPE categories. To measure the correlation between automated BPE values to the radiologists’ assessments, we computed Spearman’s rho as a measure of correlation. According to our results, the new segmentation method obtained an average DSC of 0.81 ±0.09, which was significantly higher (p<0.001) compared to the previous method (0.76±0.10). The highest correlation values between automated BPE categories and radiologists’ assessments were obtained with the BPE_rf measurement (r=0.55, r=0.49, p<0.001 for both), while the correlation between the scores given by the two radiologists was 0.82 (p<0.001). The presented framework can be used to systematically investigate the correlation between BPE and risk in large screening cohorts.

9785-21, Session 4

Parenchymal texture measures weighted by breast anatomy: preliminary optimization in a case-control study

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We assess the hypothesis that breast cancer risk factors are not uniformly expressed in the breast parenchymal tissue and, therefore, breast-anatomy-weighted parenchymal texture descriptors, where different breasts ROIs have non uniform contributions, may enhance breast cancer risk assessment. We introduce an automated breast-anatomy-driven methodology which generates a breast atlas, which is then used to produce a weight map that reinforces the contributions of the central and upper-out breast areas. We incorporate this methodology to our previously validated lattice-based strategy for parenchymal texture analysis. In the framework of a pilot case-control study, including digital mammograms from 424 women, our proposed breast-anatomy-weighted texture descriptors are optimized and evaluated against non weighted texture features, using regression analysis with leave-one-out cross validation. The classification performance is assessed in terms of the area under the curve (AUC) of the receiver operating characteristic. The collective discriminatory capacity of the weighted texture features was maximized (AUC=0.87) when the central breast area was considered more important than the upper-out area, with significant performance improvement (DeLong’s test, p-value<0.05) against the non-weighted texture features (AUC=0.82). Our results suggest that breast-anatomy-driven methodologies have the potential to further upgrade the promising role of parenchymal texture analysis in breast cancer risk assessment and may serve as a reference in the design of future studies towards image-driven personalized recommendations regarding women’s cancer risk evaluation.

9785-22, Session 4

Automated linking of suspicious findings between automated 3D breast ultrasound volumes

Albert Gubern-Mérida, Tao Tan, Jan van Zelst, Ritse M. Mann, Nico Karssemeijer, Radboud Univ. Medical Ctr. (Netherlands)

Automated breast ultrasound (ABUS) is a 3D imaging technique which is rapidly emerging as a safe and relatively inexpensive modality for screening of women with dense breasts. However, reading ABUS examinations is very time consuming task since radiologists need to manually identify suspicious findings in all the different ABUS volumes available for each patient. Image analysis techniques to automatically link findings across volumes are required to speed up clinical workflow and make ABUS screening more efficient. In this study, we propose an automated system to, given the location in the ABUS volume being inspected (source), find the corresponding location in a target volume. The target volume can be a different view of the same study or the same view from a prior examination. The algorithm was evaluated using 118 linkages between suspicious abnormalities annotated in a dataset of ABUS images of 27 patients participating in a high risk screening program. The distance between the predicted location and the center of the annotated lesion in the target volume was computed for evaluation. The mean ± stdev and median distance error achieved by the presented algorithm for linkages between volumes of the same study was 7.75 ± 6.71 mm and 5.16 mm, respectively. The performance was 9.54 ± 7.87 and 8.00 mm (mean ± stdev and median) for linkages between volumes from current and prior examinations. The proposed approach has the potential to minimize user interaction for finding correspondences among ABUS volumes.

9785-23, Session 5

Radiomics: there is more than meets the eye in medical imaging (Keynote Presentation)

Hugo Aerts, Dana-Farber Cancer Institute (United States) and Brigham and Women’s Hospital (United States) and Harvard Medical School (United States)

No Abstract Available

9785-24, Session 5

Deep convolutional networks for automated detection of posterior-element fractures on spine CT

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Injuries of the spine, and its posterior elements in particular, are a common occurrence in trauma patients, with potentially devastating consequences. Computer-aided detection (CADe) could assist in the detection and classification of spine fractures. Furthermore, CAD could help assess the stability and chronicity of fractures, as well as facilitate research into optimization of treatment paradigms.

In this work, we apply ConvNets for the automated detection of posterior element fractures of the spine. First, the vertebra bodies of the spine with its posterior elements are segmented in spine CT using multi-atlas label fusion. Then, an edge map of the posterior elements is computed. These edge maps serve as candidate regions for predicting a set of probabilities for fractures along an image edge using ConvNets in a 2.5D fashion. We explore three different methods for training the ConvNet using 2.5D patches (5 orthogonal patches in axial, coronal and sagittal planes) along the edge maps of ‘positive’, i.e. fractured posterior-elements and ‘negative’, non-fractured elements.

An experienced radiologist retrospectively marked the location of 55 displaced posterior-element fractures in 18 trauma patients. We randomly split the data into training and testing cases. In testing, we achieve an area-under-the-curve of 0.857. This corresponds to an 81% sensitivity at 0.2 false-positives per posterior process. Results from analysis of our set of
trauma patients demonstrate the feasibility of detecting posterior-element fractures in spine CT images using computer vision techniques such as deep convolutional networks.

9785-25, Session 5
Increasing CAD system efficacy for lung texture analysis using a convolutional network
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The infiltrative lung diseases are a class of irreversible, non-neoplastic lung pathologies requiring regular follow-up with CT imaging. Quantifying the evolution of the patient status imposes the development of automated classification tools for lung texture. For the large majority of CAD systems, such classification relies on a two-dimensional analysis of axial CT images. In a previously developed CAD system, we proposed a fully-3D approach exploiting a multi-scale morphological analysis which showed good performance in detecting diseased areas, but with a major drawback consisting of sometimes overestimating the pathological areas and mixing different type of lung patterns. This paper proposes a combination of the existing CAD system with the classification output provided by a convolutional network, specifically tuned-up, in order to increase the specificity of the classification and the confidence to diagnosis. The advantage of using a deep learning approach is a better regularization of the classification output (because of a deeper insight into a given pathological class over a large series of samples) where the previous system is extra-sensitive due to the multi-scale response on patient-specific, localized patterns. In a preliminary evaluation, the combined approach was tested on a 30 patient database of various lung pathologies, showing a sharp decrease of false alerts.

9785-26, Session 6
Increasing cancer detection yield of breast MRI using a new CAD scheme of mammograms
Maxine Tan, Faranak Aghaei, The Univ. of Oklahoma (United States); Alan B. Hollingsworth, Rebecca G. Stough, Mercy Women’s Ctr. (United States); Hong Liu, Bin Zheng, The Univ. of Oklahoma (United States)

Although breast MRI is the most sensitive imaging modality to detect early breast cancer, its cancer detection yield in breast cancer screening is quite low (< 3 to 4% even for the small group of high-risk women) to date. The purpose of this preliminary study is to test the potential of developing and applying a new computer-aided detection (CAD) scheme of digital mammograms to identify women at high risk of harboring mammography-occult breast cancers, which can be detected by breast MRI. For this purpose, we retrospectively assembled a dataset involving 30 women who had both mammography and breast MRI screening examinations. All mammograms were interpreted as negative, while 5 cancers were detected using breast MRI. We developed a CAD scheme of mammograms, which include a new quantitative mammographic image feature analysis based risk model, to stratify women into two groups with high and low risk of harboring mammography-occult cancer. Among 30 women, 9 were classified into the high risk group by CAD scheme, which included all 5 women who had cancer detected by breast MRI. All 21 low risk women remained negative on the breast MRI examinations. The cancer detection yield of breast MRI applying to this dataset substantially increased from 16.7% (5/30) to 55.6% (5/9), while eliminating 84% (21/25) unnecessary breast MRI screenings. The study demonstrated the potential of applying a new CAD scheme to significantly increase cancer detection yield of breast MRI, while simultaneously reducing the number of negative MRIs in breast cancer screening.

9785-27, Session 6
Identification, segmentation, and characterization of microcalcifications on mammography
Karen Drukker, The Univ. of Chicago (United States); Serghei Malkov, Jesus Avila, Karla Kerlikowske, Bonnie Joe, Gregor Krings, Jennifer Creasman, Univ. of California, San Francisco (United States); Jennifer S. Drukteinis, Malesa M. Pereira, H. Lee Moffitt Cancer Ctr. & Research Institute (United States); Leila Kazemi, John A. Shepherd, Univ. of California, San Francisco (United States); Maryellen L. Giger, The Univ. of Chicago (United States)

The purpose was to develop a characterization method for breast lesions visible only as microcalcifications in digital mammography. The method involved 4 steps: 1) image preprocessing through morphological filtering, 2) un-supervised identification of microcalcifications in the region surrounding the radiologist-indicated location through k-means clustering, 3) segmentation of the identified microcalcifications using an active contour model, and 4) characterization by image-based phenotypes describing properties of individual microcalcifications, cluster, and surrounding parenchyma. The individual image-based phenotypes were investigated for their ability to distinguish – without a classifier – between invasive and in-situ (non-invasive) breast cancers, fibroadenomas, and other benign-type lesions. The data set contained diagnostic mammograms of 82 patients with 2 views per patient (CC and MLO views of the affected breast with a single biopsy-proven finding indicated per view) with 7 invasive cancers, 14 in situ cancers, 13 fibroadenomas, and 48 other benign-type lesions. Analysis was performed per finding and calculated phenotypes were averaged over views. Performance was assessed using ROC analysis with individual phenotypes as decision variables in the tasks of a) pair-wise distinction among the 4 finding types, b) distinction between each finding type and all others, and c) distinction between cancer and non-cancer. Different phenotypes (calcification size, inter-calcification distance and X-ray attenuation-based) emerged as the best performers with areas under the ROC curve ranging from 0.69 (0.05) to 0.92 (0.09) depending on the task. We obtained encouraging preliminary results beyond the classification of cancer versus non-cancer in the distinction between different types of breast lesions visible as mammographic calcifications.

9785-28, Session 6
Predicting Ki67% expression from DCE-MR images of breast tumors using textural kinetic features in tumor habitats
Baishali Chaudhury, Mu Zhou, Dmitry B. Goldgof, Lawrence O. Hall, Univ. of South Florida (United States); Robert A. Gatenby, Robert J. Gillies, Jennifer S. Drukteinis, H. Lee Moffitt Cancer Ctr. & Research Institute (United States)

The use of Ki67% expression, a cell proliferation marker, as a predictive and prognostic factor has been widely studied in the literature. Yet its usefulness is limited due to inconsistent cut off scores for Ki67% expression, subjective differences in its assessment in various studies, and spatial variation in expression, which makes it difficult to reproduce as a reliable independent prognostic factor. Previous studies have shown that there are significant spatial variations in Ki67% expression, which may limit its clinical prognostic utility after core biopsy. These variations are most evident when examining the periphery of the tumor vs. the core. To date, prediction of Ki67% expression from quantitative image analysis of DCE-MRI is very limited. This work presents a novel computer aided diagnosis framework to use textural kinetics to (i) predict the ratio of periphery Ki67% expression to core Ki67% expression, and (ii) predict Ki67% expression from individual tumor habitats. The pilot cohort
consists of T1 weighted fat saturated DCE-MR images from 17 patients. Support vector regression with a radial basis function was used for predicting the Ki67% expression and ratios. The initial results show that texture features from individual tumor habitats are more predictive of the Ki67% expression ratio and spatial Ki67% expression than features from the whole tumor. The Ki67% expression ratio could be predicted with a root mean square error (RMSE) of 1.67%. Thus quantitative image analysis of DCE-MRI using textural kinetic habitats, has the potential to be used as a non-invasive method for predicting Ki67% percentage and ratio.

9785-29, Session 6

Applying quantitative adiposity feature analysis models to predict benefit of bevacizumab-based chemotherapy in ovarian cancer patients

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How to rationally identify epithelial ovarian cancer (EOC) patients who will benefit from bevacizumab or other antiangiogenic therapies is a critical issue in EOC treatments. The motivation of this study is to quantitatively measure adiposity features from CT images and investigate the feasibility of predicting potential benefit of EOC patients with or without receiving bevacizumab-based chemotherapy treatment using multivariate statistical models and quantitative adiposity features. A dataset involving CT images from 59 advanced EOC patients were included in this study. Among them, 32 patients received maintenance bevacizumab after primary chemotherapy and the remaining 27 patients did not. We developed a computer-aided detection (CAD) scheme to automatically segment visceral fat areas (SFA) and subcutaneous fat areas (VFA) and then extracted 7 adiposity-related quantitative features. Three multivariate data analysis models (linear regression, logistic regression and Cox proportional hazards regression) were performed respectively to investigate the potential association between the model-generated prediction results and the patients’ progression-free survival (PFS) and overall survival (OS). The results show that using all 3 statistical models, a statistically significant association was detected between the model-generated results and both of the two clinical outcomes in the group of patients receiving maintenance bevacizumab (p<0.01), while there were no significant association for both PFS and OS in the group of patients without receiving maintenance bevacizumab. Therefore, this study demonstrated the feasibility of using quantitative adiposity-related CT image features based statistical prediction models to generate a new clinical marker and predict the clinical outcome of EOC patients receiving maintenance bevacizumab-based chemotherapy.

9785-30, Session 6

Radiogenomics of glioblastoma: a pilot multi-institutional study to investigate a relationship between tumor shape features and tumor molecular subtype

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Genomic subtype has been shown to be an important predictor of therapy response for patients with glioblastomas. Unfortunately, obtaining the genomic subtype is an expensive process that is not typically included in the standard diagnostic workup. It is therefore of interest to investigate potential surrogates of molecular subtypes that use standard diagnostic data such as magnetic resonance (MR) imaging. In this study, we analyze the relationship between tumor genomic subtypes, proposed by Verhaak et al, 2008, and novel features that capture the shape of abnormalities as seen in fluid attenuated inversion recovery (FLAIR) MR images. In our study, we used data from 88 patients with glioblastomas from four institutions provided by The Cancer Genome Atlas (TCGA). We explored five shape features calculated by computer algorithms implemented in our laboratory that assess shape both in individual slices and rendered three dimensional tumor volumes. The association between each feature and molecular subtype was assessed using a Fisher’s exact test. Our results indicate that margin fluctuation, which characterizes the complexity of a tumor’s outer edge, is significantly associated with subtype (p < 0.02). These preliminary findings show promise for an imaging-based surrogate of molecular subtype and contribute to the understanding of the relationship between tumor biology and its radiology phenotype.

9785-31, Session 6

Prognosis classification in glioblastoma multiforme using multimodal MRI derived heterogeneity textural features: impact of pre-processing choices

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Heterogeneity image-derived features of Glioblastoma multiforme (GBM) tumors from multimodal MRI sequences may provide higher prognostic value than standard parameters used in routine clinical practice. We developed a framework for the extraction and combination of textural features through support vector machines (SVM). The results in a cohort of 40 GBM suggested these features could be used to identify patients with poorer outcome. However, extraction of these features is a delicate multi-step process and their values may therefore depend on the pre-processing of images. The original developed workflow included skull removal, bias homogeneity correction, and multimodal tumor segmentation, followed by textural features computation, and lastly ranking, selection and combination through a SVM-based classifier. The goal of the present work was to specifically investigate the potential benefit and respective impact of several MRI pre-processing steps (spatial resampling of voxels, intensities quantization and normalization) to be added before textural features computation, on the resulting accuracy of the classifier. Eighteen new patients datasets were also added. A classification accuracy of 71% (sensitivity 79%, specificity 62%) was obtained using the original framework. The addition of the new pre-processing steps increased it to 81% (sensitivity 86%, specificity 76%). Spatial resampling had the most important impact on the resulting accuracy. This shows the crucial importance of investigating appropriate image pre-processing steps to be used for methodologies based on textural features extraction in medical imaging.

9785-32, Session 7

Detection of soft tissue densities from digital breast tomosynthesis: comparison of conventional and deep learning approaches

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Computer-aided detection (CAD) has been used in screening mammography for many years and is likely to be utilized for digital breast tomosynthesis (DBT). High detection performance is desirable as it may have an impact on radiologist’s decisions and clinical outcomes. Recently the algorithms based on deep convolutional architectures have been
shown to achieve state of the art performance in object classification and detection. Similarly, we trained a deep convolutional neural network directly on patches sampled from two-dimensional mammography and reconstructed DBT volumes and compared its performance to a conventional CAD algorithm that is based on computation and classification of hand-engineered features. The detection performance was evaluated on the same independent test set of 344 DBT reconstructions (GE SenoClaire 3D, iterative reconstruction algorithm) containing 328 suspicious and 115 malignant soft tissue densities including masses and architectural distortions. Detection sensitivity was measured on a region of interest (ROI) basis at the rate of five detection marks per volume. Moving from conventional to deep learning approach resulted in increase of ROI sensitivity from 0.832 ± 0.040 to 0.893 ± 0.033 for suspicious ROIs; and from 0.852 ± 0.065 to 0.930 ± 0.046 for malignant ROIs. These results indicate the high utility of deep feature learning in the analysis of DBT data and high potential of the method for broader medical image analysis tasks.

9785-33, Session 7

Deep learning convolution neural network for computer-aided detection of microcalcifications in digital breast tomosynthesis
Ravi K. Samala, Heang-Ping Chan, Lubomir M. Hadjiiski, Kenny H. Cha, Mark A. Helvie, Univ. of Michigan (United States)

A deep learning convolution neural network (DLCNN) was designed to differentiate microcalcification candidates detected during the prescreening stage as true calcifications or false positives in a computer-aided detection (CAD) system for clustered microcalcifications. The microcalcification candidates were extracted from the planar projection image generated from the digital breast tomosynthesis volume reconstructed by a multiscale bilateral filtering regularized simultaneous algebraic reconstruction technique. For training and testing of the DLCNN, true microcalcifications are manually labeled for the data sets and false positives were obtained from the candidate objects identified by the CAD system at prescreening after exclusion of the true microcalcifications. The DLCNN architecture was selected by varying the number of filters, filter kernel sizes and gradient computation parameter in the convolution layers, resulting in a parameter space of 216 combinations. The exhaustive grid search method was used to select an optimal architecture within the parameter space studied using the area under the curve (AUC) as a figure-of-merit. The effects of varying different categories of the parameter space were analyzed. The selected DLCNN was compared with our previously designed CNN architecture for the test set. The AUCs of the CNN and DLCNN was 0.89 and 0.93, respectively. The improvement was statistically significant (p < 0.05).

9785-34, Session 7

Computer aided lung cancer diagnosis with deep learning algorithms
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Deep learning is considered as a popular and powerful method in pattern recognition and classification. However, there are not many deep structured applications used in medical imaging diagnosis area. In this study we tested the feasibility of using deep learning algorithms for lung cancer diagnosis with the cases from Lung Image Database Consortium (LIDC) database. The nodules on each computed tomography (CT) slice were segmented according to marks provided by the radiologists. After down sampling and rotating we acquired 174412 samples with 52 by 52 pixel each and the corresponding truth files. Three deep learning algorithms were designed and implemented, including Convolutional Neural Network (CNN), Deep Belief Networks (DBNs), Stacked Denoising Autoencoder (SDAE). To compare the performance of deep learning algorithms with traditional computer aided diagnosis (CADx) system, we designed a scheme with 28 image features and support vector machine. The accuracies of CNN, DBNs, and SDAE are 0.7976, 0.8119, and 0.7929, respectively; the accuracy of our designed traditional CADx is 0.7940, which is slightly lower than DBNs. We also noticed that the mislabeled nodules using DBNs are 4% larger than traditional CADx, this might be resulting from down sampling process lost some size information of the nodules.

9785-35, Session 7

Visualizing and enhancing a deep learning framework using patients age and gender for chest x-ray image retrieval
Yaron Anavi, Ilya Kogan, Elad Gelbart, Ofer Geva, Hayit Greenspan, Tel Aviv Univ. (Israel)

We explore the combination of text metadata, such as patients’ age and gender, with image-based features, for X-ray chest pathology image retrieval. We focus on the combination set extracted from a deep convolutional network shown in earlier work to achieve state-of-the-art results. Two distance measures are explored: a descriptor-based measure, which computes the distance between image descriptors, and a classification-based measure, which requires an initial categorization of each image followed by comparison of the corresponding SVM classification probabilities. We show that retrieval results increase once the age and gender information is included, with best results using the classification-based scheme. Visualization of the X-ray data is presented by embedding the high dimensional deep learning features in a 2-D dimensional space while preserving the pairwise distances using the t-SNE algorithm.

9785-36, Session 7

Deep convolutional neural networks for automatic coronary calcium scoring in a screening study with low-dose chest CT
Nikolas Lessmann, Ivana Isgum, Univ. Medical Ctr. Utrecht (Netherlands); Arnaud A. A. Setio, Radboud Univ. Medical Ctr. (Netherlands); Bob D. de Vos, Univ. Medical Ctr. Utrecht (Netherlands); Francesco Cioffi, Radboud Univ. Medical Ctr. (Netherlands); Pim A. de Jong, Univ. Medical Ctr. Utrecht (Netherlands); Matthijs Oudkerk, Univ. Medical Ctr. Groningen (Netherlands); Willem P. Th. M. Mali, Max A. Viergever, Univ. Medical Ctr. Utrecht (Netherlands); Bram van Ginneken, Radboud Univ. Medical Ctr. (Netherlands)

The amount of calcifications in the coronary arteries is a powerful and independent predictor of cardiovascular events and is used to identify subjects at high risk who might benefit from preventive treatment. Routine quantification of coronary calcium scores can complement screening programs using low-dose chest CT, such as lung cancer screening. We present a system for automatic coronary calcium scoring based on deep convolutional neural networks (CNNs). The system uses three independently trained CNNs to estimate a bounding box around the heart. In this region of interest, connected components above 130 HU are considered candidates for coronary artery calcifications. To separate them from other high intensity lesions, classification of all extracted voxels is performed by feeding two-dimensional 50mm x 50mm patches from three orthogonal planes into three concurrent CNNs. The networks consist of three convolutional layers and one fully-connected layer with 256 neurons.

In the experiments, 1028 non-contrast-enhanced and non-ECG-triggered low-dose chest CT scans were used. The network was trained on 797
scans. In the remaining 231 test scans, the method detected on average 194.3mm? of 199.8mm? coronary calcifications (sensitivity 97.2 %) with an average false-positive volume of 10.3mm?. Subjects were assigned to one of five standard cardiovascular risk categories based on the Agatston score. Accuracy of risk category assignment was 84.4% with a linearly weighted kappa of 0.89. The proposed system can perform automatic coronary artery calcium scoring and identify subjects undergoing low-dose chest CT screening who are at risk of cardiovascular events with high accuracy.

9785-37, Session 7
Comparison of bladder segmentation using deep-learning convolutional neural network with and without level sets
Kenny H. Cha, Lubomir M. Hadjiiski, Ravi K. Samala, Heang-Ping Chan, Richard H. Cohan M.D., Elaine M. Caoli, Univ. of Michigan Health System (United States)

We are developing a CAD system for detection of bladder cancer on CTU. In this study we investigated the application of deep-learning convolutional neural network (DL-CNN) to the segmentation of the bladder, which is a challenging problem because of the strong boundary between the non-contrast and contrast-filled regions. We trained a DL-CNN to estimate the likelihood of a pixel being inside the bladder using neighborhood information. The segmented bladder was obtained from thresholding and hole-filling of the likelihood map. We compared the segmentation performance of the DL-CNN alone and with additional cascaded 3D and 2D level sets to refine the segmentation using 3D hand-segmented contours as reference standard. The segmentation accuracy was evaluated by five performance measures: average volume intersection %, average % volume error, average absolute % error, average minimum distance, and average Jaccard index for a data set of 81 training and 92 test cases. For the training set, DL-CNN with level sets achieved performance measures of 87.2±6.1%, 6.0±9.1%, 8.7±6.1%, 3.0±1.2 mm, and 81.9±7.6%, respectively, while the DL-CNN alone obtained the values of 73.6±8.5%, 23.0±8.5%, 23.0±8.5%, 5.1±1.5 mm, and 71.5±9.2%, respectively. For the test set, the DL-CNN with level sets achieved performance measures of 81.9±12.1%, 10.1±16.2%, 14.0±13.0%, 3.6±2.0 mm, and 76.2±11.8%, respectively, while DL-CNN alone obtained 68.8±12.1%, 27.2±13.7%, 27.3±13.6%, 5.7±2.2 mm, and 66.2±11.8%, respectively. DL-CNN alone is effective in segmenting bladders but may not follow the details of the bladder wall. The combination of DL-CNN with level sets provides highly accurate bladder segmentation.

9785-65, Session PS1
Reference state estimation of breast computed tomography for registration with digital mammography
Ravi K. Samala, Heang-Ping Chan, Lubomir M. Hadjiiski, Univ. of Michigan (United States); Ruolung Ning, Unio of Rochester Medical Ctr. (United States); Kenny H. Cha, Mark A. Helvie, Univ. of Michigan (United States)

Understanding the deformation of the breast is a fundamental aspect to lesion localization in multi-view and multimodality imaging. Finite element methods (FEMs) are commonly used to model the deformation process of the breast. In FEM, ideally it would start from a reference state of the breast, with no loading conditions and apply the different imaging-modality-based loading conditions for correspondence analysis. We propose an iterative method to estimate the reference state configuration between a gravity loaded uncompressed breast computed tomography (BCT) volume and corresponding digital mammograms (DM) of the breast. The reference state breast model is compressed between two plates similar to DM to generate a DM-like image by forward ray-tracing. The iterative method applies pressure in the anterior-to-posterior direction of the breast and uses information from the DM geometry and measurements to converge on a reference state of the breast. BCT cases from small to large breast sizes and breast densities consisting of scattered, heterogeneous and extremely dense categories are evaluated. Non-linear materials based on Mooney-Rivlin models are used for homogeneous breast volume. The Fréchet distance between the edges of the DM-like image and the DM image is used as a validation method to analyze the effects of material properties on the estimation process.

9785-66, Session PS1
Improving the performance of lesion-based computer-aided detection schemes of breast masses using a case-based adaptive cueing method
Maxine Tan, Faranak Aghaei, Bin Zheng, The Univ. of Oklahoma (United States)

Current commercialized CAD schemes have high false-positive (FP) detection rates and also have high correlations in positive lesion detection with radiologists. Thus, we recently investigated a new approach to improve the efficacy of applying CAD to assist radiologists in reading and interpreting screening mammograms. Namely, we developed a new global feature-based CAD approach/scheme that can cue the warning sign on the cases with high risk of being positive. In this study, we investigate the possibility of fusing global feature or case-based scores with the local or lesion-based CAD scores using an adaptive cueing method. We hypothesize that the information from the global feature extraction (features extracted from the whole breast regions) are different from and can provide supplementary information to the locally-extracted features (computed from the segmented lesion regions only). On a large and diverse full-field digital mammography (FFDM) testing dataset with 785 cases (347 negative and 438 cancer cases with masses only), we ran our lesion-based and case-based CAD schemes “as is” on the whole dataset. To assess the supplementary information provided by the global features, we used an adaptive cueing method to adaptively adjust the original CAD-generated detection scores (Sorg) of a detected suspicious mass region based on the computed case-based score (Scase) of the case associated with this detected region. Using the adaptive cueing method, better sensitivity results were obtained at lower FP rates (≤ 1 FP per image). Namely, increases of sensitivities (in the FROC curves) of up to 6.7% and 8.2% were obtained for the ROI and Case-based results, respectively.

9785-67, Session PS1
Quantitative breast MRI radiomics for cancer risk assessment and the monitoring of high-risk populations
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Breast density is routinely assessed qualitatively in screening mammography, however, it is challenging to quantitatively determine a 3D density from a 2D image. Furthermore, dynamic contrast enhanced magnetic resonance imaging (DCE-MRI) is increasingly used in screening high-risk populations. The purpose of our study is to quantitatively segment parenchyma and determine breast density on pre-contrast axial DCE-MRI images (i.e., non-contrast) using a semi-automated quantitative approach. In this study, we retroactively examined 2D mammograms and 3D DCE-MRI images taken for breast cancer screening in a high-risk population. To date, we have analyzed 16 cases, in a database of 92 patients, with ages between 31 and 66 (mean 50.7, standard deviation 10.9). Images included FFDMs (Hologic) and DCE-MRIs (Philips 3.0 T scanner). Our semi-automated DCE-MRI algorithm includes: (a) segmentation of breast tissue from non-breast tissue using fuzzy c-means clustering (b) separation of dense and fatty tissues using Otsu’s...
between the extracted features and FP recall were assessed via odds ratios.

Our method within precision medicine may be useful for monitoring high-risk populations.

Benign-malignant mass classification in mammogram using edge weighted local texture features

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This paper introduces novel Discriminative Robust Local Binary Pattern (DRLBP) and Discriminative Robust Local Ternary Pattern (DRLTP) for the classification of mammographic masses as benign or malignant. Mass is one of the common, however, challenging evidence of breast cancer in mammography and diagnosis of masses is a difficult task. Since DRLBP and DRLTP overcome the drawbacks of Local Binary Pattern (LBP) and Local Ternary Pattern (LTP) by discriminating a brighter object against the dark background and vice-versa, in addition to the preservation of the edge information along with the texture information, several edge-preserving texture features are extracted, in this study, from DRLBP and DRLTP. Finally, a Fisher Linear Discriminant Analysis method is incorporated with discriminating features, selected by stepwise logistic regression method, for the classification of benign and malignant masses. The performance characteristics of DRLBP and DRLTP features are evaluated using a ten-fold cross-validation technique with 58 masses from the mini-MIAS database, and the best result is observed with DRLBP having an Area under the Receiver Operating Characteristic curve (AUC) of 0.982.

Parameter optimization of parenchymal texture analysis for prediction of false-positive recalls from screening mammography

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This work details a methodology to obtain optimal parameter values for a locally-adaptive texture algorithm that extracts mammographic texture features representative of breast parenchymal complexity for predicting false-positive (FP) recalls from breast cancer screening with digital mammography. The algorithm has two components: (1) adaptive selection of localized regions of interest (ROIs) and (2) Haralick texture features extraction via Gray-Level Co-Occurrence Matrices (GLCM). The following parameters were systematically varied: mammographic views used, upper limit of the ROI window size used for adaptive ROI selection, GLCM distance offsets, and gray levels (binning) used for feature extraction. Each iteration per parameter set had logistic regression with stepwise feature selection performed on a clinical screening cohort of 474 non-recalled women and 68 FP recalled women; FP recall prediction was evaluated using area under the curve (AUC) of the receiver operating characteristic (ROC) and associations between the extracted features and FP recall were assessed via odds ratios.

Automatic quantification of mammary glands on non-contrast X-ray CT by using a novel segmentation approach

Xiangrong Zhou, Takuya Kano, Gifu Univ. School of Medicine (Japan); Shuo Li, Western Univ. (Canada); Xinxin Zhou, Nagoya Bunri Univ. (Japan); Takeshi Harai, Hiroshi Fujita, Gifu Univ. School of Medicine (Japan)

This paper describes a brand new automatic segmentation method for quantifying volume and density of mammary gland regions on non-contrast CT images. The proposed method uses two processing steps: (1) breast region localization, and (2) breast region decomposition to accomplish a robust mammary gland segmentation task on CT images. The first step detects two minimum bounding boxes of left and right breast regions respectively based on a machine-learning approach that adapts to a large variance of the breast appearances on different age levels. The second step divides the whole breast region into mammary gland, fat tissue, ribs, breast muscle and air regions by using spectral decomposition that focuses on intra-region similarities of each patient that aims to overcome the image variance caused by different scan-parameters. The whole approach is designed as a unified structure with very minimum number of parameters to gain a superior robustness and computational efficiency for real clinical setting. We applied this approach to a dataset that includes 300 CT scans sampling with the equal numbers from 30 to 50 year-old-women. Comparing to human annotations, the proposed approach can measure volume and quantify mode of the CT numbers of mammary gland region accurately. The experimental results demonstrated that the proposed approach achieves results consistent with manual annotations. Through our proposed framework, an efficient and effective low cost clinical screening scheme can be easily implemented to predict breast cancer risk, especially on those already acquired scans.

Computer-aided classification of mammographic masses using the deep learning technology: a preliminary study

Yuchen Qiu, The Univ. of Oklahoma (United States); Shijiu Yan, Univ. of Shanghai for Science and Technology (China); Maxine Tan, The Univ. of Oklahoma (United States); Samuel Cheng, The Univ. of Oklahoma - Tulsa (United States); Hong Liu, Bin Zheng, The Univ. of Oklahoma (United States)

Although mammography is the only clinically acceptable imaging modality used in the population-based breast cancer screening, its efficacy is quite controversial. One of the major challenges is how to help radiologists more accurately classify between benign and malignant lesions. The purpose of this study is to investigate a new mammographic mass classification scheme based on a deep learning method. In this study, we used an image dataset involving 560 regions of interest (ROIs) extracted from digital mammograms, which includes 280 malignant and 280 benign mass ROIs, respectively. An eight layer deep learning network was applied, which employs three pairs of convolution--max-pooling layers for automatic...
feature extraction and a multiple layer perception (MLP) classifier for feature categorization. In order to improve robustness of selected features, each convolution layer is connected with a max-pooling layer. A number of 20, 10, and 5 feature maps were utilized for the 1st, 2nd and 3rd convolution layer, respectively. The convolution networks are followed by a MLP classifier, which generates a classification score to predict likelihood of a ROI depicting a malignant mass. Among 560 ROIs, 420 ROIs were used as a training dataset and the remaining 140 ROIs were used as a validation dataset. The result shows that the new deep learning based classifier yielded an area under the receiver operation characteristic curve (AUC) of 0.802±0.037. This study demonstrated the potential superiority of using a deep learning based classifier to distinguish malignant and benign breast masses without segmenting the lesions and extracting the pre-defined image features.

9785-72, Session PS1
An initial investigation on developing a new method to predict short-term breast cancer risk based on deep learning technology
Yuchun Qiu, The Univ. of Oklahoma (United States); Shiju Yan, Univ. of Shanghai for Science and Technology (China); Maxine Tan, Samuel Cheng, Hong Liu, Bin Zheng, The Univ. of Oklahoma (United States)
In order to establish a new personalized breast cancer screening paradigm, it is critically important to more accurately predict a short-term risk of a woman having image-detectable cancer after a negative screening mammography of interest. In this study, we developed and tested a novel short-term risk assessment model based on a deep learning method. During the experiment, a dataset including 270 “prior” negative screening mammography cases was selected. In the next sequential (“current”) screening mammography, 135 cases were positive and 135 remained negative. These cases were randomly divided into a training set with 200 cases and a testing set with 70 cases. A deep learning based computer-aided diagnosis (CAD) scheme was developed for the risk assessment, which consists of two modules: automatic feature extraction module and risk prediction module. The automated feature extraction module is composed of three pairs of convolution-max-pooling layers, which contains 20, 10, and 5 feature maps, respectively. The risk prediction is implemented by a MLP classifier, which produces a risk score to predict the likelihood of the woman having mammography-detectable cancer in a short-term. The result shows that new CAD-based risk model yielded a positive predictive value of 0.71 and a negative predictive value of 0.75, with a total prediction accuracy of 0.73. This study demonstrated that applying a new deep learning technology may have significant potential to develop a new short-term risk model with improved performance in detecting early abnormal symptom from the negative mammograms, which may lead to develop cancer in the near future.

9785-73, Session PS1
Computer-aided global breast MR image feature analysis for prediction of tumor response to chemotherapy: performance assessment
Faranak Aghaei, Maxine Tan, Samuel Cheng, Bin Zheng, The Univ. of Oklahoma (United States)
Dynamic contrast-enhanced breast magnetic resonance imaging (DCE-MRI) has been increasingly in breast cancer diagnosis and assessment of cancer treatment efficacy. In this study, we applied a computer-aided detection (CAD) scheme to automatically segment breast regions depicting on MR images and used the kinetic image features computed from the global breast MR images acquired before neoadjuvant chemotherapy to build a new quantitative model to predict response of the breast cancer patients to the chemotherapy. To assess performance and robustness of this new prediction model, an image dataset involving breast MR images acquired from 151 cancer patients before undergoing neoadjuvant chemotherapy was retrospectively assembled and used. Among them, 63 patients had “complete response” (CR) to chemotherapy in which the enhanced contrast levels inside the tumor volume (pre-treatment) was reduced to the level as the normal enhanced background parenchymal tissues (post-treatment), while 88 patients had “partially response” (PR) in which the high contrast enhancement remain in the tumor regions after treatment. We performed the studies to analyze the correlation among the 22 global kinetic image features and then select a set of 4 optimal features. Applying an artificial neural network trained with the fusion of these 4 kinetic image features, the prediction model yielded an area under ROC curve (AUC) of 0.83±0.04. This study demonstrated that by avoiding tumor segmentation, which is often difficult and unreliable, fusion of kinetic image features computed from global breast MR images without tumor segmentation can also generate a useful clinical marker in predicting efficacy of chemotherapy.

9785-74, Session PS1
First and second-order features for detection of masses in digital breast tomosynthesis
Ravi K. Samala, Jun Wei, Heang-Ping Chan, Lubomir M. Hadjiiski, Kenny H. Cha, Mark A. Helvie, Univ. of Michigan Health System (United States)
We are developing novel methods for prescreening of mass candidates in computer-aided detection (CAD) system for digital breast tomosynthesis (DBT). With IRB approval and written informed consent, 186 views from 94 breasts were imaged using a GE GEN2 prototype DBT system. The data set was randomly separated into training and test sets by cases. Gradient field convergence features based on first-order features were used to select the initial set of mass candidates. Eigenvales based on second-order features from the Hessian matrix were extracted for the mass candidate locations in the DBT volume. The features from the first- and second-order analysis form the feature vector which was input to a linear discriminant analysis (LDA) classifier to generate a candidate-likelihood score. The likelihood scores were ranked and the top N candidates were passed onto the subsequent detection steps. The improvement between using only first-order features and the combination of first and second-order features was analyzed using a rank sensitivity plot. 3D objects were obtained with two-stage 3D clustering followed by active contour segmentation. Morphological, gradient field, and texture features were extracted and feature selection was performed using stepwise feature selection. A combination of LDA and rule-based classifiers was used for FP reduction. The LDA classifier output a malignancy-likelihood score for each object that was used as a decision variable for FROC analysis. At breast-based sensitivities of 70% and 80%, prescreening using first-order and second-order features resulted in 0.7 and 1.0 FPs/DBT.

9785-75, Session PS1
An adaptive online learning framework for practical breast cancer diagnosis
Tianshu Chu, Stanford Univ. (United States); Jiayu Chen, GE Healthcare (United States); Jie Wang, Stanford Univ. (United States)
This paper presents an adaptive online learning (AOL) framework for supporting real-time breast cancer (BC) diagnosis. Unlike traditional data mining, our framework provides AOL models that can be adaptively updated with new incoming data, and newly discovered features. As a result, our framework can naturally perform BC risk prediction on a sequence of
Incoming patients, with increasing accuracy. For each patient, it can also adaptively adjust the prediction with more available features measured during the diagnosis procedure. Our framework maintains the model structure and the model parameters separately, for efficient management of AOL knowledge. In particular, for prediction, we build flexible fitted models, by integrating different model structures, and plugging in the corresponding parameters. For training, we update the relevant model parameters, based on the current diagnosis outcome. When new features are added, we initialize the corresponding parameters, and combine them with previous ones, for creating the new extended model without loss of the cumulative knowledge. We evaluate our framework on a real dataset from BCSC, and demonstrate that our framework can learn from sequential data and incremental features, and its performance approaches that of an oracle OL model that has unlimited access to features, after training with sufficient data. Furthermore, online decision-making models, such as reinforcement learning (RL), can be integrated to our framework, for suggesting which additional features should be prioritized and measured at each diagnosis stage. A simulation on the same dataset verifies that well-trained RL provides promising measurement suggestions given the current features and OL predictions.

9785-76, Session PS2

Computer-aided detection of polyps in optical colonoscopy images from Stony Brook University

Saad Nadeem, Arie Kaufman, Stony Brook Univ. (United States)

We present a computer-aided detection algorithm for polyps in optical colonoscopy images. Polyps are the precursors to colon cancer. In the US alone, 14 million optical colonoscopies are performed every year, mostly for screening for polyps. Optical colonoscopy has been shown to have an approximately 25% polyp miss rate due to the convoluted folds and bends present in the colon. In this work, we present an automatic detection algorithm to detect these polyps in the optical colonoscopy images. We use a machine learning algorithm to infer a depth map for a given optical colonoscopy image and then use a detailed pre-built polypl profile to detect and delineate the boundaries of polyps in this given image. We have achieved the best recall of 84.0% and the best specificity value of 83.4%.

9785-77, Session PS2

Performance evaluation of multi-material electronic cleansing for ultra-low-dose dual-energy CT colonography

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Accurate electronic cleansing for CT colonography (CTC) enables the visualization of the entire colonic surface without residual materials. In this study, we evaluated the accuracy of a novel multi-material electronic cleansing (MUMA-EC) scheme for non-cathartic ultra-low-dose dual-energy CTC (DE-CTC). The MUMA-EC performs a water-iodine material decomposition of the DE-CTC images and calculates virtual monochromatic images at multiple energies, after which a random forest classifier is used to label the images into the regions of lumen air, soft tissue, fat, fecal tagging, and two types of partial-volume boundaries based on image-based features. After the labeling, materials other than soft tissue are subtracted from the CTC images. For pilot evaluation, 384 volumes of interest (VOIs) that represented sources of EC artifacts observed in current EC schemes, were sampled from 32 ultra-low-dose DE-CTC scans. The voxels in the VOIs were labeled manually to serve as a reference standard. The metric for EC accuracy was the mean overlap ratio between the labels of the reference standard and the labels generated by the MUMA-EC, a dual-energy EC (DE-EC), and a single-energy EC (SE-EC) scheme. Statistically significant differences were observed between the performance of the MUMA-EC and the SE- and DE-EC methods (p<0.001). Visual assessment confirmed that the MUMA-EC generates less EC artifacts than do DE-EC and SE-EC. Our MUMA-EC scheme yielded superior performance over conventional DE-EC and SE-EC schemes in identifying and minimizing subtraction artifacts on non-cathartic ultra-low-dose DE-CTC images.

9785-78, Session PS2

Detection of benign prostatic hyperplasia nodules in T2W MR images using fuzzy decision forest

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Prostate cancer is the second leading cause of cancer-related death in men [6]. Consequently the detection of suspected prostate cancer in medical images has been extensively explored in the literature. Some examples of computer-aided diagnosis (CAD) of prostate cancer in the literature can be seen in [1-4]. One source of false positives in prostate CAD is the presence of benign prostatic hyperplasia (BPH) nodules [1]. These nodules have a distinct appearance with a pseudo-capsule on T2 weighted MR images but can also resemble cancerous lesions in other sequences such as the ADC or high B-value images. Describing their appearance with hand-crafted heuristics (features) that also exclude the appearance of cancerous lesions is challenging. This work develops a method based on fuzzy decision forests [7] to automatically learn discriminative features for the purpose of BPH nodule detection in T2 weighted images for the purpose of improving prostate CAD systems.

9785-79, Session PS2

Colonoscopic polyp detection on multimodality images using convolutional neural networks

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For colorectal cancer screening, colonoscopy is the primary method and considered to be the gold standard, with white light colonoscopy being widely used as the standard modality. Recently, multi-modality approaches combining white light, narrow-band and fluorescence imaging have shown promising results in clinical studies. In this paper, we present an automatic polyp detection algorithm for multi-modality colonoscopy video. We perform registration to align the modalities using mutual information as a metric. Then we derive polyp descriptors from the aligned white light colonoscopy images, narrow-band images, and fluorescence images. The features are learned automatically using a convolutional neural network that is trained on the three different image types. Finally, polyp classification on colon images is performed using a conditional random field model, using features detected in all three image modalities. The proposed method has been tested on both human and mouse colonoscopy videos.
Normalization of T2W-MRI prostate images using Rician priori

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Prostate cancer is reported to be the second most frequently diagnosed cancer of men in the world. In practise, diagnosis can be affected by multiple factors which reduces the chance to detect the potential lesions. In the last decades, new imaging techniques mainly based on MRI are developed in conjunction with Computer-Aided Diagnosis (CAD) systems to help radiologists for such diagnosis. CAD systems are usually designed as a sequential process consisting of four stages: pre-processing, segmentation, registration and classification. As a pre-processing, image normalization is a critical and important step of the chain in order to design a robust classifier and overcome the inter-patient’s intensity variations. However, little attention has been dedicated to the normalization of T2W-MRI prostate images. In this paper, we propose a method based on a Rician a priori in order to normalize T2W-MRI prostate images. A comparison with the state-of-the-art methods is also provided.

The normalization of the data is assessed by comparing the alignment of the patient Probability Density Function (PDF) in both qualitative and quantitative manners. In both evaluation, the normalization using Rician a priori outperforms the other state-of-the-art methods.

Detection and measurement of retinal blood vessel pulsatile motion

Di Xiao, Australian e-Health Research Ctr. (Australia) and Commonwealth Scientific and Industrial Research Organisation (Australia)

Benefiting from the modern medical imaging techniques, retinal images were able to provide large amounts of valuable information, especially related to eye disease diagnosis. It also enabled direct assessment of human’s body circulation system and providing information for the diagnosis of ocular and systemic vascular disease. Pulsatile properties caused by cardiac rhythm, such as spontaneous venous pulsation (SVP), pulsatile motion of small arterioles, and serpentine movement of principal arteries, can be visualized by dynamic retinal imaging techniques and provide clinical significance.

In this paper, we aim at pulsatile motion and serpentine movement detection and measurement. We propose a novel approach for pulsatile motion measurement of retinal blood vessels by applying retinal image registration, blood vessel segmentation and blood vessel pulsatile motion measurement on infrared retinal image sequences. For image registration, we adopted quadratic image region method from Dual-Bootstrap ICP. We developed blood vessel segmentation method by applying Black Top-hat and Gaussian matched filtering and local entropy thresholding. A blood vessel skeleton processing and vessel corresponding segment searching method was developed for vessel pulsatile motion measurement.

The performance of the proposed methods was tested on 8 image sequences with 240 images. A preliminary result has demonstrated the robustness of the method for blood vessel pulsatile motion observation and measurement.
Automated determination of white matter hyperintensity properties in relation to the development of Alzheimer’s disease

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Alzheimer’s disease (AD) is the most common form of dementia seen in the elderly. Unfortunately, no curing medicine for AD exists at this moment. In the search for an effective medicine, research is directed towards the prediction of conversion of mild cognitive impairment (MCI) to AD. White matter hyperintensities (WMHs) have been shown to contain information regarding the development of AD, although non-conclusive results are found in literature. These studies often use qualitative measures to describe WMHs, which is time consuming and prone to variability. To investigate the relation between WMHs and the development of AD, algorithms to automatically determine quantitative properties in terms of volume and spatial distribution of white matter hyperintensities are developed. These properties are compared between normal controls and MCI subjects. This eliminates all variabilities related to manual segmentation or scoring on a visual rating scale.

Results show that MCI subjects have a significantly higher total volume of WMHs than normal controls. This difference persists when lesions are classified according to their distance to the ventricular wall. Spatial distribution is also described by defining different brain regions based on a common coordinate system. This reveals that MCI subjects have a larger WMH volume in the upper part of the brain compared to normal controls.

In four subjects, the change of WMH properties over time is studied in detail. Although such a small dataset cannot be used to give definitive conclusions, the data suggests that progression of WMHs in subjects with a low lesion load is caused by an increase in the number of lesions and by the progression of juxtacortical lesions. In subjects with a larger lesion load, progression is caused by growth of pre-existing lesions.

Improvement of retinal blood vessel detection by spur removal and Gaussian matched filtering compensation

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Retinal photography is a non-invasive and well-accepted clinical diagnosis of ocular diseases. Qualitative and quantitative assessment of retinal images is crucial in ocular diseases related clinical application. The quality of retinal blood vessel detection influences further automatic or semi-automatic blood vessel measurements. However, the quality of blood vessel detection is variable, caused by factors of retinal image quality, individual difference, and eye disease level etc.

In this paper, we proposed two novel approaches for improving the quality of retinal blood vessel detection. First, a blood vessel spur pruning method has been developed for removing the blood vessel spurs, which are usually caused by artifacts and the side-effect of Gaussian matched filtering enhancement. Secondly, a Gaussian matched filtering compensation method has been developed for improving the blood vessel detection in the dark areas of retinal image.

40 images from publicly available database DiaretDB1 and our own automated diabetic retinopathy screening project were selected for the evaluation of the spur pruning method. From the two datasets, 30 images, which all contain partial low-illuminated areas, were selected for the evaluation of Gaussian matched filtering compensation method. Qualitative and quantitative evaluation were performed and the results demonstrated the robustness and efficiency of the proposed methods for improving the quality of retinal blood vessel detection.

Automated blood vessel extraction using local features on retinal images

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A preliminary study of automated blood vessel extraction using high-order local autocorrelation (HLAC) on retinal images is presented. Although many blood vessel extraction methods have been proposed, a technique based on the relation of neighbor pixels has not been published. HLAC features are shift-invariant; therefore, we applied HLAC features to retinal images. However, HLAC features are weak to turned image, thus a method was improved by the addition of HLAC features to a polar transformed image. The blood vessels were classified using an artificial neural network (ANN) with HLAC features using 25 mask patterns as input. To improve performance, the output value of ANN was combined with outputs values of CLAHE, Gabor filter, double ring filter, and black top-hat using a second ANN (ANN2). The retinal images used in this study were obtained from the “Digital Retinal Images for Vessel Extraction” (DRIVE) database. The ANN using HLAC output apparent white values in the blood vessel regions and could also extract blood vessels with low contrast. The outputs were evaluated using the area under the curve (AUC) based on receiver operating characteristics (ROC) analysis. The AUC of ANN2 was 0.943 as a result of our preliminary study. The best AUC in DRIVE is over 0.96, thus the proposed method should be improved.

Automated detection of retinal whitening in malarial retinopathy

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Cerebral malaria (CM) is a severe neurological complication associated with malarial infection. Malaria affects about 200 million people worldwide, and claims 584,000 lives annually, 75% of whom are African children under 5 years of age. Most of these mortalities are caused due to the high incidence of CM misdiagnosis, and therefore an accurate diagnostic to confirm the presence of CM is needed. The retinal lesions associated with malarial retinopathy (MR) are highly specific to CM, the detection of which can improve the accuracy of CM diagnosis. Retinal whitening is a unique sign of MR that appears due to ischemia as a result of CM. We propose a method to detect the whitening region in retinal color images based on features extracted from multiple color channels. First we preprocessed the image using color and textural features of CMYK and CIE-xyz color spaces to minimize the camera reflex. Next, we utilized color features of HSL, CMYK, and CIE-xyz channels, and structural features of difference of Gaussian. A watershed segmentation algorithm was used to assign each image region a probability of being inside the whitening, based on extracted features. We
applied the algorithm to a dataset of 54 images (40 with whitening and 14 controls) that resulted in an image-based (binary) classification with the AUC of 0.80 and 88% sensitivity at specificity of 65%.

9785-88, Session PS3
Finding regional models of the Alzheimer’s disease by fusing neuropsychological and structural MRI information
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Initial diagnosis of Alzheimer’s disease (AD) is based on the patient’s clinical history and a battery of neuropsychological tests. This work presents an automatic strategy that uses Structural Magnetic Resonance Imaging (MRI) to learn brain models for different stages of the disease using information from clinical assessments. Then, a comparison of the discriminant power of the models in different anatomical areas is made by using the brain region of the models as a reference frame for the classification problem by using the projection into the AD model to construct a Receiver Operating Characteristic (ROC) curve. Validation was performed using a leave-one-out scheme with 86 subjects (20 AD and 60 NC) from the Open Access Series of Imaging Studies (OASIS) database. The region with the best classification performance was the left amygdala where it is possible to achieve a sensitivity and specificity of 85% at the same time. The regions with the best performance, in terms of the AUC, are in strong agreement with those described as important for the diagnosis of AD in clinical practice.

9785-89, Session PS3
Deep learning in the small sample size setting: cascaded feed forward neural networks for medical image segmentation
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The task of automatic detection and segmentation of organs or regions of interest is fundamental to medical image analysis. Several machine learning techniques have been proposed for addressing these tasks. However, a key drawback of these methods has been the need of large quantities of training datasets. Generating this training data often requires a substantial amount of effort and time on the part of an experienced clinician. Thus, generating a large amount of such data comes at an incredibly high cost. In stark contrast to machine learning based diagnostic systems, the human visual system works perfectly well with an incredibly limited quantity of data. For instance, first year medical students may look at lungs on a single CT scan, synthesize this information and use it to identify lungs on the very next scan they see. This implies the existence of an extremely fast visual learning system which can learn with extremely limited data. In this paper, we introduce a cascaded deep learning architecture which can emulate this behavior. Our algorithm trains a cascade of deep neural networks trained to respond to raw intensity values from local image patches. Each deep net in the cascade is trained to identify a region of interest that may contain the organ of interest. This region of interest is fed to the next neural net in the cascade to further refine the search for the organ of interest. Each neural net in the cascade is 5 layers deep. The entire cascade may be conceptualized as an ultra deep network with a mutable architecture. To demonstrate the effectiveness of our approach, we train our deep network cascade for three separate segmentation tasks, on raw intensity data from a single 3D CT scan. We show that the trained network can successfully complete the same tasks on CT scans taken from other patients. This is comparable to one shot paradigm of human learning. Our fully automatic technique compares favorably with state of the art semi-automatic human guided segmentation for both tasks.

9785-90, Session PS3
A fully automatic framework for cell segmentation on non-confocal adaptive optics images
Jianfei Liu, National Institutes of Health (United States); Alfredo Dubra, Medical College of Wisconsin (United States); Johnny Tam, National Institutes of Health (United States)

By the time most retinal diseases are detected, dramatic changes to the tissue morphology have already occurred. The recent development of non-confocal adaptive optics scanning light ophthalmoscope (AOSLO) imaging [1,2] has shown that these tissue changes are often preceded by subtle changes at the single cell level. Tracking the morphological changes that occur to individual cells within the retina may lead to better ways to prevent or treat blindness. This work aims to develop a fully automatic cell segmentation framework to extract cell boundaries from noninvasive images of cone photoreceptor cells in the living human eye. Significant challenges include anisotropy, heterogeneous cell regions arising from shading effects, and low contrast between cells and background. To overcome these challenges, we propose: 1) multi-scale Hessian response to detect heterogeneous cell regions, 2) convex hull to create boundary templates, and 3) circularly-constrained geodesic active contour to refine cell regions. We acquired images from three healthy subjects at eccentric retinal regions and manually contoured cells to generate ground-truth for evaluating segmentation accuracy. Dice coefficient, relative absolute area difference, and average contour distance were $82.4 \pm 1.8\%$, $10.9 \pm 6.2\%$, and $2.0 \pm 0.2$ pixels (Mean±SD), respectively. Strong shading effects are a main factor that causes cell over-segmentation and false segmentation. Experimental results demonstrate that our segmentation algorithm can automatically and accurately segment photoreceptor cells on non-confocal AOSLO images, which is the first step in longitudinal tracking of cellular changes in the individual eye over the time course of disease progression.

9785-91, Session PS3
Automated metastatic brain lesion detection: a computer aided diagnostic and clinical research tool
Jeremy Devine, Univ. of Toronto (Canada); Arjun Sahgal, Irene Karam, Sunnybrook Health Sciences Ctr. (Canada); Anne L. Martel, Sunnybrook Research Institute (Canada)

No Abstract Available

9785-93, Session PS3
Automated detection of retinal nerve fiber layer defects on fundus images: false positive reduction based on vessel likelihood
Chisako Muramatsu, Kyoko Ishida, Akira Sawada, Gifu Univ. School of Medicine (Japan); Yuji Hatanaka, Univ. of Shiga Prefecture (Japan); Tetsuya Yamamoto, Hiroshi Fujita, Gifu Univ. School of Medicine (Japan)

Early detection of glaucoma is important to slow down or cease progression of the disease and for preventing total blindness. We have previously proposed an automated scheme for detection of retinal nerve fiber layer defect (NFLD), which is one of the early signs of glaucoma observed on retinal fundus images. In this study, a new multi-step detection scheme was included to improve detection of subtle and narrow NFLDs. In addition, new
features were added to distinguish between NFLDs and blood vessels, which are frequent sites of false positives. The result was evaluated with a new test dataset consisting of 261 cases, including 130 cases with NFLDs. Using the proposed method, the initial detection rate was improved from 82% to 98%. At the sensitivity of 80%, the number of false positives per image was reduced from 4.25 to 1.36. The result indicated the potential usefulness of the proposed method for early detection of glaucoma.

9785-94, Session PS3

Phenotypic characterization of glioblastoma identified through shape descriptors
Ahmad Chaddad, Christian Desrosiers, Matthew Toews, École de Technologie Supérieure (Canada)

This paper proposes quantitatively describing the shape of glioblastoma (GBM) tissue phenotypes in terms of nine shape features derived from volumetric tissue segmentations, with the aim of discriminating between phenotypes and monitoring GBM tumor progression. GBM patients were identified from the Cancer Genome Atlas, and quantitative MR imaging data were obtained from the Cancer Imaging Archive. Three GBM tissue phenotypes are considered including necrosis, active tumor and edema/invasion. Volumetric tissue segmentations are obtained from registered T1-weighted (T1W) contrast-enhanced T1-weighted (T1WI) post-contrast and fluid-attenuated inversion recovery (FLAIR) MRI modalities. Shape features are computed from respective tissue phenotype segmentations, and a Kruskal-Wallis test was employed to select features capable of classifying with a significance level of $p < 0.05$. Several classifier models are employed to distinguish phenotypes, where a leave-one-out cross-validation was performed. Eight features were found statistically significant for classifying GBM phenotypes with $p < 0.05$, orientation is uninformative. Quantitative evaluations show the SVM results in the highest classification accuracy of 87.50%, sensitivity of 94.59% and specificity of 92.77%.

In summary, the shape descriptors proposed in this work show high performance in predicting GBM tissue phenotypes. They are thus closely linked to morphological characteristics of GBM phenotypes and could potentially be used in a computer assisted labeling system.

9785-95, Session PS3

3D texture-based classification applied on brain white matter lesions on MR images
Marina P. Bento Leite, Univ. Estadual de Campinas (Brazil); David Gobbi, Marina Salluzi, Richard Frayne, Univ. of Calgary (Canada); Roberto A. Lotufo, Leticia Rittner, Univ. Estadual de Campinas (Brazil)

Lesions in the brain white matter are among the most frequently observed incidental findings on MR images. This paper presents a 3D texture-based classification to distinguish normal appearing white matter from white matter containing lesions, and compares it with the 2D approach. Texture analysis were based on 55 texture attributes extracted from gray-level histogram, gray-level co-occurrence matrix, run-length matrix and gradient. The results show that the 3D approach achieves an accuracy rate of 99.28%, against 97.41% of the 2D approach by using a support vector machine classifier. Furthermore, the most discriminating texture attributes on both 2D and 3D cases were obtained from the image histogram and co-occurrence matrix.

9785-96, Session PS3

Classification of SD-OCT volumes for DME detection: an anomaly detection approach
Shrinivasan Sankar, Désiré Sibidé, Univ. de Bourgogne (France); Carol Y. Cheung, Tien Y. Wong, Ecosse Lamoureux, Dan Milea, Singapore Eye Research Institute (Singapore); Fabrice Meriaudeau, Univ. de Bourgogne (France)

Diabetic Macular Edema (DME) is the leading cause of blindness amongst the diabetic patients worldwide. It is characterized by accumulation of water molecules in the macula leading to swelling. Early detection of the disease helps prevent further loss of vision. Naturally, automated detection of DME from Optical Coherence Tomography (OCT) volumes plays a key role. To this end, a pipeline for detecting DME diseases in OCT volumes is proposed in this paper. The method is based on anomaly detection using Gaussian Mixture Model (GMM). It starts with pre-processing the B-scans by resizing, flattening, filtering and extracting features from them. Both intensity and Linear Binary Pattern (LBP) features are considered. The dimensionality of the extracted features is reduced using PCA. As the last stage, a GMM is fitted with features from normal volumes. During testing, features extracted from the test volume go through the fitted model to evaluate for anomaly and classification is made based on the number of B-scans detected as outliers. The pipeline is tested on two datasets with accuracies of 90.4% and 100.0% respectively. Finally, a comparison with the Bag of Words (BoW) approach reveals better performance of the proposed method. In particular, the BoW method achieves accuracies of 87.5% and 86.76%.

9785-97, Session PS3

A toolbox to visually explore cerebellar shape changes in cerebellar disease and dysfunction
Sayed M. Abulnaga, The Univ. of British Columbia (Canada); Zhen Yang, Aaron Carass, Johns Hopkins Univ. (United States); Kalyani Kansal, Johns Hopkins Univ. School of Medicine (United States); Bruno M. Jedynek, Johns Hopkins Univ. (United States); Chiadi U. Onyike, Sarah H. Ying, Johns Hopkins Univ. School of Medicine (United States); Jerry L. Prince, Johns Hopkins Univ. (United States)

The cerebellum plays an important role in motor and cognitive functions. Cerebellar function is specialized by location, although the exact topographic functional relationship is not fully understood. The spinocerebellar ataxias are a group of neurodegenerative diseases that cause regional atrophy in the cerebellum, yielding distinct motor and cognitive problems. The ability to study the region-specific atrophy patterns can provide insight into the problem of relating cerebellar function to location. In an effort to study these structural change patterns, we developed a toolbox in MATLAB to provide researchers a unique way to visually explore the correlation between cerebellar lobule shape changes and function loss, with a rich set of visualization and analysis modules. In this paper, we outline the functions and highlight the utility of the toolbox. The toolbox takes as input landmark shape representations of subjects’ cerebellar substructures. Dimension reduction precedes a principal component analysis. Following this, a linear discriminant analysis and a regression analysis can be performed to find the discriminant direction associated with a specific disease type, or the regression line of a specific functional measure can be generated. The characteristic structural change pattern of a disease type or of a functional score is visualized by sampling points on the discriminant or regression line. The sampled points are used to reconstruct synthetic cerebellar lobule shapes. We perform a regression analysis to reveal the cerebellar atrophy patterns associated with motor and cognitive function loss and compare the results with the literature.
9785-98, Session PS3

Using support vector machines with tract-based spatial statistics for automated classification of Tourette syndrome children

Hongwei Wen, Institute of Automation (China); Yue Liu, Yun Peng, Capital Medical Univ. (China); Huiguang He, Institute of Automation (China)

Tourette syndrome (TS) is a neurological disorder that emerges in early childhood (3-8 years) and which is characterized by involuntary and repetitive motor and vocal tics. For most patients, the worst tic severity falls between 7-15 years of age. To date, the neural basis of TS is not fully understood yet and TS has a long-term prognosis that is difficult to accurately estimate. Presently no study has looked at the potential of using diffusion tensor imaging (DTI) in conjunction with machine learning algorithms in order to automate the classification of healthy children and TS children. Here we apply Tract-Based Spatial Statistics (TBSS) method to 44 TS children and 48 age and gender matched healthy children in order to extract the diffusion values from each voxel in the white matter (WM) skeleton. A feature selection algorithm (Relieff) was used to select the most salient voxels for subsequent classification with support vector machine (SVM). The highest accuracy (94.6%), sensitivity (93.2%) and specificity (95.8%) were achieved in our method as peak performance of the SVM classifier was achieved using the axial diffusivity (AD) metric with 2000 voxels feature set, demonstrating the potential of a joint TBSS and SVM pipeline for fast, objective classification of healthy and TS children. These results support the contention that our methods may be useful for the early identification of subjects with TS, and hold promise for predicting prognosis and treatment outcome for individuals with TS.

9785-99, Session PS3

A diagnosis model for early Tourette syndrome children based on brain structural network characteristics

Hongwei Wen, Institute of Automation (China); Yue Liu, Yun Peng, Capital Medical Univ. (China); Huiguang He, Institute of Automation (China)

Tourette syndrome (TS) is a childhood-onset neurobehavioral disorder characterized by the presence of multiple motor and vocal tics. Tic generation has been linked to disturbed networks of brain areas involved in planning, controlling and execution of action. The aim of our work is to select topological characteristics of structural network which were most efficient for estimating the classification models to identify early TS children. Here we employed the diffusion tensor imaging (DTI) and deterministic tractography to construct the structural networks of 44 TS children and 48 age and gender matched healthy children. We calculated four different connection matrices (fiber number, mean FA, averaged fiber length weighted and binary matrices) and then applied graph theoretical methods to extract the regional nodal characteristics of structural network. For each weighted or binary network, nodal degree, nodal efficiency and nodal betweenness were selected as features. Support Vector Machine Recursive Feature Extraction (SVM-RFE) algorithm was used to estimate the best feature subset for classification. The accuracy of 88.26% evaluated by a nested cross validation was achieved on combing best feature subset of each network characteristic. The identified discriminative brain nodes mostly located in the basal ganglia and frontal cortico-cortical networks involved in TS children which was associated with tic severity. Our study holds promise for early identification and predicting prognosis of TS children.

9785-100, Session PS3

A primitive study of voxel feature generation by multiple stacked denoising autoencoders for detecting cerebral aneurysms on MRA

Mitsutaka Nemoto, Naoto Hayashi, Shouhei Hanaoka, Yukihiro Nomura, Soichiro Miki, Takeharu Yoshikawa, Kuni Ohtomo M.D., The Univ. of Tokyo (Japan)

Purpose: We have been developing an automatic detection method for cerebral aneurysms on magnetic resonance angiogram (MRA). In this study, our previous method is improved by adding voxel features extracted by multiple stacked denoising autoencoders (SdAs). After pre-processing and detection of lesion candidate points, these candidate points are classified using not only with manually designed voxel features but also voxel features that are automatically extracted by multiple SdAs. The purpose of this study is to evaluate the feasibility of our SdA-based feature extraction approach. Methods: In this study, time-consuming manual optimization of SdA hyper-parameter is not carried out. Instead of experimentally searching the best SdA hyper-parameter set, all of multiple SdA models trained using different hyper-parameter sets are used to extract a large quantity of SdA voxel feature sets. The voxel features extracted by multiple SdAs are processed using the max-/min-/average-pooling and then used in the candidate classification step. The features actually used in the candidate classification are automatically selected by an ada-boost ensemble learning method. Results: The evaluation was performed with 100 MRA cases. Each case included at least one aneurysm of 2 mm or more in diameter. By using both previous voxel features and SdA voxel features, the classification performance was improved compared to the previous one was obtained (AUC=0.838 vs. 0.811). Conclusion: The proposed feature extraction method was shown to be effective in the aneurysm detection application.

9785-101, Session PS3

Predicting outcomes in glioblastoma patients using computerized analysis of tumor shape: preliminary data

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Glioblastoma (GBM) is the most common primary brain tumor characterized by very poor survival. However, while some patients survive only a few months, some might live for multiple years. Accurate prognosis of survival and stratification of patients allows for making more personalized treatment decisions and moves treatment of GBM one step closer toward the paradigm of precision medicine. While some molecular biomarkers are being investigated, medical imaging remains significantly underutilized for prognostication in GBM. In this study, we investigated whether computer analysis of tumor shape can contribute toward accurate prognosis of outcomes. Specifically, we implemented applied computer algorithms to extract 5 shape features from magnetic resonance imaging (MRI) for 22 GBM patients. Then, we determined whether each one of the features can accurately distinguish between patients with good and poor outcome. We found that one of the 5 analyzed features showed prognostic value of survival. The prognostic feature describes how well the 3D tumor shape fills its minimum bounding ellipsoid. Specifically, for low values (less or equal than the median) the proportion of patients that survived more than a year was 27% while for high values (higher than median) the proportion of patients with survival of more than 1 year was 82%. The difference was statistically significant (p < 0.05) even though the number of patients analyzed in this pilot study was low. We concluded that computerized, 3D analysis of tumor shape in MRI may strongly contribute to accurate prognostication and stratification of patients for therapy in GBM.

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Glioma grading using cell nuclei morphologic features in digital pathology images
Syed M. S. Reza, Khan M. Iftekharuddin, Old Dominion Univ. (United States)

This work proposes a computationally efficient cell nuclei morphologic feature analysis technique to characterize the brain gliomas in tissue slide images. In this work, our contributions are two-fold: 1) obtain an optimized cell nuclei segmentation method based on the pros and cons of the existing techniques in literature, 2) extract representative features by k-means clustering of nuclei morphologic features to include area, perimeter, eccentricity, and major axis length. This clustering based representative feature extraction avoids shortcomings of extensive tile [1] [2] and nuclear score [3] based methods for brain glioma grading in pathology images. Multilayer perceptron (MLP) is used to classify extracted features into two tumor types: glioblastoma multiforme (GBM) and low grade glioma (LGG). Quantitative scores such as precision, recall, and accuracy are obtained using 66 clinical patients’ images from The Cancer Genome Atlas (TCGA) [4] dataset. An on average -94% accuracy from 10 fold cross-validation confirms the efficacy of the proposed method.

Quantitative characterization of brain β-amyloid in 300 normal subjects using a joint PiB/FGD PET image histogram
Jon J. Camp, Dennis P. Hanson, Val J. Lowe M.D., Bradley J. Kemp, Matthew L. Senjem, Melissa E. Murray, Dennis W. Dickson M.D., Joseph E. Parisi M.D., Ronald C. Petersen M.D., Richard A. Robb, David R. Holmes III, Mayo Clinic (United States)

We have previously described an automated system for the co-registration of PiB and FGD PET images with structural MRI and a neurological anatomy atlas to produce region-specific quantification of cortical activity and amyloid burden. We also reported a global joint PiB/FGD histogram-based measure (FDG-Associated PiB Uptake Ratio – FAPUR) that performed as well as regional PiB ratio in stratifying Alzheimer’s Disease (AD) and Lewy Body Dementia (LBD) patients from normal subjects in an autopsy-verified cohort of 31. In this paper we examine results of this analysis on a clinically-verified cohort of 300 normal volunteers, where we found essentially unimodal normal distribution of all measurements in the normal cohort, with small correlations with age. We then used these measurements to construct age-weighted Z-scores for all measurements made on the original autopsy cohort. In addition we introduce a new metric – the Pearson’s correlation coefficient ($r_2$) of the joint PiB/FGD histogram. We found similar stratification using Z-scores compared to raw values; however, the $r_2$ Z-score showed the greatest stratification ability.

A novel approach for tuberculosis screening based on deep convolutional neural networks
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Tuberculosis (TB) is one of the major global health threats. 15M patients among 9M incident cases died in 2013, and the majority of the patients are from developing countries. Although newly diagnosed TB patients can be recovered with over-90% cure rate, many curable TB patients in the developing countries are obliged to die because of delayed diagnosis, partly by the lack of radiography and radiologists. Therefore, developing a computer-aided diagnosis (CAD) system for TB screening can contribute to early diagnosis of TB, which results in prevention of deaths from TB. Currently, most CAD algorithms adopt carefully-designed morphological features distinguishing different lesion types to improve classification accuracy. However, such engineered features cannot be guaranteed to be the best descriptors for TB screening.

Deep learning has become a majority in machine learning society. Especially in computer vision fields, it has been verified that deep convolutional neural networks (CNN) is a very promising algorithm for object recognition. Since deep CNN enables end-to-end training from feature extraction to classification, it does not require objective-specific manual feature engineering.

In this work, we designed CAD system based on deep CNN for automatic TB screening. To the best of our knowledge, this is the first CNN-based TB screening system without lesion-specific manual feature engineering. Based on large-scale chest X-rays on well-designed CNN architecture, we achieved viable TB screening performance of 0.97, 0.91 and 0.85 in terms of AUC for three real field datasets, respectively, by exploiting the effect of transfer learning.
Conference 9785: Computer-Aided Diagnosis

of Medical Education & Research (India); Prafulla Kumar, Dept. of Electronics and Information Technology (India)

Differentiation of malignant and benign pulmonary nodules is important for prognosis. The present work focuses on the classification of benign and malignant pulmonary nodules using several shape-based and texture-based features. The pulmonary nodules are segmented using a semi-automated technique, which requires only a seed point from the end-user. The relevant features are selected for efficient representation of the nodules in the feature space. Support vector machine is used for classification of benign and malignant nodules. The proposed classification scheme is applied on a data set of 542 nodules of Lung Image Database Consortium and Image Database Resource Initiative. Considering composite rank of malignancy “1”, “2” as benign and “4”, “5” as malignant, the proposed framework achieves an area of 0.9465 under the receiver operating characteristics curve. The proposed method outperforms the most recent technique.

9785-107, Session PS4

Differential of several interstitial lung disease patterns in HRCT images using support vector machine: role of databases on performance

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Interstitial lung disease (ILD) is complicated group of pulmonary disorders. High Resolution Computed Tomography (HRCT) considered to be best imaging technique for analysis of different pulmonary disorders. HRCT findings can be categorized in several patterns viz. Consolidation, Emphysema, Ground Glass Opacity, Nodular, Normal etc. based on their texture like appearance. Clinician often find it difficult to diagnosis these pattern because of their complex nature. In such scenario computer-aided diagnosis system could help clinician to identify patterns. Several approaches had been proposed for classification of ILD patterns. This includes computation of textural feature and training /testing of classifier such as ANN, SVM etc. In this paper, wavelet features are calculated from two different ILD database, publicly available MedGIFT ILD database and private ILD database, followed by performance evaluation of ANN and SVM classifiers in terms of average accuracy. It is found that average classification accuracy by SVM is greater than NN where trained and tested on same database. Investigation continued further to test variation in accuracy of classifier when training and testing is performed with alternate database and training and testing of classifier with database formed by merging samples from same class from two individual databases. The average classification accuracy drops when two independent databases used for training and testing respectively. There is significant improvement in average accuracy when classifiers are trained and tested with merged database. It infers dependency of classification accuracy on training data. It is observed that SVM outperforms ANN when same database is used for training and testing.

9785-108, Session PS4

Automated anatomical description of pleural thickening towards improvement of its computer-assisted diagnosis

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Pleural thickenings are caused by asbestos exposure and may evolve into malignant pleural mesothelioma. An early diagnosis plays the key role to an early treatment, and therefore helping to relieve the morbidity. The detection of pleural thickenings is today done by a visual inspection of CT data, which is time-consuming and underlies the physician’s subjective judgment. A computer-assisted diagnosis system to automatically assess pleural thickening have been developed including not only the quantitative assessment such as size and coordinate but also enhanced with the anatomical description, i.e. lung side (left, right), part of pleura (pars costalis, mediastinalis, diaphragmatica, spinalis), as well as vertical (upper, middle, lower) and horizontal (ventral, dorsal) position. For this purpose, a 3D anatomical model of lung surface has been manually constructed as a 3D atlas. Three registration sub-steps including rigid, affine, and non-rigid registration align input patient lung to the 3D anatomical atlas model of lung surface. Finally, each detected pleural thickening will be given a set of labels describing its anatomical properties. Through this added information, an enhancement to the existing computer-assisted diagnosis system is presented in order to assure a higher precision and reproducible assessment of pleural thickenings towards the diagnosis of the pleural mesothelioma in its early stage.

9785-109, Session PS4

Computer aided diagnosis for severity assessment of pneumoconiosis using CT images

Hidenobu Suzuki, Mikio Matsushiro, Yoshiki Kawata, Noboru Niki, The Univ. of Tokushima (Japan); Katsuya Kato, Kawasaki Medical School (Japan); Takumi Kishimoto, Okayama Rosai Hospital (Japan); Kazuto Ashizawa, Nagasaski Univ. (Japan)

240,000 participants have a screening for diagnosis of pneumoconiosis every year in Japan. Radiograph is used for staging of severity in pneumoconiosis worldwide. This paper presents a method for quantitative assessment of severity in pneumoconiosis using both size and frequency of lung nodules that detected by thin-section CT images. This method consists of three steps. First, thoracic organs (body, ribs, spine, trachea, bronchi, lungs, heart, and pulmonary blood vessels) are segmented. Second, lung nodules that have radius over 1.5mm are detected. These steps used functions of our developed computer aided detection system of chest CT images. Third, severity in pneumoconiosis is quantified using size and frequency of lung nodules. This method was applied to six pneumoconiosis patients. The initial results showed that proposed method can assess severity in pneumoconiosis quantitatively. This paper demonstrates effectiveness of our method in diagnosis and prognosis of pneumoconiosis in CT screening.

9785-110, Session PS4

Lung nodule detection using 3D convolutional neural networks trained on weakly labeled data

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Early detection of lung nodules is currently the one of the most effective ways to predict and treat lung cancer. As a result, the past decade has seen a lot of focus on computer aided detection for lung nodules, whose goal is to efficiently detect, segment lung nodules and classify them as being benign or malignant. Effective detection of such nodules remains a challenge due to their arbitrariness in shape, size and texture. In this paper, we propose a 3D convolutional neural network (CNN) that learns the discriminative features instead of classifying hand-tuned ones such as
geometric shape or texture. While 3D CNNs are promising tools to model the spatio-temporal statistics of data, they are limited by their need for detailed 3D labels, which is significantly more expensive than obtaining 2D labels. Existing CAD methods rely on obtaining detailed labels for lung nodules, to train models, which is also unrealistic and time consuming. Therefore, we propose a solution to work with a “point label”, i.e. the expert has to just specify a single pixel location indicating the presence of the nodule, and its largest expected size. We use unsupervision segmentation to grow out a 3D region, which is used to train the CNN. We show the network trained on the estimated labels have reasonably low false positive rates with a high sensitivity. We demonstrate its performance on the SPIE-LUNGx dataset, which does not have ground truth segment labels.

9785-111, Session PS4
Investigating the effects of majority voting on CAD systems: an LIDC case study
Miguel Carrazza, Brendan Kennedy, Alex Rasin, Jacob D. Furst, Daniela S. Raicu, DePaul Univ. (United States)

Computer Aided Diagnosis (CAD) systems can provide a second opinion for either identifying suspicious regions on a medical image or predicting the degree of malignancy for a detected suspicious region. To develop a predictive model, CAD systems are trained on low-level image features extracted from image data and the class labels acquired through radiologists’ interpretations or a gold standard (e.g., a biopsy). While the opinion of an expert radiologist is still an estimate of the answer, the ground truth may be extremely expensive to acquire. In such cases, CAD systems are trained on input data that contains of multiple expert opinions per case with the expectation that the aggregate of multiple labels will closely approximate the ground truth. Using multiple labels to solve this problem has its own challenges because of the inherent label uncertainty introduced by the variability in the radiologists’ interpretations. Most CAD systems use majority voting (e.g., average, mode) to handle label uncertainty. This paper investigates the effects that majority voting can have on a CAD system by classifying and analyzing different semantic characteristics supplied with the Lung Image Database Consortium (LIDC) dataset. Applying an iterative prediction model based on decision trees, we show that majority voting on labels that have certain types of skewed distributions can have a negative impact on the performance of a CAD system; therefore, alternative strategies for label integration are required when handling multiple interpretations.

9785-112, Session PS4
Automated lymph node segmentation in CT images using deep reconstruction
Ajay Gupta, Florida State Univ. (United States) and National Institutes of Health (United States); Ari Seff, Le Lu, National Institutes of Health (United States); Adrian Barbu, Florida State Univ. (United States); Ronald M. Summers, National Institutes of Health (United States)

The segmentation of lymph nodes (LN) or clusters of lymph nodes in 3D computed tomography (CT) images is a new problem and clinically relevant to several forms of cancer. The segmentation can be used to estimate the total volume for the lymph node mass or clusters in a specific body region (e.g., Abdomen), or full body. 1). The total LN volume estimate can potentially offer better accuracy in staging or assessing the outcome of treatment of cancers, than the current RECIST criteria where only the shortest axis diameter is measured. More severe or treatment resisted cancers generally lead to larger lymph nodes. 2). LNs often appear in adjacent spatial areas. The CT delineation among individual lymph nodes in a cluster is very ambiguous and low contrast. In our new formulation, we propose to segment all lymph node voxels in a region (i.e., 3D region of interest, ROI) as a binary foreground segmentation problem. No delineation between adjacent LNs is necessary and doctors can receive the total LN volume measurement directly which is highly efficient. We believe the method exploited here can make it feasible for a new radiology protocol with better diagnostic and treatment precision.

We propose a method of lymph node cluster segmentation from a 3D CT volume of interest by a patchwise application of reconstructive segmentation mask modeling and regression based convolutional neural networks. This method applies in a bottom-up fashion that does not require any manually-provided information even for initialization. The same general method can be applied to any region of the body that has lymph nodes. We evaluated the method on 86 abdominal CT scans collected from patients undergoing cancer treatment at the National Institutes of Health Clinical Center. We compared the estimates of the lymph node cluster segmentations and of the lymph node cluster volumes to those from the manual segmentation by an experienced radiologist. The proposed method has multiple different configurations on the reconstruction process which have been quantitatively evaluated and showed promising results and segmentation accuracy.

9785-113, Session PS4
Change descriptors for determining nodule malignancy in National Lung Screening Trial CT screening images
Benjamin E. Geiger, Samuel H. Hawkins, Lawrence O. Hall, Dmitry B. Goldgof, Univ. of South Florida (United States); Yoganand Balagurunathan, Robert A. Gatenby, Robert J. Gillies, H. Lee Moffitt Cancer Ctr. & Research Institute (United States)

Pulmonary nodules are effectively diagnosed in CT scans, but determining their malignancy has been a challenge. The rate of change of the size (and volume) of a pulmonary nodule is known to be a prognostic factor for cancer development. In this study, we propose that other changes in imaging characteristics are similarly informative. We examined the combination of image features across multiple CT scans, taken from the National Lung Screening Trial, with individual readings of the same patient separated by approximately one year. By subtracting the values of existing features in multiple readings for the same patient, we were able to improve the ability of existing classification algorithms to determine malignancy. We trained each classifier on 86 nodules determined to be malignant by biopsy and 171 nodules determined to be benign by their clinical stability through two years of no change; classifiers were tested on 79 malignant and 138 benign nodules. Preliminary feature selection was performed via test-retest stability. An accuracy of 81.57% and AUC of 0.844 were achieved with the Random Forests classifier on a subset of features determined to be stable via test-retest reproducibility analysis.

9785-114, Session PS4
Adaptive thresholding of chest temporal subtraction images in computer-aided diagnosis of pathologic change
Melanie J. Harrison, Jared Looper, Samuel G. Armato III, The Univ. of Chicago (United States)

Radiologists frequently use chest radiographs acquired at different times to diagnose a patient by identifying regions of change. Temporal subtraction (TS) images are formed when a computer warps a radiographic image to register and then subtract one image from the other, accentuating regions of change as “light” or “dark.” Therefore, TS allows the radiologist to visualize areas of pathologic change. The purpose of this study was to create a computer-aided diagnostic (CAD) system to threshold chest TS images and identify candidate regions of pathologic change. Each
thresholding technique created two different candidate regions: light and dark. Light regions have a high gray-level mean, while dark regions have a low gray-level mean; areas with no change appear as medium-gray pixels. Ten different thresholding techniques were examined and compared. By thresholding light and dark candidate regions separately, the number of properly thresholded regions improved. The thresholding of light and dark regions separately produced fewer overall candidate regions that included more regions of actual pathologic change than global thresholding of the image. Overall, the moment-preserving method produced the best results for light regions, while the normal distribution method produced the best results for dark regions. Separation of light and dark candidate regions by thresholding shows potential as the first step in creating a CAD system to detect pathologic change in chest TS images.

9785-115, Session PS4
Correlation analysis between pulmonary function test parameters and CT image parameters of emphysema
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Chronic Obstructive Pulmonary Disease (COPD), the third leading cause of death in the United States, is a progressive disease making a patient difficult to breathe. It includes two main types of diseases, namely, emphysema and chronic bronchitis. Conventionally, diagnosis and severity classification of COPD are usually based on the pulmonary function tests (PFTs). Nevertheless, not all people can accurately perform PFTs, especially, for those who have difficulty in breathing.

To reduce the need of PFT for the diagnosis of COPD, this paper proposes a correlation model between the lung CT images and the crucial index of the PFT, FEV1/FVC, a severity index of COPD distinguishing a normal subject from a COPD patient. A new lung CT image index, Mirage Index (MI), is developed to describe the severity of COPD primarily with emphysema disease. Unlike conventional Pixel Index (PI) which takes into account all voxels with HU values less than -950, the proposed approach models these voxels by different sizes of bullae balls and defines MI as a weighted sum of the percentages of the bullae balls of different sizes and locations in a lung.

To evaluate the efficacy of the proposed model, 45 emphysema subjects of different severity are involved in this study. In comparison with the conventional index, PI, the correlation between MI and FEV1/FVC is -0.75±0.08, which substantially outperforms the correlation between PI and FEV1/FVC, i.e., -0.63±0.11. Moreover, we have shown that the emphysematous lesion areas constituted by small bullae balls are basically irrelevant to FEV1/FVC.

9785-116, Session PS4
Computerized lung cancer malignancy level analysis using 3D texture features
Wenqing Sun, Xia Huang, Tzu-Liang B. Tseng, Wei Qian, The Univ. of Texas at El Paso (United States)

Based on the likelihood of malignancy, the nodules are classified into five different levels in Lung Image Database Consortium (LIDC) database. In this study, we tested the possibility of using three-dimensional (3D) texture features to identify the malignancy level of each nodule. Five groups of features were implemented and tested on 172 nodules with confident malignancy levels from four radiologists. These five feature groups are: grey level co-occurrence matrix (GLCM) features, local binary pattern (LBP) features, scale-invariant feature transform (SIFT) features, steerable features, and wavelet features. Because of the high dimensionality of our proposed features, multidimensional scaling (MDS) was used for dimension reduction. RUSBoost was applied for our extracted features for classification, due to its advantages in handling imbalanced dataset. Each group of features and the final combined features were used to classify nodules highly suspicious for cancer (level 5) and moderately suspicious (level 4). The results showed that the area under the curve (AUC) and accuracy are 0.7659 and 0.8365 when using the finalized features. These features were also tested on differentiating benign and malignant cases, and the reported AUC and accuracy were 0.8901 and 0.9353.

9785-117, Session PS4
A CAD system to detect pathologies in temporal subtraction images of chest radiographs
Jared Looper, Melanie J. Harrison, Samuel G. Armato III, The Univ. of Chicago (United States)

Radiologists often compare sequential radiographs to identify areas of pathologic change; however, this process is prone to error, as human anatomy can obscure the regions of change, causing the radiologists to overlook pathologies. Temporal subtraction (TS) images can provide enhanced visualization of regions of change in sequential radiographs and allow radiologists to better detect areas of change in radiographs. Not all areas of change shown in TS images, however, are actual pathologies. The purpose of this study was to create a computer-aided diagnostic (CAD) system that identifies which regions of change are caused by pathology and which are caused by misregistration of the radiographs used to create the TS image. The dataset used in this study contained 120 images with 74 pathologies on 54 images outlined by an experienced radiologist. High and low (“light” and “dark”) gray-level candidate regions were extracted from the images using gray-level thresholding. Then, sampling techniques were used to address the class imbalance problem between “true” and “false” candidate regions. Next, the datasets of light candidate regions, dark candidate regions, and the combined set of light and dark candidate regions were used as training and testing data for classifiers by using five-fold cross validation. Of the classifiers tested (support vector machines, discriminant analyses, logistic regression, and k-nearest neighbors), the support vector machine on the combined candidates using the synthetic minority oversampling technique (SMOTE) performed best with an area under the receiver operating characteristic curve value of 0.85, a sensitivity of 85%, and a specificity of 84%.

9785-118, Session PS5
Computer-aided diagnosis for osteoporosis using chest 3D CT images
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Sufferers of osteoporosis is increasing with the rapid aging. There is a QCT as an auxiliary role DXA has been used in the diagnosis of osteoporosis. In recent years, the effectiveness of osteoporosis diagnosis by 3D-QCT is growing. Development of osteoporosis diagnosis support system is required for this. In this report, we have carried out the extraction of the vertebral body by the code of the vertebral body from the spine of the 3-dimensional CT images. By measuring the bone density of the cancellous bone and the height of the vertebral body, to construct a system for supporting diagnosis of osteoporosis presents a decrease in bone density and fractures.
Dermatological hypercolorimetric multispectral imaging (DHMI): an advanced non invasive spectral imaging decision support system for early diagnostics and monitoring in dermatology

Marcello Melis M.D., Profilocolore Srl (Italy); Carmen Cantisani M.D., Dario Didona M.D., Stefano Calvieri Sr., Sapienza Univ. di Roma (Italy); Giovanni Pellacani M.D., Univ. degli Studi di Modena and Reggio Emilia (Italy)

Each year there are more new cases of skin cancer than the combined incidence of cancers of the breast, prostate, lung and colon. About 90 percent of skin cancers are associated with exposure to ultraviolet (UV) radiation from the sun. As incidence rises dermatologist are challenged by the need to make accurate diagnoses and to assess risk for skin cancers in such patients.

Melanoma and non-melanoma skin cancer incidence is increasing more than 2 million cases for year in the united states alone.

The aim of this study is to propose a new approach to screening, diagnostics and monitoring skin diseases that is based on non invasive high resolution imaging. The system we used is able of precisely measure the spectral reflectance in the range of 300 to 1000 nanometer pixel by pixel (imaging) with a very fast acquisition procedure, fully compatible with hospital routine. We followed a multidisciplinary approach (medicine, engineering and radiometry) achieving a practical system to read spectral signature of the skin integrated with other imaging data. At first stage we compared exact spectral reflectance to diagnostics based on visual inspection and histopathological exams. This allowed us to develop statistics and compile a spectral database of diseases. In the second stage we applied the system to new cases both for fast screening and for specific diagnostics. The results have been very encouraging of the method giving a valuable support to the dermatologist diagnosis. A number of representative clinical cases are shown in detail in our study.

Segmentation of knee MRI using structure enhanced local phase filtering

Mikhail Lim, Ilker Hacihaliloglu, Rutgers, The State Univ. of New Jersey (United States)

The segmentation of bone surfaces from magnetic resonance imaging (MRI) data has applications in the quantitative measurement of knee osteoarthritis, surgery planning for patient specific total knee arthroplasty and its subsequent fabrication of artificial implants. However, due to the problems associated with MRI imaging such as low contrast between bone and surrounding tissues, noise, bias fields, and the partial volume effect, segmentation of bone surfaces continues to be a challenging operation. In this paper, we present a new framework for the enhancement of knee MRI scans prior to segmentation in order to obtain high contrast bone images. During the first stage, a new contrast enhanced relative total variation (TV) regularization method is used in order to remove textural noise from the bone structures and surrounding soft tissue interface. This salient bone edge information is further enhanced using a sparse gradient counting method based on L0 gradient minimization, which globally controls how many non-zero gradients are resulted in order to approximate prominent bone structures in a structure-sparsity-management manner. The last stage of the framework involves incorporation of local phase bone boundary information in order to provide an intensity invariant enhancement of the contrast between the bone and surrounding soft tissue. The enhanced images are segmented using a fast random walker algorithm. Validation against expert segmentation was performed on 10 clinical knee MRI images, and achieved a mean dice similarity coefficient (DSC) of 0.975.

Automated morphological analysis of bone marrow cells in microscopic images for diagnosis of leukemia: nucleus-plasma separation and cell classification using a hierarchical tree model of hematopoiesis

Sebastian Krappe, Thomas Wittenberg, Fraunhofer-Institut für Integrierte Schaltungen (IIS) (Germany); Torsten Haferlach, MLL Münchner Leukämielabor GmbH (Germany); Christian Münzenmayer, Fraunhofer-Institut für Integrierte Schaltungen (IIS) (Germany)

The morphological differentiation of bone marrow is fundamental for the diagnosis of leukemia. Currently, the counting and classification of the different types of bone marrow cells is done manually under the use of bright field microscopy. This is a time-consuming, subjective, tedious and error-prone process. Furthermore, repeated examinations of a slide may yield intra- and inter-observer variances. For that reason a computer assisted diagnosis system for bone marrow differentiation is pursued. In this work we focus (a) on a new method for the separation of nucleus and plasma parts and (b) on a knowledge-based hierarchical tree classifier for the differentiation of bone marrow cells in 16 different classes.

Classification trees are easily interpretable and understandable and provide a classification together with an explanation. Using classification trees, expert knowledge (i.e. knowledge about similar classes and cell lines in the tree model of hematopoiesis) is integrated in the structure of the tree. The proposed segmentation method is evaluated with more than 10,000 manually segmented cells. For the evaluation of the proposed hierarchical classifier more than 140,000 automatically segmented bone marrow cells are used. Future automated solutions for the morphological analysis of bone marrow smears could potentially apply such an approach for the pre-classification of bone marrow cells and thereby shortening the examination time.

A B-spline image registration based CAD scheme to evaluate drug treatment response of ovarian cancer patients

Maxine Tan, Zheng Li, The Univ. of Oklahoma (United States); Kathleen Moore, The Univ. of Oklahoma Health Sciences Ctr. (United States); Theresa Thai, Kai Ding, Hong Liu, Bin Zheng, The Univ. of Oklahoma (United States)

Ovarian cancer is the second most common cancer amongst gynecologic malignancies, and has the highest death rate. Since the majority of ovarian cancer patients (>75%) are diagnosed in the advanced cancer stage with tumor metastasis, chemotherapy is often required after surgery to remove the primary ovarian tumors. In order to quickly assess patient response to the chemotherapy in the clinical trials, two sets of CT examinations are taken pre- and post-therapy (e.g., after 6 weeks). Treatment efficacy is then evaluated based on Response Evaluation Criteria in Solid Tumors (RECIST) guideline, whereby tumor size is measured by the longest diameter on one CT image slice and only a subset of selected tumors are tracked. However, this criterion cannot fully represent the volumetric changes of the tumors and might miss potentially problematic unmarked tumors. Thus, we developed a new CAD approach to measure and analyze volumetric tumor growth/shrinkage using a cubic B-spline deformable image registration method. In this initial study, on 14 sets of pre- and post-treatment CT scans, we registered the two consecutive scans using cubic B-spline registration in a multiresolution (from coarse to fine) framework. We used Matuss mutual information metric as the similarity criterion and the L-BFGS-B optimizer. The results show that our method can quantify volumetric changes in the tumors more accurately than RECIST, and detect (highlight) potentially...
In this research, we propose a method of acquiring a global frame-of-reference based on a local coordinate system of a specific bone which are sensitive to bone deformities. Although the approach provides reliable measurements, we measured talus-calcaneal and talus-navicular angles based on the articular surfaces for 3D angles. Conventional projection angles were also obtained from the CT image planes (sagittal, frontal, and transverse), and their standard deviation (SD) of the measured angles were compared. The results show that the proposed method has considerably reduced SD, and it was also comparable with the measurement values obtained from local coordinate systems of the bones. Unlike the local coordinates, however, the proposed method is independent from any individual local shape of a bone, and suitable for inter-subject comparison study.

Phantom-less bone mineral density (BMD) measurement using dual energy computed tomography-based 3-material decomposition

Philipp Hofmann, Siemens Healthcare GmbH (Germany) and Philips-Universitatsklinikum Marburg (Germany); Martin Sedlmair, Bernhard Krauss, Siemens Healthcare GmbH (Germany); Julian L. Wichmann, Universitätsklinikum Frankfurt (Germany) and The Medical Univ. of South Carolina (United States); Ralf W. Bauer, Universitätsklinikum Frankfurt (Germany); Thomas G. Flohr, Siemens Healthcare GmbH (Germany); Andreas H. Mahnken M.D., Philips-Universitatsklinikum Marburg (Germany)

Osteoporosis is a degenerative bone disease usually diagnosed at the manifestation of fragility fractures, which severely endanger the health of especially the elderly. To ensure timely therapeutic countermeasures, noninvasive and widely applicable diagnostic methods are required. Currently the primary quantifiable indicator for bone stability, bone mineral density (BMD), is obtained either by DEXA (Dual-energy X-ray absorptiometry) or qCT (quantitative CT). Both have respective advantages and disadvantages, with DEXA being considered as gold standard. For timely diagnosis of osteoporosis, another CT-based method is presented.

A Dual Energy CT reconstruction workflow is being developed to evaluate BMD by evaluating lumbar spine (L1-L4) DE-CT images. The workflow is ROI-based and automated for practical use. A dual energy 3-material decomposition algorithm is used to differentiate bone from soft tissue and fat attenuation. The algorithm uses material attenuation coefficients on different beam energy levels. The bone fraction of the three different tissues is used to calculate the amount of hydroxylapatite in the trabecular bone of the corpus vertebrae inside a predefined ROI. Calibrations have been performed to obtain volumetric bone mineral density (vBMD) without having to add a calibration phantom or to use special scan protocols or hardware. Accuracy and precision are dependent on image noise and comparable to qCT images. Clinical indications are in accordance with the DEXA gold standard. The decomposition-based workflow shows bone degradation effects normally not visible on standard CT images which would induce errors in normal qCT results.

Reliable measurement of 3D foot bone angles based on the frame-of-reference derived from the sole of the foot

Taeho Kim, KAIST (Korea, Republic of); Dong Yeon Lee, Seoul National Univ. Hospital (Korea, Republic of); Jinah Park, KAIST (Korea, Republic of)

Clinical management of foot pathology requires accurate and robust measurement of the anatomical angles. In order to measure a 3D angle, recent approaches have adopted a landmark-based local coordinate system to establish bone angles used in orthopedics. Although the approach provides clinically useful measurements, these are mainly relative angles based on a local coordinate system of a specific bone which are sensitive to bone deformities.

In this research, we propose a method of acquiring a global frame-of-reference for representing consistent direction of the foot by extracting the undersurface of the foot from CT data. Two lowest positions of the foot skin are identified from the surface to define the base plane, and the direction from the hallux to the fourth toe is defined together to construct the global coordinate system. We performed the experiment on 10 volumes of foot CT images of healthy subjects to verify that the proposed coordinate system provides reliable measurements. We measured talus-calcaneus and talus-navicular angles based on the articular surfaces for 3D angles. Conventional projection angles were also obtained from the CT image planes (sagittal, frontal, and transverse), and their standard deviation (SD) of the measured angles were compared. The results show that the proposed method has considerably reduced SD, and it was also comparable with the measurement values obtained from local coordinate systems of the bones. Unlike the local coordinates, however, the proposed method is independent from any individual local shape of a bone, and suitable for inter-subject comparison study.

Segmentation and JSW measurements of feet radiographs

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Joint damage in rheumatoid arthritis is frequently assessed using radiographs of hands and feet. Evaluation includes measurements of the joint space width (JSW) and detection of erosions. Current visual scoring methods are time-consuming and subject to inter- and intra-observer variability. Automated measurement methods avoid these limitations and have been fairly successful in hand radiographs. This contribution aims at foot radiographs.

Starting from an earlier proposed automated segmentation method we have developed a novel model based image analysis algorithm for JSW measurements. This method uses active appearance and active shape models to identify individual bones. The model compiles ten submodels, each representing a specific bone of the foot (metatarsals 1-5, proximal phalanges 1-5).

We have performed segmentation experiments using 20 foot radiographs, randomly selected from a large database from the rheumatology department of a local hospital. 10 for training and 10 for testing. Segmentation was considered successful if the surrounding box completely covers the phalanx, which is the case in 76% of individual bones. Within these boxes the algorithm was able to correctly find 49% of the contours of the bone. Results are expected to improve when the model is refined by increasing the number of training examples.

We tested JSW measurements on one randomly selected radiograph from the earlier mentioned set of 20. JSW values are plausible and the algorithm is ready for testing on a larger data set.

This is a first step towards automated determination of progression of RA and therapy response in feet using radiographs.

Multi-atlas segmentation of the cartilage in knee MR images with sequential volume- and bone-mask-based registrations

Han Sang Lee, KAIST (Korea, Republic of); Hyeun A. Kim, Hyeonjin Kim, Helen Hong, Seoul Women’s Univ. (Korea, Republic of); Young Cheol Yoon, Samsung Medical Ctr. (Korea, Republic of); Junmo Kim, KAIST (Korea, Republic of)

Segmentation of knee cartilage in MR images is a critical process in the
With the advent of modern machine learning methods and fully automated image analysis there is a need for very large image datasets having documented segmentations for both computer algorithm training and evaluation. Current approaches of visual inspection and manual markings do not scale well to big data. We present a new approach that depends on fully automated algorithm outcomes for segmentation documentation, requires no manual marking, and provides quantitative evaluation for computer algorithms. This method has been applied to a data set of 7452 whole-lung CT images for 6 different segmentation algorithms. The results indicate that we could show 90% to 99% successful segmentation for these algorithms on this relatively large image database. The proposed evaluation method may be scaled to much larger image databases.

9785-127, Session PS5

A new paradigm of oral cancer detection using digital infrared thermal imaging

Manashi Chakraborty, Sudipta Mukhopadhyay, Avijit Dasgupta, Swapna Banerjee, Sourav Mukhopadhyay, Indian Institute of Technology Kharagpur (India); Santanu Patsa, Jay Gopal Ray, Dr. R. Ahmed Dental College & Hospital (India); Keya Chaudhuri, CSIR-Indian Institute of Chemical Biology (India)

Histopathology is considered the gold standard for oral cancer detection. But a major fraction of patient population is incapable of accessing such healthcare facilities due to poverty. Moreover, such analysis may report false negatives when test tissue is not collected from exact cancerous location. The proposed work introduces a pioneering computer aided paradigm of fast, non-invasive and non-ionizing modality for oral cancer detection using Digital Infrared Thermal Imaging (DITI). Due to aberrant metabolic activities in carcinogenic facial regions, heat signatures of patients are different from that of normal subjects. The proposed work utilizes asymmetry of temperature distribution of facial regions as principle cue for cancer detection. Three views of a subject, viz. front, left and right are acquired using long infrared (7.5 -13μm) camera for analyzing distribution of temperature. We study asymmetry of facial temperature distribution between: a) left and right profile faces and b) left and right half of frontal face. Comparison of temperature distribution suggests that patients manifest greater asymmetry compared to normal subjects. For classification, we initially use k-means and fuzzy k-means for unsupervised clustering followed by class cluster prototype assignment based on majority voting. Average classification accuracy of 91.5% and 92.8% are achieved by k-mean and fuzzy k-mean framework for frontal face. The corresponding metrics for profile face are 93.4% and 95%. Combining features of frontal and profile faces, average accuracies are increased to 96.2% and 97.6% respectively for k-means and fuzzy k-means framework.

9785-128, Session PS5

Image segmentation evaluation for very-large data sets

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With the advent of modern machine learning methods and fully automated image analysis there is a need for very large image datasets having documented segmentations for both computer algorithm training and evaluation. Current approaches of visual inspection and manual markings do not scale well to big data. We present a new approach that depends on fully automated algorithm outcomes for segmentation documentation, requires no manual marking, and provides quantitative evaluation for computer algorithms. This method has been applied to a data set of 7452 whole-lung CT images for 6 different segmentation algorithms. The results indicate that we could show 90% to 99% successful segmentation for these algorithms on this relatively large image database. The proposed evaluation method may be scaled to much larger image databases.

9785-129, Session PS5

Automated recognition of the iliac muscle and modeling of muscle fiber direction in torso CT images

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The iliac muscle is an important skeletal muscle related to ambulatory function. The muscles related to ambulatory function are the psoas major and iliac muscles, collectively defined as the ilipsoas muscle. We have proposed an automated recognition method of the iliac muscle. Muscle fibers of the iliac muscle have a characteristic running pattern. Therefore, we used 20 cases from a training database to model the movement of the muscle fibers of the iliac muscle. In the recognition process, the existing position of the iliac muscle was estimated by applying the muscle fiber model. To generate an approximation mask by using a muscle fiber model, a candidate region of the iliac muscle was obtained. Finally, the muscle region was identified by using values from the gray value and boundary information. The experiments were performed by using the 20 cases without abnormalities in the skeletal muscle for modeling. The recognition result in five cases obtained a 76.9% average concordance rate. In the visual evaluation, overextraction of other organs was not observed in 85% of the cases. Therefore, the proposed method is considered to be effective in the recognition of the initial region of the iliac muscle. In the future, we will integrate the recognition method of the psoas major muscle in developing an analytical technique for the ilipsoas area. Furthermore, development of a sophisticated muscle function analysis method is necessary.

9785-130, Session PS5

Multispectral imaging burn wound tissue classification system: a comparison of test accuracies of several common machine learning algorithms

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Multispectral imaging (MSI) was implemented to develop a burn tissue classification system to assist burn surgeons in planning and performing debridement surgery. A swine burn model was developed to build an MSI training database and study a variety of common machine learning algorithms’ burn tissue classification abilities. The algorithms tested, from least to most complex, were: K-nearest neighbors (KNN), decision tree
(DT), linear discriminant analysis (LDA), weighted linear discriminant analysis (W-LDA), quadratic discriminant analysis (QDA), ensemble linear discriminant analysis (EN-LDA), ensemble K-nearest neighbors (EN-KNN), ensemble decision tree (EN-DT), and support vector machine (SVM). After the ground-truth database of six tissue types (healthy skin, wound bed, blood, hyperemia, partial injury, full injury) was generated by histopathological analysis, we used 10-fold cross validation to compare the algorithms’ performance based on their accuracies in classifying data against the ground truth. In order to reduce bias, each algorithm was tested 100 times with the training database. The mean test accuracy of the algorithms were KN 68.3%, DT 61.5%, LDA 70.5%, W-LDA 68.1%, QDA 68.9%, EN-LDA 56.8%, EN-KNN 49.7%, EN-DT 36.5%, and SVM 62.6%. LDA had the highest test accuracy, reflecting the bias-variance tradeoff over the range of complexities inherent to the algorithms tested. Several algorithms were able to match the current gold standard in burn tissue classification, the clinical judgment of expert burn surgeons, which has been estimated to be between 60-80%. These results will guide further development of the burn tissue classification system. Given that there are few surgeons and facilities specializing in burn care, this technology may improve the standard of burn care for patients without access to specialized facilities.

9785-131, Session PS5

Automated torso organ segmentation from 3D CT images using conditional random field

Yukitaka Nimura, Yuichiro Hayashi, Nagoya Univ. (Japan); Takeyuki Kitasaka, Aichi Institute of Technology (Japan); Kazunari Misawa, Aichi Cancer Ctr. Research Institute (Japan); Kensaku Mori, Nagoya Univ. (Japan)

This paper presents a segmentation method for torso organs using conditional random field (CRF) from medical images. A lot of methods have been proposed to enable automated extraction of organ regions from volumetric medical images. However, it is necessary to adjust empirical parameters of them to obtain precise organ regions. In this paper, we propose an organ segmentation method using structured output learning which is based on probabilistic graphical model. The proposed method utilizes CRF on three-dimensional grids as probabilistic graphical model and binary features which represent the relationship between voxel intensities and organ labels. Also we optimize the weight parameters of the CRF using stochastic gradient descent algorithm and estimate organ labels for a given training set, a template scan was selected from the positive samples and all other scans were registered to it. Each registered scan was then evenly split into 92.5±3.1% to 93.8±2.1% for the left and right transverse processes and lumbar vertebrae from 10 pathological and traumatic spine patients accuracy. Vertebra atlases produced errors where the segmentation leaks into the ribs. The use of joint vertebra-rib atlas produced a statistically significant increase in the Dice coefficient from 92.5±3.1% to 93.8±2.1% for the left and right transverse processes and decrease in mean and max surface distance from 0.75±0.60mm and 8.63±4.44mm to 0.30±0.27mm and 3.65±2.87mm, respectively.

9785-132, Session PS5

Interactive computer-assisted approach for evaluation of ultrastructural cilia abnormalities

Christoph Palm, Ostbayerische Technische Hochschule Regensburg (Germany); Heiko Siegmund, Universitätsklinikum Regensburg (Germany); Matthias Semmelmann, Ostbayerische Technische Hochschule Regensburg (Germany); Claudia Grafe, Matthias Evert, Josef A. Schroeder, Universitätsklinikum Regensburg (Germany)

Introduction – Diagnosis of abnormal cilia function is based on ultrastructural analysis of axoneme defects, especially the features of inner and outer dynein arms which are the motors of ciliary motility. Sub-optimal biopsy material, methodical, and intrinsic electron microscopy factors pose difficulty in ciliary defects evaluation. We present a computer-assisted approach based on state-of-the-art image analysis and object recognition methods yielding a time-saving and efficient diagnosis of cilia dysfunction. Method – The presented approach is based on a pipeline of basal image processing methods like smoothing, thresholding and ellipse fitting. However, integration of application specific knowledge results in robust segmentations even in cases of image artifacts. The method is build hierarchically starting with the detection of cilia within the image, followed by the detection of nine doublets within each analyzable cilium, and ending with the detection of dynein arms of each doublet. The process is concluded by a rough classification of the dynein arms as basis for a computer-assisted diagnosis. Additionally, the interaction possibilities are designed in a way, that the results are still reproducible given the completion report. Results – A first qualitative evaluation showed reasonable detection results for cilia, doublets and dynein arms. However, since a ground truth is missing, the variation of the computer-assisted diagnosis should be within the subjective bias of human diagnosticians. For such a quantitative evaluation, a suitable study will take place in the next months and will be included in the final paper.

9785-133, Session PS5

Improving vertebra segmentation through joint vertebra-rib atlases

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Accurate spine segmentation allows for improved identification and quantitative characterization of abnormalities of the vertebra, such as vertebra fractures. However, existing automated vertebra segmentation on computed tomography (CT) images result in leakage into nearby bones (such as ribs) due to the close proximity of these visibly intense structures in a 3D CT volume. To reduce this error, we propose the use of a joint vertebra-rib atlas to improve the segmentation of vertebrae via multi-atlas joint label fusion. Segmentation was performed and evaluated on CTs containing 106 thoracic and lumbar vertebrae from 10 pathological and traumatic spine patients on an individual vertebra level basis. Vertebra atlases produced errors where the segmentation leaks into the ribs. The use of joint vertebra-rib atlas produced a statistically significant increase in the Dice coefficient from 92.5±3.1% to 93.8±2.1% for the left and right transverse processes and decrease in mean and max surface distance from 0.75±0.60mm and 8.63±4.44mm to 0.30±0.27mm and 3.65±2.87mm, respectively.

9785-134, Session PS5

A machine learning approach for classification of anatomical coverage in CT

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Automatic classification of anatomical coverage of medical images such as CT has potential applications in big data mining and as a pre-processing step to automatically trigger CAD since DICOM header descriptions are not always reliable. The traditional identification of scans through DICOM headers has limitations due to manual entry of non-standardized naming conventions. In this study, we present a machine learning approach where multiple binary classifiers were used to classify different anatomical coverages of CT scans. A one-vs-rest strategy was applied. For a given training set, a template scan was selected from the positive samples and all other scans were registered to it. Each registered scan was then evenly split into 92.5±3.1% to 93.8±2.1% for the left and right transverse processes and decrease in mean and max surface distance from 0.75±0.60mm and 8.63±4.44mm to 0.30±0.27mm and 3.65±2.87mm, respectively.
Objective evaluation of medical image segmentation is one of the important steps for proving its validity and clinical applicability. Since there are many researches presenting segmentation methods on medical image, with few studying the evaluation methods on their results, this paper presents a learning evaluation method with combined measures to make it as close as possible to the clinicians’ judgment. This evaluation method is more quantitative and precise for the clinical diagnose. In our experiment, the same data sets include 120 segmentation results of lumen-intima boundary (LIB) and media-adventitia boundary (MAB) of carotid ultrasound images respectively. And the 15 measures of goodness method and discrepancy method are used to evaluate the different segmentation results alone. Furthermore, the experimental results showed that compared with the discrepancy method, the accuracy with the measures of goodness method is poor. Then, by combining with the measures of two methods, the average accuracy and the area under the receiver operating characteristic (ROC) curve of 2 segmentation groups are higher than 93% and 0.9 respectively. And the results of MAB are better than LIB, which proved that this novel method can effectively evaluate the segmentation results. Moreover, it lays the foundation for the non-supervised segmentation evaluation system.

9785-137, Session PS6

Atorvastatin effect evaluation based on feature combination of three-dimension ultrasound images

Yongkang Luo, Ming Yue Ding, Huazhong Univ. of Science and Technology (China)

In the past decades, stroke has become the worldwide common cause of death and disability. And the ischemic stroke is mainly caused by carotid atherosclerosis. As an inexpensive, convenient and fast means of detection, ultrasound technology is applied widely in the prevention and treatment of carotid atherosclerosis. Recently, many studies have focused on how to quantitatively evaluate local arterial effects of medicine treatment for carotid diseases. In this paper, an evaluation method based on feature combination was proposed to detect potential changes in the carotid arteries after atorvastatin treatment. The support vector machine (SVM) and 10-fold cross-validation protocol were utilized on a database of 5530 carotid ultrasound images of 38 patients (17 atorvastatin groups and 21 placebo groups) at baseline and after 3 months of treatment. With the combination optimization of many features (including 26 morphological and 339 texture features), the evaluation results of single feature and different combined features were compared. The experiment results show that the performance of single feature is poor and the best feature combination have good recognition ability, with the accuracy 92.81%, sensitivity 80.95%, specificity 95.52%, positive predictive value 80.47%, negative predictive value 95.65%, Matthew’s correlation coefficient 76.27%, and Youden’s index 76.48%. And the receiver operating characteristic (ROC) curve was also performed well with 0.9663 of the area under the ROC curve (AUC), which is better than all the features with 0.9423 of AUC. Thus, it is proved that this novel method can reliably and accurately evaluate the effect of atorvastatin treatment.

9785-138, Session PS6

Fully automated segmentation of left ventricle using dual dynamic programming in cardiac cine MR images

Luan Jiang, Shanghai Advanced Research Institute (China); Shan Ling, Shanghai United Imaging Healthcare Co., Ltd. (China); Qiang Li, Shanghai Advanced Research Institute (China) and Shanghai United Imaging Healthcare Co., Ltd. (China)

Cardiovascular diseases are becoming a leading cause of death all over the world. The cardiac function could be evaluated by global and regional parameters of left ventricle (LV) of the heart. The purpose of this study is to develop and evaluate a fully automated scheme for segmentation of LV in short axis cardiac cine MR images. Our fully automated method consists of three major steps, i.e., LV localization, LV segmentation at end-diastolic phase, and LV segmentation propagation to the other phases. First, the maximum intensity projection image along the time phases of the midventricular slice, located at the center of the image, was calculated to locate the region of interest of LV. Based on the mean intensity of the roughly segmented blood pool in the midventricular slice at each phase, end-diastolic (ED) and end-systolic (ES) phases were determined. Second, the endocardial and epicardial boundaries of LV of each slice at ED phase were synchronously delineated by use of a dual dynamic programming technique. The external costs of the endocardial and epicardial boundaries were defined with the gradient values obtained from the original and
volumetric estimation methods. We conclude, by providing guidance on under certain conditions our heuristics are superior to standard practice both healthy and sick subjects and contrast them to established methods.

We propose two new heuristics for the selection of the optimal axial plane for splenic volume estimation: the maximum craniocaudal dimension. We evaluate these heuristics on time-variant data derived from a newly developed deep-learning convolutional neural network in combination with level sets. The non-contrast-enhanced region was separated from the contrast-enhanced region with a maximum-intensity-projection-based method. The non-contrast region was smoothed and a gray level threshold was employed to segment the bladder wall and potential masses. The bladder wall was transformed into a straightened thickness profile, which was analyzed to identify lesion candidates as a prescreening step. The candidates were segmented using our auto-initialized cascaded level set (AI-CALS) segmentation method, and 27 morphological features were extracted for each candidate. Stepwise feature selection with simplex optimization and leave-one-case-out resampling were used for training and validation of an FP classifier. In each leave-one-case-out cycle, features were selected from the training cases and a linear discriminant analysis (LDA) classifier was designed to merge the selected features into a single score for classification of the left-out test case. A data set of 33 cases with 42 biopsy-proven lesions in the non-contrast enhanced region was collected. During prescreening, the system obtained 83.3% sensitivity at an average of 2.5 FPs/case. After feature extraction and FP reduction by LDA, the system achieved 81.0% sensitivity at 2.0 FPs/case, and 73.8% sensitivity at 1.5 FPs/case.

Maximal area and conformal welding heuristics for optimal slice selection in splenic volume estimation

Ievgeniia Gutenko, Hao Peng, Xianfeng Gu, Stony Brook Univ. (United States); Mathew Barish, Stony Brook Medicine (United States); Arie Kaufman, Stony Brook Univ. (United States)

Accurate estimation of splenic volume is crucial for the determination of disease progression and response to treatment for diseases that result in enlargement of the spleen. However, there is no consensus with respect to the use of single or multiple one dimensional, or volumetric measurement. Existing methods for human reviewers focus on measurement of cross diameters on a representative axial slice and the length of the organ in craniocaudal dimension. We propose two new heuristics for the selection of the optimal axial plane for splenic volume estimation: the maximum area axial measurement heuristic and the conformal welding shape-based heuristic. We evaluate these heuristics on time-variant data derived from both healthy and sick subjects and contrast them to established methods. Under certain conditions our heuristics are superior to standard practice volumetric estimation methods. We conclude, by providing guidance on selecting the optimal heuristic for splenic volume estimation.

Computer-aided detection of bladder mass within non-contrast-enhanced region of CT Urography (CTU)

Kenny H. Cha, Lubomir M. Hadijski, Heang-Ping Chan, Elaine M. Caoili, Richard H. Cohan M.D., Chuan Zhou, Univ. of Michigan Health System (United States)

We are developing a computer-aided detection system for bladder cancer in CT urography (CTU). We have previously developed methods for detection of bladder masses within the contrast-enhanced region of the bladder. In this study, we investigated methods for detection of bladder masses within the non-contrast-enhanced region. The bladder was first segmented using a newly developed deep-learning convolutional neural network in combination with level sets. The non-contrast-enhanced region was separated from the contrast-enhanced region with a maximum-intensity-projection-based method. The non-contrast region was smoothed and a gray level threshold was employed to segment the bladder wall and potential masses. The bladder wall was transformed into a straightened thickness profile, which was analyzed to identify lesion candidates as a prescreening step. The candidates were segmented using our auto-initialized cascaded level set (AI-CALS) segmentation method, and 27 morphological features were extracted for each candidate. Stepwise feature selection with simplex optimization and leave-one-case-out resampling were used for training and validation of an FP classifier. In each leave-one-case-out cycle, features were selected from the training cases and a linear discriminant analysis (LDA) classifier was designed to merge the selected features into a single score for classification of the left-out test case. A data set of 33 cases with 42 biopsy-proven lesions in the non-contrast enhanced region was collected. During prescreening, the system obtained 83.3% sensitivity at an average of 2.5 FPs/case. After feature extraction and FP reduction by LDA, the system achieved 81.0% sensitivity at 2.0 FPs/case, and 73.8% sensitivity at 1.5 FPs/case.

Pulmonary nodule detection using a cascaded SVM classifier

Martin Bergtholdt, Philips Technologie GmbH (Germany); Rafael Wiemker, Tobias Klinder, Philips GmbH Innovative Technologies (Germany)

Automatic detection of lung nodules from chest CT has been researched extensively over the last decades resulting also in several commercial products. However, solutions are not commonly used in daily clinical routine as many current CAD systems still potentially miss true nodules with the same time generating too many false positives (FP). While many earlier approaches had to rely on rather few cases, larger data bases become now available and can be used for algorithmic development. In this paper, we address the problem of lung nodule detection via a cascaded SVM classifier. The idea is to sequentially perform two classification tasks in order to select from an extremely large pool of potential candidates the few most likely ones. As the initial pool is allowed to contain thousands of candidates, very loose criteria could be applied during this pre-selection. In this way, the chances that a true nodule is not considered as a candidate are reduced significantly. The final algorithm is trained and tested on the full LIDC/DIAB database. Comparison is done against two previously published CAD systems. Overall, the algorithm achieved sensitivity of 0.836 at 2 FP/ volume where the other two achieved sensitivity values of 0.321 and 0.625, respectively.
Spatial context learning approach to automatic segmentation of pleural effusion in chest computed tomography images

Awais Mansoor, Children's National Medical Ctr. (United States); Rafael Casas Jr., National Institute of Health (United States); Marius G. Linguraru, Children's National Medical Ctr. (United States)

Pleural effusion is an abnormal collection of fluid within the pleural cavity. Excessive accumulation of pleural fluid is an important bio-marker for various illnesses, including congestive heart failure, pneumonia, metastatic cancer, and pulmonary embolism. Quantification of pleural effusion can be indicative of the progression of disease as well as the effectiveness of any treatment being administered. Quantification, however, is challenging due to unpredictable amounts and density of fluid, complex topology of the pleural cavity, and the similarity in texture and intensity of pleural fluid to the surrounding tissues in computed tomography (CT) scans. Herein, we present an automated method for the segmentation of pleural effusion in CT scans based on spatial context information. The method consists of two stages: first, a probabilistic pleural effusion map is created using multi-atlas segmentation. The probabilistic map assigns a priori probabilities to the presence of pleural fluid at every location in the CT scan. Second, a statistical pattern classification approach is designed to annotate pleural regions using local descriptors based on a priori probabilities, geometrical, and spatial features. Thirty-seven CT scans from a diverse patient population containing confirmed cases of minimal to severe amounts of pleural effusion were used to validate the proposed segmentation method. An average Dice coefficient of 0.82685 and Hausdorff distance of 16.2155 mm was obtained.

Lymph node detection in IASLC-defined zones on PET/CT images

Yihua Song, Jayaram K. Udupa, Dewey Odhner, Drew A. Torigian, Univ. of Pennsylvania (United States)

Lymph node detection is challenging due to the low contrast between lymph nodes and surrounding soft tissues and the variation in nodal size and shape. In this paper, we propose several novel ideas which are combined into a system to operate on PET/CT images to detect abnormal thoracic nodes. First, our previous AAR approach is modified where lymph node zones following IASLC specifications are modeled as objects arranged in a hierarchy along with key anatomic anchor objects. This fuzzy anatomy model built from diagnostic CT images is then deployed on PET/CT images for automatically recognizing the zones. A novel globular filter (g-filter) to detect blob-like objects over a specified range of sizes is designed to detect most likely locations and sizes of diseased nodes. Abnormal nodes within each automatically localized zone are subsequently detected via combined use of different items of information at various scales: lymph node zone model found at recognition indicating the geographic layout at the global level of node clusters, g-filter response which hones in on and carefully selects node-like globular objects at the node level, and CT and PET gray value but within only most plausible nodal regions for node presence at the voxel level. The models are built from 25 diagnostic CT images and refined for object hierarchy based on a separate set of 20 diagnostic CT images. Node detection is tested on an additional set of 20 PET/CT images. Our preliminary results indicate node detection sensitivity and specificity at around 90% and 85%, respectively.

Intrapulmonary vascular remodeling: MSCT-based evaluation in COPD and alpha-1 antitrypsin deficient subjects

Adeline Crosnier, Catalin Fetita, Télécom SudParis (France); Pierre-Yves Brillet, Univ. Paris 13 (France)

Whether COPD is generally known as a small airway disease, recent investigations suggest that vascular remodeling could play a key role in disease progression. This paper develops a specific investigation framework in order to evaluate the remodeling of the intrapulmonary vascular network and its correlation with other image or clinical parameters (emphysema score or FEV1) in patients with smoking- or genetic- (alpha-1 antitrypsin deficiency - AATD) related COPD. The developed approach evaluates the vessel caliber distribution per lung or lung region (upper, lower, 10%- and 20%- periphery) in relation with the severity of the disease and computes a remodeling marker given by the area under the calibration curve for radii less than 1.6 mm, AUC16. It exploits a medial axis analysis in relation with local caliber information computed in the segmented vascular network, with values normalized with respect to the lung volume (for which a robust segmentation is developed). The first results obtained on a 34-patient database (13 COPD, 13 AATD and 8 controls) showed statistically significant vascular remodeling for COPD and AATD versus controls, with a negative correlation with the emphysema degree for COPD, but not for AATD. Significant vascular remodeling at 20% lung periphery was found both for the severe COPD and AATD patients, but not for the moderate groups. Also the vascular remodeling in AATD did not correlate with the FEV1, which might suggest independent mechanisms for bronchial and vascular remodeling in the lung.

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Comprehensive eye evaluation algorithm
Carla P. Agurto Rios, Sheila C. Nemeth, Gilberto Zamora, Maria Vahtel, Peter Soliz, Simon Barriga, VisionQuest Biomedical LLC (United States)

In recent years, several research groups have developed automatic algorithms to detect diabetic retinopathy (DR) in individuals with diabetes (DM) using digital retinal images. Studies have indicated that diabetics have 1.5 times the annual risk of developing primary open angle glaucoma (POAG) as people without DM. DM patients have 1.8 times the risk of developing age-related macular degeneration (AMD). While there are numerous investigators developing automatic DR detection algorithms, there are few successful efforts to develop automatic algorithms to detect other ocular diseases as POAG and AMD. Consequently, our aim was to develop a comprehensive eye evaluation algorithm that not only detects DR in retinal images, but also automatically detects glaucoma suspects and AMD by integrating other personal medical information with the retinal features. The proposed system is fully automatic and will provide three outputs for the likelihood of presence of each eye diseases. The system was evaluated on 104 diabetic cases. For each eye, we used two non-myrdicall digital color fundus photographs (macula and optic disc centered) and information of age, duration of diabetes, cataracts presence, hypertension information, and sex. Our results showed that the combination of multimodal features has the potential to increase the detection of eye diseases. Marked improvement was achieved for AMD classification, going from an AUC of 0.77 to 0.81 by adding the medical information to the image information. For DR and glaucoma suspects, image features were sufficient to achieve excellent AUCs of 0.93 and 0.95.

Vessel discoloration detection in malaria retinopathy
Carla P. Agurto Rios, Sheila C. Nemeth, Simon Barriga, Peter Soliz, VisionQuest Biomedical LLC (United States); Ian MacCormick, Univ. of Liverpool (United Kingdom); Terrie Taylor, Michigan State Univ. (United States); Simon P. Harding, Univ. of Liverpool (United Kingdom); Susan Lewallen, Kilimanjaro Ctr. for Community of Ophthalmology (South Africa); Vinayak Joshi, VisionQuest Biomedical LLC (United States)

Cerebral malaria (CM) is a life-threatening clinical syndrome associated with malarial infection affecting about 188 million people, mostly sub-Saharan African children under 5 years of age. Malaria retinopathy (MR) is a condition where the blood vessels associated with CM appear deformed. Other unrelated diseases can present with symptoms similar to CM, therefore the highly specific nature of MR is important in avoiding a misdiagnosis which can lead to inappropriate treatment, and potentially, death. In this paper we present the first system to detect the presence of discolored vessels associated with MR. We modified and improved our previous vessel segmentation algorithm by incorporating the a channel of the CIELab color space and noise reduction. Then, we divided the segmented vasculature in vessel segments and extracted features at the wall and in the centerline of the vessel segment. Finally we used a regression classifier to classify the segments. We achieved and accuracy of 85% with sensitivity of 94% and specificity of 67% in detecting vessels which present discoloration due to CM.

Computer-aided detection of human cone photoreceptor inner segments using multi-scale circular voting
Jianfei Liu, National Institutes of Health (United States); Alfredo Dubra, Medical College of Wisconsin (United States); Johnny Tam, National Institutes of Health (United States)

Cone photoreceptors are highly specialized cells responsible for the origin of vision in the human eye. The inner segments of these cells can be noninvasively imaged in the living human eye using an adaptive optics scanning light ophthalmoscope (AOSLO) with non-confocal split detection capabilities. Monitoring the status of these cells can lead to a better understanding of human vision and disease progression. However, cell identification in split detection AOSLO images is hindered by heterogeneous cell regions arising from shading effects, weak boundaries, and image degradation due to the presence of overlying blood vessels. We present a multi-scale circular voting approach that overcomes these challenges. Our approach is based on the novel combination of three techniques: 1) iterative circular voting to identify candidate cells based on their circular structures, 2) a multi-scale strategy to identify the optimal detection response, and 3) clustering to improve robustness while removing false positives. We acquired images from three healthy subjects at various locations on the retina and manually labeled cell locations to create ground-truth for evaluating the detection accuracy. The images have a large range of cell densities. The overall recall, precision and F1 score were 91.2±5.8%, 83.6±10.1%, and 87.1±6.9% (Mean±SD). Experimental results on unlabeled images showed that our novel method for the identification of cone photoreceptor inner segments performs well even with weak cell boundaries and vessel obscuration. These encouraging results demonstrate that the proposed detection algorithm can robustly and accurately identify cells in split detection AOSLO images.

Sweet-spot training for early esophageal cancer detection
Fons van der Sommen, Svitlana Zinger, Technische Univ. Eindhoven (Netherlands); Erik J. Schoon M.D., Catharina-ziekenhuis (Netherlands); Peter H. N. de With, Technische Univ. Eindhoven (Netherlands)

Over the past decade, the imaging tools for endoscopists have improved drastically. This has enabled physicians to visually inspect the intestinal tissue for early signs of malignant lesions. Furthermore, it has paved the way for image analysis algorithms, to support the gastroenterologist in finding these early signs of developing cancer. Recent studies show the feasibility of such systems, where the problem is typically approached as a segmentation task and a binary ground truth is employed. In this study, we show that the detection of early cancerous tissue in the gastrointestinal tract cannot be approached as a binary segmentation problem and it is crucial and clinically relevant to involve multiple experts for annotating early lesions. By employing the so-called sweet spot for training purposes, a much better detection performance can be achieved. Furthermore, a multi-expert-based ground truth, i.e. a golden standard, enables an improved validation of the resulting delineations. For this purpose, we propose two novel metrics that can handle multiple ground-truth annotations. Our experiments involving these metrics and based on the golden standard show that the performance of a detection algorithm of early neoplastic lesions in Barrett’s esophagus can be increased significantly, demonstrating a 10 percent point increase in the resulting F1 detection score.
9785-47, Session 9

A single-layer network unsupervised feature learning method for white matter hyperintensity segmentation

Koen P. T. Vijverberg, Radboud Univ. Nijmegen (Netherlands) and Radboud Univ. Medical Ctr. (Netherlands); Mohsen Ghafoorian, Radboud Univ. Nijmegen (Netherlands) and Radboud Univ. Medical Ctr. (Netherlands); Inge van Uden, Frank-Erik de Leeuw, Bram Platel, Radboud Univ. Medical Ctr. (Netherlands); Tom Heskes, Radboud Univ. Nijmegen (Netherlands)

Cerebral small vessel disease (SVD) is a disorder frequently found in elderly people and is associated with deterioration in cognitive performance, parkinsonism, motor- and mood impairments. White matter hyperintensities (WMH) as well as lacunes, microbleeds and subcortical brain atrophy are part of the spectrum of image findings, related to SVD. Accurate segmentation of WMHs is important for prognosis and diagnosis of multiple neurological disorders such as MS and SVD. Almost all of the published (semi-)automated WMH detection models employ multiple complex hand-crafted features, which require in-depth domain knowledge. In this paper we propose to apply a single-layer network unsupervised feature learning (USFL) method to avoid hand-crafted features, but rather to automatically learn a more efficient set of features. Experimental results show that a computer aided detection system with USFL system outperforms a hand-crafted approach.

9785-48, Session 9

Early esophageal cancer detection using RF classifiers

Mark H. A. Janse, Fons van der Sommen, Svitlana Zinger, Technische Univ. Eindhoven (Netherlands); Erik J. Schoon M.D., Catharina-ziekenhuis (Netherlands); Peter H. N. de Wit, Technische Univ. Eindhoven (Netherlands)

One of the fastest rising forms of cancer in the Western world is esophageal cancer. Using High-Definition (HD) endoscopy, gastroenterology experts can identify esophageal cancer at an early stage. Recent research shows that early cancer can be found using a state-of-the-art computer-aided detection (CADE) system based on analyzing static HD endoscopic images. Our research aims at extending this system by applying Random Forest (RF) classification which introduces a confidence measure for detected cancer regions. To visualize this data, we propose a novel annotation system, employing the unique characteristics of the previous confidence measure. This allows reliable modeling of multi-expert knowledge and provides essential data for real-time video processing, to enable future use of the system in a clinical setting. The performance of the CADE system is evaluated on a 39-patient dataset, containing 100 images annotated by five expert gastroenterologists. The proposed system reaches a precision of 75% and recall of 90%, thereby improving the state-of-the-art results by 11 and 6 percentage points, respectively.

9785-49, Session 10

Applying a radiomics approach to predict prognosis of lung cancer patients

Nastaran Emaminejad, Shiju Yan, The Univ. of Oklahoma (United States); Wei Qian, The Univ. of Texas at El Paso (United States); Yubao Guan, Guangzhou Medical College (China); Bin Zheng, The Univ. of Oklahoma (United States)

Radiomics is an emerging technology to decode tumor phenotype based on quantitative analysis of image features computed from radiographic images. In this study, we applied Radiomics concept to investigate the association among the CT image features of lung tumors, which are either quantitatively computed or subjectively rated by radiologists, and two genomic biomarkers namely, protein expression of the excision repair cross-complementing 1 (ERCC1) genes and a regulatory subunit of ribonucleotide reductase (RRM1), in predicting disease-free survival (DFS) of lung cancer patients after surgery. An image dataset involving 94 patients was used. Among them, 20 had cancer recurrence within 3 years, while 74 patients remained DFS. After tumor segmentation, 35 image features were computed from CT images. Using the Weka data mining software package, we selected 10 non-redundant image features. Applying a SMOTE algorithm to generate synthetic data to balance case numbers in two DFS (“yes” and “no”) groups and a leave-one-case-out training/testing method, we optimized and compared a number of machine learning classifiers using (1) quantitative image (QI) features, (2) subjective rated (SR) features, and (3) genomic biomarkers (GB). Data analyses showed relatively lower correlation among the QI, SR and GB prediction results (with Pearson correlation coefficients < 0.5 including between ERCC1 and RRM1 biomarkers). By using area under ROC curve as an assessment index, the QI, SR and GB based classifiers yielded AUC = 0.89, 0.72 and 0.59, respectively, which showed that all three types of features had prediction power (AUC>0.5). Among them, using QI yielded the highest performance.

9785-50, Session 10

Radiomics versus physician assessment for the early prediction of local cancer recurrence after stereotactic radiotherapy for lung cancer

Sarah A. Mattonen, Western Univ. (Canada) and London Regional Cancer Program (Canada); Carol Johnson, London Regional Cancer Program (Canada); David A. Palma, Western Univ. (Canada) and London Regional Cancer Program (Canada); George Rodrigues, Alexander V. Louie, Western Univ. (Canada); Suresh Senan, Vrije Univ. Medical Ctr. (Netherlands); Timothy P. C. Yeung, Aaron D. Ward, Western Univ. (Canada) and London Regional Cancer Program (Canada)

Stereotactic ablative radiotherapy (SABR) has recently become a standard treatment option for patients with early-stage lung cancer, which achieves local control rates similar to surgery. Local recurrence following SABR typically presents after one year post-treatment. However, benign radiological changes mimicking local recurrence can appear on CT imaging following SABR, complicating the assessment of response. We hypothesize that subtle changes on early post-SABR CT images are important in predicting the eventual incidence of local recurrence and would be extremely valuable to support timely salvage interventions. The objective of this study was to extract radiomic image features on post-SABR follow-up images for 45 patients (15 with local recurrence and 30 without) to aid in the early prediction of local recurrence. Three blinded thoracic radiation oncologists were also asked to score follow-up images as benign injury for overall errors of 34–37%, FPRs of 0–4%, and FNRs of 100%. These results suggest that radiomics can detect early changes associated with local recurrence which are not typically considered by physicians. We aim to develop a decision support system which could potentially allow for early salvage therapy of patients with local recurrence following SABR.
**Automatic staging of bladder cancer on CT urography**

Sankeerth S. Garapati, Lubomir M. Hadjiiski, Kenny H. Cha, Heang-Ping Chan, Elaine M. Caoli M.D., Richard H. Cohan M.D., Alon Weizer, Ajaii Alva, Chintana Paramagul, Jun Wei, Chuan Zhou, Univ. of Michigan (United States)

Correct staging of bladder cancer is crucial for the decision of neoadjuvant chemotherapy treatment and minimizing the risk of under- or overtreatment. Subjectivity and variability of clinicians in utilizing available diagnostic information may lead to inaccuracy in staging bladder cancer. An objective decision support system that merges the information in a predictive model based on statistical outcomes of previous cases and machine learning may assist clinicians in making more accurate and consistent staging assessments. In this study, we developed a preliminary method to stage bladder cancer. With IRB approval, 84 bladder cancer cases with CTU scans were collected from patient files. The cases were classified into two classes based on pathological stage T2, which is the decision threshold for neoadjuvant chemotherapy treatment (i.e. for stage ≥T2) clinically. There were 43 cancers below stage T2 and 41 cancers at stage T2 or above. All 84 lesions were automatically segmented using our autoinitialized cascaded level sets (AI-CALS) method. Morphological features were extracted, which were selected and merged by an LDA classifier. The classification accuracy was quantified using the area under the ROC curve (Az2). The dataset was split into Set 1 and Set 2 for two-fold cross validation. The Az was 0.91 for training on Set 1 and 0.81 for testing on Set 2. The Az was 0.97 for training on Set 2 and 0.90 for testing on Set 1. The classifier consistently selected the lesion volume, a gray level feature and a contrast feature. This predictive model shows promise for assisting in assessing the bladder cancer stage.

**Signal intensity analysis of ecological defined habitat in soft tissue sarcomas to predict metastasis development**

Hamidreza Farhizadeh, Univ. of South Florida (United States); Jacob G Scott, H. Lee Moffitt Cancer Ctr. & Research Institute (United States); Dmitry B. Goldgof, Lawrence O. Hall, Univ. of South Florida (United States); Robert A. Gatenby, Robert J. Gillies, Meera Raghavan, H. Lee Moffitt Cancer Ctr. & Research Institute (United States)

The clinical MRI imaging is the practical tool to explore the heterogeneity of the Soft Tissue Sarcomas (STS). Tumor heterogeneity is a challenging problem to quantify substantial tumor variation. Different tumors in different patients are significantly diverse in appearance. Thus, we need a system to stratify tumors outcomes. In this paper, a novel method is proposed with focus on spatial distinctive sub-regions or ‘habitat’ by using pixel signal intensity. Habitats characteristics may express potential developments within the tumor, which is clinically practical to select therapy regimen (chemotherapy or radiation). To quantify tumor heterogeneity, first we get intra-tumor segmentations based on signal intensity and then build spatial mapping scheme from MRI modalities. Finally, we predict tumor development in case of metastasis. After tumor segmentation into high and low signal intensities, a set of quantitative feature based on signal intensity is proposed to represent variation in habitat characteristics. This set of feature is utilized to predict metastasis on STS. The experimental results have been shown this framework has high capability to classify metastasis development in tumors by 72.41% for metastasis.

**Classification of recurrence free survival nasopharyngeal carcinoma tumors**

Hamidreza Farhizadeh, Univ. of South Florida (United States); Joo Y Kim, H. Lee Moffitt Cancer Ctr. & Research Institute (United States) and The Royal Australian and New Zealand College of Radiologists (New Zealand); Jacob G. Scott, H. Lee Moffitt Cancer Ctr. & Research Institute (United States); Dmitry B. Goldgof, Lawrence O. Hall, Univ. of South Florida (United States); Louis B. Harrison, H. Lee Moffitt Cancer Ctr. & Research Institute (United States)

Nasopharyngeal carcinoma is an abnormal growth of tissue which rises from top of mouth and behind the nose. It is crucial to identify tumor sub-regions that possess unfavorable functional and biological properties regions in order to optimize treatment. Assessment of the biologic properties of the tumor based on imaging, would allow physicians to initiate the most efficacious therapy regimen. Additionally, the ability to accurately assess response to therapy earlier in the disease course would allow for modification of treatment to best benefit the patient. In this paper, we assessed standard of care MRI in T1 post contrast sequences performed on 25 patients with nasopharyngeal carcinoma. Tumor tissue was identified by manually drawing a mask on contrast enhanced images in 3D. Otsu segmentation was applied to segment tumor tissue into low and high signal intensity regions on T1 and within high and low signal regions, texture features were extracted to quantify the heterogeneity of these regions. Radiologist divided the patients in two groups, the patients who developed no metastasis and are alive (recurrence free survival) vs. others. For classification, we used meta-classifiers which contained feature selectors and classifiers. Individual cases were correctly classified by 74.25% classification accuracy by wrapper + SVM.

**Decision forests for learning prostate cancer probability maps from multiparametric MRI**

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Advances in multiparametric magnetic resonance imaging (mpMRI) and ultrasound/MRI fusion imaging offer a powerful alternative to the typical undirected approach to diagnosing prostate cancer, but it requires the time and expertise needed to interpret multiparametric MRI image scenes. In this paper, a machine learning framework for automatically detecting and localizing cancerous lesions within the prostate is developed and evaluated. Two studies were performed to gather MRI and pathology data. In both, patients underwent an MRI session to obtain structural, diffusion-weighted, and dynamic contrast enhanced image volumes of the prostate. For the 12 patients in the first study, regions suspected of being cancerous from the MRI data were manually contoured by radiologists. Pseudo-whole mount slices of the prostate were obtained for the patients in the second study, in addition to MRI data, for pathologic verification. A 3-D feature set for voxel-wise appearance description combining intensity data, textural operators, and zonal approximations was generated. Voxels in a test set were classified as normal or cancer using a joint Gaussian discriminant analysis and decision forests approach. A leave-one-patient-out cross-validation scheme was used to assess the predictions against the expert manual tracings. We achieved an area under the average receiver-operator characteristic curve of 0.9228 for the first study, and visual assessment of the probability maps showed 21 out of 22 tumors were identified while a high level of specificity was maintained. In addition to evaluating the model against related approaches, the effects of the individual MRI channels were explored, and pathological verification using whole-mount slices is underway. The results of this paper show that the combination of mpMRI and machine learning is a powerful tool for quantitatively diagnosing prostate cancer.
Conference 9785: Computer-Aided Diagnosis

9785-55, Session 12

Fusion of multi-parametric MRI and temporal ultrasound for characterization of prostate cancer: in vivo feasibility study
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Recently, multi-parametric Magnetic Resonance Imaging (mp-MRI) has been used along with transrectal ultrasound (TRUS) to improve the sensitivity of detecting high-risk prostate cancer (PCa). mp-MRI, however, is not as sensitive in detecting low-risk or low volume as high-risk cancer. In this paper, for the first time, we present a fused mp-MRI-temporal-ultrasound framework for characterization of PCa, in vivo. Cancer classification results obtained using temporal ultrasound are fused with those achieved using consolidated mp-MRI maps determined by multiple observers. We verify the outcome of our study using histopathology following deformable registration of ultrasound and histology images. Fusion of temporal ultrasound and mp-MRI for characterization of the PCa results in an area under the receiver operating characteristic curve (AUC) of 0.82 for cancerous regions with Gleason scores (GSs)≥3+3 and AUC of 0.88 for those with GSs≥3+4 versus benign tissue.

9785-56, Session 12

An integrated classifier for computer-aided diagnosis of colorectal polyps based on random forest and location index strategies
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INTRODUCTION
The main task of computer-aided diagnosis (CADx) is to differentiate the pathological stages to which each detected lesion belongs. For the classification part, we have widely explored the RF classifier, which is one of the strong classifiers and have played a good performance in computer-aided detection (CADx) and also shown to be strong in CADx of colorectal polyps [2]. In addition, we also derived a location index measure for the kNN and wkNN classifiers and demonstrated the measure can be also play a strong classifier role and improve computing efficiency [1]. In this paper, we integrate the location index measure and RF to take their advantages for CADx of colorectal polyps.

2. METHODOLOGY
2.1 Data and feature used in this experiment
A computed tomography colonography (CTC) database of 114 scans from 67 patients with polyps of size 8mm and larger, which include 153 lesions with 37 no-risk lesions (hyperplastic) and 116 risky lesions (adenoma). Based on these lesions and the Haralick’s texture feature model [3], we extract the 3D high-order texture features [2] from all lesions to perform the classification.

2.2 Random Forest
The RF is constructed by many classification and regression trees (CART) [4]. Each tree in is grown as follows:
Suppose there are M features for each data, we randomly choose m<= M features (with replacement) every time to build a tree and the best split on these m is used to split the node (here we use Gini importance as the criterion when split the node). Each tree is grown to the largest extent possible. There is no pruning.
To classify a new object from an input feature vector, put the input vector down each of the trees in the forest. Each tree gives a label, and we say the tree “votes” for that class. The forest chooses the classification having the most votes (over all the trees in the forest).

We evaluate the RF algorithm here by the use of the R package: randomForest.

2.3 Location index
The location index in my previous SPIE paper was defined as follows, based on mainly the “distance-weighted inside disc” classifier [1].
Definition 1: Location index
For each test point x, the location index of x is a score or posterior probability p_x=(∑_i y_i/d(·,x_i))/(|x|/d(·,x)).
In the formula above, y_i is the label of each training point, d(·,:) is the Euclidean distance between the test point x and training point x_i.
We can see many obvious properties from the location index in the following:
If the label of all “inside disc” training point is 0, the score for this test point will be 0. If the label of all “inside disc” training point is 1, the score for this test point will be 1. Then the score for each test point will be between 0 and 1.
The nearer is the training point to the test point, the larger is the weight of that training point. The further is the training point to the test point, the smaller is the weight of that training point.
Based on property 2, when a test point is falling into the area with many points of class 1 and far from points of class 0, the location index will be close to 1. Simply, the location index reflects the distribution of training points of both classes surrounded by the test point.

For a simple example as shown above, the location index p_x=A=0.6046, the location index p_y=B=0.4652, the location index p_z=C=0.2281. This result shows that the larger location index for a test point is, the more points with class 1 are surrounded by this test point.
Furthermore, the location index itself can be served as a good classifier, since the input is just the training set and the output score is the index value for each test point. After obtaining all the scores, it could be evaluated by the ROC analysis and the AUC value.

2.4 Location index embedded Random Forest

From the example in Figure 1, we can see that there are two types of points:
Points located inside one class (like points A and C), which should be classified correctly.
Points located on the boundary between two classes (like point B) are pretty hard to classify.
Therefore, our idea is to classify those two types of points differently. For each test point, we first decide which type the point is and this step could be realized by computing its location index value. If the location index is very large or small, the point belongs to type 1 points set, otherwise, it belongs to type 2 points set. It is obvious that the location index, as a classifier, itself have a good performance for type 1 points, while not so good for type 2 points. Moreover, RF is a strong classifier which has a better performance on classifying type 2 points, So we embed the location index into the RF to help RF classify type 1 points, where RF might have some errors. The algorithm is demonstrated below:
Location index embedded Random Forest classifier
Divide our dataset H into training set H_1 and test set H_2.
Build a RF model by the training set.
Decide two threshold parameters: α and β. (α>β)
For each test point
Deep learning for electronic cleansing in dual-energy CT colonography

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We developed a novel deep-learning-based electronic cleansing (EC) method for dual-energy CT colonography (DE-CTC). In the method, an ensemble of deep convolutional neural networks (DCNNs) is used to classify each voxel of a DE-CTC image volume into five classes: luminal air, soft tissue, tagged fecal materials, and partial-volume boundaries between air and tagging, and those between soft tissue and tagging. Each DCNN acts as a pixel classifier. At each voxel, a region-of-interest (ROI) centered at the voxel is extracted. After mapping the pixels of a ROI to the input layer of a DCNN, a series of convolutional and max-pooling layers are used to extract features with increasing levels of abstraction. The output layer produces the probabilities at which the input voxel belongs to one of the five classes. Multiple DCNNs were trained based on the multi-material image volumes derived from the DE-CTC images, including material decomposition images and virtual monochromatic images. An ensemble DCNN was developed by combining the outputs of these DCNNs by means of a meta-classifier for precise classification of the voxels. The electronically cleansed CTC images were generated by removing regions that were classified as other than soft tissue, followed by colon surface reconstruction. Preliminary results based on 184,320 images sampled from 30 clinical CTC cases showed a higher accuracy in labeling these classes than that of our previous machine-learning-based method, suggesting that the deep-learning-based EC can accurately remove residual fecal materials from CTC images without generating major EC artifacts.

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9785-58, Session 12

Colitis detection on abdominal CT scans by rich feature hierarchies

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Colitis is inflammation of the colon due to neutropenia, inflammatory bowel disease (such as Crohn disease), infection and immune compromise. Colitis is often associated with thickening of the colon wall. The wall of a colon afflicted with colitis is much thicker than normal. For example, the mean wall thickness in Crohn disease is 11-13 mm compared to the wall of the normal colon that should measure less than 3 mm. Colitis can be debilitating or life threatening, and early detection is essential to initiate proper treatment. In this work, we apply high-capacity convolutional neural network (CNNs) to bottom-up region proposals to detect potential colitis on CT scans. Our method first generates around 3000 category-independent region proposals for each slice of the input CT scan using selective search. Then, a fixed-length feature vector is extracted from each region proposal using a CNN. Finally, each region proposal is classified and assigned a confidence score using linear SVMs. We applied the detection method to 260 images from 26 CT scans of patients with colitis for evaluation. The detection system can achieve a 0.85 sensitivity at 1 false positive per image.

9785-59, Session 13

Automatic detection of ureter lesions in CT urography

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We are developing a CAD system for automated detection of ureter abnormalities in multi-detector row CT urography (CTU). Our CAD system consists of two stages. The first stage automatically tracks the ureter via the...
Segmentation of hepatic arteries in multi-phase liver CT using directional dilation and connectivity analysis

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Segmentation of hepatic arteries in multi-phase computed tomography (CT) images is indispensable in liver surgery planning. During image acquisition, the hepatic artery is enhanced by the injection of contrast agent. The enhanced signals are often not stably acquired due to non-optimal contrast timing. Other vascular structures, such as hepatic vein or portal vein, can be enhanced as well in the arterial phase, which can adversely affect the segmentation results. Furthermore, the arteries might suffer from partial volume effects due to their small diameter. To overcome these difficulties, we propose a framework for robust hepatic artery segmentation requiring a minimal amount of user interaction. First, an efficient multi-scale Hessian-based vesselness filter is applied on the artery phase CT image, aiming to enhance vessel structures with specified diameter range. Second, the vesselness response is processed using a Bayesian classifier to identify the most probable vessel structures. Considering the vesselness filter normally performs not ideally on the vessel bifurcations or the segments corrupted by noise, two vessel-reconnection techniques are proposed. The first technique uses a directional morphological operator to dilate vessel segments along their centerline directions, attempting to fill the gap between broken vascular segments. The second technique analyzes the connectivity of vessel segments and reconnects disconnected segments and branches. Finally, a 3D vessel tree is reconstructed. The algorithm has been evaluated using 18 CT images of the liver. To quantitatively measure the similarities between segmented and reference vessel trees, the skeleton coverage and mean symmetric distance are calculated to quantify the agreement between reference and segmented vessel skeletons, resulting in an average of 0.55 ± 0.27 and 12.7 ± 7.9 mm (mean ± standard deviation), respectively.

Machine-learning based comparison of CT-perfusion maps and dual energy CT for pancreatic tumor detection

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Perfusion CT is well-suited for diagnosis of pancreatic tumors but tends to be associated with a high radiation exposure. Dual-energy CT (DECT) might be an alternative to perfusion CT, offering correlating contrasts while being acquired at lower radiation doses. While previous studies compared intensities of Dual Energy iodine maps and CT-perfusion maps, no study has assessed the combined discriminative power of all information that can be generated from an acquisition of both functional imaging methods. We therefore propose the use of a machine learning algorithm for assessing the amount of information that becomes available by the combination of multiple images. For this, we train a classifier on both imaging methods, using a new approach that allows us to train only from small regions of interests (ROIs). This makes our study comparable to other - ROI-based analysis - and still allows comparing the ability of both classifiers to discriminate between healthy and tumorous tissue. We were able to train classifiers that yield DICE scores over 80% with both imaging methods. This indicates that Dual Energy iodine maps might be used for diagnosis of pancreatic tumors instead of Perfusion CT, although the detection rate is lower. We also present tumor risk maps that visualize possible tumorous areas in an intuitive way and can be used during diagnosis as an additional information source.
9785-63, Session 13

**Automatic anatomy recognition on CT images with pathology**

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Body-wide anatomy recognition on CT images with pathology becomes crucial for quantifying body-wide disease burden. This, however, is a challenging problem because various diseases result in various abnormalities of objects such as shape and intensity patterns. We previously developed an automatic anatomy recognition (AAR) system [3] whose applicability was demonstrated on near normal diagnostic CT images in different body regions on 35 organs. The aim of this paper is to investigate strategies for adapting the previous AAR system to diagnostic CT images of patients with various pathologies as a first step toward automated body-wide disease quantification. The AAR approach consists of three main steps - model building, object recognition, and object delineation. In this paper, we describe a new strategy for object recognition to handle abnormal images. In the model building stage an optimal threshold interval is learned from near-normal training images for each object. This threshold is optimally tuned to the pathological manifestation of the object in the test image. Recognition is performed following a hierarchical representation of the objects. Experimental results based on 50 near-normal abdominal images for model building and 20 abnormal images of the same body region show that object localization accuracy within 2 voxels for liver and spleen and 3 voxels for kidney can be achieved with the new strategy.

9785-64, Session 13

**Differentiating bladder carcinoma from bladder wall using 3D textural features: an initial study**

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The textural features embedded in the images are a very useful tool in the task of image classification and carcinoma detection. Recent literatures indicate that many textural features between carcinomatous tissues and bladder wall in two-dimensional (2D) images show significant differences. However, whether these features still show significant differences in three-dimensional (3D) image data is unclear. So in this study, the widely used 6 Tamura features was firstly wholly extended to 3D, and then different types of 3D textural features including 3D features derived from grey level co-occurrence matrices (GLCM) and grey level-gradient co-occurrence matrix (GLGCM), as well as 3D Tamura features, were extracted from 23 VOIs of bladder tumors and 21 volumes of interest (VOI) of bladder wall, which were obtained from MR datasets of 20 patients with bladder cancer. Statistical result indicates that 30 out of 47 features are significantly different between two groups; suggesting that for the MR sequence used, the 3D textural pattern of carcinomatous tissues is quite different from that of bladder wall. Preliminary classification with a SVM classifier demonstrates that combinations of different sets of 3D features outperform the performance of using only one set of 3D features. The result not only validates the feasibility of 3D textural features in differentiating the malignancy from bladder wall, it also demonstrates the potential of 3D textural features on the detection of bladder carcinoma.
Improved image guidance technique for minimally invasive mitral valve repair using tracked 3D ultrasound

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In the past ten years, numerous new surgical and interventional techniques have been developed for treating heart valve disease without the need for cardiopulmonary bypass. Heart valve repair or replacement is now being performed in a blood-filled environment, reinforcing the need for accurate and intuitive imaging techniques. Previous work has demonstrated how augmenting ultrasound with virtual representations of specific anatomical landmarks can greatly simplify interventional navigation challenges and increase patient safety. These techniques often complicate interventions by requiring extra time taken to manually define or initialize virtual models. In addition, they introduce the need to monitor for invalidation of the image-sensor calibration due to sensor dehiscence. In an effort to reduce the complexity of the intervention workflow, a system was developed to minimize this reliance on virtual elements, while attempting to maintain image guidance capabilities equivalent to augmented reality tracked 2D ultrasound guidance. This system consists of magnetically tracked tools and 3D ultrasound presented in an augmented reality environment. In phantom studies simulating the navigation stage of a NeoChord mitral valve procedure, safety and cognitive load metrics have achieved similar success compared to more involved augmented reality techniques, and considerable improvement over standard of care ultrasound guidance.

Cognitive tools pipeline for assistance of mitral valve surgery

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For cardiac surgeons, mitral valve reconstruction (MVR) surgery is a highly demanding procedure, where an artificial ring is implanted onto the mitral valve annulus to re-enable the valve’s proper closing functionality. For a successful operation the surgeon has to keep track of a variety of relevant impact factors, such as patient-individual geometries and tissue properties of the surgical target, and deduce type and size of the ring prosthesis according to practical surgery experience.

Dynamic tracking of prosthetic valve motion and deformation from bi-plane x-ray views: feasibility study

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Transcatheter aortic valve replacement (TAVR) requires navigation and deployment of a prosthetic valve within the aortic annulus under fluoroscopic guidance. To support improved device visualization in this procedure, this study investigates the feasibility of frame-by-frame 3D reconstruction of a moving and expanding prosthetic valve structure from simultaneous bi-plane x-ray views. In the proposed method, a dynamic 3D model of the valve is used in a 2D/3D registration framework to obtain a reconstruction of the valve from bi-plane x-ray images. For each frame, valve model parameters describing position, orientation, expansion state, and deformation are iteratively adjusted until forward projections of the model match both bi-plane views. Simulated bi-plane imaging of a valve at different signal-difference-to-noise ratio (SDNR) levels was performed to test the approach. The valve structure was modeled as sinusoidal curves wrapped around a cylinder, which was allowed to expand and deform to the shape of a truncated cone. 2D image sequences with 50 frames of valve deployment were simulated at each SDNR. The simulation achieved a target registration error (TRE) of the estimated valve model of 0.93 ± 2.6 mm (mean ± S.D.) for the lowest SDNR of 2. For higher SDNR (5 to 50) a TRE of 0.04 mm ± 0.23 mm was achieved in >99% of frames. Results indicate that it is feasible to use bi-plane imaging to recover the 3D structure of deformable catheter devices.

Classification of calcium in intravascular OCT images for the purpose of intervention planning

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The presence of extensive calcification is a primary concern when planning and implementing a vascular percutaneous intervention such as stenting. If the balloon does not expand, the interventionist must blindly apply high balloon pressure, use an atherectomy device, or abort the procedure. As part of a project to determine the ability of Intravascular Optical Coherence Tomography (IVOCT) to aid intervention planning, we developed a method for automatic classification of calcium (appearing as a low intensity region with sharply delineated borders) in coronary IVOCT images. We developed an approach where plaque texture is modeled by the joint probability distribution of maximum response bank of filter responses (MR8) where the filter bank was chosen to reflect the qualitative characteristics of the calcium. This distribution is represented by the frequency histogram of filter response cluster centers. IVOCT image data was obtained on cadaver specimens. Ground truth was obtained from brightfield and fluorescence microscopic cryo-image volumes which were accurately registered using a specialized algorithm. In this initial study, sub-images were selected that included calcium, fibrous, and lipid tissues. We manually optimized algorithm parameters such as choice of filter bank, size of the dictionary, etc. Splitting samples into training and testing data, we achieved calcium classification accuracy of 97.8±2.8% with recall of ≥95% and a precision of ≥94%, in this idealized scenario. The automated algorithm performed in close-to-real-time (0.27 seconds) suggesting possible on-line use. This promising preliminary study indicates that computational IVOCT might automatically identify calcium in IVOCT coronary artery images.

9786-5, Session 1

Fusion of CTA and XA data using 3D centerline registration for plaque visualization during coronary intervention

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Coronary Artery Disease (CAD) results in the buildup of plaque below the intima layer inside the vessel wall of the coronary arteries causing narrowing of the vessel and obstructing blood flow. Percutaneous coronary intervention (PCI) is usually done to enlarge the vessel lumen and regain back normal flow of blood to the heart. During PCI, X-ray images are acquired to assist guide wire movement through the vessels to the area of stenosis. While X-ray imaging allows for good lumen visualization, information on plaque type is unavailable. Also due to the projection nature of the X-ray imaging, additional drawbacks such as foreshortening and overlap of vessels limit the efficacy of the cardiac intervention.

Reconstruction of 3D vessel geometry from biplane X-ray acquisitions helps to overcome some of these projection drawbacks, however the plaque type information remains an issue. In contrast, imaging using computed tomography angiography (CTA) can provide us with information on both lumen and plaque type and allows to generate a complete 3D coronary vessel tree unaffected by the foreshortening and overlap problems of the X-ray imaging.

In this paper, we combine x-ray biplane images with CT angiography to visualize three plaque types (dense calcium, fibrous fatty and necrotic core) on x-ray images. 3D registration using three different registration methods is done between coronary centerlines available from x-ray images and CTA volume along with 3D plaque information available from CTA. We compare the different registration methods i.e. iterative closest point algorithm, Gaussian mixture modelling and coherent point drift (and its two modifications) and evaluate their performance based on 3D root mean squared errors (RMSE). Two methods are used to project this 3D information onto 2D plane of the x-ray biplane images. Validation of our approach is performed using artificial x-ray datasets in 3D and 2D space. Finally, a graphical user interface (GUI) is developed to automate the registration and visualization process. We observe that coherent point drift and its modifications yield the best RMSE results for our datasets with mean (µ) = 1.29 mm and standard deviation (σ) = 0.49 mm. Validation study also yields the best results for CPD and its modifications.

9786-6, Session 2

Random walk based segmentation for the prostate on 3D transrectal ultrasound images

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This paper proposes a new semi-automatic segmentation method for the prostate on 3D transrectal ultrasound images (TRUS) by combining the region and classification information. We use a random walk algorithm to express the region information efficiently and flexibly because it can avoid segmentation leakage and shrinking bias. We further use the decision tree as the classifier to distinguish the prostate from the non-prostate tissue due to its fast speed and superior performance, especially for a binary classification problem. Our segmentation algorithm is initialized with the user roughly marking the prostate and non-prostate points on the mid-gland slice which are fitted into an ellipse for obtaining more points. Based on these fitted seed points, we run the random walk algorithm to segment the prostate on the mid-gland slice. The segmented contour and the information from the decision tree classification are combined to determine the initial seed points. The random walk algorithm is then used to segment the prostate on the adjacent slice. We propagate the process until all slices are segmented. The segmentation method was tested in 32 3D transrectal ultrasound images. Manual segmentation by a radiologist serves as the gold standard for the validation. The experimental results show that the proposed method achieved a Dice similarity coefficient of 91.37±0.05%. The segmentation method can be applied to 3D ultrasound-guided prostate biopsy and other applications.

9786-7, Session 2

Resection planning for robotic acoustic neuroma surgery

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Acoustic neuroma surgery is a procedure in which a benign mass is removed from the Internal Auditory Canal (IAC). Currently this surgical procedure requires the manual drilling of the temporal bone followed by exposure and removal of the acoustic neuroma. This procedure is physically and mentally taxing to the surgeon. Our group is working to develop an Acoustic Neuroma Surgery Robot (ANSR) to perform the initial drilling procedure. Planning the ANSR’s drilling region using pre-operative CT requires expertise and around 35 minutes’ time. We propose an approach for automatically producing a resection plan for the ANSR that would avoid damage to sensitive ear structures and requires minimal editing by the surgeon. We first compute an atlas-based segmentation of the mastoid section of the temporal bone, refine it based on the position of anatomical landmarks, and apply a safety margin to the result to produce the automatic resection plan. In experiments with CTs from 4 subjects, our automated process resulted in a resection plan that was verified to be safe.
in every case. Approximately 5 minutes time was required in each case for the surgeon to edit the plan to permit functional access to the IAC. We measured a mean Dice coefficient of 0.93 and surface error of 0.38 mm between the final and automatically proposed plans. These preliminary results indicate that our approach is a viable method for resection planning for the ANSR and drastically reduces the surgeon’s planning effort.

9786-8, Session 2
Fat segmentation on chest CT images via fuzzy models
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Fat quantification in the thorax is important, especially for lung transplant candidates since obesity and being underweight are contraindications to lung transplantation due to their association with mortality. Common approaches for thoracic fat segmentation are interactive requiring significant manual effort to draw the interfaces between fat and muscle with low efficiency and poor repeatability. The goal of this paper is to explore a practical way based on automatic anatomy recognition (AAR) for chest subcutaneous (SAT) and visceral (VAT) fat segmentation. AAR is a recently proposed approach for whole body object segmentation. AAR mainly involves 3 steps: fuzzy object model building, object recognition, and object delineation. AAR recognition is to find the general whereabouts of the target object, which is done by searching the best “pose” for placing fuzzy object models in the test images. AAR delineation is performed to determine the exact object outline or boundary in test images. Overall, unenhanced CT images from 40 lung transplant candidates were used in our experiments. The first 20 were used for model building and the remaining 20 were used for testing (recognition and delineation) and then switch them to use the first 20 for testing and the second 20 for model building. New objects, SatIn and VatIn which represent interfaces of SAT and VAT regions with other tissues, can be effectively used in AAR model building and recognition, rather than the SAT and VAT objects directly, with mean location error less than 2 voxels and scale error around 1. Object delineation achieved segmentation of SAT with TPVF 0.90, FPVF 0.07 and of VAT with TPVF around 0.8, and FPVF 0.04.

9786-9, Session 2
Automatic masking for robust 3D-2D image registration in image-guided spine surgery
Michael D. Ketcha, Tharinu De Silva, Ali Uneri, Johns Hopkins Univ. (United States); Gerhard Kleinszig, Siemens AG (Germany); Sebastian Vogt, Siemens Medical Solutions USA, Inc. (Germany); Jean-Paul Wollinsky, Jeffrey H. Siewerdsen, Johns Hopkins Univ. (United States)
During spinal neurosurgery, information such as vertebral labels can be mapped from preoperative 3D CT to intraoperative 2D radiographs via image-based 3D-2D registration. Such registration has been shown to provide a potentially valuable means of decision support in target localization as well as quality assurance of the surgical product. However, robust registration can be challenged by mismatch in image content between the preoperative CT and intraoperative radiographs, arising, for example, from anatomical deformation or the presence of surgical tools within the radiograph. In this work, we develop and evaluate methods for automatically mitigating the effect of content mismatch by leveraging the surgical planning data to assign greater weight to anatomical regions known to be reliable for registration and vital to the surgical task while removing problematic regions that are highly deformable or often occluded by surgical tools. We investigated two approaches to assigning variable weight (i.e., “masking”) to image content and/or the similarity metric: (1) masking the preoperative 3D CT; and (2) masking within the 2D similarity metric calculation. The accuracy of registration was evaluated in 61 cases of an IRB-approved clinical study using projection distance error (PDE). The best performing of the masking techniques was found to reduce the rate of gross failure (PDE > 20 mm) from 12.46% to 5.25%. These approaches provided robustness to content mismatch and eliminated distinct failure modes of registration. Such improvement was gained without additional workflow and has motivated incorporation of the masking methods within a system under development for prospective clinical studies.

9786-10, Session 2
Robust patella motion tracking using intensity-based 2D-3D registration on dynamic bi-plane fluoroscopy: toward quantitative assessment in MPFL reconstruction surgery
Yoshito Otake, Matthieu Esnault, Nara Institute of Schience and Technology (Japan); Robert Grupp, Johns Hopkins Univ. (United States); Shinichi Kosugi, Nara Prefecture Western Medical Ctr. (Japan); Yoshinobu Sato, Nara Institute of Science and Technology (Japan)
The determination of in vivo motion of multiple-bones using dynamic fluoroscopic images and computed tomography (CT) is useful for post-operative assessment of orthopaedic surgeries such as medial patellofemoral ligament reconstruction. We propose a robust method to measure the 3D motion of multiple rigid objects with high accuracy using a series of bi-plane fluoroscopic images and a multi-resolution, intensity-based, 2D-3D registration. A Covariance Matrix Adaptation Evolution Strategy (CMA-ES) optimizer was used with a gradient correlation similarity metric. Four approaches to register three rigid objects (femur, Tibia-fibula and patella) were implemented: 1) an individual bone approach registering one bone at a time, each with optimization of a six degrees of freedom (6DOF) parameter; 2) a sequential approach registering one bone at a time but using the previous bone results as the background in DRR generation, 3) a simultaneous approach registering all the bones together (18DOF) and 4) a combination of the sequential and the simultaneous approaches. These approaches were compared in experiments using simulated images generated from the CT of a healthy volunteer and measured fluoroscopic images. Over the 120 simulated frames of motion, the simultaneous approach showed improved registration accuracy compared to the individual approach: with less than 0.68mm root-mean-square error (RMSE) for translation and less than 1.2° RMSE for rotation. A robustness evaluation was conducted with 45 trials of a randomly perturbed initialization showed that the sequential approach improved robustness significantly (74% success rate) compared to the individual bone approach (34% success) for patella registration (femur and tibia-fibula registration had a 100% success rate with each approach).

9786-11, Session 2
Fast generation of digitally reconstructed radiograph through an efficient preprocessing of ray attenuation values
Soheil Ghafurian, Dimitris Metaxas, Virak Tan, Kang Li, Rutgers, The State Univ. of New Jersey (United States)
Digitally reconstructed radiographs (DRR) are a simulation of radiographic images produced through a perspective projection of the three-dimensional (3D) image (volume) onto a two-dimensional (2D) image plane. The traditional method for the generation of DRRs, namely ray-casting, is a
9786-12, Session 3

**Accurate biopsy-needle depth estimation in limited-angle tomography using multi-view geometry**

Fons van der Sommen, Svitlana Zinger, Peter H. N. de With, Technische Univ. Eindhoven (Netherlands)

Recently, compressed-sensing based algorithms have enabled volume reconstruction from projection images acquired over a relatively small angle. These methods enable accurate depth estimation of surgical tools with respect to anatomical structures. However, they are computationally expensive and time consuming, rendering them unattractive for image-guided interventions. We propose an alternative approach for depth estimation of biopsy needles during image-guided interventions, in which we split the problem into two parts and solve them independently: needle-depth estimation and volume reconstruction. The complete proposed system consists of three steps: (1) needle extraction, (2) depth estimation and (3) volume reconstruction. First, we detect the biopsy needle in the projection images and remove it by interpolation. Next, we exploit epipolar geometry to find point-to-point correspondences in the projection images to triangulate the 3D position of the needle in the volume. Finally, we use the interpolated projection images to reconstruct the local anatomical structures and indicate the position of the needle within this volume. For validation of the algorithm, we have recorded a full CT scan of a phantom with an inserted biopsy needle. The performance of our approach ranges from a median error of 2.94 mm for a distributed viewing angle of 1 degree down to an error of 0.30 mm for an angle larger than 10 degrees. Based on the results of the initial phantom experiment, we conclude that multi-view geometry offers an alternative attractive to time-consuming iterative methods for the depth estimation of surgical tools during C-arm-based image-guided interventions.

9786-13, Session 3

**Automatic geometric rectification for patient registration in image-guided spinal surgery**

Yunliang Cai, Jonathan Olson, Xiaoyao Fan, Thayer School of Engineering at Dartmouth (United States); Linton Evans, Dartmouth Hitchcock Medical Ctr. (United States); Keith D. Paulsen, Thayer School of Engineering at Dartmouth (United States) and Dartmouth Hitchcock Medical Ctr (United States); David Roberts, Sohail Mirza, Stuart S. Lollis, Dartmouth Hitchcock Medical Ctr. (United States); Songbai Ji, Thayer School of Engineering at Dartmouth (United States) and Dartmouth Hitchcock Medical Ctr. (United States)

Accurate and efficient patient registration is crucial for the success of image-guidance in spinal surgery. Recently, we have established the feasibility of using intraoperative stereovision (ISV) to perform patient registration with respect to preoperative CT (pCT) in human subjects undergoing spinal surgery. Although a desired accuracy was achieved, this technique required manual segmentation and placement of feature points on reconstructed ISV and pCT surfaces. In this study, we present an improved registration pipeline with automatic geometric rectification to restore spine structures in both pCT and ISV into regular symmetric shapes. Non-linear principal component analysis (NPCA) was used to extract the overall spinal shape and individual vertebral poses. Rectified shapes were then obtained by locally projecting the 3D shapes in the original coordinates into a new local NPCA coordinate system. Using the rectified shapes, the initial alignment between the 3D ISV and pCT surfaces is reduced to a 2D image registration, which builds up the point-point correspondences between ISV and pCT. With the guidance of these correspondences, the final high accurate resulting registration is achieved by an iterative closest point (ICP) algorithm over the correlated SV-pCT point sets. The technique was successfully applied to two explanted porcine spine samples. The computational cost of the whole ISV-pCT registration pipeline was less than 1 min with RMS registration error less than 2.2 mm. These preliminary results suggest great potential for the pose-free rectification-based registration in clinical human subjects in image-guided spine surgery.

9786-15, Session 3

**Study into clinical workflow for spinal curvature measurement with portable ultrasound**

Reza Tabanfar, Queen’s Univ. (Canada) and Lab. for Percutaneous Surgery (Canada); Christina Yan, Lab. for Percutaneous Surgery (Canada); Michael Kempston, Daniel Borschneck, Queen’s Univ. (Canada); Tamas Ungi, Gabor Fichtinger, Lab. for Percutaneous Surgery (Canada)
Purpose: Spinal curvature monitoring is essential in making treatment decisions in scoliosis. Monitoring entails radiographic examinations, however repeated ionizing radiation exposure has been shown to increase cancer risk. Ultrasound does not emit ionizing radiation and is safer for spinal curvature monitoring. We investigated a clinical sonography protocol and challenges associated with position-tracked ultrasound in spinal curvature measurement in scoliosis.

Methods: Transverse processes were landmarked along each vertebra using tracked ultrasound snapshots. The transverse process angle was used to determine the orientation of each vertebra. We tested our methodology on five patients in a local pediatric scoliosis clinic, comparing ultrasound to radiographic curvature measurements. Results: Despite strong correlation between radiographic and ultrasound curvature angles in phantom studies, we encountered new challenges in the clinical setting. Our main challenge was differentiating transverse processes from ribs and other structures during landmarking. We observed up to 13° angle variability for a single vertebra and a 9.85 ± 10.81° difference between ultrasound and radiographic Cobb angles for thoracic curvatures. Additionally, we were unable to visualize anatomical landmarks in the lumbar region where soft tissue depth was 25-35mm. In volunteers with large Cobb angles (greater than 40° thoracic and 60° lumbar), we observed spinal protrusions resulting in incomplete probe-skin contact and partial ultrasound images not suitable for landmarking. Conclusion: Spinal curvature measurement using tracked ultrasound is viable on phantom spine models. In the clinic, new challenges were encountered which must be resolved before a universal sonography protocol can be developed.

MIND Demons for MR-to-CT deformable image registration in image-guided spine surgery

Sureerat Reaungamornrat, Tharindu De Silva, Ali Uneri, Johns Hopkins Univ. (United States); Jean-Paul Wolinsky, The Johns Hopkins Hospital (United States); Akhil J. Khanna, Johns Hopkins Health Care & Surgery Ctr. (United States); Gerhard Kliensing, Sebastian Vogt, Siemens AG (Germany); Jerry L. Prince, Jeffrey H. Siewerdsen, Johns Hopkins Univ. (United States)

Purpose: Intraoperative localization of target and normal anatomy can be achieved through multi-modality deformable image registration to resolve planning data (e.g., tumor boundaries and adjacent vital structures) defined in preoperative MR in up-to-date intraoperative CT. We propose a new symmetric diffeomorphic deformable registration method to align preoperative MR to intraoperative CT using a modality-independent neighborhood descriptor (MIND), a Huber metric, and a Gauss-Newton optimization for robust MR-CT registration.

Method: The method estimates symmetric time-dependent diffeomorphisms with smoothness priors on both the velocity fields and the diffeomorphisms using a Demons framework. Analysis of parameter sensitivity and registration performance was assessed in simulation and phantom experiments, and the performance was compared to that of free-form deformation (FFD) with mutual information (MI) and local MI (LMI) and Demons with normalized MI (NMI).

Results: The method yielded reliable and invertible viscoelastic deformations capable of preserving anatomical structures with non-singular spatial Jacobian and sub-voxel inverse consistency of 0.008 mm. The estimated viscoelastic diffeomorphisms were able to resolve large deformations, achieving mean target registration error TRE = 1.5 mm compared to 10.9 mm for MI FFD, 2.3 mm for LMI FFD, and 4.6 mm for NMI Demons.

Conclusions: A promising method for MR-to-CT image registration has been developed for image-guided spine surgery. The approach could facilitate visualization of preoperative planning data with respect to the intraoperative CT images and localization of target and critical tissues in support of safer, high-precision spine surgery.

Automatic detection of a hand-held needle in ultrasound via phased-based analysis of the tremor motion

Parmida Beigi, Septimiu E. Salcudean, Robert Rohling, The Univ. of British Columbia (Canada); Gary C. C慌g, Philips Ultrasound, Inc. (United States)

This paper presents an automatic localization method for a standard hand-held needle in ultrasound based on temporal motion analysis of spatially decomposed data. Subtle displacement arising from tremor motion has a periodic pattern which is usually imperceptible in the intensity image but may convey information in the phase image. Our method aims to detect such periodic motion of a hand-held needle and distinguish it from intrinsic tissue motion, using a technique inspired by video magnification. Complex steerable pyramids allow specific design of the wavelets’ orientations according to the insertion angle as well as the measurement of the local phase. We therefore use steerable pairs of even and odd Gabor wavelets to decompose the ultrasound B-mode sequence into various spatial frequency bands. Variations of the local phase measurements in the spatially decomposed input data is then temporally analyzed using a finite impulse response bandpass filter to detect regions with tremor motion pattern. Results obtained from different pyramid levels are then combined and thresholded to generate the binary mask input for the Hough transform, which determines an estimate of the direction angle and discards some of the outliers. Polynomial fitting is used at the final stage to remove any remaining outliers and improve the trajectory detection. The detected needle is finally added back to the input sequence as an overlay of a cloud of points. We demonstrate the efficiency of our approach to detect the needle from subtle tremor motion in ex-vivo images and in cases where intrinsic motion is also present.

Ultrasound to video registration using a bi-plane transrectal probe with photoacoustic markers

Alexis Cheng, Hyun Jae Kang, Russell H. Taylor, Emad M. Doctor, Johns Hopkins Univ. (United States)

Modern surgical scenarios typically provide surgeons with additional information through fusion of video and other imaging modalities. To provide this information, the tools and devices used in surgery must be registered together with interventional guidance equipment and surgical navigation systems. In this work, we focus explicitly on registering ultrasound with a stereocamera system using photoacoustic markers. Previous work has shown that photoacoustic markers can be used to facilitate this registration task to achieve target registration errors lower than the current available systems. Photoacoustic markers are defined as a set of non-collinear laser spots projected onto some surface. They can be simultaneously visualized by a stereocamera system and an ultrasound transducer because of the photoacoustic effect. In more recent work, the three-dimensional ultrasound volume was replaced by images from a single ultrasound image pose from a convex array transducer. The feasibility of this approach was demonstrated, but the accuracy was lacking due to the physical limitations of the convex array transducer. In this work, we propose the use of a bi-plane transrectal ultrasound transducer. The main advantage of using this type of transducer is that the ultrasound elements are no longer restricted to a single plane. While this development would be limited to prostate applications, liver and kidney applications are also feasible if a suitable transducer is built. This work is demonstrated in two experiments, one without photoacoustics and one with. The resulting target registration error for these experiments were 1.07mm±0.35mm and 1.82mm±0.87mm respectively, which is better than current available systems.
Classification of prostate cancer grade using temporal ultrasound: in vivo feasibility study

Sahar Ghavidel, Queen’s Univ. (Canada); Farhad Imani, Purang Abolmaesumi, Siavash Khallaghi, The Univ. of British Columbia (Canada); Eli Gibson, Western Univ. (Canada); Amir Khojaste, Queen’s Univ. (Canada); Mena Gaed M.D., Western Univ. (Canada); Madeleine Moussa, José A. Gomez, London Health Sciences Ctr. (Canada); D. Robert Siemens, Michael Leveridge, Kingston General Hospital (Canada); Silvia Chang, Vancouver General Hospital (Canada); Aaron Fenster, Aaron D. Ward, Western Univ. (Canada); Parvin Mousavi, Queen’s Univ. (Canada)

Temporal ultrasound has been shown to be an efficient tissue classification approach for detection of cancer. Previous studies of this method have demonstrated high classification accuracy in differentiating cancer from benign tissue. In this paper, we extend the temporal ultrasound method to classify lower grades (tissues with Gleason Score 3+3 Prostate Cancer (PCa)) from all other grades (Gleason Score 3+4). We use a group of 9 patients with mostly lower grade PCa. To resolve the problem of imbalanced dataset, we use Synthetic Minority Oversampling Technique (SMOTE) to generate synthetic samples for the minority class (which is higher grades PCa in our case). We calculate spectral features of temporal ultrasound data and perform feature selection using Random Forests. In leave-one-patient-out cross-validation strategy, an area under ROC curve of 0.73 is achieved with overall sensitivity and specificity of 73% and 61%, respectively. This work represents promising results to classify lower and higher grade PCa using temporal ultrasound.

Deformable registration of x-ray to MRI for post-implant dosimetry in prostate brachytherapy

Seyoun Park, The Johns Hopkins Hospital (United States); Danny Y. Song, Sidney Kimmel Comprehensive Cancer Ctr. (United States); Junghoon Lee, Johns Hopkins Univ. (United States)

Post-implant dosimetric assessment in prostate brachytherapy is typically performed using CT as the standard imaging modality. However, poor soft tissue contrast in CT causes significant variability in target contouring, resulting in incorrect dose calculations for organs of interest. CT-MR fusion-based approach has been advocated taking advantage of the complementary capabilities of CT (seed identification) and MRI (soft tissue visibility), and has proved to provide more accurate dosimetry calculations. However, seed segmentation in CT requires manual review, and the accuracy is limited by the reconstructed voxel resolution. In addition, CT deposits considerable amount of radiation to the patient. In this paper, we propose an X-ray and MRI based post-implant dosimetry approach. Implanted seeds are localized using three X-ray images by solving a combinatorial optimization problem, and the identified seeds are registered to MR images by an intensity-based points-to-volume registration. We pre-process the MR images using geometric and Gaussian filtering. To accommodate potential soft tissue deformation, our registration is performed in two steps, an initial affine transformation and local deformable registration. An evolutionary optimizer in conjunction with a points-to-volume similarity metric is used for the affine registration. Local prostate deformation and seed migration are then adjusted by the deformable registration step with external and internal force constraints. We tested our algorithm on four patient data sets, achieving registration error of (1.2±0.8)mm in <30s. With high accuracy and speed, our proposed approach has the potential to be a cost-effective solution for post-implant dosimetry with equivalent accuracy as CT-MR fusion-based approach.

Evaluation of a CT-based electro-anatomical cochlear implant model

Ahmet Cakir, Benoit M. Dawant, Jack H. Noble, Vanderbilt Univ. (United States)

Cochlear implants (CIs) are considered standard treatment for patients who experience sensory-based hearing loss. Although these devices have been remarkably successful at restoring hearing, it is rare to achieve natural fidelity, and many patients experience poor outcomes. Previous studies have shown that outcomes can be improved when optimizing CI processor settings using an estimation of the CI’s neural activation patterns found by detecting the distance between the CI electrodes and the nerves they stimulate in pre- and post-implantation CT images. We call this method Image-Guided CI Programming (IGCIP). More comprehensive electro-anatomical models (EAMs) might better estimate neural activation patterns than using a distance-based estimate, potentially leading to selection further optimized CI settings. Our goal in this study is to investigate whether CT-based EAMs can accurately estimate neural stimulation patterns. For this purpose, we have constructed EAMs of N=5 specimens. We analyzed the sensitivity of our model to design parameters such as field-of-view, resolution, and tissue resistivity. Our results show that our model is stable to parameter changes. To evaluate the utility of patient-specific modeling, we identify the difference in estimated neural activation patterns across specimens for identically located electrodes. The average computed coefficient of variation (COV) across specimens is 0.262, suggesting patient-specific models are necessary and that the accuracy of a generic model would be insufficient. Our results suggest that development of in vivo patient-specific CIs could lead to better methods for selecting CI settings, which would ultimately lead to better hearing outcomes with CIs.

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detected based on their distance to the nerves, and these electrodes are deactivated from the patient’s map [2]. A large clinical study by our group has shown statistically significant improvement in average outcomes when implants are programmed using this approach [3].

While our studies have shown that our IGCIP approach already leads to improved outcomes, our current method for detecting channel interaction relies on an indirect estimation of each electrode’s neural activation pattern based purely on the distance from the electrodes to the neural stimulation sites. This approach may be less accurate than a more comprehensive model of electrical stimulation such as a high-fidelity finite element model (FEM) of the electrically stimulated cochlea. Kakman et al. [4] and Whiten [5] have constructed cochlear EAMs using histological imaging. We are interested in constructing EAMs using μCTs of cochlear specimens. In this study, we investigate whether μCT-based EAMs can accurately estimate neural stimulation patterns. If such EAMs prove useful, it may be possible to fit those EAMs to new patient CT images by leveraging active-shape model-based techniques we have previously developed [6]. These techniques are designed to localize intra-cochlear anatomy in patient CT images by fitting a high resolution model of cochlear geometry constructed using μCTs of a set of specimens. Such an approach would permit creating EAMs that use patient CT images to account for patient-specific cochlear shape.

To evaluate the use of μCT-based EAMs for our application, we have constructed EAMs for N=5 specimens. For each specimen, the EAM is used to estimate neural activation patterns for each of a number of different simulated electrode locations. To evaluate the accuracy of the estimated activation patterns, we evaluate the sensitivity of the results to the resolution and scope of the EAM. To evaluate the utility of patient-specific modeling, we quantify the difference in estimated neural activation patterns across specimens for identically located electrodes.

METHODS: EAMs were designed based on our μCT images in a similar fashion to those designed with histological images by Whiten et al. [5]. The tissue was assumed to be electrically linear. A uniform 3D grid of nodes was defined over the field of view of the μCT image. Nodes were assigned tissue resistivity classes, including air, bone, soft tissue, neural tissue, and electrolytic fluid (see Figure 1). The μCT was used to determine the class of each node. Manual segmentation of the modiolus and the scala tympani and vestibuli in the μCT were used to label nodes as neural tissue and electrolytic fluid, respectively. Intensity thresholding of the μCT was used to classify the remaining nodes into air, bone, and soft tissue classes. Electrical resistivity values for each class were selected as values found by other groups [7], with air, bone, neural tissue, soft tissue, and electrolytic fluid being assigned resistivity values of $\approx 5000$, 300, 300 and 50 $\Omega\text{cm}$, respectively.

We computed the voltage at each node that results from cochlear implant activation using Ohm's Law, $V=IR$. This is done by solving a system of linear equations describing the flow of current to and from each node. For each node, an equation is designed to describe the current flow between that node and each of its 6-connected neighbor nodes. Using the formulation of Whiten et al. [5], the current in the $\chi$ direction for the node located at $i,j,k$ can be defined using

$$\text{where } o_1, o_2, o_3 \text{ is the conductivity of the node at } i,j,k \text{ and is defined as the inverse of the node's resistivity, } q_0, q_1, q_2 \text{ is the voltage of the same node, and } \Delta x, \Delta y, \Delta z \text{ are dimensions of the node. An equation for the sum of currents entering and leaving the node can be defined as } I_1 + I_2 + I_3 + I_4 + I_5 + I_6 \text{. This equation is set equal to } \eta_1 A \text{ if the node contains a stimulating electrode, } \eta_2 A \text{ for the ground node, and zero for every other node, representing the fact that the sum of currents entering and leaving a tissue node must be equal.}$$

We then solve the system of all the equations using the formulation $A\phi = b$, where $A$ is a sparse matrix containing coefficients of the linear sum of currents equations, $\phi$ are the set of node voltages that are being determined and are concatenated into a vector, and $b$ is a vector containing the sum of current for each node equation. After solving for the voltage map $\phi$, it is possible to estimate neural activation patterns.

To simulate various electrode positions, we place a stimulating electrode at 90, 180, 270, 360, 450 and 540 degrees along the length of the scala tympani (see Figure 1). Angular-depth within the cochlea is defined by angle along the cochlea’s spiral with $0^\circ$ being defined by the location of the round window membrane of the cochlea. The simulated electrode locations were chosen at these angles because they are representative of the typical range of electrode locations with CIs. A node in the internal auditory canal (IAC) was defined as the ground as it is thought that nearly all current returning to the CI ground travels through the IAC.

We evaluated the performance of the model by testing the sensitivity of model estimations to design parameters, including field-of-view (FOV) of the mesh, resolution of the mesh, and tissue resistivity values. A more limited FOV mesh improves computational efficiency but may decrease accuracy. Similarly, coarser resolution of the mesh can improve efficiency but may decrease accuracy. Measuring the sensitivity of the model to changes in tissue resistivity will help in understanding the limits of the model’s accuracy. To test sensitivity to FOV, EAMs were built with FOV at the full 7CT FOV and at a limited FOV containing approximately 5 mm of space around the cochlea. To test sensitivity to resolution, EAMs were built at the full resolution of the 7CT as well as at a resolution downscaled by a factor of 2 and of 4 in each direction. Further EAMs were constructed with resistivity values halved and doubled for each of the electrolytic fluid, nervous tissue, and bone resistivity values. We also evaluated the importance of patient-specific design of the EAM by comparing model estimations across the EAMs built for each specimen. The sensitivity of the model to different conditions is evaluated by comparing the resulting estimated current density profile (CDP) along the length of RC (see Figure 1) across conditions.

RESULTS: The average percent differences in estimated CDP along RC based on model and limited FOV and varied resolution models are shown in Table 1. As can be seen in the table, limiting the FOV or reducing model resolution by a factor of two results in relatively small -4% differences in estimations of current density profiles. However, further model resolution reduction results in larger differences of -25%. The effect of the changes to resistivity values can be seen in Figure 2. CDPs for specimen 4 and 3 for the different tissue resistivity conditions for an electrode located at 180 degree depth are shown. These results show that the model is relatively insensitive to changes in the resistivity of bone but is sensitive to changes in fluid and nerve tissue resistivity.

To measure difference in model predictions across specimens, we compute the coefficient of variation (COV) in the estimated CDPs across specimens for identically located simulated electrodes. Since we are interested in using the model to estimate the relation in CDP between electrodes, a groupwise change in scale of the CDPs among electrodes from one cochlea to another is not important, and a direct comparison of CDPs across specimens would not be appropriate. Thus, prior to comparing CDP across specimens, for each specimen, the electrode with the maximum total current density (mCD) along RC is identified, and the CDPs for all electrodes for that specimen are normalized by rescaling them by $1/mCD$. mCD is chosen as the normalization factor because perception levels are thought to be related to total current density in RC. After normalization, the COV of the CDPs across specimens for each electrode can be measured to quantify inter-model differences, and these results are shown in Table 2. As seen in the table, the mean and maximum COV of current density, computed at each of the densely sampled sites along the length of the RC across specimens, are relatively large values of 0.26 and 0.36, respectively. This suggests that patient-specific factors such as height and body mass index can affect CDPs. We are interested in constructing EAMs using histological imaging. We are interested in constructing EAMs using histological imaging. We are interested in constructing EAMs using histological imaging. We are interested in constructing EAMs using histological imaging. We are interested in constructing EAMs using histological imaging.
method. Results showed that the proposed method efficiently estimated landmark-based metrics being used for the parameter optimization process. In addition, registration accuracy improved with both image-based and the registration process occurs only during the treatment planning stage. To achieve the best registration performance with the specific algorithm. In this paper, we investigated a parameter optimization strategy for Optical-deformable image registration of 4DCT lung anatomy. A novel fast simulated annealing strategy. Audiology & Neurotology 2014, 19(6), 400-411 (2014)


9786-22, Session 5

Fast simulated annealing and adaptive Monte Carlo sampling based parameter optimization for dense optical-flow deformable image registration of 4DCT lung anatomy

Tai Dou, Yugang Min, John Neylon, David Thomas, Patrick Kupelian, Anand Santhanam, Univ. of California, Los Angeles (United States)

Deformable image registration (DIR) is an important step in radiotherapy treatment planning. An optimal input registration parameter set is critical to achieve the best registration performance with the specific algorithm. In this paper, we investigated a parameter optimization strategy for Optical-flow based DIR of the 4DCT lung anatomy. A novel fast simulated annealing with adaptive Monte Carlo sampling algorithm (FSA-AMC) was investigated for solving the complex non-convex parameter optimization problem. The method for registration error for a given parameter set was computed using both a landmark-based mean target registration error (mTRE) as well as an image-based metric, Entropy Correlated Coefficient (ECC), between a given segmentation of intra-cochlear anatomy in conventional CT”. IEEE Trans. on Biomedical Eng., Vol. 58, No. 9, pp. 2625-32, 2011.


9786-23, Session 5

Automatic pose correction for image-guided nonhuman primate brain surgery planning

Soheil Ghashfuran, Merck & Co., Inc. (United States) and Rutgers Univ. (United States); Antong Chen, Catherine Hines, Belma Dogdas, Ashleigh Bone, Kenneth Lodge, Stacey O’Malley, Merck & Co., Inc. (United States); Christopher T. Winkelmann, Pfizer Inc. (United States); Ansuman Bagchi, Laura S. Lubbers, Jason M. Uslaner, Colena Johnson, John Renger, Hatim A. Zariwala, Merck & Co., Inc. (United States)

Intracranial delivery of recombinant DNA and neurochemical analysis in nonhuman primate (NHP) requires precise targeting of various brain structures via imaging derived coordinates in stereotactic surgeries. To attain targeting precision, the surgical planning needs to be done on preoperative three dimensional (3D) CT and/or MR images, in which the animal’s head is fixed in a pose identical to the pose during the stereotactic surgery. The matching of the image to the pose in the stereotactic frame can be done manually by detecting key anatomical landmarks on the 3D MR and CT images such as ear canal and ear bar zero position. This is not only time intensive but also prone to error due to the varying initial poses in the images which affects both the landmark detection and rotation estimation. We have introduced a fast, reproducible, and semi-automatic method to detect the stereotactic coordinate system in the image and correct the pose. The method begins with a rigid registration of the subject images to an atlas and proceeds to detect the anatomical landmarks through a sequence of optimization, deformable and multimodal registration algorithms. The results showed similar precision (maximum difference of 1.7º in average in-plane rotation) to a manual pose correction.
segments and automatic segmentations are 3.70±2.30(B-spline), 1.25±1.78(demons), 0.93±1.14(optical flow), and 4.39±3.86(VelocityAI). The proposed method significantly reduced the estimation error by 9%(B-spline), 38%(demos), and 51%(optical flow) over the results using VelocityAI. Although demonstrated only on HN nodal GTVs, the results imply that the proposed method can produce improved segmentation of other critical structures over conventional methods.

9786-25, Session 6

Toward disparity joint upsampling for robust stereoscopic endoscopic scene reconstruction in robotic prostatectomy

Xiongbiao Luo, A. Jonathan McLeod, Terry M. Peters, Western Univ. (Canada)

Three-dimensional (3D) scene reconstruction from stereoscopic binocular laparoscopic videos is an effective way to expand the limited surgical field and augment the structure visualization of the organ being operated in minimally invasive surgery. However, currently available reconstruction approaches possibly limit themselves to image noise, occlusions, textureless and blurred structures. In particular, the endoscope going inside the body only has the limited light source that makes illumination nonuniform in visualizing the surgical field. These limitations unavoidably deteriorate the stereo image quality and hence lead to low-resolution and inaccurate disparity map with blurring edge structures in 3D scene reconstruction. This paper proposes a new stereo correspondence framework that integrates cost-volume filtering with joint upsampling for robust disparity map estimation. Joint bilateral upsampling, joint geodesic upsampling, and tree filtering upsampling were compared to enhance the disparity accuracy. The experimental results demonstrate that joint upsampling provides an effective way to boost the disparity estimation and hence to improve the surgical endoscopic scene 3D reconstruction. Moreover, the bilateral upsampling generally outperforms other two upsampling methods in disparity estimation.

9786-26, Session 6

Endoscopes and robots for tight surgical spaces: use of pre-curved elastic elements to enhance curvature

Andria A. Remirez, Robert J. Webster III, Vanderbilt Univ. (United States)

In this paper we show how pre-curved elastic elements used inside devices like endoscopes and endoscope-like robots can be used in conjunction with axial rotation of the overall device to increase workspace and maximum curvature. These capabilities are useful for surgeries in small spaces, and we provide examples in the context of retroflexed endoscopy and total hip revision procedures involving the removal of osteolytic lesions. The use of precurvature effectively biases the workspace of the device within the bending plane, so that its configuration ranges between straight and a very tight curve on one side of the entry axis, in contrast to the traditional paradigm of bending in both directions to a lower maximum curvature. Used in conjunction with axial rotation, this increases the volume of points accessible to the device. In this paper, we will present the design and construction of a simple prototype illustrating this concept, and compare it to the same design without precurvature in terms of workspace volume under both strain- and actuation force-based limits. Experiments will be used to validate our theoretical comparison, and we will provide results of experiments testing the prototype to failure, describing failure modes.

9786-27, Session 6

Disposable patient-mounted geared robot for image-guided needle insertion

Charles Watkins, Takahisa Kato, Nobuhiko Hata, Brigham and Women’s Hospital (United States)

Patient-mounted robotic needle guidance is an emerging method of needle insertion in percutaneous ablative therapies. During needle insertion, patient-mounted robots can account for patient body movement, unlike gantry or floor mounted devices, and still increase the accuracy and precision of needle placement. Patient-mounted robots, however, require repeated sterilization, which is often a difficult process with complex devices; overcoming this challenge is therefore key to the success of a patient mounted robot. To eliminate the need for repeated sterilization, we have developed a disposable patient-mounted robot with a two-ring structure: an angled upper ring both rotates and revolves about the lower ring. Using this structure, the robot has a clinically suitable range of needle insertion angles with a remote center of motion. To achieve disposability, our structure applies a disposable gear transmission component which detachably interfaces with non-disposable driving motors. With a manually driven prototype of the gear transmission component, we assessed whether manual knobs could control rotation and revolution of the upper ring, and measured this transmission of rotation between the manual knobs and rotating rings to evaluate consistent needle placement. Our tests confirmed that the manual knobs were able to create both rotation and revolution in the upper ring. We also determined that with any rotation of the upper ring, the manual knobs’ rotation varied by an acceptable degree from their expected rotation. Our robot introduces a novel approach to patient-mounted robots, and has potential to enable sterile and accurate needle guidance in percutaneous ablation therapies.

9786-29, Session 6

Image-guided preoperative prediction of pyramidal tract side effect in deep brain stimulation

Clément Baumgarten, Yulong Zhao, INSERM (France) and Lab. Traitement du Signal et de l’Image (France); Paul Saulieu M.D., Cecile Malrain M.D., Ctr. Hospitalier Univ. de Rennes (France); Pierre Jannin, Univ. de Rennes 1 (France) and Lab. Traitement du Signal et de l’Image (France); Claire Haegelen M.D., Ctr. Hospitalier Univ. de Rennes (France) and INSERM (France) and LTSI (France)

Deep brain stimulation of the medial globus pallidus is a surgical procedure for treating patients suffering from Parkinson’s disease. Its therapeutic effect may be limited by the presence of pyramidal tract side effect (PTSE). PTSE is a contraction time-locked to the stimulation when the current spreading reaches the motor fibers of the pyramidal tract within the internal capsule. The lack of side-effect predictive model leads the neurologist to secure an optimal electrode placement by iterating clinical testing on an awake patient during the surgical procedure. The objective of the study was to propose a preoperative predictive model of PTSE. A machine learning based method called PyMAN (for Pyramidal tract side effect Model based on Artificial Neural network) that accounted for the current of the stimulation, the 3D electrode coordinates and the angle of the trajectory, was designed to predict the occurence of PTSE. Ten patients implanted in the medial globus pallidus have been tested by a clinician to create a labeled dataset of the stimulation parameters that trigger PTSE. The kappa index value between the data predicted by PyMAN and the labeled data was .78. Further evaluation studies are desirable to confirm whether PyMAN could be a reliable tool for assisting the surgeon to prevent PTSE during the preoperative planning.
Rapid virtual stenting for intracranial aneurysms

Liang Zhao, Danyang Chen, Zihe Chen, Xiangyu Wang, Nikhil Paliwal, Univ. at Buffalo (United States); Jianping Xiang, Hui Meng, Toshiba Stroke and Vascular Research Ctr. (United States); Jason J. Corso, Jinhui Xu, Univ. at Buffalo (United States)

The rupture of Intracranial Aneurysms is the most severe form of stroke with high rates of mortality and disability. One of its primary treatments is to use stunt or Flow Diverter to divert the blood flow away from the IA in a minimal invasive manner. To optimize such treatments, it is desirable to provide an automatic tool for virtual stenting before its actual implantation. In this paper, we propose a novel method, called ball-sweeping, for rapid virtual stenting. Our method sweeps a maximum inscribed sphere through the aneurysmal region of the vessel and directly generates a stunt surface. First, we compute a guideline on the vessel. Then we compute the Voronoi Diagram of the vessel geometry. We choose some of the Voronoi vertices as our candidate points for centerline according to the guideline on the vessel. Based on this idea, to make the stunt deployment more realistic, we also consider the smoothness of the centerline and the density of the stunt. Our resulting stunt mesh has guaranteed smoothness and variable pore density to achieve an enhanced occlusion performance. This is achieved by Dynamic Programming based on the candidate points for the centerline using constraints on the smoothness of the centerline and the smoothness of the stunt (difference between the radii of consecutive maximum inscribed spheres). Comparing to existing methods, our technique is computationally much more efficient.

Surface-driven biomechanical breast image registration

Bjoern Eiben, Vasileios Vavourakis, John H. Hipwell, Univ. College London (United Kingdom); Sven Kabus, Cristian Lorenz, Thomas Buelow, Philips Research (Germany); David J. Hawkes, Univ. College London (United Kingdom)

Biomechanical modelling enables large deformation simulations of breast tissues under different loading conditions. Such simulations can be utilised to transform prone MR images into a different patient position, such as upright or supine. We present a novel integration of biomechanical modelling with a surface registration algorithm which optimises the unknown material parameters of a biomechanical model and performs a subsequent regularised surface alignment. This allows deformations induced by effects other than gravity, such as those due to contact of the breast and MR coil, to be reversed. Correction displacements are applied to the biomechanical model enabling transformation of the original pre-surgical images to the corresponding target position. The algorithm is evaluated for the prone-to-supine case using prone MR images and the skin outline of supine CT scans for three patients. This allows a mean target registration error (TRE) of 10.6mm for internal structures to be achieved. For the prone-to-upright scenario, an optical 3D surface scan of one patient is used as a registration target and the nipple distances after alignment between the transformed MRI and the surface are 10.1mm and 6.3mm respectively.

Modeling and simulation of tumor-influenced high-resolution real-time physics-based breast models for model-guided robotic interventions

John Neylon, Katelyn Hasse, Anand Santhanam, Univ. of California, Los Angeles (United States)

Breast radiation therapy is typically delivered to the patient in either supine or prone position. Each of these positioning systems has its limitations in terms of tumor localization, dose to the surrounding normal structures, and patient comfort. We focus on developing a pneumatically controlled breast immobilization device that will enable the benefits of both supine and prone positioning. In this paper, we present a physics-based breast deformable model that aids in both the design of the breast immobilization device as well as act as control module for the device during every day positioning. The model geometry is generated from a subject’s CT scan acquired during the treatment planning stage. A GPU based deformable model is then generated for the breast. A mass-spring-damper approach is then employed for the deformable model. Each voxel of the CT scan is then associated with a mass element, which gives the model its high resolution nature. The subject specific elasticity is then estimated from a CT scan in prone position. Our results show that the model can deform at >30 deformations per second, which satisfies the real-time requirement for robotic positioning. The model interacts with a computer designed immobilization device to position the breast and tumor anatomy in a reproducible location. The elasticity estimation was systematically verified to be 98% accuracy. The design of the immobilization device was also systematically varied based on the breast geometry, tumor location, elasticity distribution and the reproducibility of the desired tumor location.

Accuracy of lesion boundary tracking in navigated breast tumor excision

Emily Heffernan, Tamas Ungi M.D., Thomas Vaughan, Padina Pezeshki, Andras Lasso, Evelyn Morin, Gabor Fichtinger, Gabrielle Gauvin, Jay Engel M.D., John Rudan M.D., Queen’s Univ. (Canada)

Purpose: An electromagnetic navigation system for tumor excision in breast conserving surgery has recently been developed. Preoperatively, a hooked needle is positioned in the tumor and the tumor boundaries are defined in the needle coordinate system. The needle is tracked electromagnetically throughout the procedure to localize the tumor. However, the needle may move and the tissue may deform, leading to errors in maintaining a correct excision boundary. It is imperative to quantify these errors so the surgeon can choose an appropriate resection margin. Methods: A commercial breast biopsy phantom with several inclusions was used. Location and shape of a lesion before and after mechanical deformation were determined using 3D ultrasound. Tumor location and shape were estimated from the initial contours and tracking data. The difference in estimated and actual location and shape of the lesion after deformation was quantified using the Hausdorff distance. Data collection and analysis were done using our 3D Slicer software application and PLUIIS toolkit. Results: The deformation of the breast resulted in 3.72 mm (STD 0.67 mm) average boundary displacement for an isoelectric lesion and 3.88 mm (STD 0.43 mm) for a hyperelastic lesion. The difference between the actual and estimated tracked tumor boundary was 0.88 mm (STD 0.20 mm) for the isoelectric and 1.78 mm (STD 0.18 mm) for the hyperelastic lesion. Conclusion: The average lesion boundary tracking error was below 2mm, which is clinically acceptable. We suspect that stiffness of the phantom tissue effected the error measurements. This will be validated in patient studies.
Diaphragm motion characterization using chest motion data for biomechanics-based lung tumor tracking during EBRT

Elham Karami, Western Univ. (Canada) and Robarts Research Institute (Canada); Stewart Gaede, Western Univ. (Canada) and London Regional Cancer Program (Canada); Ting-Yim Lee, Western Univ. (Canada) and Robarts Research Institute (Canada) and Lawson Health Research Institute (Canada); Abbas Samani, Western Univ. (Canada) and Robarts Research Institute (Canada)

Despite recent advances in image-guided interventions, lung cancer External Beam Radiation Therapy (EBRT) is still highly challenging due to respiration induced tumor motion. Real-time tumor tracking is known to be the optimal solution for this problem. As such, we propose a biomechanics-based real-time tumor tracking method for effective lung cancer EBRT. In the proposed algorithm, the required boundary conditions for the lung Finite Element model, including diaphragm motion, are obtained using the chest surface motion as a surrogate signal. The primary objective of this paper is to demonstrate the feasibility of developing a function which is capable of inputting the chest surface motion data and outputting the diaphragm motion in real-time. For this purpose, after quantifying the diaphragm motion with a Principle Component Analysis (PCA) model, correlation coefficients between the model parameters of diaphragm motion and chest motion data were obtained through linear regression. Preliminary results obtained in this study indicate that more than one external fiducial marker is required to accurately obtain the PCA-based diaphragm motion parameters through chest surface motion tracking. Multiple linear regression analysis indicates that when 5 chest motion signals are combined, the PCA-based diaphragm motion parameters are highly correlated with the combined signal with R-squared value of 0.996±0.003.

Determination of surgical variables using an android application for a brain shift correction pipeline used in image guided neurosurgery

Rohan C. Vijayan, Rebekah H. Conley, Logan W. Clements, Reid C. Thompson M.D., Michael I. Miga, Vanderbilt Univ. (United States)

Brain shift describes the deformation that the brain undergoes from mechanical and physiological effects typically during a surgical or interventional procedure. With respect to image guidance techniques, brain shift has been shown to compromise the fidelity of these approaches. In recent work, a computational pipeline was developed to predict “brain shift” based on preoperatively determined surgical variables (such as head orientation), and subsequently correct preoperative images to more closely match the intraoperative state of the brain. However, a clinical workflow difficulty in the execution of this pipeline has been acquiring the surgical variables by the neurosurgeon prior to surgery. In order to simplify and expedite this process, an Android, Java-based application designed for tablets was developed to provide the neurosurgeon with the ability to orient 3D computer graphic models of the patient’s head, determine expected location and size of the craniotomy, and provide the trajectory into the tumor. These variables are exported for use as inputs for the biomechanical models of the preoperative computing phase for the brain shift correction pipeline. The accuracy of the application’s exported data was determined by comparing it to data acquired from the physical execution of the surgeon’s plan on a phantom head. Results indicated good overlap of craniotomy predictions, craniotomy centroid locations, and estimates of patient’s head orientation with respect to gravity. With respect to the mock intraoperative setup for testing, improvement in the medial-lateral axis rotation of the head phantom is needed.

Non-rigid point set registration of curves: registration of the superficial vessel centerlines of the brain

Filipe M. Marreiros, Linköping Univ. (Sweden) and Ctr. for Medical Image Science and Visualization (Sweden); Chunliang Wang, KTH Royal Institute of Technology (Sweden); Sandro Rossitti, Region Östergötland (Sweden); Örjan Smedby, KTH Royal Institute of Technology (Sweden)

In this study we evaluate the registration of 3D superficial vessels of the brain. Non-rigid registration methods were used to match vessel centerline points. A combination of the Coherent Point Drift (CPD) and the Thin-Plate Spline (TPS) semilandmarks is proposed. The CPD is used to perform the initial matching of centerline 3D points, while the semilandmark method iteratively relaxes/slides the points.

For the evaluation, a Magnetic Resonance Angiography (MRA) image was used. Deformations were applied to the extracted vessels centerlines to simulate brain bulging and sinking, using a TPS deformation where a few control points were manipulated to obtain the desired transformation (T1). Once the correspondences are known, the corresponding points are used to define a new TPS deformation(T2). The errors are measured in the deformed space, by transforming the original points using T1 and T2 and measuring the distance between them. To simulate cases where the deformed vessel data is incomplete, parts of the reference vessels were cut and then deformed. Furthermore, anisotropic normally distributed noise was added. The results show that the error estimates (root mean square deviation and average error) are below 1 mm, even in the presence of noise and incomplete data.

A novel craniotomy simulation system for evaluation of stereo-pair reconstruction fidelity and tracking

Xiaochen Yang, Logan W. Clements, Rebekah H. Conley, Reid C. Thompson M.D., Benoit M. Dawant, Michael I. Miga, Vanderbilt Univ. (United States)

Brain shift compensation using computer modeling strategies is an important research area in the field of image-guided neurosurgery (iGNS). One important source of available sparse data during surgery to drive these frameworks is deformation tracking of the visible cortical surface. Possible methods to measure intra-operative cortical displacement include laser range scanners (LRS), which typically complicate the clinical workflow, and reconstruction of cortical surfaces from stereo pairs acquired with the operating microscopes. In this work, we propose and demonstrate a craniotomy simulation device that permits simulating realistic cortical displacements designed to measure and validate proposed intra-operative cortical shift measurement systems. The device permits 3D deformations of a mock cortical surface which consists of a membrane made of a Dragon Skin® high performance silicone rubber on which vascular patterns are drawn. We then use this device to validate our stereo pair-based surface reconstruction system by comparing landmark positions and displacements measured with our systems to those positions and displacements as measured by a stylus tracked by a commercial optical system. Our results show a 1mm average difference in localization error and a 1.2mm average difference in displacement. These results suggest that our stereo-pair technique is accurate enough for estimating intra-operative displacements in near real-time without affecting the surgical workflow.
Structure sensor for mobile markerless augmented reality

Thomas Kilgus, Deutsches Krebsforschungszentrum (Germany); Roland Bux, Ruprecht-Karls-Univ. Heidelberg (Germany); Alfred M. Franz, Wibke Johnen, Eric Heim, Markus Fangerau, Michael Müller, Deutsches Krebsforschungszentrum (Germany); Kathrin Yen, Ruprecht-Karls-Univ. Heidelberg (Germany); Lena Maier-Hein, Deutsches Krebsforschungszentrum (Germany)

3D Visualization of anatomical data is an integral part of diagnostics and treatment in many medical disciplines, such as radiology, surgery and forensic medicine. To enable intuitive interaction with the data, we recently proposed a new concept for on-patient visualization of medical data which involves rendering of subsurface structures on a mobile display that can be moved along the human body. The data fusion is achieved with a range imaging device attached to the display. The range data is used to register static 3D medical imaging data with the patient body based on a surface matching algorithm. However, our previous prototype was based on the Microsoft Kinect camera and thus required a cable connection to acquire color and depth data. The contribution of this paper is two-fold. Firstly, we replace the Kinect with the Structure Sensor - a novel cable-free range imaging device - to improve handling and user experience and show that the resulting accuracy (target registration error: 4.8 ± 1.5 mm) is comparable to that achieved with the Kinect. Secondly, a new approach to visualizing complex 3D anatomy based on this device, as well as 3D printed models of anatomical surfaces, is presented. We demonstrate that our concept can be applied to in-vivo data and to a 3D printed skull of a forensic case. Our new device is the next step towards clinical integration and shows that the concept can be applied for a wide range of applications such as presentation of forensic data to laypeople in court or medical education.

Visual design and verification tool for collision-free dexterous patient specific neurosurgical instruments

Margaret A. Hess, Lab. for Percutaneous Surgery (Canada); Kyle W. Eastwood, Univ. of Toronto (Canada); Bence Linder, Queen’s Univ. (Canada); Vivek Bodani, Univ. of Toronto (Canada); Andras Lasso, Queens Univ. (Canada); Thomas Looi, The Hospital for Sick Children (SickKids) (Canada); Gabor Fichtinger, Queen’s Univ. (Canada); James Drake, The Hospital for Sick Children (SickKids) (Canada)

Many minimally invasive neurosurgical (MIN) procedures require surgeons to perform complex maneuvers within small, convoluted workspaces using straight instruments with limited dexterity. For example, patients with pineal region tumors and swelling of the cerebral ventricles are treated through a single entry point with a rigid tool. It is difficult for surgeons to reach the multiple surgical targets required for treatment. To address this problem, continuum tools made from multiple pre-curved tubes are under development to create highly dexterous instruments. Designing these devices is not trivial and relies heavily upon surgeon input. Thus, a user friendly design process is essential. Methods: We propose a method to design patient and procedure specific continuum tools through simulation, allowing visual verification. Our software allows for input and visualization of pre-operative scans and patient models. In the virtual patient, a trocar with multiple continuum tools is modeled. Design parameters for the tools, such as segment number, can be specified in the user interface. By modifying points on the tool models, the tools are automatically re-shaped and reconfigured. The tool shape and entry points are then optimized. Results:

Tool models were designed for two intraventricular endoscopic procedures. The software was tested and validated by two neurosurgeons. Conclusion: Our software enables user-friendly visual design and verification of custom MIN instruments.

Kinect based real-time position calibration for nasal endoscopic surgical navigation system

Jingfan Fan, Jian Yang, Yakui Chu, Shaodong Ma, Yongtian Wang, Beijing Institute of Technology (China)

Unanticipated, reactive motion of the patient during skull based tumor resective surgery is the source of the consequence that the nasal endoscopic tracking system is compelled to be recalibrated. To accommodate the calibration process with patient’s movement, this paper developed a Kinect based Real-time positional calibration method for nasal endoscopic surgical navigation system. In this method, a Kinect scanner was employed as the imaging device attached to the display. The range data is used to register static 3D medical imaging data with the patient body based on a surface matching algorithm. However, our previous prototype was based on the Microsoft Kinect camera and thus required a cable connection to acquire color and depth data. The contribution of this paper is two-fold. Firstly, we replace the Kinect with the Structure Sensor - a novel cable-free range imaging device - to improve handling and user experience and show that the resulting accuracy (target registration error: 4.8 ± 1.5 mm) is comparable to that achieved with the Kinect. Secondly, a new approach to visualizing complex 3D anatomy based on this device, as well as 3D printed models of anatomical surfaces, is presented. We demonstrate that our concept can be applied to in-vivo data and to a 3D printed skull of a forensic case. Our new device is the next step towards clinical integration and shows that the concept can be applied for a wide range of applications such as presentation of forensic data to laypeople in court or medical education.

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Tool models were designed for two intraventricular endoscopic procedures. The software was tested and validated by two neurosurgeons. Conclusion: Our software enables user-friendly visual design and verification of custom MIN instruments.
An improved robust hand-eye calibration for endoscopy navigation system

Wei He, Kumsok Kang, Yanfang Li, Weili Shi, Yu Miao, Fei He, Fei Yan, Huamin Yang, Changchun Univ. of Science and Technology (China); Kensaku Mori, Nagoya Univ. (Japan); Zhengang Jiang, Changchun Univ. of Science and Technology (China)

Endoscopy is widely used in clinical application, and surgical navigation system is an extremely important way to enhance the safety of endoscopy. The key to improve the accuracy of the navigation system is to solve the positional relationship between the camera and tracking marker precisely. The problem can be solved by the hand-eye calibration method based on dual quaternions. However, because of the tracking error and the limited motion of the endoscope, the sample motions algorithm needs may contain some parallel and coaxial motions. Those motions can lead to the algorithm becomes unstable and inaccurate. Therefore the advanced selection rule of sample motion is proposed in this paper to avoid these problems. Three thresholds are proposed to filter out the parallel and coaxial motions from all possible motions composed of any two different poses.

In order to assess the effect of the selection rule of sample motions, the dual quaternions hand-eye calibration algorithm and one non dual quaternions algorithm have been implemented in our experiments. Then, these two algorithms have been assessed in two ways. In the first way, the coordinates of cross points of the chess-grid on the chess-grid frame have been computed, which do not take into account the intrinsic parameter and distortion of camera. In the second way, the coordinates of the center of five markers in the optical sensor frame have been compared by considering the intrinsic parameter and distortion of camera.

The experimental results show that the accuracy and stability of algorithm have been effectively improved by selecting sample motion data automatically.

Toward robust specularity detection and inpainting in cardiac images

Samar Alsaled, The George Washington Univ. (United States); Angelica Aviles, Pilar Sobrevilla, Alicia Casals, Univ. Politècnica de Catalunya (Spain)

Computer-assisted cardiac surgeries had major advances throughout the years and are gaining more popularity over conventional cardiac procedures as they offer many benefits to both patients and surgeons. One obvious advantage is that they enable surgeons to perform delicate tasks on the heart while it is still beating avoiding the risks associated with cardiac arrest. Consequently, the surgical system needs to accurately compensate the physiological motion of the heart which is a very challenging task in medical robotics since there exist different sources of disturbances. One of which is the bright light reflections, known as specular highlights, that appear on the glossy surface of the heart and partially occlude the field of view. This work is focused on developing a robust approach that accurately detects and removes those highlights to reduce their disturbance to the surgeon and the motion compensation algorithm. As a first step, we exploit color attributes and wavelet modulus maxima jointly to detect specular regions in each acquired image frame. These two techniques together work as restricted thresholding and are able to accurately identify specular regions. Then, in order to eliminate the specularity artifact and give the surgeon better perception of the heart, the second part of our solution is dedicated to correct the detected regions using a two level inpainting to propagate and smooth the boundary. Our experimental results, which we carry out in realistic datasets, reveal how efficient and precise the proposed solution is, as well as demonstrate its robustness and real-time performance.

Real-time mosaicing of fetoscopic images

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Fetoscopic laser photo-coagulation of the placental vascular anastomoses remains the most effective therapy for twin-to-twin transfusion syndrome (TTTS) in monochorionic twin pregnancies. However, to ensure the success of the intervention, complete closure of all anastomoses is needed. This is made difficult by the limited field of view of the fetoscopic video guidance, which hinders the surgeon’s ability to locate all the anastomoses. A potential solution to this problem is to expand the field of view of the placental surface by creating a mosaic from overlapping fetoscopic images. This mosaic can then be used for anastomoses localization and spatial orientation during surgery. However, this requires accurate and fast algorithms that can operate within the real-time constraints of fetal surgery. In this work, we present an image mosaicing framework that leverages the parallelism of modern GPUs and can process clinical fetoscopic images in real time. Initial qualitative results indicate that the proposed framework can generate clinically useful mosaics from fetoscopic videos in real time.

Multiple video sequences synchronization during minimally invasive surgery

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Since the introduction of laparoscopy in 1902, minimally invasive surgery (MIS) has been evolving and has expanded dramatically over the past two decades. This expansion can mainly be attributed to the exponential growth in technology and the evolution of laparoscopic instrumentation over this period of time. In order to assist the surgeons during such surgery, the augmented reality technology is integrated into an operating room (OR). To perform that, the information data flowing in OR and gathered from different medical devices should be collected. In this paper, we propose a hardware platform dedicated to multiple video sequence synchronization. This latter is necessary for any computer vision application that integrates data from multiple simultaneously recorded video sequences. With the increased availability of video cameras in OR, a large volume of video data is available for processing by a growing range of computer vision applications that process multiple video sequences. To ensure that the output of these applications is correct, accurate video sequence synchronization is essential. A hardware synchronization approach is implemented which can embed timestamps into each sequence on-the-fly and requires no post-processing. However, it requires specialized hardware and it is necessary to set up the camera network in advance. In this paper, we discuss its performances.

Visualization framework for colonoscopy videos from Stony Brook University

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We present a visualization framework for annotating and comparing colonoscopy videos and these annotations can also be used for semi-
automatic report generation at the end of the procedure. Currently, in the US there are approximately 14 million colonoscopies every year. In this work, we create a visualization tool to deal with the deluge of colonoscopy videos in a more effective way. We present an interactive visualization framework for the annotation and tagging of colonoscopy videos in an easy and intuitive way. These annotations and tags can later be used for report generation for EMR purposes and for comparison at an individual as well as group level. We also present important use cases and medical expert feedback for our visualization framework.

9786-65, Session PSMon

High-performance computing (HPC) enabled real-time remote processing of laparoscopic surgery

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Small incisions, such as those in laparoscopic surgery, have a disadvantage of limited visualization of subsurface tissues. Image-guided surgery (IGS) uses pre-operative and intra-operative images to map subsurface structures. One particular laparoscopic system is the da Vinci-si robotic surgical system, which uses stereo high-definition (HD) laparoscopic cameras. The video streams generate approximately 360 megabytes of data per second. Real-time processing this large stream of data on a bedside PC, single or dual node setup, has become challenging and a high-performance computing (HPC) environment may not always be available at the point of care. To process this data on remote HPC clusters at the typical 30 frames per second rate, it is required that each 11.9 MB video frame be processed by a server and returned within 1/30th of a second.

We have implemented and compared performance of compression, segmentation and registration algorithms on Clemson's Palmetto supercomputer with 2 NVIDIA K40 GPUs per node. Our computing framework will also enable reliability using replication of computation. We will securely transfer the files to remote HPC clusters using an OpenFlow-based network service, Steroid OpenFlow Service (SOS) that can increase performance of large data transfers over long-distance and high bandwidth networks. As a result, using high-speed OpenFlow-based network to access computing clusters with GPUs will improve surgical procedures by providing real-time medical image processing and laparoscopic data.

9786-66, Session PSMon

Content-based retrieval in videos from laparoscopic surgery

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In the field of medical endoscopy more and more surgeons are changing over to record and store videos of their endoscopic procedures for long-term archival. These endoscopic videos are a good source of information for explanations to patients and follow-up operations. As the endoscope is the "eye of the surgeon", the video shows the same information the surgeon has seen during the operation, and can describe the situation inside the patient much more precisely than an operation report would do. Recorded endoscopic videos can also be used for training young surgeons and in some countries the long-term archival of video recordings from endoscopic procedures is even enforced by law (e.g., The Netherlands). A big problem, however, is to efficiently use these videos for later purposes since multimedia systems with sufficient support are not available yet. One problem, for example, is to locate specific images in the videos that show important situations, which are typically also captured as static images during the procedure. This work addresses this problem and focuses on content-based video retrieval in data from laparoscopic surgery. We propose to use special version of feature signatures, which can appropriately and concisely describe the content of laparoscopic images, and show that by using this content descriptor with an appropriate metric, we are able to efficiently perform content-based retrieval in laparoscopic videos. In a dataset with 600 captured static images from 33 hours recordings, we are able to find the correct video segment for more than 95% of these images.

9786-67, Session PSMon

Cost-effective surgical registration using consumer depth cameras

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The high costs associated with technological innovation have been previously identified as both a major contributor to the rise of healthcare expenses, and as a limitation for widespread adoption of new technologies. In this work we evaluate the use of two consumer grade depth cameras, the Microsoft Kinect v1 and 3DSystems' Sense, as a means for acquiring point clouds for registration. These devices have the potential to replace professional grade laser range scanning devices in medical interventions that do not require sub-millimetric registration accuracy, and may do so at a significantly reduced cost. To facilitate the use of these devices we have developed a near real-time (1-4 sec/frame) rigid registration framework combining several initialization approaches with the Iterative Closest Point algorithm. Using surface registration error as our evaluation criterion we found the optimal scanning distances for the Sense and Kinect to be 50-60cm and 70-80cm respectively. When imaging a skull phantom at these distances, RMS error values of 1.35mm and 1.14mm were obtained. The registration framework was then evaluated using two clinical cranial MR scans. On the first subject, the average (n=70 depth images) RMS error using the Sense was 1.22mm. Using the Kinect this error was 1.24mm (n=108 depth images). On the second subject, whose MR scan was significantly corrupted by metal implants, the errors increased to 1.82mm (n=81) and 1.74mm (n=90), which are still within the clinically acceptable error range.

9786-68, Session PSMon

Exploring the effects of dimensionality reduction in deep networks for force estimation in robotic-assisted surgery

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Robotic-Assisted Surgery approach overcomes the limitations of the traditional laparoscopic and open surgeries. However, one of its major limitations is the lack of force feedback. Since there is no direct interaction between the surgeon and the tissue, there is no way of knowing how much force the surgeon is applying which can result in irreversible injuries. The use of force sensor is not practical since they impose different constraints. Thus, we make use of a neuro-visual approach to estimate the applied forces, in which the 3D shape recovery together with geometry of motion are used as input to a deep network based on LSTM-RNN architecture. When deep networks are used in real-time, pre-processing of data is a key factor to reduce complexity and improve the network performance. A common pre-processing is dimensionality reduction which attempts to eliminate redundant and insignificant information by selecting a subset of relevant features to use in model construction. In this work, we show the effects of dimensionality reduction in a real-time application: estimating the applied force in Robotic-Assisted Surgeries. According to the results, we
demonstrate positive effects on the deep network including faster training, improved network performance, and overfitting prevention. We also show a significant percentage of accuracy improvement, ranging from about 54% to 78%, over existing approaches related to force estimation.

9786-69, Session PSMon

Current sensing for navigated electrosurgery: proof of concept

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PURPOSE: Tracked power-tools are routinely used in computer-assisted intervention and surgical systems. In order to properly perform temporal and spatial monitoring of the tracked tool with the navigation system, it is important to know when the tool, such as an electrosurgical cautery, is being activated during surgery. We have developed a general purpose current sensor that can be augmented to tracked surgical devices in order to inform the surgeon and the navigation system when the tool is activated.

METHODS: Two non-invasive AC current sensors, two peak detector circuits, one voltage comparator circuit, and a microcontroller were used to detect when an electrosurgical cautery is being powered on and differentiate between the cut and coagulation modes. The system was tested by comparing various substances at varied power ratings. RESULTS: By comparing the ratio of amplitudes as well as the frequencies of the signals, the current sensing system is able to differentiate between on/off, cut/coagulation, as well as when a cautery is being powered on and in the future could be integrated with a navigation system in order to easily temporally monitor the electrosurgical tool.

9786-70, Session PSMon

Characterization of a phantom setup for breast conserving cancer surgery

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The purpose of this work is to develop an anatomically and mechanically representative breast phantom for the validation of breast conserving surgical therapies, specifically, in this case, image guided surgeries. Using three patients scheduled for lumpectomy and four healthy volunteers in mock surgical presentations, the magnitude, direction, and location of breast deformations was analyzed. A phantom setup was then designed to approximate such deformations in a mock surgical environment. Specifically, commercial and custom-built polyvinyl alcohol (PVA) phantoms were created to mimic breast tissue during surgery. A custom designed deformation apparatus was then created to reproduce deformations seen in typical clinical setups of the pre- and intra-operative breast geometry. Quantitative analysis of the human subjects yielded a positive correlation between breast volume and amount of breast deformation. Phantom results reflected similar behavior with the custom-built PVA phantom outperforming the commercial phantom. Material property improvements are necessary to better match clinical conditions.

9786-71, Session PSMon

Image-guided intracranial cannula placement for awake in vivo microdialysis in nonhuman primates

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Intracranial microdialysis is used for sampling neurochemicals and large peptides along with their metabolites from the interstitial fluid (ISF) of the brain. The ability to perform this in nonhuman primates (NHP) for e.g., rhesus could improve the prediction of pharmacokinetic (PK) and pharmacodynamics (PD) action of drugs in humans. However, microdialysis in rhesus brain is not as routinely performed as in rodents. One of the challenges is that the precise intracranial probe placement in NHP brains is made difficult due to the richness of anatomical structure and variability of size and shape of brains across animals. Also a repeatable and reproducible ISF sampling from the same animal is highly desirable when combined with cognitive behaviors or other longitudinal study end points. Toward that end, we have developed a semi-automatic flexible neurosurgical method employing MR and CT imaging to (a) derive coordinates for permanent guide cannula placement in mid brain structures and (b) fabricate a custom recording chamber to implant above the skull for enclosing and safeguarding the access to the cannula for repeated experiments. In order to place the intracranial guide cannula in each subject the entry points in the skull and the depth in the brain was derived using co-registered images acquired from MR and CT scans. The anterior / posterior (A/P) and medio-lateral (M/L) rotation in the pose of the animal was corrected in the 3D image to appropriately represent the pose used in the stereotactic frame. An array of implanted fiducial markers was used to transform stereotactic coordinates to the images and vice versa. The recording chamber was custom fabricated using computer-aided design (CAD), such that it would fit the contours of the individual skull with minimum error. The chamber also helped in guiding the cannula through the entry points down a trajectory into the depth of the brain. We have validated our method in three animals and our results indicate average placement error of cannula to be 1.03 mm (+/- SEM) of the target area. The method employed here for generation of the coordinates, surgical implantation and post implant validation is built using traditional access to surgical and imaging methods without the necessity of intra-operative imaging. The validation of our method lends support to its wider application in most nonhuman primate laboratories with onsite MR and CT imaging capabilities.

9786-72, Session PSMon

Patch-based label fusion for automatic multi-atlas-based prostate segmentation in MR images

Xiaofeng Yang, Peter J. Rossi, Ashesh B. Jani, Hui Mao, Walter J. Curran, Tian Liu, Emory Univ. (United States)

We propose a 3D multi-atlas-based prostate segmentation method for MR images, which is based on patch-based label fusion strategy. The atlases with the most similar appearance are selected to serve as the best subjects in the label fusion. A local patch-based atlas fusion is performed using voxel weighting based on anatomical signature. Our segmentation technique was validated with a clinical study of 13 patients. The accuracy of our approach was assessed using the manual segmentation (gold standard). Dice volumetric overlapping accuracy was used to quantify the difference between the automatic and manual segmentation. We have developed a
new prostate MR segmentation approach based on nonlocal patch-based label fusion, demonstrated its clinical feasibility, and validated its accuracy with manual segmentation.

9786-73, Session PSMon
Phantom-based ground truth generation for cerebral vessel segmentation and pulsatile deformation analysis
Daniel Schetelig, Dennis Säring, Till Illies, Jan Sedlacik, Fabian Kording, René Werner, Univ. Medical Ctr. Hamburg-Eppendorf (Germany)

Hemodynamic and mechanical factors of the vascular system are assumed to play a major role in understanding, e.g., initiation, growth and rupture of cerebral aneurysms. Among those factors, cardiac cycle-related pulsatile motion and deformation of cerebral vessels currently attract much interest. However, imaging of those effects requires very high spatial and temporal resolution and remains challenging – and similarly does the analysis of the acquired images: Flow velocity changes and contrast media inflow cause vessel intensity variations in related temporally resolved computed tomography angiography and magnetic resonance angiography data over the cardiac cycle and impede application of intensity threshold-based segmentation and subsequent motion analysis.

In this work, a flow phantom for generation of ground-truth images for evaluation of appropriate segmentation and motion analysis algorithms is developed. The acquired ground-truth data is used to illustrate the interplay between intensity fluctuations and (erroneous) motion quantification by simple threshold-based segmentation, and an adaptive threshold-based segmentation approach is proposed that alleviates respective issues. The results of the phantom study are further demonstrated to be transferable to patient data.

9786-74, Session PSMon
A general approach to liver lesion segmentation in CT images
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Lesion segmentation has remained a challenge in different body regions. Generalizability is lacking in published methods as such variability in results is common, even for a given organ and modality, and it becomes difficult to establish standardized methods of disease quantification and reporting. This paper makes an attempt at a generalizable method based on classifying lesions along with their background into groups using clinically used visual attributes. Using an Iterative Relative Fuzzy Connectedness (IRFC) delineation engine, the ideas are implemented for the task of liver lesion segmentation in CT images. For lesion groups with the same background properties, a few subjects are chosen as the training set to obtain the optimal IRFC parameters for the background tissue components. For lesion groups with similar foreground properties, optimal foreground parameters for IRFC are set as the median intensity value of the training lesion subset. To segment liver lesions belonging to a certain group, the devised method requires manual loading of the corresponding parameters, and correct setting of the foreground and background seeds. The segmentation is then completed in seconds. Segmentation accuracy and repeatability with respect to seed specification are evaluated. Accuracy is assessed by the assignment of a delineation quality score (DQS) to each case. Inter-operator repeatability is assessed by the difference between segmentations carried out independently by two operators. Experiments on 80 liver lesion cases show that the proposed method achieves a mean DQS score of 4.03 and inter-operator repeatability of 92.3%.

9786-75, Session PSMon
A comparison study of atlas-based 3D cardiac MRI segmentation: global versus local and global transformations
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Magnetic Resonance Imaging (MRI) is a standard-of-care imaging modality for cardiac function assessment and guidance of cardiac interventions due to the high image quality and lack of exposure to ionizing radiation. Cardiac health parameters such as left ventricular volume, ejection fraction, myocardial mass, thickness, and strain can be assessed by segmenting the heart from cardiac MRI images. Furthermore, the segmented pre-operative and post-operative cardiac models can be used to precisely identify regions of interest during the minimally invasive therapy. Hence, the use of accurate and computationally efficient segmentation techniques is critical, especially for intra-procedural guidance applications that rely on the peri-operative segmentation of subject-specific datasets without delaying the procedure workflow. Atlas-based segmentation incorporates the prior knowledge of the anatomy of interest from expertly annotated image datasets. Typically, the ground truth atlas label is propagated to a test subject as a segmentation mask via non-rigid registration. The high computational cost of non-rigid registration motivated us to obtain an initial segmentation using global transformations based on an atlas of the left ventricle from a population of patient MRI images and refine it using well-developed techniques such as Level Set or Graph Cuts. Here we quantitatively compare the segmentations obtained from the global and global plus local atlases with the expert segmentations according to several similarity metrics, including Dice correlation coefficient, Hausdorff distance, and Mean absolute distance error.

9786-76, Session PSMon
Surface mesh to voxel data registration for patient-specific anatomical modelling
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Virtual Physiological Human (VPH) models are frequently used for training, planning, and performing medical procedures. We suggest patient-specific VPH models that are composed by registering the general mesh-based models with patient voxel data-based recordings. The processing pipeline is composed of different freely available toolboxes such as MatLab, the open Simulation framework (SOFA), and MeshLab. The approach of Gilles is applied for mesh-to-voxel registration. Personalized VPH models include anatomical as well as mechanical properties of the tissues. Specifically, the pelvis region has been focused for the femoral nerve block. Here, patient-specific models are used in virtual and augmented reality for training and assistance, respectively. Individualized models enrich the virtual training tools for learning and improving regional anaesthesia (RA) skills. The Regional Anaesthesia Simulator and Assistant (RASimAs) project has the goal of increasing the application and effectiveness of RA by combining a simulator ultrasound-guided and electrical nerve-stimulated through an integration of image processing, physiological models, and subject-specific data, and virtual reality. Two commercial VPH models (Zygote and Anatomy) were used together with 34 MRI datasets. Results are presented for the skin surface and pelvic bones. Future work will extend the registration procedure to cope with all model tissue (i.e. skin, muscle, bone, vessel, nerve, fascia) in a one-step procedure and extrapolating the personalized models to body regions actually being out of the captured field of view.
9786-77, Session PSMon

**Estimation of line-based target registration error**

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We present a method for estimating target registration error (TRE) in point-to-line registration. We develop a spatial stiffness model of the registration problem and derive the stiffness matrix of the model which leads to an analytic expression for predicting the root-mean-square TRE. Under the assumption of isotropic localization noise, we show that the stiffness matrix for line-based registration is equal to the difference of the stiffness matrices for fiducial registration and surface-based registration. The expression for TRE is validated in the context of freehand ultrasound calibration performed using a tracked line fiducial as a calibration phantom. Measurements taken during calibration of a tracked linear ultrasound probe were used in simulations to assess TRE of point-to-line registration and the results were compared to the values predicted by the analytic expression. The difference between predicted and simulated TRE magnitude for targets near the registration point centroid was less than 2.4% of the simulated magnitude when using more than 5 registration points. When using an approximately uniform spatial sampling of registration points, the minimum TRE magnitude was found near the centroid of the registration points and the isocontours of TRE were elliptical in shape. For \( n \geq 12 \) registration points, the number of registration points has only a small effect on the RMS TRE for targets near the registration point centroid; however, the rate at which TRE increases as the target location moves away from the centroid is affected by the number of registration points.

9786-78, Session PSMon

**Learning-based MRI-CT registration using patch-deformation dictionary for image-guided prostate radiotherapy**

Xiaofeng Yang, Peter J. Rossi, Hui Mao, Ashesh B. Jani, Walter J. Curran, Tian Liu, Emory Univ. (United States)

We propose a new patch-based initial deformation prediction framework for prostate MRI-CT registration to improve the performance of the existing registrations. The sparse representation technique is used to estimate the initial deformation between MR and CT in a patch-wise fashion. This method provides a predicted field for initializing prostate MR-CT registration. Our proposed registration was compared with the current intensity-based registration technique. We have developed a new prostate MR-CT registration approach based on patch-deformation dictionary, demonstrated its clinical feasibility, and validated its accuracy with some identified landmarks.

9786-79, Session PSMon

**Model-based deformable registration of compressed and uncompressed MRI breast images**

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A model-based method for non-rigid registration of single-modality magnetic resonance images of normal and compressed breast tissue - capturing in the same position- in breast cancer diagnostic/interventional imaging is presented. First, based on segmented pre-operative images, a deformation model of the breast tissue is developed and discretized in the spatial domain using the method of finite element. The compression of the pre-operative image is modeled by applying smooth normal forces on the surface of the breast where compression plates are placed. The applied forces are approximated within a Gaussian summation. Image registration is accomplished by solving an optimization problem. The cost function is a similarity measure between the deformed preoperative image and intra-operative image computed at some control points and the decision variables are the tissue interaction forces. An extension of the Speeded Up Robust Features to 3D is employed to extract control feature points. Sum of squared differences of the image intensities at the control points is the similarity measure minimized in the optimization. Application of the algorithm to clinical breast MR images demonstrates its effectiveness in solving the registration problem.
estimated from iSV using a “trial-and-error” approach, and the cortical shift was measured from iSV through a surface registration method using projected images and an optical flow motion tracking algorithm. The measured displacements were employed to drive the biomechanical brain deformation model, and the estimated whole-brain deformation was subsequently used to deform pMR and produce uMR. We illustrate the method using one patient example. The results show that the uMR aligned well with iSV and the overall misfit between model estimates and measured displacements was 1.46 mm. The overall computational time was ~15 min. including iSV image acquisition, surface registration, modeling, and image warping, with minimal interruption to the surgical flow. Furthermore, we compare uMR against intraoperative MR (iMR) that was acquired following iSV acquisition. Effort is underway to incorporate intraoperative ultrasound (iUS) together with iSV to guide the FEM model.

9786-82, Session PSMon

A fully automatic image-to-world registration method for image-guided procedure with intraoperative imaging updates

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Image-guided procedure with Intraoperative imaging updates has made a big impact on minimally invasive surgery. It allows surgeons to conduct precise operations on updated anatomical structures and improve surgical outcomes. VISIUS Surgical Theater (IMRIS Inc., Minnetoka, MN, USA) is a typical application of this technology, but its huge cost becomes a big hurdle to expand its applications. Mobile CT imaging device combining with current commercial available image guided navigation system is a legitimate and cost-efficient solution for a typical operating room setup. However, the process of manual fiducial-based registration between image and physical spaces (image-to-world) is troublesome for surgeons during the procedure, which results in much procedure interruptions and is the main source of registration errors. A robust registration approach is highly preferred. In this study, we developed a novel method to eliminate the manual registration process. Instead of using probe to manually localize the fiducials during the surgery, a tracking plate with known fiducial positions relative to the reference coordinates is designed and fabricated through 3D printing technique, in which, the orientation of fiducial markers relative to the tracking sensor in physical space was defined through a pre-calibration process and its corresponding orientation in image space was determined through image processing. We also developed an easy-to-use approach for pre-calibration of the tracking plate. The workflow and feasibility of this method has been studied through a phantom experiment. Fiducial registration errors of 0.28-0.39mm were achieved with the calibrated tracking plate and target registration errors were measured on the phantom.

9786-83, Session PSMon

Optimal atlas construction through hierarchical image registration

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Atlases (digital or otherwise) are common in medicine. However, there is no standard framework for creating them. One traditional approach is to pick a representative subject and then proceed to label structures/regions of interest. Another is to create a “mean” or average subject. Atlases may also contain more than a single representative (e.g., the Visible Human contains both a male and a female data set). Other criteria beside gender may be used as well, and the atlas may contain many examples for a given criterion. In this work, we propose that atlases be created in an optimal manner using a well-established graph theoretic approach using a min spanning tree (or more generally, a collection of them). The resulting atlases may contain many examples for a given criterion. In fact, our framework allows for the addition of new subjects to the atlas to allow it to evolve over time. Furthermore, one can apply segmentation methods to the graph (e.g., graph-cut, fuzzy connectedness, or cluster analysis) which allow it to be separated into “sub-atlases” as it evolves. We demonstrate our method by applying it to 50 3D CT data sets of the chest region, and by comparing it to a number of traditional methods using measures such as Mean Squared Difference, Mattes Mutual Information, and Correlation, and for a variety of registration methods such as rigid, affine, and deformable. Our results demonstrate that optimal atlases can be constructed in this manner and they outperform other methods of construction using freely available software.

9786-84, Session PSMon

Fast single slice US-MRI registration for neurosurgical MRI-guided US

Utsav Pardasani, John S. H. Baxter, Terry M. Peters, Ali R. Khan, Robarts Research Institute (Canada)

Image-based ultrasound to magnetic resonance image (US-MRI) registration can be an invaluable tool in image-guided neuronavigation systems. State-of-the-art commercial and research systems utilize image-based registration to assist in functions such as brain-shift correction, image fusion, and probe calibration. Since traditional US-MRI registration uses reconstructed US volumes or a series of tracked US slices, the functionality of this approach can be compromised by the limitations of optical or magnetic tracking systems in the neurosurgical operating room. These drawbacks include ergonomic issues, line-of-sight/magnetic interference, and maintenance of the sterile field. For those seeking a US vendor-agnostic system, these issues are compounded with the challenge of instrumenting the probe without permanent modification and calibrating the probe face to the tracking tool. To address these challenges, this paper explores the feasibility of a real-time US-MRI volume registration in a small virtual craniotomy site using a single slice. We employ the Linear Correlation of Linear Combination (LC2) similarity metric in its patch-based form on data from the Brain Images for Tumour Evaluation (BiTE) dataset as a PyCUDA enabled Python module in Slicer. Though we have not yet achieved near-real-time speeds, we are encouraged by the preliminary results which suggest that future improvements in computation speed may bring us to the goal of trackerless US-MR fusion.

9786-85, Session PSMon

Rapidly-steered single-element ultrasound for real-time volumetric imaging and guidance

Mark Stauber, Craig Western, Stanford Univ. (United States); Roman Solek, Interson, Inc. (United States); Kenneth Salisbury, Stanford Health Care (United States); Dmitri Hristov, Stanford Univ. (United States); Jeffrey Schlosser, SoniTrack Systems (United States)

Volumetric ultrasound (US) imaging has the potential to provide real-time anatomical imaging with high soft-tissue contrast in a variety of diagnostic and therapeutic guidance applications. However, existing volumetric US machines utilize “wobbling” linear phased array or matrix phased array transducers which are costly to manufacture and necessitate bulky external processing units. To drastically reduce cost, improve portability, and reduce footprint, we propose a rapidly-steered single-element volumetric US imaging device. The device uses a multi-directional raster-scan technique to generate a series of two-
We now propose a full multimodal image-based methodology for guiding EBUS. The complete methodology involves two components: 1) a procedure planning protocol that gives bronchoscope movements appropriate for live EBUS positioning; and 2) a guidance strategy and associated system graphical user interface (GUI) designed for image-guided EBUS. We present results demonstrating the operation of the system.

9786-88, Session PSMon

A motorized ultrasound system for MRI-ultrasound fusion guided prostatectomy

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Purpose: This study presents MoTRUS, a motorized transrectal ultrasound system, to enable remote navigation of a transrectal ultrasound (TRUS) probe during da Vinci assisted prostatectomy. MoTRUS not only provides a stable platform to the ultrasound probe, but also allows the physician to navigate it remotely while sitting on the da Vinci console. This study also presents intraoperative MRI-US image fusion capability to bring preoperative MR images to the operating room for the best visualization of the gland, boundaries, nerves, etc. Method: A two degree-of-freedom probe holder is developed to insert and rotate a bi-plane transrectal ultrasound transducer. A custom joystick is made to enable remote navigation of MoTRUS. Safety features have been considered to avoid inadvertent risks (if any) to the patient. Custom design software has been developed to fuse pre-operative MR images to intraoperative ultrasound images acquired by MoTRUS. Results: MoTRUS was evaluated on a patient after taking required consents during prostatectomy. It took 10 min to setup the system in OR. MoTRUS provided similar capability in addition to remote navigation and stable imaging. No complications were observed. Image fusion was evaluated on a commercial prostate phantom. Conclusions: Motorized navigation of the TRUS probe during prostatectomy is safe and feasible. Remote navigation provides physician with a more precise and easier control of the ultrasound image while removing the burden of manual manipulation of the probe. Image fusion improved visualization of the prostate and boundaries in phantom study.

9786-89, Session PSMon

Visualization of hepatic arteries with 3D ultrasound during intra-arterial therapies

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Liver cancer represents the second most common cause of cancer-related mortality worldwide. The prognosis is quite poor with an overall mortality of 95%. Moreover, most hepatic tumors are unreatachable due to the advanced stage of the tumor or an insufficient underlying liver function. Tumor embolization by intra-arterial approaches is currently the standard therapeutic approach for advanced cases of hepatocellular carcinoma. These therapies rely on the fact that the blood supply of these tumors is for the most part of arterial origin. Real-time feedback on blood flow velocities in the hepatic arteries is crucial to insure maximal treatment efficiency on the targeted masses. Depending on those velocities, a modulation of the injection rate is performed to allow for an optimal infusion of intra-arterial chemotherapy into the tumorous tissue. While Doppler ultrasound is a well-documented technique for the assessment of blood flow, 3D visualization of vascular anatomy with ultrasound remains challenging. In this paper we present an image-guidance pipeline that enables the localization of the hepatic arterial branches within a 3D ultrasound image of the liver. A diagnostic MR angiography (MRA) is first processed to automatically...
segment the hepatic arteries. A non-rigid registration method is then applied on the portal phase of the MRA volume with a 3D ultrasound to enable the visualization of the 3D mesh of the hepatic arteries in the Doppler images. To evaluate the performance of the proposed workflow, we illustrate initial results on porcine models and patient images.

9786-90, Session PSMon

Comparison of portable and conventional ultrasound imaging in spinal curvature measurement

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PURPOSE: In scoliosis monitoring, tracked ultrasound has been explored as a safer imaging alternative to traditional radiography. Use of ultrasound in spinal curvature measurement requires identification of vertebral landmarks, but bones have reduced visibility in ultrasound imaging and high quality ultrasound machines are often expensive and not portable. In this work, we investigate the image quality and measurement accuracy of a low cost and portable ultrasound machine in comparison to a standard ultrasound machine in scoliosis monitoring. METHODS: Two ultrasound machines were tested on three human subjects, using the same position tracker and software. Spinal curves were measured in the same reference coordinate system using both ultrasound machines. Lines were defined by connecting two symmetric landmarks identified on the left and right transverse process of the same vertebrae, and spinal curvature was defined as the transverse process angle between two such lines, projected on the coronal plane. RESULTS: Three healthy volunteers were scanned by both ultrasound configurations. The mean difference per transverse process angle measured was 2.95 ± 2.09°. Inter-observer error in the Telemed was 4.48° and 4.30° in the Sonix Touch. 88% of transverse processes visualized in the Sonix Touch were also visible in the Telemed. CONCLUSION: Price, convenience and accessibility suggest the Telemed to be a viable alternative in scoliosis monitoring, however further improvements in measurement protocol and image noise reduction must be completed before implementing the Telemed in the clinical setting.

9786-91, Session PSMon

3D shape tracking of minimally invasive medical instruments using optical frequency domain reflectometry

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The guidance of minimally invasive medical instruments such as needles or catheters (ex. by adding them a piezoelectric coating) has been the focus of extensive research in the past decades. Real-time tracking of instruments in medical interventions facilitates the insertion of these instruments and help the user to reach a pre-localized target more precisely. Image-guided systems using ultrasound imaging and shape sensors based on fiber Bragg gratings (FBG) embedded optical fibers can provide retroactive feedback to the user in order to reach the targeted areas with even more precision. However, ultrasound imaging with electro-magnetic tracking cannot be used in the MR suite, while shape sensors based on FBG embedded optical fibers gives discrete values of the instrument position, which mean approximations are needed to evaluate its global shape. Here, we propose a new alternative to provide real-time device tracking during minimally invasive interventions using a truly-distributed strain sensor based on optical frequency domain reflectometry (OFDR) in optical fibers. Since the strain is proportional to the curvature radius of the fiber, a distributed strain sensor can provide the three-dimensional shape of medical instruments by simply inserting fibers inside the devices. To orientate the shape of the needle in the tracking frame, 3 fibers glued in a specific geometry are used, providing 3 degrees of freedom along the fiber. Real-time tracking of medical instruments is thus obtained and can clearly be of clinical value for monitoring the remotely controlled catheter or needle. We present results demonstrating the promising aspects of this approach. The advantages as well as the limitations of using the very simple OFDR technique as a high-precision truly-distributed strain sensor are discussed.

9786-92, Session PSMon

Measurement of electromagnetic tracking error in a navigated breast surgery setup

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PURPOSE: The measurement of tracking error is crucial to ensure the safety and feasibility of electromagnetically tracked, image-guided procedures. Measurement should occur in a clinical environment because electromagnetic field distortion highly depends on positioning relative to the field generator and metal objects in the field. Concurrent optical tracking is suitable to estimate electromagnetic tracking error, as it is not impacted by electromagnetic field distortion. However, we could not find an accessible and open-source system for calibration, error measurement, and visualization. We developed such a system and tested it in an ultrasound-guided, navigated breast surgery setup. METHODS: A pointer tool was designed for concurrent electromagnetic and optical tracking. Software modules were developed for automatic calibration of the measurement system, real-time error visualization, and analysis. The system was taken to an operating room to test for field distortion in a navigated breast surgery setup. Positional and rotational electromagnetic tracking errors were then calculated using optical tracking as ground truth. RESULTS: Field distortion was measured in the presence of various surgical equipment. Positional and rotational error in a clean field was approximately 0.90 mm and 0.31 degrees. The presence of a surgical table, an electrosurgical cautery, and anesthesia machine increased the error by up to a few tenths of a millimeter and tenth of a degree. CONCLUSION: In a navigated breast surgery setup, measurement and visualization of tracking error defines a safe working area in the presence of surgical equipment. Our system is available as a module for the open-source 3D Slicer platform.

9786-93, Session PSMon

Image-guided navigation surgery for pelvic malignancies using electromagnetic tracking

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The purpose of this study was to implement and evaluate a surgical navigation system for pelvic malignancies. For tracking an NDI Aurora tabletop field generator and in-house developed navigation software were used. For patient tracking three EM-sensor stickers were used, one on the back and two on the superior iliac spines. During surgery a trackable pointer was used. One day before surgery a CT scan was acquired with the stickers in-place and marked. From the CT scan the EM-sensors, tumor and normal structures were segmented. During surgery, accuracy was independently checked by pointing at the aorta bifurcation,
and the common iliac artery bifurcations. Subsequently, the system was used to localize the ureters and the tumor.

Seven patients were included, three rectal tumors with lymph node-involvement, three lymph node recurrences, and one rectal recurrence. The average external marker registration accuracy was 0.75 cm RMSE (range 0.31-1.58 cm). The average distance between the pointer and the articular bifurcations was 1.55 cm (1SD=0.63 cm). We were able to localize and confirm the location of all ureters. Twelve out of thirteen lymph nodes were localized and removed. All tumors were removed radically. In all cases the surgeons indicated that the system aided in better anatomical insight, and faster localization of malignant tissue. In 2/7 cases surgeons indicated that radical resection was only possible with navigation.

The navigation accuracy was limited due to the use of skin markers. Nevertheless, preliminary results indicated potential clinical benefit due to better utilization of pre-treatment 3D imaging information.

9786-94, Session PSMon
Feasibility of tracked electrodes for use in epilepsy surgery
David R. Holmes III, Benjamin Brinkmann, Dennis P. Hanson, Gregory Worrell, Richard A. Robb, Mayo Clinic (United States); Leslie Holton, Medtronic Navigation (United States)

Subdural electrode recording is commonly used to evaluate intractable epilepsy. In order to accurately record electrical activity, however, electrodes must be positioned precisely near targets of interest (as generally indicated pre-operatively through imaging studies). To achieve accurate placement, a large craniotomy is used to expose the brain surface. With the intent of limiting the size and improving the location of craniotomy for electrode placement, we examined magnetic tracking for localization of electrode strips. Commercially available electrode strips were attached to specialized magnetic tracking sensors developed by Medtronic plc. In a rigid phantom we evaluated the strips to determine the accuracy of electrode placement on targets. We further conducted an animal study to evaluate the impact of magnetic field interference during data collection. The measured distance between the physical fiducial and lead coil of the electrode strip was 1.32 ± 1.03mm in the phantom experiments. The tracking system induces a very strong signal in the electrodes in the Very Low Frequency, an International Telecommunication Union (ITU) designated frequency band, from 3 kHz to 30 kHz. The results of the animal experiment demonstrated both tracking feasibility and data collection.

9786-95, Session PSMon
4D cone-beam CT imaging for guidance in radiation therapy: setup verification by use of implanted fiducial markers
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The use of 4D cone-beam computed tomography (CBCT) in combination with fiducial markers for guidance during radiation therapy is hindered by the trade-off between image quality, imaging dose, and scanning time. We investigated the visibility of markers and feasibility of marker-based 4D registration for different CBCT acquisition settings. A dynamic thorax phantom and a patient with implanted gold markers were used for this purpose. For both phantom and patient, the peak-to-peak amplitudes of marker motions in the cranial-caudal direction ranged from 5.3mm to 14.0mm. The results indicate that these motion amplitudes did not affect the marker visibility and associated marker-based registration feasibility. While using a medium field of view (FOV) and the same total imaging dose as is applied for the 3D CBCT scanning in our clinic, it was feasible to attain improved marker visibility for marker-based 4D registration by reducing the dose per projection image and increasing the number of projections. For a small FOV with a smaller rotation arc but similar total imaging dose, reducing the gantry rotation speed could efficiently reduce streak artifacts. The scanning time of these 4D CBCTs was ~4min. Further, the use of a small FOV allowed to reduce the total imaging dose and scanning time (~2.5min) almost without loss of marker visibility. In conclusion, by use of 4D CBCT with identical or lower total imaging dose and a reduced gantry speed (as compared to standard 3D acquisition), it is feasible to attain sufficient visibility of gold markers for 4D CBCT marker-based setup verification.

9786-96, Session PSMon
Effects of voxelization on dose volume histogram accuracy
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PURPOSE: In radiotherapy treatment planning systems, structures of interest such as targets and organs at risk are stored as 2D contours on evenly spaced planes. In order to be used in various different algorithms, the contours must first be converted into binary labelmap volumes through voxelization. The process of voxelization results in a loss of information, which has a small effect on the volume of large structures, but can have significant impact on small structures, which may only contain a few voxels. The accuracy of these segmented structures affects metrics, such as dose volume histograms (DVH), which are used for treatment planning. Our goal is to evaluate the effect that varying voxelization resolutions has on the DVH for each structure. METHODS: We implemented tools for analysis as modules in the SlicerRT toolkit based on the 3D Slicer platform with which we create a series of implicit functions, representing simulated structures. These structures are then sampled at varying resolutions, which are compared to a labelmap with a high sub-millimeter resolution, in order to calculate Hausdorff distance and Dice similarity coefficient between the labelmaps. We use both labelmaps to generate DVH and evaluate voxelization error for the same structures at different resolutions by calculating the agreement acceptance percentage between the DVH. RESULTS: We found that there was a large DVH variation from the baseline for small structures located in regions with a high dose gradient. CONCLUSION: Labelmap and dose volume voxel size was found to be an important factor in DVH accuracy.

9786-97, Session PSMon
Partition-based acquisition model for speed-up navigated Beta-probe surface imaging
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Although gross total resection in low-grade glioma surgery leads to a better patient outcome, the in-vivo control of resection borders remains challenging. For this purpose, navigated beta-probe systems combined with FDG radiotracer, relying on activity distribution surface estimation, have been proposed to generate reconstructed images. The clinical relevance has been outlined by early studies where intraoperative functional information is leveraged although inducing low spatial resolution in reconstruction. To improve reconstruction quality, acquisition models have been suggested. They involve the definition of attenuation matrix for designing radiation detection physics. Yet, they require high computational power for an efficient intraoperative usage. To address the problem, we propose a new acquisition model called Partition Model (PM) considering an existing model where coefficients of the matrix are taken from a look-up table (LUT). Our
model is based upon the division of the LUT into particular homogeneous values for assigning attenuation coefficients. To validate our model, we ran multiple experiments using in-vitro data sets. Three spatial configurations of grown cancer cells using Petri dish as phantom, simulating tumors and peri-tumoral tissues, have been acquired. We compared our acquisition model with the off-the-shelf LUT and the raw method. Acquisition models outperformed the raw method in terms of tumor contrast (7.9:1 mean T:B) but with an impossibility of real time usage.

Both acquisition models reached the same detection performances with reference (0.8 mean AUC and 0.77 mean NCC). Yet PM slightly improves the mean tumor contrast up to 10.1:1 vs 9.9:1 with the LUT model and more importantly reduces the mean computation time by 7.5%.

9786-98, Session PSMon

**Stent enhancement in digital x-ray fluoroscopy using an adaptive feature enhancement filter**

Yuhao Jiang, Josey Zachary, Univ. of Central Oklahoma (United States)

Fluoroscopic images belong to the classes of low contrast and high noise. Simply lowering radiation dose will render the images unreadable. Feature enhancement filters can reduce patient dose by acquiring images at low dose settings and then digitally restoring them to the original quality. In this study, a stent contrast enhancement filter is developed to selectively improve the contrast of stent contour without dramatically boosting the image noise including quantum noise and clinical background noise. Gabor directional filter banks are implemented to detect the edges and orientations of the stent. A high orientation resolution of 9? is used. To optimize the use of the information obtained from Gabor filters, a computerized Monte Carlo simulation followed by ROC study is used to find the best nonlinear operator. The next stage of filtering process is to extract symmetrical parts in the stent. The global and local symmetry measures are used. The information gathered from previous two filter stages are used to generate a stent contour map. The contour map is then scaled and added back to the original image to get a contrast enhanced stent image. We also apply a spatio-temporal channelized Hotelling observer model and other numerical measures to characterize the response of the filters and contour map to optimize the selections of parameters for image quality. The results are compared to those filtered by an adaptive unsharp masking filter previously developed. It is shown that stent enhancement filter can effectively improve the stent detection and differentiation in the interventional fluoroscopy.

9786-99, Session PSMon

**Evaluation of left ventricular scar identification from contrast enhanced magnetic resonance imaging for guidance of ventricular catheter ablation therapy**

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Patients with ventricular arrhythmias typically exhibit myocardial scarring, which is believed to be an important anatomic substrate for reentrant circuits, thereby making these regions a key target in catheter ablation therapy. In ablation therapy, a catheter is guided into the left ventricle and radiofrequency energy is delivered into the tissue to interrupt arrhythmic electrical pathways. Low bipolar voltage regions are typically localized during the procedure through point-by-point construction of an electroanatomical map by sampling the endocardial surface with the ablation catheter and are used as a surrogate for myocardial scar. This process is time consuming, requires significant skill, and has the potential to miss low voltage sites. This has led to efforts to quantify myocardial scar preoperatively using delayed, contrast-enhanced MRI. In this paper, we evaluate the utility of left ventricular scar identification from delayed contrast enhanced magnetic resonance imaging for guidance of catheter ablation of ventricular arrhythmias. The left ventricle and myocardial core and border scar is segmented from preoperative MRI images and sampled points from the procedural electroanatomical map are registered to the segmented endocardial surface. Sampled points with low bipolar voltage points visually align with the segmented scar regions and have significantly smaller distances as compared with other sampled points to both core and border scar regions (p<.02 and p<.03 respectively). This work demonstrates the potential utility of using preoperative delayed, enhanced MRI to identify myocardial scarring for guidance of ventricular catheter ablation therapy.

9786-100, Session PSMon

**Interactive visualization for scar transmurality in cardiac resynchronization therapy**

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Heart failure is a global pandemic with an estimated 23 million patients affected worldwide. Cardiac resynchronization therapy is used to treat patients with symptomatic heart failure, a severely depressed left ventricular function and electrical delay. However, 30-50% patients still do not derive clinical benefit. One of main causes is suboptimal (and empirical) placement of the epicardial left ventricular lead. Pacing in areas of myocardial scar correlates with poor clinical outcomes. Therefore precise knowledge of the individual patient’s scar characteristics is critical for delivering tailored treatments capable of improving response rates. Current research methods for scar assessment either map information to an alternative, non-anatomical coordinate system or they use the image coordinate system but lose critical information about scar transmurality. This paper proposes two interactive methods for visualizing scar transmurality. A 2D slice based approach with a scar mask overlaid on a 16 segment heart model and a 3D layered mesh visualization which allows physicians to scroll through layers of scar from epicardium to endocardium. These complementary methods enable physicians to evaluate scar location and transmurality during planning and guidance. Six physicians evaluated the proposed system by identifying target regions for lead placement. With the proposed method more target regions could be identified.

9786-101, Session PSMon

**A robust, automated left ventricle region of interest localization technique using a cardiac cine MRI atlas**

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Region of interest detection is a precursor to many medical image processing and analysis applications, including segmentation, registration and other image manipulation techniques. The optimal region of interest is often selected manually, based on empirical knowledge and features of the image dataset. However, if inconsistently identified, the selected region of interest may greatly affect the subsequent image analysis or interpretation.
steps, in turn leading to incomplete assessment during computer-aided diagnosis or incomplete visualization or identification of the surgical targets, if employed in the context of pre-procedural planning or image-guided interventions. Therefore, the need for robust, accurate and computationally efficient region of interest localization techniques is prevalent in many modern computer-assisted diagnosis and therapy applications. Here we propose a fully automated, robust, a priori learning-based approach that provides reliable estimates of the left ventricle features from cine cardiac MR images. The proposed approach leverages the temporal frame-to-frame motion extracted across a range of short axis left ventricle slice images to first identify an initial region of interest depicting the left and right ventricles that exhibits the greatest extent of cardiac motion. This region is correlated to the homologous region belonging to the training dataset that best matches the test image using feature vector correlation techniques. Lastly, the optimal left ventricle region of interest of the test image is identified based on the correlation of HOG features of known ground truth segmentation associated with the training dataset deemed closest to the test image. The proposed approach was tested using several combinations consisting of 25 training datasets and 75 testing datasets from a population of 100 patients datasets and was validated against the ground truth region of interest of the test images manually annotated by experts. This tool successfully identified the bounding box around the LV and RV and furthermore the minimal region of interest that fully enclosed the left ventricle from all testing datasets.

9786-102, Session PSMon

Classification of coronary artery tissues using optical coherence tomography imaging in Kawasaki disease

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Evaluation of coronary artery layers and early detection of coronary abnormalities is significant for preventing myocardial infarction and other cardiac problems in young children and infants affected with Kawasaki disease. Thickness of the arterial wall is an active process which increases the risk of future atherosclerosis and plaque rupture if it is not diagnosed and treated in acute phase of the disease. Intravascular imaging modalities, such as Optical Coherence Tomography (OCT) allow nowadays to improve diagnosis, treatment, follow-up, and even prevention of coronary artery disease. More importantly, OCT is promising for tissue quantification of the inner vessel wall. The goal of this study is to classify the coronary artery layers to evaluate the effects of Kawasaki disease on the arterial wall. Our approach is focused on developing a robust Random Forest classifier built on the idea of randomly selecting a subset of features at each node and based on second- and higher-order statistical texture analysis which estimates the gray-level spatial distribution of images by specifying the local features of each pixel and extracting the statistics from their distribution. The average classification accuracy for intima and media are 76.36% and 73.72% respectively. Random forest classifier with texture analysis promises for classification of coronary artery tissue.

9786-38, Session 8

Biplane reconstruction and visualization of virtual endoscopic and fluoroscopic views for interventional device navigation

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Biplane fluoroscopic imaging is an important tool for minimally invasive procedures for the treatment of cerebrovascular diseases. However, finding a good working angle for the C-arms of the angiography system as well as navigating based on the 2D projection images can be a difficult task. The purpose of this work is to propose a novel 4D reconstruction algorithm for interventional devices from biplane fluoroscopy images and to propose new techniques for a better visualization of the results. The proposed reconstruction methods binarizes the fluoroscopic images using a dedicated noise reduction algorithm for curvilinear structures and a global thresholding approach. A topology preserving thinning algorithm is then applied and a path search algorithm minimizing the curvature of the device is used to extract the 2D device centerlines. Finally, the 3D device path is reconstructed using epipolar geometry. The point correspondences are determined by a monotonic mapping function that minimizes the reconstruction error. The results are used to render synchronized virtual endoscopic and glass pipe views. Path and camera position visualization as well as automatic camera positioning are used to further improve the spatial orientation. The proposed techniques could considerably improve the workflow of minimally invasive procedures for the treatment of cerebrovascular diseases.

9786-39, Session 8

Visual feedback mounted on surgical tool: proof of concept

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PURPOSE: When using surgical navigation systems in the operating room, feedback is typically displayed on a computer monitor. The surgeon’s attention is usually focused on the tool and the surgical site, so the display is typically out of the direct line of sight. The purpose is to develop a virtual feedback device mounted on an electromagnetically tracked electrosurgical cautizer which will provide navigation information for the surgeon in their field of view. METHODS: A study was conducted to determine the usefulness of the visual feedback in adjunct to the navigation system currently in use. Subjects were asked to identify tumor contours with the tracked cautizer using 3D screen navigation with the mounted visual feedback and the 3D navigation screen alone. The movements of the cautizer were recorded. RESULTS: The study showed a significant decrease in the subjects’ distance from the tumor margin, a significant increase in the subjects’ confidence to avoid cutting the tumor and a statistically significant reduction in the subjects’ perception of the need to look at the screen when using the visual feedback device compared to without. DISCUSSION: The LED feedback device mounted on the cautizer helped the subjects feel confident in their ability to identify safe margins and minimize the amount of healthy tissue removed in the tumor resection. CONCLUSION: Good potential for the visual LED feedback has been shown. With additional training, this approach promises to lead to improved resection technique, with fewer cuts into the tumor and less healthy tissue removed.

9786-40, Session 8

CT thermometry for cone-beam CT guided ablation

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Monitoring temperature during a cone-beam CT (CBCT) guided ablation procedure is important for prevention of over-treatment and under-treatment. In order to accomplish ideal temperature monitoring, a thermometry map must be generated. Previously, this was attempted
using CBCT scans of a pig shoulder undergoing ablation. We are extending this work by using CBCT scans of real patients and incorporating more processing steps. We register the scans before comparing them due to the movement and deformation of organs. We then automatically locate the needle tip and the ablation zone. We employ a robust change metric to address image noise and artifacts. This change metric takes windows around each pixel and uses an equation inspired by Time Delay Analysis to calculate the error between windows with the assumption that there is an ideal spatial offset. Once the change map is generated, we correlate change data with measured temperature data at the key points in the region. This allows us to transform our change map into a thermal map. This thermal map is then able to provide an estimate as to the size and temperature of the ablation zone. We evaluated our procedure on a data set of 12 patients who had a total of 24 ablation procedures performed. We were able to generate reasonable thermal maps with varying degrees of accuracy. The average error ranged from 2.7 to 16.2 degrees Celsius. In addition to providing estimates of the size of the ablation zone for surgical guidance, 3D visualizations of the ablation zone and needle are also produced.

9786-41, Session 8

A computational model for estimating tumor margins in complementary tactile and 3D ultrasound images

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While traditional open surgical methods are effective treatments for lung tumors detected at an early stage, they impose high trauma and pain to patients. Minimally invasive surgery (MIS) is a safer alternative requiring much smaller incisions to reach the target organ; however, there exists a challenge as a result of inadequate intraoperative tumor localization. To address this issue, a mechatronic palpation device was developed that incorporates both tactile and ultrasound imaging sensors capable of capturing surface and cross sectional images of palpated tissue, respectively. Initial work focused on tactile image segmentation followed by fusion of position-tracked tactile images, resulting in reconstruction of the palpated surface; however, it only provided the spatial location of an underlying tumor. This paper presents an enhancement of this method by integrating an adaptive pattern classification technique that can segment suspicious regions in both tactile and ultrasound images via a computational model. Furthermore, an algebraic model, derived by combining the device kinematics, image poses and the geometric interaction of complementary image planes in 3D, is presented to compute tumor depth margins within the thickness of the palpated tissue. The proposed models have been tested on a set of tactile and ultrasound images of ex vivo porcine liver tissue injected with iodine-agar tumors. The tumor margins computed from the processed images were then compared against the corresponding physical measurements on fluoroscopy images of the liver tissue. The results show a 91.5 % match with an average error of 1.29 mm between the two sets of measurements.

9786-42, Session 8

Freehand 3D-US reconstruction with robust visual tracking with application to ultrasound-Augmented laparoscopy

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Background:

3D reconstruction of ultrasound volumes from tracked 2D frames is a cost effective intraoperative 3D imaging strategy. The reconstructed volumes can be visualized in-situ if the probe is tracked with respect to the camera during laparoscopic interventions. To this end, efficient, image-based intrinsic pose tracking methods are preferred over well-established extrinsic tracking methods. However, the potential of these intrinsic tracking methods as means of tracking in freehand 3D ultrasound reconstruction has not been investigated to-date. In this paper, we demonstrate that a recently proposed, image-based, robust pose tracking method can be used to achieve high quality, geometrically accurate reconstructions.

Methods:

A tissue-mimicking phantom with structures resembling anatomical targets, and plastic beads to help in a validation study, is constructed. An in-corporeal US probe tracked by a state-of-the-art, robust, image-based method smoothly scanned the phantom to reconstruct a 3D volume using a state-of-the-art algorithm. The plastic beads were manually localized in the ultrasound volumes and distances between them were compared to the ground truth measured from a micro-CT of the phantom.

Results and Conclusions:

The mean absolute distance error measured was 0.75mm while the maximum absolute error was 0.8mm. Structures resembling anatomical targets were clearly visible in a direct volume rendering of the reconstructed volumes. These results suggest that the 3D US volumes reconstructed with the robust, image-based method were of high quality and geometrically accurate. They further suggest that, in the future, the image-based pose tracking methods may be a comparable alternative to popular magnetic tracking-based methods.

9786-43, Session 9

Superpixel-based structure classification for laparoscopic surgery

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Minimally-invasive interventions offers multiple benefits for patients, but also entails drawbacks for the surgeon. The goal of context-aware assistance systems is to alleviate some of these difficulties. Localizing and identifying anatomical structures, malign tissue and surgical instruments through endoscopic image analysis is paramount for an assistance system, making online measurements and augmented reality visualizations possible. Furthermore, such information can be used to assess the progress of an intervention, hereby allowing for a context-aware assistance. In this work, we present an approach for such an analysis. First, a given laparoscopic image is divided into groups of connected pixels, so-called superpixels, using the SEEDS algorithm. The content of a given superpixel is then described using information regarding its color and texture. Using a Random Forest classifier, we determine the class label of each superpixel. We evaluated our approach on a publicly available dataset for laparoscopic instrument detection and achieved a DICE score of 0.69.

9786-44, Session 9

Tissue classification for laparoscopic image understanding based on multispectral texture analysis

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Intra-operative tissue classification is one of the prerequisites for providing context-aware visualization in computer-assisted interventions. As many anatomical structures are difficult to differentiate in conventional RGB medical images, we propose classification based on multispectral image patches. In a comprehensive ex-vivo study we show that multispectral imaging data is superior to RGB data for organ tissue classification when used in conjunction with widely applied feature descriptors and that combining the tissue texture with the reflectance spectrum can improve the classification performance. Overall, our study suggests that multispectral imaging data can be used for accurate organ classification in computer-assisted endoscopic interventions.

9786-45, Session 9

Endoscopic feature tracking for augmented-reality assisted prosthesis selection in mitral valve repair

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Mitral valve annuloplasty describes a surgical procedure where an artificial prosthesis is sutured onto the anatomical structure of the mitral annulus to re-establish the valve’s functionality. Choosing an appropriate commercially available ring size and shape is a difficult decision the surgeon has to make intraoperatively according to his experience. In our augmented-reality framework, we superimpose digitalized ring models onto endoscopic image streams without using any additional hardware. To place the ring model on the proper position within the endoscopic image plane, a pose estimation is performed that depends on the localization of sutures placed by the surgeon around the leaflet origins and punctured through the stiffer structure of the annulus.

In this work, the tissue penetration points are tracked by the realtime capable Lucas Kanade optical flow algorithm. The accuracy and robustness of this tracking algorithm is investigated with respect to the question whether outliers influence the subsequent pose estimation. Our results suggest that optical flow delivers very stable results for a variety of different endoscopic scenes and erroneous results do not affect the position of the superimposed virtual objects in the scene, making this approach a viable candidate for annuloplasty augmented reality-enhanced decision support.

9786-46, Session 9

Method for endobronchial video parsing

Patrick D Byrnes, William E. Higgins, The Pennsylvania State Univ. (United States)

Endoscopic examination of the lungs during bronchoscopy produces a considerable amount of endobronchial video. A physician uses the video stream as a guide to navigate the airway tree for various purposes such as general airway examinations, collecting tissue samples, or administering disease treatment. Aside from its intraoperative utility, the recorded video provides high-resolution detail of the airway mucosal surfaces and a record of the endoscopic procedure. Unfortunately, due to a lack of robust automatic videoanalysis methods to summarize this immense data source, it is essentially discarded after the procedure. To address this problem, we present a fully-automatic method for parsing endobronchial video for the purpose of summarization. Endoscopic-shot segmentation is first performed to parse the video sequence into structurally similar groups according to a geometric model. Bronchoscope-motion analysis then identifies motion sequences performed during bronchoscopy and extracts relevant information. Finally, representative key frames are selected based on the derived motion information to present a drastically reduced summary of the processed video. The potential of our method is demonstrated on four endobronchial video sequences from both phantom and human data. Preliminary tests show that, on average, our method reduces the number of frames required to represent an input video sequence by approximately 96% and consistently selects salient key frames appropriately distributed throughout the video sequence, enabling quick and accurate post-operative review of the endoscopic examination.

9786-47, Session 9

Uncalibrated stereo rectification and disparity range stabilization: A comparison of different feature detectors

Xiongbiao Luo, A. Jonathan McLeod, Terry M. Peters, Robarts Research Institute (Canada)

This paper studies uncalibrated stereo rectification and stable disparity range determination for surgical scene three-dimensional (3D) reconstruction. Stereoscopic endoscope calibration sometimes is not available and also increases the complexity of the operating-room environment. Stereo from uncalibrated endoscopic cameras is an alternative to reconstruct the surgical field visualized by binocular endoscopes within the body. Uncalibrated rectification is usually performed on the basis of a numeric matched feature points (semi-dense correspondence) between the left and the right images of stereo pairs. After uncalibrated rectification, the corresponding feature points can be used to determine the proper disparity range that helps to improve the reconstruction accuracy and reduce the computational time of disparity map estimation. Therefore, the corresponding or matching accuracy and robustness of feature point descriptors is important to surgical field 3D reconstruction. This work compares four feature detectors: (1) scale invariant feature transform (SIFT), (2) speeded up robust features (SURF), (3) affine scale invariant feature transform (ASIFT), and (4) gauge speeded up robust features (GSURF) with applications to uncalibrated rectification and stable disparity range determination.

We performed our experiments on surgical endoscopic video images that were collected during robotic prostatectomy. The experimental results demonstrate that ASIFT with less dynamic error outperforms other feature detectors in the uncalibrated stereo rectification and also provides a stable disparity range for surgical scene reconstruction.

9786-48, Session 9

Position-based adjustment of landmark-based correspondence finding in electromagnetic sensor-based colonoscope tracking method

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We propose a colonoscope tracking method that can utilize suitable correspondence finding condition for each position in the colon.
electromagnetic sensor-based colonoscope tracking method have been proposed. The method performs a landmark-based correspondence finding and a length-based fine correspondence finding processes to find the colonoscope tip position. The previous method used the same condition in the landmark-based correspondence finding for each position in the colon. In this paper, we newly propose a colonoscope tracking method that performs different correspondence finding depending on positions. Our method needs parameter settings that reduces tracking errors. We measured tracking errors at 52 points in a colon phantom to clarify relationships between parameters and tracking errors. From the experimental results, small tracking errors were obtained when we set small values to the parameters.

9786-49, Session 10

Robot-assisted tumor resection: palpation, incision, debridement and adhesive closure (Keynote Presentation)

Kenneth Y. Goldberg, Univ. of California, Berkeley (United States); W. Douglas Boyd, Univ. of California, Davis (Uruguay)

No Abstract Available

9786-50, Session 10

Toward automated cochlear implant insertion using tubular manipulators

Josephine Granna, Leibniz Univ. Hannover (Germany); Thomas S. Rau, Medizinische Hochschule Hannover (Germany); Thien-Dang Nguyen, Leibniz Univ. Hannover (Germany); Thomas Lenarz, Omid Majdani, Medizinische Hochschule Hannover (Germany); Jessica Burgner-Kahrs, Leibniz Univ. Hannover (Germany)

During manual cochlear implant electrode insertion the surgeon is at risk to damage the intracochlear fine-structure, as the electrode array is inserted through a small opening in the cochlea blindly with little force-feedback. This paper addresses a novel concept for cochlear electrode insertion using tubular manipulators to reduce risks of causing trauma during insertion and to automate the insertion process.

We propose a tubular manipulator incorporated into the electrode array composed of an inner wire within a tube, both elastic and helical shaped. It is our vision to use this manipulator to actuate the initially straight electrode array during insertion into the cochlea by actuation of the wire and tube, i.e. translation and slight axial rotation. We evaluate the geometry of the human cochlea in 22 patient datasets in order to derive design requirements for the manipulator. An optimization algorithm is presented to determine the tube set parameters (curvature, torsion, diameter, length) for an ideal final position within the cochlea. To prove our concept, we further demonstrate that insertion can be realized in a follow-the-leader fashion for 19 out of 22 cochleas.

9786-51, Session 10

Increasing safety of a robotic system for inner ear surgery using probabilistic error modeling near vital anatomy

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Safe and effective planning for robotic surgery that involves cutting or ablation of tissue must consider all potential sources of error when determining how close the tool may come to vital anatomy. A pre-operative plan that does not adequately consider potential deviations from ideal behavior of the system may lead to patient injury. Conversely, a plan that is overly conservative may result in ineffective or incomplete performance by the robot. Enforcing simple uniform-thickness safety margins around vital anatomy is insufficient in the presence of spatially varying, anisotropic error. Prior work has used registration error to determine a variable-thickness safety margin around vital structures that must be approached during the procedure but ultimately preserved. In this paper, these methods are extended to incorporate additional image processing errors and physical robot errors, including kinematic/positioning errors as well as deflections of the robot based on expected forces during surgery. These additional sources of error are discussed and stochastic models for a bone-attached robot for otologic surgery are developed. An algorithm for generating appropriate safety margins based on a desired probability of preserving the underlying anatomical structure is presented. Simulations are performed on a CT scan of a cadaver head and safety margins are calculated around several critical structures for planning of a robotic mastoidectomy.

9786-52, Session 11

A comparison of needle tip localization accuracy using 2D and 3D-guided ultrasound for high-dose-rate prostate brachytherapy treatment planning

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Background: High-dose-rate brachytherapy (HDR-BT) is a prostate cancer treatment option involving the insertion of hollow needles into the gland through the perineum to deliver a radioactive source. Conventional needle imaging involves indexing a trans-rectal ultrasound (TRUS) probe in the superior/inferior (S/I) direction, using the axial transducer to produce an image set for organ segmentation. These images have limited resolution in the needle insertion direction (S/I), so the sagittal transducer is used to identify needle tips, requiring a manual registration with the axial view. This registration introduces a source of uncertainty in the final segmentations and subsequent treatment plan. Our lab has developed a device enabling 3D-TRUS guided insertions with high S/I spatial resolution, eliminating the need to align axial and sagittal views.

Purpose: To compare HDR-BT needle tip localization accuracy between 2D and 3D-TRUS.

Methods: 5 prostate cancer patients underwent conventional 2D TRUS guided HDR-BT, during which 3D images were also acquired for post-operative registration and segmentation. Needle end-length measurements were taken, providing a gold standard for insertion depths.

Results: 73 needles were analyzed from all 5 patients. Needle tip position differences between imaging techniques was found to be largest in the S/I direction with mean±SD of -2.52±4.01 mm. End-length measurements indicated that 3D TRUS provided significantly lower mean±SD insertion depth error of -0.22±3.42 mm versus 2.28±3.72 mm with 2D guidance (p < .001).

Conclusions: 3D TRUS may provide more accurate HDR-BT needle localization than conventional 2D TRUS guidance for the majority of HDR-BT needles.
An MRI guided system for prostate laser ablation with treatment planning and multi-planar temperature monitoring

Sheng Xu, National Institutes of Health (United States); Harsh Agarwal, Philips Research (United States); Marcelino Bernardo, Baris Turkbey, National Institutes of Health (United States); Ari Partanen, Philips Healthcare (United States); Ayele Negussie, National Institutes of Health (United States); Neil Glossop, Traxtal Technologies (Canada); Peter Choyke, Peter Pinto, Bradford J. Wood, National Institutes of Health (United States)

Prostate cancer is currently over treated with standard treatment options which often impact the patients’ quality of life. Laser ablation has emerged as a new approach to treat prostate cancer while sparing the healthy tissue around the tumor. Since laser ablation has a small treatment zone with high temperature, it is necessary to use accurate image guidance and treatment planning to enable full ablation of the tumor. Intraoperative temperature monitoring is also desirable to protect critical structures from being damaged in laser ablation. In response to these problems, we developed a navigation platform and integrated it with a clinical MRI scanner and a side firing laser ablation device. The system allows imaging, image guidance, treatment planning and temperature monitoring to be carried out on the same platform. Temperature sensing phantoms were developed to demonstrate the concept of iterative treatment planning and intraoperative temperature monitoring. Retrospective patient studies were also conducted to show the clinical feasibility of the system.

How does prostate biopsy guidance error impact pathologic cancer risk assessment?

Peter R. Martin, Mena Gaed, José A. Gómez, Madeleine Moussa, Western Univ. (Canada); Eli Gibson, Univ. College London (United Kingdom) and Radboud Univ. Medical Ctr. (Netherlands); Derek W. Cool, Joseph L. Chin, Stephen Pautler, Aaron Fenster, Aaron D. Ward, Western Univ. (Canada)

Magnetic resonance imaging (MRI)-targeted, 3D transrectal ultrasound (TRUS)-guided “fusion” prostate biopsy aims to reduce the 21-47% false negative rate of clinical 2D TRUS-guided sextant biopsy, but still has a substantial false negative rate. This could be improved via biopsy needle target optimization, accounting for uncertainties due to guidance system errors, image registration errors, and irregular tumor shapes. As an initial step toward the broader goal of optimized prostate biopsy targeting, in this study we elucidated the impact of biopsy needle delivery error on the probability of obtaining a tumor sample, and on the core involvement. These are both important parameters to patient risk stratification and the decision for active surveillance vs. definitive therapy. We addressed these questions for cancer of all grades, and separately for high grade (≥ Gleason 4+3) cancer. We used expert-contoured gold-standard prostatectomy histology to simulate targeted biopsies using an isotropic Gaussian needle delivery error from 1 to 6 mm, and investigated the amount of cancer obtained in each biopsy core as determined by histology. Needle delivery error resulted in variability in core involvement that could influence treatment decisions; the presence or absence of cancer in 1/3 or more of each needle core can be attributed to a needle delivery error of 4 mm. However, our data showed that by making multiple biopsy attempts at selected tumor foci, we may increase the probability of correctly characterizing the extent and grade of the cancer.

Impact of contouring variability on focal therapy coverage assessment

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Motivation: Focal therapy is an emerging low-morbidity treatment option for low-intermediate risk prostate cancer; however, challenges remain in accurately delivering treatment to specified targets and determining treatment success. Registered multi-parametric magnetic resonance imaging (MPMRI) acquired before and after treatment can support focal therapy evaluation and optimization; however, contouring variability, when defining the prostate, the clinical target volume (CTV) and the ablation region in images, reduces the precision of quantitative image-based focal therapy evaluation metrics. To inform the interpretation and clarify the limitations of such metrics, we investigated inter-observer contouring variability and its impact on four metrics. Methods: Pre-therapy and 2-week-post-therapy standard-of-care MPMRI were acquired from 5 focal cryotherapy patients. Two clinicians independently contoured, on each slice, the prostate (pre- and post-treatment) and the dominant index lesion CTV (pre-treatment) in the T2-weighted MRI, and the ablated region (post-treatment) in the dynamic-contrast-enhanced MRI. For each combination of clinician contours, post-treatment images were registered to pre-treatment images using a 3D biomechanical-model-based registration of prostate surfaces, and four metrics were computed: the proportion of the target tissue region that was ablated and the target:ablated region volume ratio for each of two targets (the CTV and an expanded planning target volume). Variance components analysis was used to measure the contribution of each type of contour to the variance in the therapy evaluation metrics. Conclusions: 14–23% of evaluation metric variance was attributable to contouring variability (including 6-12% from ablation region contouring); reducing this variability could improve the precision of focal therapy evaluation metrics.
These scans keep radiation doses low while maximizing the detection of suspicious lung lesions. Tube current modulation (TCM) is one technique used to optimize dose, however limited work has been done to assess TCM’s effect on detection tasks. In this work the effect of TCM on detection is investigated throughout the lung utilizing several different model observers (MO). 131 lung nodules were simulated at mm intervals in each lung of the XCAT phantom. A Sensation 64 TCM profile was generated for the XCAT phantom and noise realizations were created using both TCM and a fixed TC. All nodules and noise realizations were reconstructed for a total of 262 (left and right lungs) nodule reconstructions and 4800 XCAT lung reconstructions. Single-slice Hotelling (HO) and channelized Hotelling (CHO) observers, as well as a multislice CHO were used to assess area-under-the-curve (AUC) as a function of slice location in both the fixed TC and TCM cases. As expected with fixed TC, nodule detectability was lowest through the shoulders and leveled off below mid-lung; with TCM, detectability was unexpectedly highest through the shoulders, dropping sharply near the mid-lung and then increasing into the abdomen. Trends were the same for all model observers.

These results suggest that TCM could be further optimized for detection and that detectability maps present exciting new opportunities for TCM optimization on a patient-specific level.

The purpose of this study was to determine radiologists’ diagnostic performance on different image reconstruction algorithms that could be used to optimize image-based model observers. We included a total of 102 pathology proven breast computed tomography (CT) cases (63 malignant). An iterative image reconstruction (IIR) algorithm was used to obtain 28 reconstructions with different image appearance for each image. Using quantitative image feature analysis, three IIRs and one clinical reconstruction of 50 lesions (25 malignant) were selected for a reader study. The reconstructions spanned a range of smooth-low noise to sharp-high noise image appearance. The trained classifiers’ AUCs on the above reconstructions ranged from 0.66 (for smooth reconstruction) to 0.96 (for sharp reconstruction). Six experienced MQSA radiologists read 200 cases (50 lesions times 4 reconstructions) and provided the likelihood of malignancy of each lesion. Radiologists’ diagnostic performances (AUC) ranged from 0.7 to 0.89. However, there was no agreement amongst the six radiologists on which image appearance was the best, in terms of radiologists having the highest diagnostic performance. Specifically, for two radiologists sharper image appearance was diagnostically superior, while for two radiologists smoother image appearance was diagnostically superior, and for two radiologists all image appearances were diagnostically similar to each other. Due to the poor agreement among radiologists on the diagnostic ranking of images, it may not be possible to develop a model observer for this particular imaging task.
Applying the J-optimal channelized quadratic observer to a SPECT phantom for myocardial perfusion defect detection

Meredith K. Kupinski, College of Optical Sciences, The Univ. of Arizona (United States); Eric W. Clarkson, The Univ. of Arizona (United States); Michael Ghaly, Eric C. Frey, Johns Hopkins Univ. (United States)

We apply the J-optimal channelized quadratic observer (J-CQO) to a myocardial perfusion single-photon emission computed tomography (SPECT) defect detection task. Implementing an optimal quadratic observer for detection requires the first- and second-order statistics of the image data from both classes. The dimensionality reduction from this data is accomplished using a channel matrix which yields better estimates of these statistical estimates from smaller sample sizes, and since the channelized covariance matrix is LxL, the inverse easier to compute. We consider a linear data reduction described by an LxM channel matrix and introduce an iterative gradient-based method for calculating the channel matrix. The novelty of our approach is the use of Jeffreys' figure of merit (FOM) for optimizing the channel matrix. We previously showed that the J-optimal channels are also the optimum channels for the AUC and the Bhattacharyya distance when the channel outputs are Gaussian distributed with equal means. This work evaluates the use of J as a surrogate FOM for AUC when these statistical conditions are not satisfied. The J-CQO is calculated using a finite testing and training set of cardiac SPECT phantom data. The phantom data are not equal mean, non-Gaussian, and are designed to simulate the defect variability of a realistic patient population. We compare AUC values of the linear Hotelling observer and J-CQO when the defect location is fixed and when it occurs in one of two locations.

Identification of error making patterns in lesion detection on digital breast tomosynthesis using computer-extracted image features

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Digital breast tomosynthesis (DBT) can improve lesion visibility by eliminating the issue of overlapping breast tissue present in mammography. However, this new modality likely requires new approaches to training. Our hypothesis is that the trainees’ educational outcomes will improve if they are presented with cases individually selected to address their weaknesses. In this study, we focus on the issue of selecting such cases. Specifically, we propose an algorithm that based on previously acquired reading data predicts which lesions will be missed by the trainee for future cases (i.e., we focus on false negative error). A logistic regression classifier was used to predict the likelihood of trainee error and computer-extracted features were used as the predictors. Reader data from 3 expert breast imagers was used to establish the ground truth and reader data from 5 radiology trainees was used to evaluate the algorithm performance with repeated holdout cross validation. Receiver operating characteristic (ROC) analysis was applied to measure the performance of the proposed individual trainee models. The preliminary experimental results for 5 trainees showed the individual trainee models were able to distinguish the lesions that would be detected from those that would be missed with a large enough AUROC (=0.698). The proposed algorithm can be used to identify difficult cases for individual trainees.

Location- and lesion-dependent estimation of background tissue complexity for anthropomorphic model observer

Ali R. N. Avanaki, Barco, Inc. (United States)

In the framework of virtual clinical trials (VCT), we plan to design a model observer that can track the performance of a human observer with changes in background tissue complexity (BTC). Such a model observer will be especially useful in design, and pre-clinical validation and optimization of contrast-enhanced imaging systems using VCTs. To that aim, a notion of BTC as perceived by a human observer is specified that is suited for use with model observers and is a function of image location as well as lesion shape and size. Next, we propose two predictors to quantify BTC one based on the assumption of BTC on pre- and post-lesion images and the other based on the conjecture that a conspicuous lesion should be brighter than its immediate surround. Spatiotemporal version of the proposed methods may be used for viewing breast tomosynthesis sequences in cine mode. To validate the BTC predictors, we plan a human observer study (to be conducted), where the observer’s task is to adjust the insertion contrast to achieve the threshold conspicuity for lesions of various shapes and sizes, and at different locations. Our initial analysis indicates that one of the proposed methods is correlated with local image energy (Spearman rank correlation of 0.85 for 658 images). Nonetheless, it is observed that the proposed method is more accurate than the local energy in predicting the perceived BTC in example images.

Task-based optimization of flip angle for texture analysis in MRI

Jonathan F. Brand, College of Optical Sciences, The Univ. of Arizona (United States); Lars R. Furenlid, The Univ. of Arizona College of Medicine (United States) and College of Optical Sciences, The Univ. of Arizona (United States); Maria I. Albach, Jean-Philippe Galons, Puneet Sharma, Achyut Bhattacharyya M.D., Tulshi Bhattacharyya, Ali Bilgin, Diego R. Martin M.D., The Univ. of Arizona College of Medicine (United States)

Chronic liver disease (CLD) is a worldwide health problem and hepatic fibrosis (HF) is one of the hallmarks of the disease. The current gold standard for diagnosing HF is biopsy, however this method is limited by sampling error and risks of patient complication. Biopsy diagnosis of HF is based on the textural change in the liver as a lobular collagen network that grows from hepatic arteries. The scale of collagen lobules is on the order of 1mm which is close to the resolution limit of in-vivo Gd-enhanced MR at the delayed phase, a technique used routinely in the clinic to look at changes in the liver due to HF. Formalin fixed liver samples can mimic the textural contrast of in-vivo Gd-enhanced imaging systems using VCTs. To that aim, a notion of background tissue complexity for MRI observer that can track the performance of a human observer with changes in background tissue complexity (BTC). Such a model observer will be especially useful in design, and pre-clinical validation and optimization of contrast-enhanced imaging systems using VCTs. To that aim, a notion of BTC as perceived by a human observer is specified that is suited for use with model observers and is a function of image location as well as lesion shape and size. Next, we propose two predictors to quantify BTC one based on the conjecture that a conspicuous lesion should be brighter than its immediate surround. Spatiotemporal version of the proposed methods may be used for viewing breast tomosynthesis sequences in cine mode. To validate the BTC predictors, we plan a human observer study (to be conducted), where the observer’s task is to adjust the insertion contrast to achieve the threshold conspicuity for lesions of various shapes and sizes, and at different locations. Our initial analysis indicates that one of the proposed methods is correlated with local image energy (Spearman rank correlation of 0.85 for 658 images). Nonetheless, it is observed that the proposed method is more accurate than the local energy in predicting the perceived BTC in example images.

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Semi-parametric estimation of the area under the precision-recall curve

Berkman Sahiner, Weijie Chen, Aria X. Pezeshk, Nicholas A. Petrick, U.S. Food and Drug Administration (United States)

Precision and recall are two common metrics used in the evaluation of information retrieval systems. By changing the number of retrieved documents, one can obtain a precision-recall curve. The area under the precision-recall curve (AUCPR) has been suggested as a performance measure for information retrieval systems, in a manner similar to the use of the area under the receiver operating characteristic curve (AUC) in binary classification. Limited work has been performed in the literature to investigate the bias and variance of AUCPR estimators. The goal of our study was to investigate the bias and variability of a semi-parametric binormal method for estimating the AUCPR, and to compare it to other techniques, such as average precision (AP) and lower trapezoid (LT) approximation. We show how AUCPR can be obtained given the binormal model parameters, and how its variance can be estimated using the delta method. We performed simulation experiments with non-normal data, and investigated the effect of sample size and prevalence. Our results indicated that the semi-parametric binormal approach provided AUCPR estimates with small bias and confidence intervals with acceptable coverage when the sample size was large, and the performance of the binormal model was comparable to or better than alternative methods evaluated in this study when the sample size was small. We conclude that the semi-parametric binormal model can be used to accurately estimate the AUCPR, and that the confidence intervals derived from the model can be at least as accurate as from other alternatives, even for non-normal decision variable distributions.
9787-13, Session 3

Quality metrics can help the expert during neurological clinical trials
Laure Mahé, Univ. de Nantes (France) and KEOSYS (France); Florent Autrusseau, Hubert Desal, Jean-Pierre V. Guédon, Yves Le Tournier, Univ. de Nantes (France); Henri Der Sarkissian, Sylvie Davila, Jérôme Beranger, KEOSYS (France)

Carotid surgery is a frequent act and corresponds to 15 to 20 thousands operations per year in France. Cerebral perfusion has to be tracked before and after carotid surgery. In this paper, a retroengineering using quality metrics has been done for the clinical trial EMOCAR involving more than 800 patients. This paper studies a comparison between the result of visual inspection made by the neuroradiologist and an equivalent software developed by our team. The primary goal is to help the neuroradiologist to better and faster make his work. The secondary goal was to explore the cost risk-benefits for the patient if medical imaging is included or not into the clinical trial.

Objective quality metrics (OQM) are methods whose goal is to predict the perceived quality. Here, we used both standard OQM as PSNR, RMSE, or SSIM, and advanced Human Visual System-based OQMs such as VIF or VSNR which exploit some properties of the human visual system. A study with 30 patients with or without injuries has been made and is presented. The cost risk-benefits for the clinical trial are finally discussed both for the patient and for the expert.

9787-14, Session 3

Performance comparison of semantics and lung-RADS in the National Lung Screening Trial
Qian Li, Tianjin Medical Univ. (China) and H. Lee Moffitt Cancer Ctr. & Research Institute (United States); Yoganannd Balagurunathan, H. Lee Moffitt Cancer Ctr. & Research Institute (United States); Ying Liu, Tianjin Medical Univ. (China) and H. Lee Moffitt Cancer Ctr. & Research Institute (United States); Matthew Schabath, Robert J. Gillies, H. Lee Moffitt Cancer Ctr. & Research Institute (United States)

Background: Lung-RADS is the new oncology classification guideline proposed by American College of Radiology (ACR), which provides recommendations for further follow up in lung cancer screening. However, only one texture (solid/non-solid) and one size (average diameters) feature were included in this system. We hypothesize that additional semantic features can be used to better characterize lung nodules and diagnose cancer.

Objective: We propose to develop and characterize a systematic methodology to more accurately predict occurrence of cancerous nodules.

Methods: 25 radiological image traits were systematically scored on a point scale (up to 5) by a trained radiologist, and lung-RADS was independently scored. A multivariate linear predictor model was used on the semantic features to access their performance in predicting cancer status. The semantic predictors were then compared to lung-RADS (scale 4 or above called positive) classification in National Lung Screening Trial data.

Result: A total of 60 patients diagnosed as cancer and 139 normal patients were included in our study. There were different combinations of semantic features that were good predictive candidates of cancer status. Of these, contour, texture, distribution, size and nodules in primary tumor lobe/non-tumor lobe came as top candidates. The average AUC using three best semantic features was 0.94 (± 0.036), whereas lung-RADS had an AUC of 0.89.

Conclusion: We propose that a semantics-based discrimination approach is superior to lung-RADS in classifying the presence of cancer. Hence, a quantitative radiological semantic approach to predict cancer status may act as a surrogate to the lung-RADS system.

9787-15, Session 4

The classification of normal screening mammograms
Zoey Z. Y. Ang, Mohammad A. Rawashdeh, Robert Heard, Patrick C. Brennan, Warwick B. Lee, Sarah J. Lewis, The Univ. of Sydney (Australia)

Rationale and objectives: To understand how breast screen readers classify the difficulty of normal screening mammograms using common lexicon describing normal appearances. Cases were also assessed on their suitability for a single reader strategy.

Materials and Methods: 15 breast readers were asked to interpret a test set of 29 normal screening mammogram cases and classify them by rating the difficulty of the case on a five-point Likert scale, identifying the salient features and assessing their suitability for single reading. Using the False Positive Fractions from previous study, the 29 cases were classified into 10 “low”, 10 “medium” and nine “high” difficulties. Data was analyzed with descriptive statistics. Spearman’s correlation was used to test the strength of association between the difficulty of the cases and the readers’ recommendation for single reading strategy.

Results: The ratings from readers in this study corresponded to the known difficulty level of cases for the ‘low’ and ‘high’ difficulty cases. Uniform ductal pattern and density, symmetrical mammographic features and the absence of micro-califications were the main reasons associated with ‘low’ difficulty cases. The ‘high’ difficulty cases were described as having ‘dense breasts’. There was a statistically significant negative correlation between the difficulty of the cases and readers’ recommendation for single reading (r = -0.475, P=0.009).

Conclusion: The findings demonstrated that certain salient mammographic features have a major influence on the difficulty for readers to classify mammograms as normal. The standard Australian practice of double reading was deemed more suitable for most cases. There was an inverse moderate association between the difficulty of the cases and the recommendations for single reading.

9787-16, Session 4

The potential of pigeons as surrogate observers in medical image perception studies
Elizabeth A. Krupinski, The Univ. of Arizona (United States); Richard M. Levenson, UC Davis Medical Ctr. (United States); Victor Navarro, Edward A. Wasserman, The Univ. of Iowa (United States)

Assessment of medical image quality and how changes in image appearance impact performance are critical but assessment can be expensive and time-consuming. Could an animal (pigeon) observer with well-known visual skills and documented ability to distinguish complex visual stimuli serve as a surrogate for the human observer? Using sets of whole slide pathology (WSI) and mammographic images we trained pigeons (cohorts of 4) to detect and/or classify lesions in medical images. Standard training methods were used. A chamber equipped with a 15" display with a resistive touchscreen was used to display the images and record responses (pecks). Pigeon pellets were dispensed for correct responses. The pigeons readily learned to distinguish benign from malignant breast cancer histopathology in WSI (mean % correct responses rose 50% to 85% over 15 days) and generalized readily from 4X to 10X and 20X magnifications; to detect microcalcifications (mean % correct responses rose 50% to over 85% over 25 days); to distinguish benign from malignant breast masses (3 of 4 birds learned this task to around 80% and 60% over 10 days);
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and ignore compression artifacts in WSI (performance with uncompressed slides averaged 95% correct; 15:1 and 27:1 compression slides averaged 92% and 90% correct). Pigeons models may help us better understand medical image perception and may be useful in quality assessment by serving as surrogate observers for certain types of studies.

9787-17, Session 4

The impact of radiology expertise upon the localization of subtle pulmonary lesions

John W. Robinson, Patrick C. Brennan, Claudia R. Mello-Thoms, Sarah J. Lewis, The Univ. of Sydney (Australia)

Rationale and objectives: This study investigates the influence of radiology expertise and the correct localization of lesions when radiologists are requested to perform two different observer tasks. Specifically, the ability to detect lesions of different subtleties is explored in relation to radiologists' reported specialty.

Materials and Methods: Institutional ethics was granted. Ten radiologists (5 thoracic and 5 non-thoracic) undertook an interpretation task involving a set of 40 posterior-anterior (PA) chest x-rays (CXRs) consisting of 21 normal and 19 abnormal (solitary pulmonary nodule). Radiologists read the test set twice and were asked to firstly report on all abnormalities (Unframed Task) and secondly, were asked to report only on pulmonary lesions (Framed Task). The identification of any pulmonary nodule/s was marked using a 2-5 confidence scale (2=least confident case contains a pulmonary nodule and 5=highest confidence case contains a pulmonary lesions). The cases were randomized for each reader.

Results: Using a Wilcoxon Signed Rank test, there is a significant difference in TP decisions between thoracic and non-thoracic radiologists when undertaking a framed task (P=0.048) however there is no difference between thoracic and non-thoracic radiologists when detecting lesions in an unframed task. For both the framed and unframed task, thoracic radiologists were able to detect TP lesions for all subtlety categories (P=0.004). Further analysis is currently being undertaken to investigate the effect of subtlety ranges upon lesion detection using a Kruskal-Wallis test across expertise groups.

Conclusion: Preliminary results indicate that expertise in chest radiology allows radiologists to detect lesions of varying subtlety more consistently than non-thoracic radiologist regardless of the task framing.

9787-18, Session 4

Quantitative imaging features to predict cancer status in lung nodules

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Purpose: Low dose computed tomography has evolved as the primary modality to detect lung nodules. Visual characteristics of lung nodules are most often considered by the radiologist to be heuristic measures to distinguish malignancy. We propose a systematic methodology to quantify nodules based on observed radiological traits on a point scale and these measures were then used to build a classification model to predict cancer status.

Methods: In our study we identified 25 radiological image traits that describes size, shape, texture and associated findings of the lung. We then built a machine learning classifier based on a linear model to find the best predictive imaging features to differentiate cancerous nodules from non-cancer nodules. Using exhaustive searching, several multivariate predictor pairs (up to 3 dimensions) were formed with error of the classifier estimated using a hold out cross validation approach.

Results: A total of 42 patients with 42 nodules confirmed as lung cancer and 50 patients with benign 90 nodules were included in our study. Multiple combinations of radiological image traits were found to be predictive of cancer status. Of these, size based features, concavity, spiculation, lymphadenopathy and vascular convergence were most predictive for presence of cancer. By holdout cross validation, the 3 best feature pairs had an average AUC of 89.3% (Accuracy 85.3%, Sensitivity 71.4%, Specificity 94.4%) in predicting cancer in the primary nodule.

Conclusions: Radiological image traits are useful in differentiating malignant lung nodules from non-malignant nodules, which could be collectively used in clinical workflow to better diagnose malignancy.

9787-19, Session 4

Shapelet analysis of pupil dilation for modeling visuo-cognitive behavior in screening mammography

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Our objective is to understand and model visuo-cognitive behavior of radiologists during mammographic screening. In this study, we analyzed the pupillary responses of 10 readers (three breast-imaging radiologists and seven radiology residents). Using a head-mounted eye-tracking device, we recorded the pupil response and diagnostic decisions from each reader for 100 screening mammograms. The corpus of mammograms comprised cases of varied pathology and breast parenchymal density. We applied time series shapelet analysis to extract discriminative patterns in pupillary response for each individual radiologists during the diagnostic process. Using a small set of features from shapelet primitives, we built a Random Forest (RF) classifier. We used ten-fold cross-validation for training and testing the RF classifier to evaluate the effectiveness of pupillary response in discriminating between individual radiologists, radiologists' experience level, case pathology, breast parenchyma density, and diagnostic decision. Our results suggest that the pattern of pupillary response, as characterized by time series shapelets, in combination with machine learning can be used both as a biometric as well as to predict diagnostic error for individual radiologists.

9787-20, Session 4

Image similarity ranking of focal computed tomography liver lesions using a 2AFC technique

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Content-based image retrieval (CBIR) for radiological images has experienced massive growth over the past two decades, and shows great potential as a tool for use in precision medicine. A recurring challenge in CBIR evaluation has been in obtaining reference sets of images from human viewers of the system. Our work seeks to determine the feasibility...
of creating a reference set from images ranked by similarity from human viewers of the images. We obtained 2 sets each of 10 images of CT focal liver lesions from a database of open-access publications with and without markings showing the region containing the lesions, respectively. We created 2 sets of all 45 pair-wise combinations of the images, and displayed them to 10 volunteers, of which 2 had medical training. We used a Two-Alternative Forced Choice (2AFC) paradigm to obtain complete rankings of similarity levels in these image pairs. Analysis showed that inter-reader agreement for rankings ranged from Tau=0.21-0.69 (median=0.37) for the image pairs without any markings, and Tau=0.21-0.57 (median=0.33) for the image pairs with markings. A comparison of the regions of interests drawn by the study participants outlining the lesions in images without markings showed that participants tended to agree on images containing a single focal lesion of a single density, and inter-reader agreement for image rankings in which the regions of interest agree ranged from Tau=0.39-0.85 (median=0.58). These results show that the use of image ranking using 2AFC may be a feasible method for creating reference sets for CBIR system validation.

9787-43, Session PWed

Breast ultrasound lesions classification: a performance evaluation between manual delineation and computer segmentation

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Breast cancer is a threat to women worldwide. Manual delineation (MD) on breast ultrasound lesions is time-consuming and operator dependent. Computer segmentation (CS) of ultrasound breast lesions can be a challenging task due to the ill-defined lesions boundaries and issues related to the speckle noise in ultrasound images. The main contribution in this paper is to compare the performance of the computer classifier on the MD and CS in malignant and benign lesions classification. This paper we implement CS using multifractal approach on a database consists of 120 images (50 malignant lesions, and 70 benign lesions). The CS result is compared with the MD using Jaccard Similarity Index (JSI). The result shows that the average JSI of 0.5010 (±0.2088) for malignant lesions and the average JSI of 0.6787 (±0.1290) for benign lesions. These results indicate lower agreement in malignant lesions due to the irregular shape while the higher agreement in benign lesions with regular shape. Further, we extract the feature descriptors for the lesions. These include shape descriptors and texture descriptors. By using logistic regression with 10 fold cross validation, the classification rates of MD and CS are computed. The CS produced results with sensitivity 0.780 and specificity 0.871. However, the MD produced sensitivity of 0.520 and the specificity of 0.800. The results show that there are no clear differences between the delineation in MD and CS in benign lesions but the delineation in malignant lesions using CS was more suitable for computer classifier.

9787-45, Session PWed

Impact of patient photos on visual search during radiograph interpretation

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To increase detection of mislabeled medical imaging studies evidence shows it may be useful to include patient photographs during interpretation. This study examined how inclusion of photos impacts visual search. Ten radiologists viewed 21 chest radiographs with and without a photo of the patient while search was recorded. Their task was to note tube/line placement. Eye-tracking data revealed that presence of the photo reduced the number of fixations (chest image only mean 98.68; chest with photo present 25.68; photo 3.93) on the chest image as a result of periodically looking at the photo. Overall time viewing the cases did not differ as time not spent on the radiograph was spent on the photo. On average readers scanned to the photos about 4 times during search. Men and non-cardiothoracic radiologists spent significantly more time looking at all the images including the photos. Average preference for having photos was 6.10 on 0-10 scale and neck and chest were preferred as areas to include. Photos may help with certain image interpretation tasks.

9787-46, Session PWed

Changes in frequency of recall recommendations of examinations depicting cancer with the availability of either priors or digital breast tomosynthesis

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Performance changes in a binary environment when using additional information is affected only when changes in recommendations are made due to the additional information in question. In a recent study, we have shown that, contrary to general expectation, introducing prior examinations improved recall rates, but not sensitivity. In this study, we assessed cancer detection differences when prior examinations and/or digital breast tomosynthesis (DBT) were made available to the radiologist. We identified a subset of 21 cancer cases with differences in the number of radiologists who recalled these cases after reviewing either a prior examination or DBT. For the cases with differences in recommendations after viewing either priors or DBT, separately, we evaluated the total number of readers that changed their recommendations, regardless of the specific radiologist in question. Confidence intervals for the number of readers and a test for the hypothesis of no difference was performed using the non-parametric bootstrap approach addressing both case and reader-related sources of variability by resampling cases and readers. With the addition of priors, there were 14 cancer cases (out of 15) where the number of “recalling radiologists” decreased. With the addition of DBT, the number of “recalling radiologists” decreased in only five cases (out of 15) while increasing in the remaining 9 cases. Unlike most new approaches to breast imaging DBT seems to improve both recall rates and cancer detection rates. Changes in recommendations were noted by all radiologists for all cancers by type, size, and breast density.

9787-47, Session PWed

The study of surgical image quality evaluation system by subjective quality factor method

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GreenLightTM procedure is an effective and economical way of treatment of benign prostate hyperplasia (BPH); it counts for more than 50% of BPH surgical procedures. During the surgical procedure, the surgeon or physician will rely on the monitoring video system to survey and confirm the surgical progress. There are a few obstructions that could greatly affect the image quality of the monitoring video, like laser glare by the tissue and body fluid,
air bubbles and debris generated by tissue evaporation, and bleeding, just to name a few. In order to improve the physician's visual experience of a laser surgical procedure, the system performance parameter related to image quality needs to be well defined. However, since image quality is the integrated set of perceptions of the overall degree of excellence of an image, or in other words, image quality is the perceptually weighted combination of significant attributes (contrast, graininess ...) of an image when considered in its marketplace or application, there is no standard definition on overall image or video quality especially for the no-reference case (without a standard chart as reference). In this study, Subjective Quality Factor (SQF) and acutance are used for no-reference image quality evaluation. Basic image quality parameters, like sharpness, color accuracy, size of obstruction and transmission of obstruction, are used as sub-parameter to define the rating scale for image quality evaluation or comparison. Sample image groups were evaluated by human observers according to the rating scale. Surveys of physician groups were also conducted with lab generated sample videos. The study shows that human subjective perception is a trustworthy way of image quality evaluation. More systematic investigation on the relationship between video quality and image quality of each frame will be conducted as a future study.

9787-48, Session PWed

Inter-observer variability within BI-RADS and RANZCR mammographic density assessment schemes

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Mammographic density (MD) is known to increase breast cancer risk of women with dense breasts. Variability in assessment of MD can potentially influence the individualized breast cancer screening pathway of a woman. This study compares variability associated with two visual MD assessment methods using two separate samples of radiologists. The image test-set comprised of images obtained from 20 women (age 42–89 years) imaged on two imaging systems, GE and Hologic, one year apart. The images were assessment for their MD by twenty American Board of Radiology (ABR) examiners and twenty-six Royal Australian and New Zealand College of Radiologists (RANZCR) registered radiologists. Images were assessed using the same technology and conditions, however the ABR radiologists used the BI-RADS and the RANZCR radiologists used the RANZCR breast density synoptic. Both synoptics use a 4-point assessment scale. The images were then grouped as low and high density (named binary classification), with low including BI-RADS 1 & 2 (RANZCR 1 & 2 in study 2) and high including BI-RADS 3 & 4 (RANZCR 3 & 4 in study 2). The mean BI-RADS for the images was lower than RANZCR (2.13 versus 2.18; p<0.843). BI-RADS and RANZCR showed no or negligible correlation (r=0.029; p>0.859). The average inter-observer agreement on BI-RADS had a Kappa of 0.565; [95% CI = 0.519 – 0.610], and ranged between 0.328–0.669 while the inter-observer agreement on RANZCR had a Kappa of 0.360; [95% CI = 0.308 – 0.412] and a range of 0.078-0.499.

9787-49, Session PWed

Observer study to evaluate the simulation of mammographic calcification clusters

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The detection of calcification clusters in mammograms is of great importance for early diagnosis of breast cancer. For this reason, a large number of breast phantoms have been developed posibiliting the insertion of calcifications in simulated background images, which needs to be as realistic as possible to ensure the accuracy of results and a greater range of applications. In this study, we simulated three different densities of the breast parenchyma using paraffin gel, acrylic plates and PVC films and inserted hydroxyapatite grains above to simulate six calcification clusters. From the images acquired with a GE Senographe DR equipment, we selected an equal number of regions of interest (ROIs) with and without a calcification cluster added, totalizing a quantity of 136 ROIs. For comparison, and to validate the phantom simulation, the same number of ROIs was selected from the University of South Florida's Digital Database for Screening Mammography (DDSM). Two observer experiments were performed by seven experienced readers using a high-resolution quality monitor where the observers had to try to identify which was a phantom or real image and if it had or not a calcification cluster inserted. Results shown that the hydroxyapatite calcifications are well hidden in the breast parenchyma simulated which has meant that the observers had more difficulty to identify the presence of the clusters for phantom images. However, there is the need to adapt the simulation of the image background so that it becomes more realistic.

9787-50, Session PWed

A four-alternative forced choice (4AFC) software for observer performance evaluation in radiology

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Four-alternative forced choice (4AFC) method is widely used in observer studies in radiology. To tackle various difficulties in performing 4AFC tests in practice with DICOM image data, we propose a software that is efficient and easy to use. The software is suitable for any experimental design that follows the 4AFC approach. It has a powerful DICOM viewing system that well simulates the clinical reading environment. Its graphical interface allows the observer to adjust the viewing parameters with simple operations. The automated sampling process involved in 4AFC as well as the speed and accuracy of the choice made by the observer is precisely monitored in the background and can be easily exported for further analysis. The software has also a smart instruction and warning mechanism that minimizes possible user mistakes. This software can largely facilitate the 4AFC tests in radiological observer studies and is expected to have widespread applicability.

9787-51, Session PWed

The study on the color reproduction by illumination source for disposable endoscope

Sang Kyeong Park, Young Jae Won, Osong Medical Innovation Foundation (Korea, Republic of)

Most of cameras like CCTV cameras or video cameras are shoot in available light or lightings. But the medical cameras like endoscope or laparoscopy are shoot in the situation in vivo. Generally, inside ad body is lightless and moist. So we can shoot the inside with a single light from outside the body. The study on the color reproduction by illumination source for disposable endoscope needs to be well defined. However, image quality is the perceptually weighted combination of significant attributes (contrast, graininess ...) of an image when considered in its marketplace or application. Basic image quality parameters, like sharpness, color accuracy, size of obstruction and transmission of obstruction, are used as sub-parameter to define the rating scale for image quality evaluation or comparison. Sample image groups were evaluated by human observers according to the rating scale. The automated sampling process involved in 4AFC as well as the speed and accuracy of the choice made by the observer is precisely monitored in the background and can be easily exported for further analysis. The software has also a smart instruction and warning mechanism that minimizes possible user mistakes. This software can largely facilitate the 4AFC tests in radiological observer studies and is expected to have widespread applicability.

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9787-52, Session PWed

**Cellular automata segmentation of the boundary between the compacta of vertebral bodies and surrounding structures**

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Due to the aging population, spinal diseases get more and more common nowadays; e.g., lifetime risk of osteoporotic fracture is 40% for white women and 13% for white men in the United States. Thus the numbers of surgical spinal procedures are also increasing with the aging population and precise diagnosis plays a vital role in reducing complication and recurrence of symptoms. Spinal imaging of vertebral column is a tedious process subjected to interpretation errors. In this contribution, we aim to reduce time and error for vertebral interpretation by applying and studying the GrowCut-algorithm for boundary segmentation between vertebral body compacta and surrounding structures. GrowCut is a competitive region growing algorithm using cellular automata. For our study, vertebral T2-weighted Magnetic Resonance Imaging (MRI) scans were first manually outlined by neurosurgeons. Then, the vertebral bodies were segmented in the medical images by a GrowCut-trained physician using the semi-automated GrowCut-algorithm. Afterwards, results of both segmentation processes were compared using the Dice Similarity Coefficient (DSC) and the Hausdorff Distance (HD) which yielded to a DSC of 82.99±5.03% and a HD of 18.9±7.2 voxel, respectively. In addition, the times have been measured during the manual and the GrowCut segmentations, showing that a GrowCut-segmentation – with an average time of less than six minutes (5.77±0.73) – is significantly shorter than a pure manual outlining.

9787-53, Session PWed

**New conversion factors between human and automatic readouts of the CD Mam phantom for CR systems**

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Mammography screening programs rely on highly accurate image quality (IQ) assessment to guarantee their screening success. The European protocol for the quality control of the physical and technical aspects of mammography screening (EPQC M) requires a contrast detail phantom such as the CD Mam to evaluate IQ. Since human and automatic readouts differ systematically conversion factors were published by the official reference organisation (EUREF). As we experienced a significant difference for these factors for Computed Radiography (CR) systems we developed an objectifying analyses software which presents the cells including the gold disks randomly in thickness and rotation. This allows to overcome the problem of an inevitable learning effect where observers know the position of the disks in advance. We found a conversion factor of 1.01 with the diameter of 0.1 mm compared to 1.59 mm suggested by the EUREF group. We also concluded that the commonly used inverse third degree polynomial fit adds an additional bias to the results.

9787-54, Session PWed

**Variability amongst radiographers in the categorization of clinical acceptability for digital trauma radiography**

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Introduction: According to the literature, radiographers use anatomical criteria when evaluating the clinical acceptability of a radiograph. If it is acceptable for diagnosis or not, may vary between individuals and contexts. The individual character of this decision causes variation in acceptability and retake rate. To minimise variations, definitions of acceptability, such as in RadLex, were developed. It is however unknown on what basis radiographers or other professionals attribute a RadLex score to a radiograph.

Methods: Four radiographers evaluated the visibility of five anatomical structures on, and the exposure of, 25 lateral cervical spine radiographs on a secondary class display using a Visual Grading Analysis (VGA) approach. They judged the clinical acceptability of each radiograph using RadLex and rated their confidence. Relationships between the variables and the RadLex score were analysed with Kendall’s Tau correlation and Nagelkerke pseudo-R2.

Results: The overall VGA score (VGAS) and the RadLex score correlate (r²=0.62, p<0.01, R2=0.72) strongly. The observers’ evaluation of contrast between bone, air (trachea) and soft tissue has low value in predicting (r²=0.55, p<0.01, R2=0.63) the RadLex score. The reproduction of spinous processes (r²=0.67, p<0.01,R2=0.31) and the evaluation of the exposure (r²=0.65, p<0.01, R2=0.56) have a strong correlation with high predictive value for the RadLex score.

Conclusion: RadLex scores and VGAS correlate positively, strongly and significantly. The high predictive value of bony structures, compared to other general criteria such as contrast, may support the use of these anatomical structures in the judgement of clinical acceptability.

9787-55, Session PWed

**A utility/cost analysis of breast cancer risk prediction algorithms**

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Risk prediction algorithms are used in breast cancer screening to identify sub-populations at increased risk for developing breast cancer. They can be based on many different sources of data such as demographics, relatives with cancer, gene expression, and various phenotypic features such as breast density. Women who are identified as high risk will often undergo a more extensive (and expensive) screening process that includes MRI or ultrasound imaging in addition to the standard full-field digital mammography (FFDM) exam.

Given that there are many ways that risk prediction may be accomplished, it is of interest to evaluate them in terms of expected cost, which includes the costs of diagnostic outcomes. In this work we perform an expected-cost analysis of risk prediction algorithms that is based on a published model.
Development and application of a channelized Hotelling observer for digital breast tomosynthesis optimization on structured background test images with mass simulating targets

Dimitar Petrov, UZ Leuven (Belgium); Koen Michaelsen, KU Leuven (Belgium); Lesley Cockmartin, Gouzhi Zhang, UZ Leuven (Belgium); Kenneth C. Young, The Royal Surrey County Hospital NHS Trust (United Kingdom); Nicholas W. Marshall, Hilde Bomsans, UZ Leuven (Belgium)

Digital breast tomosynthesis is a relatively new 3D mammography technique that promises better visualization of low contrast lesions than conventional 2D mammography. A wide range of parameters influence the diagnostic information present in DBT images and a systematic means of DBT system optimization is needed. The gold standard for image quality assessment is to perform an human observer experiment with experienced readers. Using human observers for optimization is time consuming and not feasible given the large parameter space. Our goal was to develop a model observer (MO) that can predict human reading performance for standard tasks contained within an anthropomorphic phantom. This was formed from an acrylic semi-circular vessel containing acrylic spheres of different sizes with the remaining space filled by water. Three types of lesions were included: 3D printed spiculated and non-spiculated and mass lesions along with calcification clusters. The images of the two mass lesion types were reconstructed with 3 different reconstruction methods (FBP, FBP with SRSAR, MLTRpr) and read by human readers. An initial channelized Hotelling observer was created for the non-spiculated lesion detection task using five Laguerre-Gauss channels, matched to the lesion diameter. There was linear relation between the MO and human observer results, with a correlation coefficients of 0.991 for FBP with SRSAR and 0.999 for MLTRpr.

The work for the spiculated mass lesions is still in progress using novel channel architectures. The first results are promising and will be included in the final paper, as well as the results for the images of non-spiculated lesions reconstructed with standard FBP.

Evaluation of image quality of MRI data for brain tumor surgery

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3D medical images are important components of modern medicine. Their usefulness for the physician depends on their quality, though. Only high-quality images allow accurate and reproducible diagnosis and appropriate support during treatment.

We have analyzed 202 MRI images for brain tumor surgery in a retrospective study. Both an experienced neurosurgeon and an experienced neuroradiologist rated each available image with respect to its role in the clinical workflow, its suitability for this specific role, various image quality characteristics, and imaging artifacts.

Our results show that MRI data acquired for brain tumor surgery does not always fulfill the required quality standards and that there is a significant disagreement between the surgeon and the radiologist, with the surgeon being more critical. Noise, resolution, as well as the coverage of anatomical structures were the most important criteria for the surgeon, while the radiologist was mainly disturbed by motion artifacts.

Evaluation of the possibility to use thick slabs of reconstructed outer breast tomosynthesis slices

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The large image volumes in breast tomosynthesis (BT) lead to large amounts of data and increased workload. A possible way to decrease the number of slice images is to combine adjacent image planes, so called slabbing, but the decrease in depth resolution can considerably affect the detection of lesions. The purpose of this work was to assess if slabbing of the outer slice images (where lesions are seldom present) could be a viable alternative in order to reduce the number of slice images in BT image volumes.

The consequences of the suggested slabbing (an image volume with thick outer slabs and thin slices between) were evaluated in two steps. Firstly, a survey of the depth of 65 cancer lesions within the breast was performed to estimate how many lesions would be affected by slabbing of outer slices with varying thickness. Secondly, a selection of 24 lesions was reconstructed with various slab thicknesses to evaluate how the appearance of lesions located in the slabbed region would be affected.

Preliminary results indicate that few malignant breast lesions are located at a depth less than 10 mm from the skin (especially for breast thicknesses of 50 mm and above). Reconstruction of BT volumes with 5 mm slabbing yields an image quality that is sufficient for lesion detection in the majority of the investigated cases. Together this shows that slabbing of the outer slice images is a promising option in order to reduce the number of slice images in BT image volumes.

Automatic and accurate: Quantra reproduces BI-RADS assessment on a two-point scale

Ernest U. Ekpo, Mark F. McEntee, The Univ. of Sydney (Australia); Mary Rickard, The Univ. of Sydney (Australia) and Sydney Breast Clinic (Australia); Patrick C. Brennan, Claudia R. Mello-Thoms, The Univ. of Sydney (Australia)

PURPOSE: To assess the performance of Quantra in reproducing BI-RADS assessment and the cut off value for Quantra that best differentiates high and low-grade BI-RADS categories.

METHODS: Two methods of mammographic breast density measurement were used (Quantra and BI-RADS). Volumetric breast density measurement from 292 raw projection images was performed using Quantra software. Brieﬂy, Quantra employs a physical modeling of mammographic systems to calculate volumetric breast density and segments the estimated VBD to
generate pseudo-BI-RADS categories. BI-RADS assessment was performed by three radiologists and a majority report was generated. Inter-reader agreement (?) and the sensitivity, specificity, and accuracy (Area Under Receiver Operating Characteristic Curve) of Quantra in reproducing the majority BI-RADS report were calculated.

RESULTS: The majority report consisted of 9.6% (n = 28), 35.3% (n = 103), 27.1% (n = 79), and 28.1% (n = 82) for BI-RADS 1, 2, 3, and 4 respectively. Inter-reader agreement (?) ranged from 0.76 to 0.85 on a four-grade scale and substantial to almost perfect (0.79 – 0.91) on a two-grade scale. Quantra correctly classified 35.7%, 91.2%, 88.6%, and 50.5% of BI-RADS 1, 2, 3, and 4 respectively on a four-grade scale and 83.6% of BI-RADS 1-2 and 91.3% of BI-RADS 3-4 on a two-grade scale, and a cut off value of 20.5% allowed for better differentiation between low- and high-grade BI-RADS categories using Quantra.

CONCLUSION: Quantra has limited accuracy in reproducing BI-RADS categories on a four-grade scale, however accurately reproduces BI-RADS assessment on a dichotomous scale that is used in clinical decision-making.

9787-22, Session 5

Validated novel software to measure the conspicuity index of focal lesions within DICOM images

Katy Szczepura, Univ. of Salford (United Kingdom); David J. Manning, Lancaster Univ. (United Kingdom)

Description of purpose
A novel software programme and associated Excel spreadsheet has been developed to provide an objective measure of the expected visual detectability of focal abnormalities within DICOM images.

Method
ROIs are drawn around the abnormality, the software then fits the lesion using a least squares method to recognise the edges of the lesion based on the full width half maximum. 180 line profiles are then plotted around the lesion, giving 360 edge profiles.

The co-ordinates of the edge profiles are captured, as well the standard deviation of the pixel values within the background and lesion (representing anatomical noise and lesion noise respectively). An Excel spreadsheet has been developed to allow variables to be calculated, including SNR and CNR. A conspicuity index has also been developed.

Results
The software has been validated using the GAMMEX ACR CT accreditation phantom and results have been found to give a linear response

New work to be presented
Both the software and the analysis of conspicuity index will be presented with proof of concept observer results.

Conclusion
A novel software programme has been validated to allow calculation of many physical properties of lesions. Additionally, a new measure of conspicuity index has been developed for focal lesions. The analysis could be further developed to incorporate JAFROC and eye-tracking data allowing correlations between physical and perception measures to be made beyond basic CNR calculations, it could also be used as a tool to distinguish between perceptual and cognitive error.

Further refinements could lead to measures of the detectability of more diffuse disease features.

9787-23, Session 5

Impact of two types of image processing on cancer detection in mammography

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The impact of image processing on cancer detection is still a concern to radiologists and physicists. This work aims to evaluate the effect of two types of image processing on cancer detection in mammography. An observer study was performed in which three radiologists inspected 349 cases (a mixture of normal cases, benign lesions and cancers) processed with two types of image processing. The observers marked areas they were suspicious were cancers. JAFROC analysis was performed to determine if there was a significant difference in cancer detection between the two types of image processing. Cancer detection was not significantly different with the standard setting image processing compared with one that provides enhanced image contrast for masses, focal asymmetries and architectural distortions (p=0.17) and calcification clusters (p=0.18). By September 2015 seven observers will have completed reading the images and their results will be included in the full paper and presentation if accepted.

9787-24, Session 5

Discriminatory power of common genetic variants in personalized breast cancer diagnosis

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Technology advances in genome-wide association studies (GWAS) and successes with cost reduction in genome-sequencing have engendered optimism that we have entered a new age of precision medicine, in which the risk of breast cancer can be predicted on the basis of a person’s genetic variants. The goal of this study is to demonstrate the discriminatory power of common genetic variants in breast cancer risk estimation. We conducted a retrospective case-control study drawing from an existing personalized medicine data repository. We collected variables that predict breast cancer risk: 153 high-frequency/low-penetrance genetic variants, reflecting the state-of-the-art GWAS on breast cancer, mammography descriptors and assessment categories recorded prospectively in the Breast Imaging Reporting and Data System (BI-RADS) lexicon. We trained and tested three naïve Bayes models by using these predictive variables. We generated ROC curves and used the area under the ROC curve (AUC) to quantify predictive performance. We found that genetic variants achieved comparable predictive performance to BI-RADS assessment categories in terms of AUC (0.655 vs. 0.646, p-value = 0.742), but significantly lower predictive
performance than the combination of BI-RADS assessment categories and mammography descriptors (0.655 vs. 0.750, p-value < 0.001). A better understanding of relative predictive capability of genetic variants and mammography data may benefit clinicians and patients to make appropriate decisions of breast cancer screening, prevention, and treatment in the era of precision medicine.

9787-25, Session 5

Potential workflow advantages with single 8MP versus dual 5MP displays

Elizabeth A. Krupinski, The Univ. of Arizona (United States)

This study compared an 8MP vs dual-5MP displays for diagnostic accuracy, reading time, number of times readers zoomed/panned images, and visual search. Six radiologists viewed 60 mammographic cases, once on each display, 15 with eye-tracking. For viewing time, there was significant difference (F = 13.901, p = 0.0002), with 8MP taking less time (62.04 sec vs 68.99). There was no significant difference (F = 0.254, p = 0.6145) in zoom/pan use (1.94 vs 1.89). Total number of fixations was significantly (F = 4.073, p = 0.0466) lower with 8MP (134.47 vs 154.29). Number of times readers scanned between images was significantly fewer (F = 10.305, p = 0.0018) with single (6.83 vs 8.22). Time to first fixate lesion did not differ (F = 0.126, p = 0.7240). It did not take any longer to detect the lesion as a function of the display configuration. Total time spent on lesion did not differ (F = 0.097, p = 0.7567) (8.59 vs 8.39). Overall the single 8MP display yielded the same diagnostic accuracy as the dual 5MP displays. The lower resolution did not appear to influence the readers’ ability to detect and view the lesion details, as the eye-position study showed no differences in time to first fixate or total time on the lesions. Nor did the lower resolution result in significant differences in the amount of zooming and panning that the readers did while viewing the cases.

9787-26, Session 6

Ranking inconsistencies in the assessment of digital breast tomosynthesis (DBT) reconstruction algorithms using a location-known task and a search task

Xin He, Rongping Zeng, Frank W. Samuelson, Berkman Sahiner, U.S. Food and Drug Administration (United States)

In this work, we validate task-based evaluations by investigating ranking inconsistencies. We applied previously developed theory to assess digital breast tomosynthesis (DBT) image quality using a scanning channelized Hotelling observer (CHHO) on a simulated DBT dataset. We compared the performance of five reconstruction algorithms: FBP, ML, SART, TVLS with strong and mild regularization settings. The results showed that the location-known-exactly (LKE) detection performance for the reconstruction techniques was almost identical. However the search characteristic, as described by effective set size (M*), was different. We attempted to use the differences in M* to explain the significantly different AUC values in the search task. To falsify/corroborate our evaluations on the search characteristic, we conducted an image-size test. This test demonstrated agreement between theoretical predictions and empirically measured observer performance in absolute performance levels, except for the ML algorithm. We concluded that evidence corroborated our evaluations, except that for the ML algorithm our evaluation was invalid. Subsequently we observed a ranking inconsistency, in terms of AUC values, between the ML and the other algorithms as the image size changes, further confirming our evaluation on the ML algorithm was indeed invalid. An investigation of the invalid evaluation showed that ranking inconsistencies existed, even using ROC analysis without M*. The falsifiable nature of M* allowed such inconsistencies to be identified, which further enabled mitigation approaches to be implemented. We concluded that LKE and search tasks may lead to inconsistent performance rankings, as well as that search tasks of different settings (e.g., image ROI size) may lead to inconsistent performance rankings.

9787-27, Session 6

Model observer design for detecting multiple abnormalities in anatomical background images

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As psychophysical studies are resource-intensive to conduct, model observers are commonly used to assess or optimize medical imaging quality. Existing model observers were typically designed to detect at most one signal. However, in clinical practice, there may be multiple abnormalities in a single image set (e.g., multifocal and multicentric breast cancers), which can have a huge impact on treatment planning. Prevalence of signals can be different across anatomical regions, and human observers do not know the number or location of signals a priori. As new imaging techniques have the potential to improve multiple-signal detection (e.g., digital breast tomosynthesis may find MRI-ocult multifocal invasive lobular carcinomas), image quality assessment approaches addressing such tasks are desirable. In this study, we present a model-observer mechanism to detect multiple signals in the same image dataset. To handle the high dimensionality of images, a novel implementation of partial least squares (PLS) was developed to estimate different sets of efficient channels directly from the images. Without any prior knowledge of the background or the signals, the PLS channels are expected to capture interactions between signals and the background which provide discriminant image information. Corresponding linear decision templates were then employed for generating both image-level and location-specific scores regarding the presence of signals. Our preliminary results show that the model observer using PLS channels, compared to our first attempts with Laguerre-Gauss channels, can achieve high performance with a reasonably small number of channels, and the optimal design of the model observer may vary as the tasks of clinical interest change.

9787-28, Session 6

Visual-search observers for SPECT simulations with clinical backgrounds

Howard C. Gifford, Univ. of Houston (United States)

The purpose of this work was to test the ability of several visual-search (VS) model observers to mimic the lesion-detection performance of human observers with hybrid SPECT images. These images consist of clinical backgrounds with simulated abnormalities. The application of existing scanning model observers to hybrid images is complicated by the need for extensive statistical information, whereas VS models based on a two-stage search-and-analysis process operate with reduced knowledge. A VS observer generates decision discriminants from morphological feature data that contain implicit anatomical information. A localization ROC (LROC) study involved the detection and localization of solitary pulmonary nodules in Tc-99m lung images. The study was aimed at optimizing the number of iterations and the postfiltering of four rescaled block-iterative (RBI) reconstruction strategies with various combinations of attenuation correction, scatter correction, and system resolution correction. Multifeature versions of the VS observer were tested, as were adaptive versions which can select the features of interest either on a set-specific or location-specific basis. A comparison of these model results against previously acquired human-observer data is presented.
Three scenarios of location-known detection and search performance ranking inconsistencies: a collection of experimental findings after an initial exploration of the underlying mechanism

Xin He, Frank W. Samuelson, Rongping Zeng, Berkman Sahiner, U.S. Food and Drug Administration (United States)

We previously proposed a falsifiable search assessment theory, which revealed a mechanism for search and detection ranking inconsistencies. In this work, we identified four publications from two groups of authors (He, Samuelson, Zeng and Sahiner JOSA 2014 and SPIE 2016; Park, Kupinski, Clarkson and Barrett, IPMI 2003 and JOSA 2005). These publications compared LKE and search performance for a variety of observers using the AUC value as the performance criterion (human, CHOs for detection and scanning CHOs for search, and the Markov Chain Monte Carlo ideal observer for detection and search). We categorize the experimental findings into three types of ranking inconsistencies: 1) Ranking inconsistencies in LKE and search tasks in system comparisons; 2) human/ideal observer ranking inconsistencies; and 3) LKE/search ranking inconsistency in the presence of signal variability. The empirical evidence presented in this work suggests that ranking inconsistencies for imaging systems exist, but are often not identified in the literature.

Investigation on location-dependent detectability of a small mass for digital breast tomosynthesis evaluation

Changwoo Lee, Jongduk Baek, Yonsei Univ. (Korea, Republic of); Subok Park, U.S. Food and Drug Administration (United States)

Digital breast tomosynthesis (DBT) is an emerging imaging modality for improved breast cancer detection and diagnosis. Numerous efforts [1-3] have been made to find quantitative metrics associated with mammographic image quality assessment, such as value of anatomical noise power spectrum, glandularity, contrast, etc. In addition, with the use of the Fourier-domain detectability index for a task-based assessment of DBT, a stationarity assumption on reconstructed image statistics was often made, resulting in the use of multiple regions-of-interest (ROIs) from different locations in order to increase sample size [4-5]. While all these metrics provide some information on mammographic image characteristics and signal detection, the relationship between these metrics and detectability in DBT evaluation has not been fully understood. In this work, we investigated spatial-domain detectability trends and levels as a function of the number of slices Ns at three different ROI locations on the same image slice, where background statistics differ in terms of the aforementioned metrics. Detectabilities for the three ROIs were calculated using multi-slice channelized Hotelling observers with 2D/3D Lg channels. Our simulation results show that detectability levels and trends as a function of Ns vary across the three ROI locations. They also show that the values of ?, mean glandularity, and mean attenuation coefficient vary across the three ROI locations but they do not necessarily predict the ranking of detectability levels and trends across these ROI locations.

Machine-learning model observer for detection and localization tasks in clinical SPECT-MPI

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In this work we propose a machine-learning MO based on Naive-Bayes classification (NB-MO) for the diagnostic tasks of detection, localization and assessment of perfusion defects in SPECT Myocardial Perfusion Imaging (MPI), with the goal of evaluating several reconstruction methods in both simulated and clinical SPECT-MPI data. NB-MO uses polar-map image features in order to predict lesion detection, localization and severity scores given by five human readers in a series of 3D SPECT-MPI simulated cases. Simulated projections were reconstructed using two image reconstruction methods (FBP and OSEM), using a range of smoothing levels that we aim to optimize using the proposed MO. For validation, a multi-reader multi-case (MRMC) analysis of alternative free-response ROC (AFROC) curve is performed for NB-MO and human observers. Results show good generalization to reconstruction methods not used during training, as well as optimal smoothing values whose ranges agree with those used in clinical practice. Next, in a second experiment, we apply the same NB-MO (trained with simulated cases) to predict human perfusion scores on a set of clinical SPECT-MPI polar maps, with the goal of assessing three scatter compensation methods, namely: no scatter correction, Triple Energy Window (TEW) method, and Effective Source Scatter Estimation (ESSE). The clinical population comprises healthy individuals and patients suffering from coronary artery disease (CAD) in three possible regions, namely: LAD, LCx and RCA. AFROC-MRMC analysis shows that NB-MO predicts higher human performance for scatter-compensated reconstructions, in agreement with what reported in published literature.

Varying performance in mammographic interpretation across two countries: Do results indicate reader or population variances?

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Aim: To compare the performance of Australia and Singapore breast readers interpreting a single test-set that consisted of mammographic examinations collected from an Australia population.

Background: In the tele-radiology era, breast readers are interpreting mammographic examinations from different populations. The question arises whether two groups of readers with similar training backgrounds, demonstrate the same level of performance when presented with a population familiar only to one of the groups.

Methods: Fifty-three Australian and 15 Singaporean breast radiologists participated in this study. All radiologists were trained in mammogram interpretation and had a median of 9 and 15 years of experience in reading mammograms respectively. Each reader interpreted the same BREASt test-set consisting of sixty de-identified mammographic examinations arising from an Australian population. Performance parameters including JAFROC,
25% higher cancer detection rate and 20% reduction in the recall rate for cancer screening have been published in a large number of studies with advantages of two projections over single MLO mammogram for breast later the cranio-caudal (CC) was proposed as a subsequent projection. The (MLO) mammography of each breast was the routine examination and radiologists mammogram projection among populations of radiologists. The influence of reading images that are different from those that radiologists normally encounter cannot be ruled out and requires further investigation, particularly in the light of increasing international outsourcing of radiologic reporting.

9787-33, Session 7

Luminance level of a monitor: influence on detectability and detection rate of breast cancer in 2D mammography
Frédéric Bemelmans, KU Leuven (Belgium); Alaleh Rashid Nasab, KU Leuven (Belgium) and Univ. College London (United Kingdom); Frédérique Chesterman, Tom R. L. Kimpe, Barco N.V. (Belgium); Hilde Bomsans, KU Leuven (Belgium) and UZ Leuven (Belgium)

Purpose: To evaluate lesion detectability and reading time as a function of luminance level of the monitor.

Material and Methods: 3D mass models and microcalcification clusters were simulated into ROIs of normal raw ('for processing') mammograms. Randomly selected ROIs were subdivided in three groups according to their background glandularity (using Volpara): high (>30%), medium (15-30%) and low (<15%). 6 non-spiculated masses (9 – 11mm), 6 spiculated masses (5 – 7mm) and 6 microcalcification clusters (2 – 4mm) were scaled in 3D to create a range of sizes. The linear attenuation coefficient (AC) of the masses was adjusted from 100% glandular tissue to 90%, 80%, 70%, to create different contrasts. A new software tool organized segments with and without signal in a 4-AFC experiment. Six physicists read the full database on a Barco Coronis Unit monitor for four different luminance levels (300, 800, 1000 and 1200 Cd/m2); Percentage correct (PC) and reading time per session were computed for all different conditions. A paired t-test was performed to evaluate the effect of luminance on PC and time. A multi-factorial analysis was performed using MANOVA.

Results: Paired t-test indicated a statistically significant difference for the average time per session between 300 and 1000; 300 and 1200; 800 and 1200 Cd/m2, for all participants combined. There was no effect on PC for different luminance levels. MANOVA denoted a significant influence of background glandularity and inter reader variability on time and PC.

Conclusion: These results demonstrate a significant decrease in reading time, while detectability remained constant.

9787-34, Session 7

The effectiveness of the cranio-caudal mammogram projection among radiologists
Phuong Dung Trieu, Warwick B. Lee, Kriscia A. Tapia, Patrick C. Brennan, The Univ. of Sydney (Australia)

When breast screening was firstly applied, a single medio-lateral oblique (MLO) mammography of each breast was the routine examination and later the cranio-caudal (CC) was proposed as a subsequent projection. The advantages of two projections over single MLO mammogram for breast cancer screening have been published in a large number of studies with 25% higher cancer detection rate and 20% reduction in the recall rate for assessment being reported. However, these studies also showed that 26% of cancers that required two projections were described as normal or benign on the oblique mammograms but suspicious or probably malignant on the CC projection. Although these studies indicated the contribution of the CC as part of the total examination, information about radiologists’ performance on the single CC projection alone was not available. The aim of this study is to compare the diagnostic accuracy of readers on single CC projection versus traditional two projection mammograms to assess the specific capabilities of single CC approaches when required in certain economic or cultural circumstances.

Sixteen radiologists were invited to report a set of 60 two projection mammograms of left and right breasts. These images were retrospectively collected from the BreastScreen New South Wales digital library, among them were 20 cancer cases. The task of participants was to search for the presence of breast lesions on images and rate the confidence levels of their decisions where 2 represented a benign lesion; 3-5 represented the possibility of a malignancy with a higher value indicating a higher confidence. The reader performance in detecting cancer cases and normal cases were evaluated via sensitivity, lesion sensitivity and specificity. The results demonstrated that BreastScreen readers or radiologists who read more than 150 cases per week demonstrated the same level of diagnostic accuracy on the single CC mammogram as two projection mammography. The implications and value of these findings will be discussed as well the caution that should be exercised.

9787-35, Session 7

Investigating the link between the radiological experience and the allocation of an equivocal finding
Mohammad A. Rawashdeh, Camila Vidotti, Warwick B. Lee, Sarah J. Lewis, Claudia R. Mello-Thoms, Warren M. Reed, Kriscia A. Tapia, Patrick C. Brennan, The Univ. of Sydney (Australia)

Rationale and Objectives: This study will investigate the link between radiologists’ experience in reporting mammograms, their caseloads and the decision to give a classification of Royal Australian and New Zealand College of Radiologists (RANZCR) category ‘3’ (indeterminate or equivocal finding).

Methods: A test set of 60 mammograms comprising of 20 abnormal and 40 normal cases were shown to 92 radiologists. Each radiologist was asked to identify and localize abnormalities and provide a RANZCR assessment category. Details were obtained from each reader regarding their experience, qualifications and breast reading activities. ‘Equivocal fractions’ were calculated by dividing the number of ‘equivocal findings’ given by each radiologist in the abnormal and normal cases by the total number of cases analyzed: 20 and 40 respectively. The ‘equivocal fractions’ for each of the groups (normal vs abnormal) were calculated and independently correlated with age, number of years since qualification as a radiologist, number of years reading mammograms, number of mammograms read per year, number of hours reading mammograms per week and number of mammograms read over lifetime (the number of years reading mammograms multiplied by the number of mammograms read per year).

The non-parametric Spearman test was used.

Results: Statistically negative correlations were noted between ‘equivocal fractions’ for the following groups:
• For abnormal cases: hours per week (r = -0.38 P = 0.0001)
• For normal cases: total number of mammograms read per year (r = -0.29, P = 0.006); number of mammograms read over lifetime (r = -0.21, P = 0.049); hours reading mammograms per week (r = -0.20, P = 0.05).

Conclusion: Radiologists with greater reading experience assign fewer RANZCR category 3 or equivocal classifications. The findings have implications for screening program efficacy and recall rates. This work is still in progress and further data will be presented at the conference.
The interplay of attention economics and CAD marks interpretation in screening mammography

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Introduction: According to attention economists, overabundant information leads to decreased attention for individual pieces of information. Computer-aided detection (CAD) alerts radiologists to findings potentially associated with breast cancer but is notorious for creating an overabundance of false-positive marks. We suspected that increased CAD marks do not lengthen mammogram interpretation time, as radiologists will selectively disregard these marks when present in larger numbers. We explore the relevance of attention economics in mammography by examining how number of CAD marks affects interpretation time.

Methods: We performed a retrospective review of bilateral digital screening mammograms obtained between January 1, 2011 and February 28, 2014, using only weekend interpretations to decrease distractions and the likelihood of trainee participation. We stratified data according to reader and used ANOVA to test the relationship between number of CAD marks and interpretation time.

Results: Ten radiologists, with median experience after residency of 12.5 years (range 6 to 24) interpreted 1849 mammograms. When accounting for number of images, Breast Imaging Reporting and Data System category, and breast density, increasing numbers of CAD marks was correlated with longer interpretation time only for the three radiologists with the fewest years of experience (median 7 years.)

Conclusion: For the 7 most experienced readers, increasing CAD marks did not lengthen interpretation time. We surmise that as CAD marks increase, the attention given to individual marks decreases. Experienced radiologists may rapidly dismiss larger numbers of CAD marks as false-positive, having learned that devoting extra attention to such marks does not improve clinical detection.

Importance of the grayscale in early assessment of image quality gains with iterative CT reconstruction

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Iterative reconstruction methods have become an important research topic in X-ray computed tomography (CT), due to their ability to yield improvements in image quality in comparison with the classical filtered backprojection method. There are many ways to design an effective iterative reconstruction method. Moreover, for each design, there may be a large number of parameters that can be adjusted. Thus, early assessment of image quality, before clinical deployment, plays a large role in identifying and refining solutions. Currently, there are few publications reporting on early, task-based assessment of image quality achieved with iterative reconstruction methods. We report here on such an assessment, and we illustrate at the same time the importance of the grayscale used for image display when conducting this type of assessment. Our results further support observations made by others that the edge preserving penalty term used in iterative reconstruction is a key ingredient to improve image quality in terms of detection task. Our results also provide a clear demonstration of an implication made in one of our previous publication, namely that the grayscale window plays an important role in image quality comparisons involving iterative CT reconstructions.

Validation of no-reference image quality index for the assessment of digital mammographic images

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To ensure optimal clinical performance of digital mammography, it is necessary to obtain images with high spatial resolution and low noise, using as little radiation as possible. These requirements directly affect the performance of radiologists. The quality of a digital image can be assessed using objective measurements. In general, these methods measure the similarity between an image and its reference without degradation (ground-truth). However, for digital mammography, an objective method to assess the quality of images must be performed without reference measurements, as ground-truth is not available in clinical practice. This study proposes a no-reference index to assess mammography images, by using the correlation between Rényi entropy in the pseudo-Wigner domain to evaluate spatial resolution and quantum noise degradation based on the human visual system (HVS). The method was validated using synthetic images from a digital phantom and clinical exposures on a physical anthropomorphic breast phantom at different radiation doses. The results reported by the blind index follow the same behavior as other well-established metrics, e.g., the peak signal-to-noise ratio (PSNR) and structural similarity index (SSIM). Thus, this index may be used in clinical practice as an image quality indicator to improve the quality assurance programs in mammography; hence, the proposed method reduces the subjectivity inter-observers in the reporting of image quality assessment.

Impact of large beam collimation on image quality

Damien Racine, Alexandre H. Ba, Julien G. Ott, François O. Bochud, Francis R. Verdun, Ctr. Hospitalier Univ. Vaudois (Switzerland)

Large beam collimation in computed tomography opens the way to a new form of examination and improves patient management for several clinical indications. The systems that offer large collimation enable a whole region of interest to be investigated with an excellent temporal resolution. One of the potential drawbacks of this option might be a noticeable difference in image quality along the z-axis. The aim of this project is to investigate the impact of the use of large beam collimation and new iterative algorithms on noise properties, spatial resolution and low contrast detectability (LCL). An anthropomorphic phantom and a custom made phantom were scanned on a GE Revolution CT and a GE HD 750. The images were reconstructed respectively with ASIR-V at 0% and 50% and FBP. Noise power spectrum to evaluate the noise properties and the Target Transfer Function to evaluate the spatial resolution were computed. Then the Channelized Hotelling Observer with Dense Difference of Gaussian was used to evaluate the LCL (quantified using the area under the ROC curve as a figure of merit). Noticeable differences of 2D noise power spectrum have been recorded; however no significant difference appeared when dealing with spatial resolution criteria and slightly difference appeared when dealing with the LCL criteria. As expected the use of iterative reconstruction allowed a
Predicting radiologists’ true and false positive decisions in reading mammograms by using gaze parameters and image-based features

Ziba Gandomkar, Kevin Tay, William J. Ryder, Patrick C. Brennan, Claudia R. Mello-Thoms, The Univ. of Sydney (Australia)

Radiologists’ gaze-related parameters combined with image-based features were utilized to classify suspicious mammographic areas identified by radiologists as True Positives (TP) and False Positives (FP). Eight breast radiologists read 120 two-view digital mammograms of which 59 had biopsy proven cancer. Eye tracking data were collected and nearby fixations were clustered together. Suspicious areas on mammograms were independently identified based on thresholding intensity saliency map followed by automatic segmentation and pruning steps. For each radiologist reported area, radiologists’ fixation clusters in the area as well as neighboring suspicious areas within 2.50 of the center of fixation were found. A 45-dimensional feature vector containing gaze parameters of the corresponding cluster along with image-based characteristics was constructed. Gaze parameters included total number of fixations in the cluster, dwell time, time to hit the cluster for the first time, maximum number of consecutive fixations, and saccade magnitude of the first fixation in the cluster. Image-based features consisted of intensity, shape, and texture descriptors extracted from the neighboring suspicious area, its surrounding tissue, and the entire breast. For each radiologist, a user-specific Support Vector Machine (SVM) model was built to classify the reported areas as TPs or FPs. Leave-one-out cross validation was utilized to avoid over-fitting. Feature selection step was embedded in SVM training procedure by allowing radial basis function kernels to have 45 scaling factors. The proposed method was compared with the radiologists’ performance using the jackknife alternative free-response receiver operating characteristic (JAFROC). The JAFROC figure of merit increased significantly for six radiologists.

Effect of anatomical backgrounds on detectability in volumetric cone beam CT images

Minah Han, Yonsei Univ. (Korea, Republic of); Subok Park, U.S. Food and Drug Administration (United States); Jongduk Baek, Yonsei Univ. (Korea, Republic of)

Previously we compared the effects of reconstruction noise on signal detection in axial and coronal planes of volumetric cone beam CT (CBCT). As anatomical noise is often a dominating factor affecting signal detection in medical imaging, in this work we investigate the effects of anatomical backgrounds on signal detection in volumetric CBCT images. Signal detection performances are compared between axial and coronal planes with either uniform or anatomical backgrounds. Sphere objects with diameters of 1 mm, 5 mm, 8 mm, and 11 mm are used as the signals. Three-dimensional (3D) anatomical backgrounds are generated using an anatomical noise power spectrum, $1/f^{\beta}$, with $\beta=3$. The mean voxel value of the 3D anatomical backgrounds is used as an attenuation coefficient of the uniform background. Noisy projection data are acquired by the forward projection of the uniform and anatomical 3D backgrounds with/without sphere lesions and by the addition of quantum noise. Then, images are reconstructed by FDK algorithm. For each signal size, signal detection performances in axial and coronal planes are measured by calculating the task-SNR of a channelized Hotelling observer with difference-of-Gaussian channels. In the uniform background case, axial planes yield higher task-SNR values for all sphere diameters and 3 mm. In the anatomical background case, coronal planes yield higher task-SNR values for all signal diameters. The results indicate that it is beneficial to use coronal planes to detect spherical signals in anatomical backgrounds.

Quantitative image quality evaluation for cardiac CT reconstructions

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Maintaining or even improving image quality while in motion is always desirable in clinical Cardiac CT imaging. Various image-reconstruction algorithms are available on current commercial CT systems. It is now clear that image-quality assessment should be task-based and the image quality evaluation process should involve a specific task, observer, and associated figure of merit. In this work, the observer performance on a task that involves estimation of percentage of plaque in a vessel was evaluated. We compared task performance of Cardiac CT image data reconstructed using a conventional FBP reconstruction algorithm and SnapShot Freeze (SSF) algorithm, each at default and optimal reconstruction phases. The purpose of this work is to design an approach of quantitative image-quality evaluation of temporal resolution for Cardiac CT systems. To simulate heart motion, a moving coronary type phantom synchronized with an ECG signal was used. Three different percentage plaques imbedded in a 3 mm vessel phantom were imaged multiple times under motion free, 60 bpm, and 80 bpm heart rates to obtain better statistics. Static (no motion) images of this phantom were taken as reference images for image template generation. Independent signal present ROIs of 60 bpm and 80 bpm were generated by vessel tracking for the estimation observer testing. Ensemble mean square error (EMSE) was used as the figure of merit. Results suggest that better image quality can be achieved in higher heart rate scans if SSF algorithm is applied.

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9787-40, Session 8

Predicting radiologists’ true and false positive decisions in reading mammograms by using gaze parameters and image-based features

9787-41, Session 8

Quantitative image quality evaluation for cardiac CT reconstructions

9787-42, Session 8

Effect of anatomical backgrounds on detectability in volumetric cone beam CT images
Alzheimer's disease imaging biomarkers using small-angle x-ray scattering

Mina Choi, Nadia Halam, Tajdar Warraich, Bahaa Ghammraoui, Aldo Badano, U.S. Food and Drug Administration (United States)

The proteins beta amyloid (Aβ) and tau are biological hallmarks of Alzheimer’s disease (AD) and have been extensively studied in an in vitro setting under various solvent conditions. Well-characterized x-ray cross sections of these proteins could potentially be used as AD biomarkers for small-angle x-ray scattering (SAXS) imaging.

We report the SAXS profiles of Aβ(43) at temperatures between -10 and 37°C, in solvents of varying pH values. Preliminary results show that SAXS provides distinct profiles for characterizing the level of aggregation of these proteins. In addition, this work provides coherent scattering cross sections of AD biomarkers useful for Monte Carlo x-ray transport simulations. Using these simulations, we can assess the performance of SAXS imaging in locating these biomarkers at varying aggregation levels within complex sample geometries.

Investigation of signal thresholding to reduce the effects of instrument noise of an EMCCD based micro-CT system

Alexander R. Podgorsak, Sumukh Bysani Krishnakumar, Univ. at Buffalo (United States) and Toshiba Stroke and Vascular Research Ctr. (United States); Swetadri Vasen Setlur Nagesh, Daniel R. Bednarek, Toshiba Stroke and Vascular Research Ctr. (United States); Stephen Rudin, Toshiba Stroke and Vascular Research Ctr. (United States) and Univ. at Buffalo (United States); Ciprian N. Ionita, Univ. at Buffalo (United States) and Toshiba Stroke and Vascular Research Ctr. (United States)

This project investigated the signal thresholding effectiveness at reducing the instrument noise of an electron multiplying CCD (EMCCD) based micro-CT system at low x-ray exposure levels. Scans of a mouse spine were taken using an EMCCD detector coupled with a micro-CT system. An iodine filter of 4 mg/cm² area density was placed in the beam to shape the spectrum. The output signal was thresholded at 0.5σ and 1.0σ, where σ is the root mean square of the inherent background instrument noise. For each threshold, 100, 200, and 300 frames were summed for each projection to evaluate the effect on the reconstructed image. The projection images from the scans were compared using line profiles and their signal to noise ratio (SNR). Our results indicate that, as the threshold was increased, the line profiles of the projection images showed less statistical variation, but also lower signal levels, so that the SNR of the projection images decreased as the threshold increased. When the line profile of a projection image obtained using a signal threshold is compared with one obtained using energy integrating mode, the profile obtained using thresholding had less variation than that obtained using energy integration, which indicates less instrument noise. The SNR at the edges of the bone is higher in the thresholded images when compared with the energy integrated projection images. In conclusion, thresholding the output signal from an EMCCD detector at low x-ray exposure levels is an effective method to reduce the instrument noise of an EMCCD detector. Supported by NIH grant 2R01EB002873.

High-resolution dynamic speech imaging with joint low-rank and atlas-driven sparsity constraints

Maojing Fu, Univ. of Illinois at Urbana-Champaign (United States); Jonghye Woo, Ctr. for Advanced Medical Imaging Sciences, Massachusetts Genral Hospital (United States); Zhi-Pei Liang, Bradley P. Sutton, Univ. of Illinois at Urbana-Champaign (United States)

Dynamic speech magnetic resonance imaging (DS-MRI) has been recognized as a promising technique for visualizing articulatory motion in real time. Recent work has enabled increased imaging speed and image quality in DS-MRI, resulting in challenges to interpret speech data sets with varying aggregation levels within complex sample geometries.

This work describes a methodology for efficient removal of scatter radiation in digital mammography by introducing a spatiotemporal atlas and using it as prior information in the reconstruction. This method is achieved by integrating a novel sparsity constraint, based on deviations from the spatiotemporal atlas, into a Partial Separability (PS) model-based imaging framework. The proposed method allows high-quality reconstruction of the articulatory motion with a spatial resolution of 2.2 mm x 2.2 mm, a nominal frame rate of 100 frames per second (fps), and integrated registration to the atlas. Also, the method allows quantitative comparison of the articulatory motion with the atlas for both a single subject or across all subjects. DS-MRI in vivo experiments were performed on human volunteers and the practical utility of the method has been systematically examined and demonstrated.

Design and evaluation of a grid reciprocation scheme for use in digital breast tomosynthesis

Tushita Patel, Helen Sporkin, Heather Peppard, Mark B. Williams, Univ. of Virginia (United States)

This work describes a methodology for efficient removal of scatter radiation during digital breast tomosynthesis (DBT). The goal of this approach is to enable grid image obscuration without an increase in radiation dose by minimizing misalignment of the grid focal point (GFP) and x-ray focal spot (XFS) during grid reciprocation. Hardware for the motion scheme was built and tested on the dual modality breast tomosynthesis (DMT) scanner, which combines DBT and mammography on a single gantry. The DMT scanner uses fully isocentric rotation of tube and x-ray detector for maintaining a fixed tube-detector alignment during DBT imaging. A cellular focused copper prototype grid with 80 cm focal length, 3.85 mm height, 0.1 mm thick lamellae, and 1.1 mm hole pitch was tested. Primary transmission of the grid at 28 kV tube voltage was 74% with the grid stationary and aligned for maximum transmission. It fell to 72% during grid reciprocation by the proposed method. Residual grid line artifacts (GLAs) in projection views and reconstructed DBT images are characterized and methods for reducing the visibility of GLAs in the reconstructed volume through projection image flat-field correction and frequency-based filtering of the DBT slices are described and evaluated. The described software correction method reduces the visibility of these artifacts in the reconstructed volume, making this design a viable option for a more efficient grid reciprocation method.
9788-5, Session 1

**Performance modeling of a wearable Brain PET (BET) camera**

Charles R. Schmidtlein, Memorial Sloan-Kettering Cancer Ctr. (United States); James N. Turner, Binghamton Univ. (United States); Michael O. Thompson, Cornell Univ. (United States); Krishna C. Mandal, Univ. of South Carolina (United States); Jiahian Zhang, Syracuse Univ. (United States); John L. Humm, Memorial Sloan-Kettering Cancer Ctr. (United States); David H. Feiglin, Andrzej Krol, SUNY Upstate Medical Univ. (United States)

We explored by means of analytical and Monte Carlo modeling performance of a novel wearable helmet-shaped Brain PET (BET) camera based on thin-film digital Geiger Avalanche Photo Diode (dGAPD) and LYSO scintillator for imaging in vivo human brain processes of freely moving and acting subjects.

We assessed a spherical cap BET and cylindrical brain PET (CYL) device, 25 cm diameter and the same mass of LYSO scintillator. We also considered a clinical whole body (WB) LYSO PET/CT scanner. BET consisted of distributed Autonomous Detector Arrays (ADAs) integrated into Intelligent Autonomous Detector Blocks (IADBs). The ADA comprised of an array of small LYSO scintillator voxels with reflective layers on its five sides and sixth side optically coupled to the matching array of thin-film dGAPDs and processing electronics with total thickness of 50um. The total thickness of the detector was in the 5-25mm range. Simulated energy resolution was in the 10-50% range, with the discriminator setting in the 250-350keV and 650-750keV the lower and upper discriminator level, respectively. The timing resolution was 100-250ps. The coincidence window was set at 1ns.

We observe that BET has higher and very different sensitivity and scatter pattern, as compared to CYL and WB. The mean NEC is much higher for BET, as compared to CYL and WB. BET with 0.5x0.5mm2 scintillator crystals can provide 0.78mm FWHM spatial resolution. We conclude that ultra-high-resolution and sensitivity, parallax-free, low-cost wearable brain PET (BET) with LYSO scintillator mass of about 12 kg is feasible.

9788-6, Session 2

**3D choroid neovascularization growth prediction based on reaction-diffusion model**

Shuxia Zhu, Xinjian Chen, Dehui Xiang, Fei Shi, Soochow Univ. (China); Haoyu Chen, Shantou Univ. (China); Weifang Zhu, Soochow university (China)

In this paper, we seek to find a method to predict the growth of choroid neovascularization (CNV) based on 3D longitudinal optical coherence tomography (OCT) images. A reaction-diffusion model based finite-element-method (FEM) is proposed for prediction. The model consists of four phases: pre-processing, meshing, CNV growth modeling and prediction. We not only apply the reaction-diffusion model to disease region, but also take the surrounding tissues into consideration including outer retinal layer, inner retinal layer and choroid layer. The diffusion in these tissues is considered as isotropic. The FEM is used to solve the partial differential equations(PDE) in the diffusion model. The curve of CNV growth with treatment were fitted by estimated parameters from OCT images, then we can predict the CNV status in a future time point. The preliminary results demonstrate that our proposed method is accurate and the feasibility of our model based on COMSOL Multiphysics is obvious.

9788-7, Session 2

**Automatic classification of endoscopic images for premalignant conditions of the esophagus**

Davide Boschietto, IMT Institute for Advanced Studies Lucca (Italy) and Univ. degli Studi di Padova (Italy); Gianluca Di Claudio, Univ. degli Studi di Padova (Italy); Hadis Mirzaei, Rupert W. L. Leong, The Univ. of New South Wales (Australia); Enrico Grisan, Univ. degli Studi di Padova (Italy)

Barrett’s esophagus (BE) is a precancerous complication of gastroesophageal reflux disease in which normal stratified squamous epithelium lining the esophagus is replaced by intestinal metaplastic columnar epithelium. Repeated endoscopies and multiple biopsies are often necessary to establish the presence of intestinal metaplasia. Narrow Band Imaging (NBI) is an imaging technique commonly used with endoscopies that enhances the contrast of vascular pattern on the mucosa. We present a computer-based method for the automatic normal/metaplastic classification of endoscopic NBI images. Superpixel segmentation is used to identify and cluster pixels belonging to uniform regions. From each uniform clustered region of pixels, eight features maximizing differences among normal and metaplastic epithelium are extracted for the classification step. For each superpixel, the three mean intensity of each color channel are firstly selected as features. Three added features are the mean intensity for each superpixel after separately applying to the red-channel image three different morphological filters (top-hat filtering, entropy filtering and range filtering). The last two features require the computation of the Grey-Level Co-Occurrence Matrix (GLCM), and are reflective of the contrast and the homogeneity of each superpixel. The classification step is performed using an ensemble of 50 classification tree, with a 10-fold cross-validation scheme by training the classifier at each step on a random 70% of the images and testing on the remaining 30% of the dataset. Sensitivity and Specificity are respectively of 79.2% and 87.3%, with an overall accuracy of 83.9%.

9788-8, Session 2

**Automatic classification of endoscopic images for premalignant conditions of the esophagus**

Davide Boschietto, IMT Institute for Advanced Studies Lucca (Italy) and Univ. degli Studi di Padova (Italy); Gianluca Di Claudio, Univ. degli Studi di Padova (Italy); Hadis Mirzaei, Rupert W. L. Leong, The Univ. of New South Wales (Australia); Enrico Grisan, Univ. degli Studi di Padova (Italy)

Celiac disease (CD) is an immune-mediated enteropathy triggered by exposure to gluten and similar proteins, affecting genetically susceptible persons, increasing their risk of different complications. Small bowels mucosa damage due to CD involves various degrees of endoscopically relevant lesions, which are not easily recognized: their overall sensitivity and positive predictive values are poor even when zoom-endoscopy is used. Conofocal Laser Endomicroscopy (CLE) allows skilled and trained experts to qualitative evaluate mucosa alterations such as a decrease in goblet cells density, presence of villous atrophy or crypt hypertrophy. We present a method for automatically classifying CLE images into three different classes: normal regions, villous atrophy and crypt hypertrophy. This classification is performed after a features selection process, in which four features are extracted from each image, through the application of homomorphic filtering and border identification through Canny and Sobel operators. Three different classifiers have been tested on a dataset of 67 different images labeled by experts in three classes (normal, VA and CH): linear approach, Naïve-Bayes quadratic approach and a standard quadratic analysis, all validated with a ten-fold cross validation scheme. Linear classification achieves 82.09% accuracy (class accuracies: 90.32% for normal villi, 82.35% for CH, 68.42% for VA, 68.42% for CH, sensitivity: 0.68, specificity 0.98). Naïve Bayes analysis returns 83.58% accuracy (87.10% for normal villi, 76.47% for VA and 84.21% for CH)
for CH, sensitivity: 0.84 specificity: 0.94), while standard quadratic analysis achieves a final accuracy of 94.03% (96.77% accuracy for normal, 94.12% for VA and 89.47% for CH, sensitivity: 0.89, specificity: 0.98).

9788-9, Session 2
Non-rigid estimation of cell motion in calcium time-lapse images
Siham Hachi, Edinson Lucumi Moreno, Luxembourg Ctr. for Systems Biomedicine (Luxembourg); An-Sofie Desmet, Pieter Vanden Bergh, KU Leuven (Belgium); Ronan M. T. Fleming, Luxembourg Ctr. for Systems Biomedicine (Luxembourg)

Calcium imaging is a widely used technique in neuroscience to simultaneously monitor neural function of hundreds of neurons at single cell resolution. Identification of neuronal activity requires rapid and reliable image analysis techniques, especially when neurons fire and move simultaneously over time. Traditionally, image segmentation is performed to extract individual neurons in the first frame of a calcium sequence. Then, the mean intensity is calculated from the same region of interest in each frame to infer calcium signals. However, when the cells move, deform and fire, the segmentation on its own provides biased neuronal activity. Therefore, an efficient cell tracking technique is required to cope with this issue. Here we present a novel vision-based cell tracking scheme using a thin-plate spline (TPS) deformable model. This model is used to estimate the non-rigid motion of cells. The TPS warping is based on control points detected using Fast from Accelerated Segment Test descriptor. The movement of these points is then tracked over the calcium sequence frames using the Lucas-Kanade optical flow. Our method is able to track neurons in calcium time-series in real-time. In addition, the large changes in intensity indicating a firing event induce a high bending energy of the TPS warp, thus allowing us to detect firing neurons. The robustness and efficiency of the proposed approach is validated on real calcium time-lapse images of a neuronal population.

9788-10, Session 3
Automated reconstruction of standing posture panoramas from multi-sector long limb x-ray images
Linzey Miller, Rochester Institute of Technology (United States); Caroline Trier, Washington Univ. in St. Louis (United States); Kfir Y. Ben-Zikri, Cristian A. Linte, Rochester Institute of Technology (United States)

Due to the limited field of view of the digital X-ray imaging system, several individual sector images are required to capture the posture of an individual in standing position. These images are then “stitched together” to reconstruct the standing posture. We have created an image processing application that automates the stitching, therefore minimizing user input, optimizing workflow, and reducing human error. The application begins by pre-processing the input images through artifact removal, filtering out isolated noisy regions, and amplifying a seamless bone edge. The resulting binary images are then registered together using a rigid-body intensity based registration algorithm. The identified registration transformations are then used to map the original sector images into a panorama image. Our method focuses primarily on the use of the anatomical content of the images to generate the panoramas as opposed to using external markers employed to aid with the alignment process. Currently, results show robust edge detection prior to registration. We have tested our approach by comparing the resulting automatically-stitched panoramas to the manually stitched panoramas in terms of registration parameters, target registration error of homologous markers, and the homogeneity of the digitally subtracted automatically- and manually-stitched images using 27 patient datasets.

9788-11, Session 3
Patellar segmentation from 3D magnetic resonance images using guided recursive ray-tracing for edge pattern detection
Ruida Cheng, Jennifer Jackson, Evan S. McCreedy, William Gandler, National Institutes of Health (United States); Joost J. F. A. Eijkenboom, Marienke van Middelkoop, Erasmus MC (Netherlands); Matthew J. McAuliffe, Frances T. Gavelli, National Institutes of Health (United States)

The paper presents an automatic segmentation methodology for the patellar bone based on 3D gradient recalled echo and gradient recalled echo with fat suppression magnetic resonance images. Constricted search space outlines are incorporated into recursive ray-tracing to segment the outer cortical bone. A statistical analysis based on the dependence of information in adjacent slices is used to limit the search in each image to between and outer and inner search region. A section based recursive ray-tracing mechanism is used to skip inner noise regions and detect the edge boundary. The proposed method achieves higher segmentation accuracy than the current state-of-the-art methods with the average dice similarity coefficient of 96.0% (SD 1.3%) agreement between the auto-segmentation and ground truth surfaces.

9788-12, Session 3
Unsupervised segmentation of MRI knees using image partition forests
Marija Marcan, Irina Voiculescu, Univ. of Oxford (United Kingdom)

Nowadays many people are affected by arthritis, a condition of the joints with limited prevention measures, but with various options of treatment the most radical of which is surgical. In order for surgery to be successful, it relies on careful analysis of patient-based models generated from medical images, usually by manual segmentation.

In this work we show how to automate the segmentation of a crucial and complex joint - the knee. To achieve this goal we rely on our novel way of representing a 3D voxel volume as a hierarchical structure of partitions which we have named Image Partition Forest (IPF). The IPF contains several partition layers of increasing coarseness, with partitions nested across layers in the form of adjacency graphs. On the basis of a set of properties (size, mean intensity, coordinates) of each node in the IPF we classify nodes into different features. Values indicating whether or not any particular node belongs to the femur or tibia are assigned through node filtering and node-based region growing.

So far we have evaluated our method on 15 MRI knee scans. Our unsupervised segmentation compared against a hand-segmented gold standard has achieved an average Dice similarity coefficient of 0.87 for femur and 0.88 for tibia, and an average symmetric surface distance of 3.77 mm for femur and 1.52 mm for tibia. The paper also discusses ways to introduce stricter morphological and spatial conditioning in the bone labelling process.

9788-13, Session 3
Trabecular bone texture classification using wavelet leaders
Zilong Zou, Temple Univ. (United States) and Beihang Univ. (China); Jie Yang, Temple Univ. (United States); Vasileios Megaloookonoumou, Univ. of Patras (Greece); Rachid Jennane, Univ. d’Orléans (France); Erkang Cheng, Broncus Medical, Inc. (United States); Haibin Ling, Temple Univ.
In this paper we propose to use Wavelet Leader (WL) transformation for studying trabecular bone patterns. Given an input image, its WL transformation is defined as the cross-channel-layer maximum pooling of an underlying wavelet transformation. WL inherits the advantage of the original wavelet transformation in capturing spatial-frequency statistics of texture images, while being more robust against scale and orientation thanks to the maximum pooling strategy. These properties make WL an attractive alternative to replace wavelet transformations which are used for trabecular analysis in previous studies. In particular, after extracting wavelet leader descriptors from a trabecular texture patch, we feed them into two existing statistic texture characterization methods, namely the Gray Level Co-occurrence Matrix (GLCM) and the Gray Level Run Length Matrix (GLRLM). The most discriminative features, Energy of GLCM and Gray LevelNon-Uniformity of GLRLM, are retained to distinguish two different populations between osteoporotic patients and control subjects. Then Receiver Operating Characteristics (ROC) curves are used to measure performance of classification. Experimental results on a recently released benchmark dataset show that WL significantly boosts baseline wavelet transformations.

Intensity-based femoral atlas 2D/3D registration using Levenberg-Marquardt optimisation

Ondrej Klima, Petr Kleparnik, Brno Univ. of Technology (Czech Republic); Michal Spanel, 3Dim Laboratory s.r.o. (Czech Republic); Pavel Zemcik, Brno Univ. of Technology (Czech Republic)

The reconstruction of the patient-specific 3D anatomy is a crucial step in the computer-aided preoperative planning based on plain X-ray images. The reconstruction is performed by 2D/3D registration of a shape prior into the set of X-ray images. We propose the robust and fast intensity-based 2D/3D registration method of fitting the statistical shape and intensity model of a femoral bone into two orthogonal X-ray images. A user provides a rough initial pose estimation and segmentation of the input X-ray images. We formulate the registration as a non-linear least squares problem, allowing involvement of Levenberg-Marquardt optimisation and combining more similarity metrics at the same time. The GP-GPU acceleration is used for time-consuming parts of the registration. The proposed method has been evaluated on a set of 96 virtual X-ray images ray-casted from CT data sets of eight different bones and using a shape model constructed from 22 bones. The difference between reconstructed and ground truth bone polygonal models has been measured using a symetric Hausdorff distance. The method converged in all tested cases, the accuracy of the reconstruction was 1.28±1.68mm on average, which is comparable with other published methods. The pose estimation reached sub-millimeter accuracy in translation and less than 0.5° rotation error around frontal and sagittal axes on average. The error in rotation around the longitudinal axis was less than 2.3° on average.

Interesting in vivo magnetic resonance experiments that are not quite ready for prime time and some that are (Keynote Presentation)

Joseph J.H. Ackerman, Washington Univ. in St. Louis (United States)

No Abstract Available

Surface displacement based change in shape of central brain structures with pre-term birth

Amanmeet Garg, Simon Fraser Univ. (Canada); Ruth E. Grunau, The Univ. of British Columbia (Canada); Steven Miller, Univ. of Toronto (Canada); Bruce Bjornson, Kenneth J. Poskitt, The Univ. of British Columbia (Canada); Mirza Faisal Beg, Simon Fraser Univ. (Canada)

Many studies using T1 magnetic resonance imaging (MRI) data have found associations between changes in global metrics (e.g. volume) of brain structures and preterm birth. In this work, we use the surface displacement feature extracted from the deformations of the surface models of the third ventricle, fourth ventricle and brainstem to capture the variation in shape in these structures that may be due to differences in trajectory of brain development as a result of premature birth. Understanding the spatial patterns of shape alterations in these structures in children who were born prematurely as compared to those who were born at full-term may lead to better insights into mechanisms of brain development between these two groups.

The T1 MRI data for the brain was acquired from children born full-term (FT, n=14, 8 males) and pre-term (PT, n=51, 22 males) at 8-years of age. Accurate segmentation labels for these structures were obtained via a multi-template registration based segmentation method. A high dimensional non-regular registration algorithm was utilized to register the target segmentation labels to a set of segmentation labels defined on an average-template. The surface displacement data thus obtained was found to be significantly different (p<0.05) between the PT and FT groups. Further, spatially localized clusters with inward and outward deformation were found to be associated with lower gestational age. The results from this study present a shape analysis method for pediatric MRI data and reveal shape changes that may be due to premature birth.

Modeling the brain morphology distribution in the general aging population

Wyke Huizinga, Erasmus MC (Netherlands); Dirk H. J. Poot, Erasmus MC (Netherlands) and Technische Univ. Delft (Netherlands); Gennady Roshchupkin, Esther E. Bron, Arfan M. Ikram, Meike W. Vernooij, Erasmus MC (Netherlands); Daniel Rueckert, Imperial College London (United Kingdom); Wiro J. Niessen, Erasmus MC (Netherlands) and Technische Univ. Delft (Netherlands); Stefan Klein, Erasmus MC (Netherlands)

Both normal aging and neurodegenerative diseases such as Alzheimer’s disease cause morphological changes of the brain. To better distinguish between normal and abnormal cases, it is necessary to model changes in brain morphology owing to normal aging. To this end, we developed a method for analyzing and visualizing these changes for the entire brain morphology distribution in the general aging population. The method is applied to 1000 subjects from a large population imaging study in the elderly, from which 900 were used to train the model and 100 were used for testing. The results of the 100 test subjects show that the model generalizes to subjects outside the model population. Smooth percentile curves showing the brain morphology changes as a function of age and spatiotemporal atlases derived from the model population are publicly available via an interactive web application at agingbrain.bitbucket.org.
Enhancing genetic correlations between blood and brain using latent factors of correlated blood measures

Neda Jahanshad, The Univ. of Southern California (United States)

Neuroimaging genetics offers new insights into the degree with which genetics underlie variability in brain structure and put the brain at a genetic predisposition to disease risk. It is possible to find genes that influence one trait, such as brain microstructure measured through DTI that also influence more readily obtainable measures such as blood markers. Knowing the degree of genetic overlap between two traits, particularly those of the blood and brain, can help identify genetic factors with multiple roles and those that may be modifiable directly through the blood to help guide changes in the brain. However, multitudes of measures can be obtained in single blood panel, many of them correlated with one another so determining independent genetic correlations can be confounded. Here we used a novel information-theoretic learning method called Correlation Explanation, or CorEx for short, to construct latent factors that reflect multivariate relationships in the data. The phenotypic correlations between DTI-FA and the latent factors were observed. Within significantly correlated regions, a cross-twin cross-trait model was fitted to discover tracts pleiotropic with basic blood markers. We found the genetic correlation to be stronger when latent factors were considered as opposed to individual univariate blood markers.

Mutual connectivity analysis (MCA) using generalized radial basis function neural networks for nonlinear functional connectivity network recovery in resting-state functional MRI

Adora M. D’Souza, Anas Z. Abidin, Mahesh B. Nagarajan, Axel Wismüller M.D., Univ. of Rochester Medical Ctr. (United States)

We investigate the applicability of a computational framework, called mutual connectivity analysis (MCA), for directed functional connectivity analysis in both synthetic and resting-state functional MRI data. This framework comprises of first evaluating non-linear cross-predictability between every pair of time series prior to recovering the underlying network structure using community detection algorithms. We obtain the non-linear cross-prediction score between time series using Generalized Radial Basis Functions (GRBF) neural networks. These cross-prediction scores characterize the underlying functionally connected networks within the resting brain, which can be extracted using non-metric clustering approaches, such as the Louvain method. We first test our approach on synthetic models with known directional influence and network structure. Our method is able to capture the directional relationships between time series (with an area under the ROC curve = 0.92 ± 0.037) as well as the underlying network structure (Rand index = 0.87 ± 0.063) with high accuracy. Furthermore, we test this method for network recovery on resting-state fMRI data, where results are compared to the motor cortex network recovered from a motor stimulation sequence, resulting in a strong agreement between the two (Dice coefficient = 0.45). We conclude that our MCA approach is effective in analyzing non-linear directed functional connectivity and in revealing underlying functional network structure in complex systems.

Large-scale Granger causality analysis on resting state functional MRI

Adora M. D’Souza, Anas Z. Abidin, Univ. of Rochester Medical Ctr. (United States); Lutz Leistritz, Friedrich-Schiller-Univ. Jena (Germany); Axel Wismüller M.D., Univ. of Rochester Medical Ctr. (United States)

We demonstrate an approach to measure the information flow between each pair of time series in resting-state functional MRI (fMRI) data of the human brain and subsequently recover its underlying network structure. By integrating dimensionality reduction into predictive time series modeling, our Large-scale Granger Causality (IsGC) analysis method can reveal directed information flow suggestive of causal influence at an individual voxel level, unlike other multivariate approaches. This method quantifies the influence each voxel time series has on every other voxel time series in a multivariate sense and hence contains information about the underlying dynamics of the whole system, which can be used to reveal functionally connected networks within the brain. To identify such networks, we perform non-metric network clustering, such as accomplished by the Louvain method. We demonstrate the effectiveness of our approach to recover the motor and visual cortex from resting state human brain fMRI data and compare it with the network recovered from a visuomotor stimulation experiment, where the similarity is measured by the Dice Coefficient (DC). The best DC obtained was 0.59 implying a strong agreement between the two networks. In addition, we thoroughly study the effect of dimensionality reduction in IsGC analysis on network recovery. We conclude that our approach is capable of detecting causal influence between time series in a multivariate sense, which can be used to segment functionally connected networks in the resting-state fMRI.

Specific frequency bands of fMRI signal oscillations with motor symptoms, depression, and their interactions in Parkinson’s disease

Xiaopeng Song, Peking Univ. (China); Xiao Hu, The Affiliated Brain Hospital, Nanjing Medical Univ. (China); Shuqin Zhou, Peking Univ. (China); Yijun Liu, Peking Univ. (China); Weiguuo Liu, The Affiliated Brain Hospital, Nanjing Medical Univ. (China)

Depression is prevalent among patients with Parkinson’s disease (PD), however the pathophysiology of depression in PD is not well understood. We adopted a novel application of the Empirical Mode Decomposition method to investigate how depression and motor impairments differentially and interactively affect specific brain regions in Parkinson’s disease (PD). The resting-state BOLD-fMRI data of 59 PD subjects were first decomposed into characteristic frequency bands. The main effects of motor severity and depression, and their interaction on the BOLD oscillation energy in these frequency bands were evaluated with a multivariate linear regression model. The results show that the severity of motor symptoms is negatively correlated with the energy in the frequency band of 0.10-0.25Hz in the bilateral thalamus, but positively correlated with 0.01-0.027Hz band energy in the bilateral postcentral gyrus. Conversely, the severity of depression is positively correlated with the energy of 0.10-0.25Hz but negatively with 0.01-0.027Hz in the bilateral subgenual gyrus. Notably, the interaction between motor and depressive symptoms is negatively correlated with the energy of 0.10-0.25Hz in the substantia nigra, hippocampus, inferior orbitofrontal cortex, and temporoparietal junction, but positively correlated with 0.02-0.05Hz in the same regions. These findings indicate unique associations of fMRI band signals with motor and depressive symptoms in PD in specific brain regions, which may underscore the neural impact of the dissociative and interactive relations between the two PD-related disorders.
9788-22, Session 5

Detecting altered connectivity patterns in HIV-associated neurocognitive impairment using mutual connectivity analysis

Anas Z. Abidin, Adora M. D’Souza, Mahesh B. Nagarajan, Axel Wismüller M.D., Univ. of Rochester Medical Ctr. (United States)

The use of functional Magnetic Resonance Imaging (fMRI) has provided interesting insights into our understanding of the brain. This method has been used to detect and study changes in brain network properties associated with various neurological disorders. A large percentage of subjects infected with HIV present cognitive deficits, which are known as HIV associated neurocognitive disorder (HAND). In this study we propose to use a novel technique named Mutual Connectivity Analysis (MCA) to detect differences in brain networks in subjects with and without HIV infection. Resting state functional MRI scans acquired from 10 subjects (5 HIV+ and 5 HIV−) were subject to standard pre-processing routines. Subsequently, the average time-series for each brain region of the Automated Anatomic Labeling (AAL) atlas were extracted and used with the MCA framework to obtain a graph characterizing the interactions between them. The network graphs obtained for different subjects were then compared using Network-Based Statistics (NBS), which is an approach to detect differences between graph edges while controlling for the family-wise error rate when mass univariate testing is performed. Applying this approach on the graphs obtained yields a single network encompassing 42 nodes and 65 edges, which is significantly different between the two subject groups. Specifically, the strength of connections to the regions within and adjacent to the basal ganglia is significantly decreased. Also some nodes corresponding to the posterior cingular cortex are affected. These results are in line with our current understanding of pathophysiological mechanisms of HAND and other HIV based MRI connectivity studies. Hence, we illustrate the applicability of our novel approach with network-based statistics in a clinical case-control study to detect differences in connectivity patterns.

9788-23, Session 5

Evaluating effects of methylphenidate on brain activity in cocaine addiction: a machine-learning approach

Irina Rish, IBM Thomas J. Watson Research Ctr. (United States); Pouya Bashivan, The Univ. of Memphis (United States); Guillermo A. Cecchi, IBM Thomas J. Watson Research Ctr. (United States); Rita Goldstein, Mount Sinai Hospital (United States)

The objective of this study is to investigate effects of methylphenidate on brain activity in individuals with cocaine use disorder (CUDs) using functional MRI. Methylphenidate hydrochloride (MPH) is an indirect dopamine agonist commonly used for treating attention deficit/hyperactivity disorders; it was also shown to have some positive effects on CUD subjects: improved stop signal reaction times associated with better control/inhibition (LiPNAS2010), as well as normalized task-related brain activity (GoldsteinPNAS2010) and resting-state functional connectivity in specific areassite(KonovaJAMA2013). While prior fMRI studies of MPH in CUDs have focused on mass-univariate statistical hypothesis testing, this paper evaluates multivariate, whole-brain effects of MPH as captured by the generalization (prediction) accuracy of different classification techniques applied to resting-state functional network properties. Our preliminary results based on resting-state data from cite(KonovaJAMA2013) suggest that MPH tends to normalize network properties such as voxel degrees in CUD subjects, thus providing additional evidence for potential benefits of MPH in treating cocaine addiction.

9788-24, Session 6

Voxel based morphometry in optical coherence tomography: validation and core findings

Bhavna J. Antony, Johns Hopkins Univ. (United States); Min Chen, Univ. of Pennsylvania (United States); Aaron Carass, Bruno M. Jedyak, Omar Al-Louzi, Sharon D. Solomon, Shiv Saidha, Peter A. Calabresi, Jerry L. Prince, Johns Hopkins Univ. (United States)

Optical coherence tomography (OCT) of the human retina is now becoming established as an important modality for the detection and tracking of various ocular diseases. Voxel based morphometry (VBM) is a long standing neuroimaging analysis technique that allows for exploration of the regional differences in the brain. There has been limited work done in developing registration based methods for OCT, which has hampered the advancement of VBM analyses in OCT based population studies. Following on from the recent development of an OCT registration method by Chen et al., we explore the potential benefits of VBM analysis in cohorts of healthy controls (HCs) and multiple sclerosis (MS) patients. Specifically, we validate the stability of VBM analysis in two pools of HCs showing no significant difference between the two populations. Additionally, we present a retrospective study of age and sex matched HCs and relapsing remitting MS patients, demonstrating consistent results with the reported literature while providing insight into the retinal changes associated with this MS subtype.

9788-25, Session 6

Multiple pinhole collimator based microscopic x-ray luminescence computed tomography

Wei Zhang, Dianwen Zhu, Changqing Li, Univ. of California, Merced (United States)

X-ray luminescence computed tomography (XLCT) is a new hybrid imaging modality, which has the capability to improve optical spatial resolution up to hundreds of micrometers for deep targets. In this paper, we reported a multi-pinhole collimator based microscopic x-ray luminescence computed tomography (microXLCT) system. Superfine x-ray pencil beams are used to excite deeply embedded phosphor particles, allowing us to obtain sub-millimeter optical spatial resolution in deep tissues. We have previously reported that the spatial resolution of XLCT can achieve several hundreds of micrometers by using a super fine single pinhole collimator. However, the single pinhole collimator based system has very low utilization of x-ray photons, which results in long measurement time. In the new system, multiple superfine x-ray beams are generated by mounting an array of pinholes in the front of a powerful x-ray tube. The collimated x-ray beams can scan multiple positions simultaneously, which will increase utilization of the x-ray photons and shorten the imaging time. The emitted optical photons will be measured with an electron multiplying charge-coupled device (EMCCD) camera. Meanwhile, an x-ray detector will be used to determine x-ray beams’ size and position, which will be used as structural guidance in the microXLCT image reconstruction. Numerical simulation and phantom experiments with multi-targets are used to evaluate the performance of the proposed multiple pinhole based microXLCT imaging system.

9788-26, Session 6

Optimization and performance evaluation of a conical mirror-based fluorescence molecular tomography imaging system

Yue Zhao, Wei Zhang, Dianwen Zhu, Changqing Li, Univ. of Pennsylvania (United States); Bruno M. Jedynak, Omar Al-Louzi, Sharon D. Solomon, Shiv Saidha, Peter A. Calabresi, Jerry L. Prince, Johns Hopkins Univ. (United States)

Multi-photon excitation microscopy (MPM) is a powerful optical microscopic technique that has been used to detect and study changes in brain network properties associated with various neurological disorders. A large percentage of subjects infected with HIV present cognitive deficits, which are known as HIV associated neurocognitive disorder (HAND). In this study we propose to use a novel technique named Mutual Connectivity Analysis (MCA) to detect differences in brain networks in subjects with and without HIV infection. Resting state functional MRI scans acquired from 10 subjects (5 HIV+ and 5 HIV−) were subject to standard pre-processing routines. Subsequently, the average time-series for each brain region of the Automated Anatomic Labeling (AAL) atlas were extracted and used with the MCA framework to obtain a graph characterizing the interactions between them. The network graphs obtained for different subjects were then compared using Network-Based Statistics (NBS), which is an approach to detect differences between graph edges while controlling for the family-wise error rate when mass univariate testing is performed. Applying this approach on the graphs obtained yields a single network encompassing 42 nodes and 65 edges, which is significantly different between the two subject groups. Specifically, the strength of connections to the regions within and adjacent to the basal ganglia is significantly decreased. Also some nodes corresponding to the posterior cingular cortex are affected. These results are in line with our current understanding of pathophysiological mechanisms of HAND and other HIV based MRI connectivity studies. Hence, we illustrate the applicability of our novel approach with network-based statistics in a clinical case-control study to detect differences in connectivity patterns.

Evaluating effects of methylphenidate on brain activity in cocaine addiction: a machine-learning approach

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The objective of this study is to investigate effects of methylphenidate on brain activity in individuals with cocaine use disorder (CUDs) using functional MRI. Methylphenidate hydrochloride (MPH) is an indirect dopamine agonist commonly used for treating attention deficit/hyperactivity disorders; it was also shown to have some positive effects on CUD subjects: improved stop signal reaction times associated with better control/inhibition (LiPNAS2010), as well as normalized task-related brain activity (GoldsteinPNAS2010) and resting-state functional connectivity in specific areassite(KonovaJAMA2013). While prior fMRI studies of MPH in CUDs have focused on mass-univariate statistical hypothesis testing, this paper evaluates multivariate, whole-brain effects of MPH as captured by the generalization (prediction) accuracy of different classification techniques applied to resting-state functional network properties. Our preliminary results based on resting-state data from cite(KonovaJAMA2013) suggest that MPH tends to normalize network properties such as voxel degrees in CUD subjects, thus providing additional evidence for potential benefits of MPH in treating cocaine addiction.

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Wei Zhang, Dianwen Zhu, Changqing Li, Univ. of California, Merced (United States)

X-ray luminescence computed tomography (XLCT) is a new hybrid imaging modality, which has the capability to improve optical spatial resolution up to hundreds of micrometers for deep targets. In this paper, we reported a multi-pinhole collimator based microscopic x-ray luminescence computed tomography (microXLCT) system. Superfine x-ray pencil beams are used to excite deeply embedded phosphor particles, allowing us to obtain sub-millimeter optical spatial resolution in deep tissues. We have previously reported that the spatial resolution of XLCT can achieve several hundreds of micrometers by using a super fine single pinhole collimator. However, the single pinhole collimator based system has very low utilization of x-ray photons, which results in long measurement time. In the new system, multiple superfine x-ray beams are generated by mounting an array of pinholes in the front of a powerful x-ray tube. The collimated x-ray beams can scan multiple positions simultaneously, which will increase utilization of x-ray photons and shorten the imaging time. The emitted optical photons will be measured with an electron multiplying charge-coupled device (EMCCD) camera. Meanwhile, an x-ray detector will be used to determine x-ray beams’ size and position, which will be used as structural guidance in the microXLCT image reconstruction. Numerical simulation and phantom experiments with multi-targets are used to evaluate the performance of the proposed multiple pinhole based microXLCT imaging system.
We have performed numerical and experimental experiments with a conical mirror based fluorescence molecular tomography (FMT) imaging system to optimize its performance. We carried out Monte Carlo ray tracing simulations to calculate multiple reflection photons caused by the conical mirror. Our experimental results indicated that the FMT system doesn’t suffer from back reflected photons. To include the effects of surface geometry in the FMT image reconstruction, we have created a look-up table according to the Monte Carlo simulations. We have also tested different measuring modes, including whole surface and half surface of the object. To improve the measurement dynamic range, we have applied neutral density (ND) filters with different transmittances. Furthermore, we used different laser illumination patterns in FMT experiments, including point and line patterns, and their effects in the FMT reconstruction accuracy combining with different FMT reconstruction approaches have been studied. For both numerical simulations and experimental studies, we used two capillary tube targets filled with fluorescence dyes with different concentrations at different depths. The factors, including measurements modes, illumination patterns, emission wavelengths, geometry of illumination, and reconstruction methods, have been investigated systematically to optimize our conical mirror based FMT imaging system. Experiments of euthanized mice with embedded targets will be performed to further validate the optimized FMT imaging system.

9788-27, Session 6
Compressive sensing-based preclinical molecular optical tomography
Xavier Intes, Rensselaer Polytechnic Institute (United States)

Time-resolved imaging techniques in optical tomography have long been established as the imaging approach providing the most comprehensive information in optical imaging. The time resolved measurements (usually referred to as Temporal Point Spread Function (TPSF)) can provide a wealth of information allowing the efficient separation of absorption and scattering in functional imaging and lifetime sensing in fluorescence measurements. The data types derived from temporal measurements therefore provide a very powerful measurement in optical tomography. Several studies in the recent years have employed time-resolved techniques for functional and molecular imaging studies (namely diffuse optical tomography (DOT) and fluorescence molecular tomography (FMT)) of both clinical and preclinical models. However, current instrumental implementations are based on point source illumination that provide sparse sampling, leading to long acquisition times and are typically limited to cross-section imaging in small animals. To overcome these limitations, we have proposed to a novel instrumental approach based on structured light illumination and detection. Such instrumental implementation allows compressive imaging for fast and robust whole-body optical tomography of small animals. In this presentation, we will report on our current instrumental and theoretical implementations for wide-field time resolved optical tomography. We will summarize our imaging platforms design and characterization. We will also report on the implementation of compressive sensing based approach in the optical inverse problem to improve tomographic performances. More precisely, we will describe the compressive sensing-based preconditioning method applied to structured light illumination and detection field. We will also present the benefits of implementing sparsity constraints.

9788-28, Session 6
A novel reconstruction algorithm for bioluminescent tomography based on Bayesian compressive sensing
Yaqi Wang, Jinchao Feng, Kebin Jia, Zhonghua Sun, Huijun Wei, Beijing Univ. of Technology (China)

Bioluminescence tomography (BLT) is becoming a promising tool because it can resolve the biodistribution of bioluminescent reporters associated with cellular and subcellular function through several millimeters with a centimeters of tissues in vivo. However, BLT reconstruction is an ill-posed problem. By incorporating sparse a priori information about bioluminescent source, enhanced image quality is obtained for sparsity based reconstruction algorithm. Therefore, sparsity based BLT reconstruction algorithm has a great potential. Here, we proposed a novel reconstruction method based on Bayesian compressive sensing and investigated its feasibility and effectiveness with a heterogeneous phantom. The results demonstrate the potential and merits of the proposed algorithm.

9788-29, Session 6
Biocompatibility of pure protein nanoprobes composed of ferritin and fluorescent protein
Gun Hyuk Jang, Sungwook Park, Kwan Yong Lee, Kwan Hyi Lee, Korea Institute of Science and Technology (Korea, Republic of) and Univ. of Science & Technology (Korea, Republic of)

Studies on highly sensitive nanoprobes for disease diagnosis are one of the essential researches in the field of medical examination. The emergence of various new nanoprobes has profoundly contributed to improving disease diagnostic techniques. However, the toxic effect of the nanoparticles’ harmful chemical components in the organism remains as a huge obstacle. We developed a pure protein nanoprobe of ferritin structure, consisting of 24 subunits, with fluorescent proteins, such as AcGFP or DsRed introduced. To verify the biological advantages of pure protein nanoprobes, we identified in-vitro and in-vivo toxicity using Human Umbilical Vein Endothelial Cells (HUVEC) and zebrafish embryos. In this study, we suggested that it is possible to produce highly applicable nanoprobes with outstanding biocompatibility for the diagnostic field.

9788-53, Session PS1
PDMS microwell device as a cancer diagnosis kit via fluorescent imaging
Keon Yong Lee, Kwan Hyi Lee, Korea Institute of Science and Technology (Korea, Republic of)

Current method of monitoring tumors and metastasis is limited to taking invasive-biopsies directly from tumor tissues, and this method is often considered non-practical. During recent few years, the circulating tumor cells (CTCs) emerged as a novel topic for the cancer diagnosis studies. CTCs originate from the primary tumors and enter the bloodstream to circulate within human blood vessels, possibly to trigger the growth of tumor tissues at distal organs. Therefore, CTCs offer a new approach to detecting tumors and metastasis through a simple blood draw, referred as ‘liquid biopsy’. Despite its immense possibility for clinical use, CTC’s extremely low concentration within blood – one CTC in 10 million blood cells – thwarts the immediate clinical application. We designed a polydimethylsiloxane (PDMS) microwell device with 84,672 (504 X 168, each well: 50 μm x 50 μm) microwells to capture and individually isolate cells from a solution of cells. Melanoma cells, SK-MEL-2 and A375, were used to demonstrate the capture and isolation process. A capture rate for the process was approximately 70%, which is quiet promising for the simple 30 minute process. Upon staining the cells with fluorescent dyes, we could easily visualize the captured and isolated cells from the microwell device. This study demonstrated that the PDMS microwell device can be utilized for the cancer diagnosis from a liquid biopsy of CTCs.
9788-76, Session PS1

**Regional placental BOLD changes with gestational age in normally developing pregnancies using long duration R2* mapping in utero**

Manjiri Dighe, Yun Jung Kim, Sharmishtaa Sheshamani, Ania Blazejewska, Susan McKown, Jason Caucutt, Christopher Gatenby, Colin Studholme, Univ. of Washington (United States)

The aim of the study was to examine the use of R2* mapping in maternal and fetal sub-regions of the placenta with the aim of providing a reference for blood oxygenation levels during normative development. There have been a number of MR relaxation studies of placental tissues in utero, but none have reported R2* value changes with age, or examined differences in sub-regions of the placenta. Here specialized long-duration R2* imaging was used to create a stable estimate for R2* values in different placental regions. 16 pregnant subjects were recruited and scanned up to 3 times during their pregnancy. A dual Echo EPI based BOLD acquisition was employed and repeated between 90 and 150 times over 3 to 5 minutes to provide a high accuracy estimate of the R2* signal level. Acquisitions were also repeated in 13 cases within a visit to evaluate reproducibility of the method in a given subject. Experimental results showed R2* measurements were highly repeatable within a visit with standard deviation of (0.76). Plots of all visits against gestational age indicated clear correlations showing decreases in R2* with age. This increase was consistent also consistent over time in multiple visits of the same volunteer during their pregnancy.

9788-54, Session PS2

**A novel Kalman filter based video image processing scheme for two-photon fluorescence microscopy**

Wenqing Sun, Xia Huang, Chunqiang Li, Chuan Xiao, Wei Qian, The Univ. of Texas at El Paso (United States)

Two-photon fluorescence microscopy (TPFM) is a perfect optical imaging equipment to monitor the interaction between fast moving viruses and hosts. However, due to the strong unavoidable background noise from the culture, videos obtained by this technique are too noisy to elaborate this fast infection process without video image processing. To the best of our knowledge, no video processing systems designed for TPFM has been reported. In this study, we developed a novel scheme to eliminate the noise, recover the background bacteria images and improve the video qualities. In our scheme, we modified and implemented the following methods for both host and virus videos: correlation method, round identification method, tree-structured nonlinear filters, Kalman filters, and object tracking. After these procedures, most of the noises were eliminated and host images were recovered with their moving directions and speed highlighted in the videos. From the analysis of the processed videos, 93% bacteria and 98% viruses were correctly detected in each frame on average.

9788-55, Session PS2

**Definition and automatic anatomy recognition of lymph node zones in the abdomen and pelvis on CT images**

Yu Liu, Univ. of Pennsylvania (United States) and Jilin Univ. (China); Jayaram K. Udupa, Dewey Odhner, Univ. of Pennsylvania (United States); Yubing Tong, Univ. of Pennsylvania School of Medicine (United States); Drew A. Torigian, Univ. of Pennsylvania (United States)

Currently, unlike IALSC-defined thoracic lymph node zones, no explicitly provided definitions for abdominal and pelvic lymph nodes are available. Yet, explicit definition of the abdominal and pelvic lymph node zones is critical for standardizing the recognition, delineation, quantification, and reporting of lymphadenopathy in these body regions. This paper, therefore, proposes standardized definition of the grouping of abdominal and pelvic lymph nodes into 10 zones in each of these two body regions. We subsequently used our earlier AAR framework designed for body-wide organ modeling, recognition, and delineation to actually implement these zonal definitions where the zones are treated as anatomic objects. Firstly, all 20 zones and key anatomic organs used as anchors are manually delineated under expert supervision for constructing fuzzy anatomy models of the assembly of organs together with the zones. Then, optimal hierarchical arrangement of these objects is constructed for the purpose of achieving best zonal recognition. For actual localization of the objects, two strategies are used – optimal thresholded search for organs and one-shot method for the zones where the known relationship of the zones to key organs is exploited. Based on 50 CT image data sets for each of the two body regions and equal division into training and test subsets, object localization within 1-3 voxels is achieved. The localization accuracy appears to be slightly better for pelvic lymph node zones compared to abdominal lymph node zones.

9788-56, Session PS2

**Comparison of volume estimation methods for pancreatic islet cells**

Jiri Dvorak, Jan Vihlik, Jan Kybic, Czech Technical Univ. in Prague (Czech Republic); David Habart M.D., Institute for Clinical and Experimental Medicine (Czech Republic)

In this contribution we study different methods of volume estimation for pancreatic islets which can be used in the quality control step prior to the islet transplantation. The total islet volume is an important criterion in the quality control. Also, the individual islet volume distribution is interesting - it has been indicated that smaller islets can be more effective. We assume two-dimensional observations - sections or projections of the islets. We consider both the heuristically motivated methods used in practice (assuming the islets have spherical or ellipsoidal shape) and a rigorous, local stereological method, the nucleator (not relying on any shape assumptions and providing unbiased estimates if isotropic sections through the islets are observed). We present a simulation study comparing the performance of the volume estimation methods. It turned out that if isotropic sections through the islets are observed, the nucleator is the method of choice - it is unbiased and has small variability. If orthogonal projections of the islets are observed, all the considered methods exhibit a significant bias and variability. In such a scenario, the method assuming the islets are in fact prolate ellipsoids performed the best.

In an experimental study with samples of rat islets it turned out that all the estimation methods provide estimates which are almost perfectly correlated with the DNA content in the sample measured in nanograms (this provides an independent measure of the islet volume). However, the methods provide different values of DNA content per unit islet volume, implying the volume estimation methods are not equivalent.

9788-57, Session PS2

**Natural image classification driven by human brain activity**

Dai Zhang, Hanyang Peng, Jinqiao Wang, Ming Tang, National Lab. of Pattern Recognition (China); Zhentao Zuo, Rong Xue, Institute of Biophysics (China); Yong Fan, Univ. of Pennsylvania School of Medicine (United States)

Natural image classification has been a hot topic in computer vision and...
pattern recognition research field. Since the performance of an image classification system can be improved by feature selection, many image feature selection methods have been developed. However, the existing supervised feature selection methods are typically driven by the class label information that are identical for different samples from the same class, ignoring within-class image variability and therefore degrading the feature selection performance. In this study, we propose a novel feature selection method, driven by human brain activity signals collected using fMRI technique when human subjects were viewing natural images of different categories. The fMRI signals associated with subjects viewing different images encode the human perception of natural images, and therefore may capture image variability within- and cross- categories. We then select image features with the guidance of fMRI signals from brain regions with active response to image viewing. Particularly, bag of words features based on GIST descriptor are extracted from natural images for classification, and a sparse regression base feature selection method is adopted to select image features that can best predict fMRI signals. Finally, a classification model is built on the select image features to classify images without fMRI signals. The validation experiments for classifying images from 4 categories have demonstrated that our method could achieve much better classification performance than classifiers built on image features selected by traditional feature selection methods.

9788-58, Session PS2
Iterative weighted average diffusion as a novel external force in the active contour model
Ilya S. Mirov, The Univ. of Alabama at Birmingham (United States) and Univ. of Richmond (United States); Arie Nakhmani, The Univ. of Alabama at Birmingham (United States)

The active contour model has good performance in boundary extraction for medical images; particularly, Gradient Vector Flow (GVF) active contour model shows good performance at concavity convergence and insensitivity to initialization, yet it is susceptible to edge leaking, deep and narrow concavities, and has some issues handling noisy images. This paper proposes a novel external force, called Iterative Weighted Average Diffusion (IWAD), which used in tandem with parametric active contours, provides superior performance in images with high values of concavity. The image gradient is first turned into an edge image, smoothed, and modified with enhanced corner detection, then the IWAD algorithm diffuses the force at a given pixel based on its 3x3 pixel neighborhood. A forgetting factor, ?, is employed to ensure that forces being spread away from the boundary of the image will attenuate. The experimental results show better behavior in high curvature regions, faster convergence, and less edge leaking than GVF when both are compared to expert manual segmentation of the images.

9788-59, Session PS2
Ultrafast superpixel segmentation of large medical datasets
Antoine Leblond, Claude Kauffmann, Ctr. Hospitalier de l’Univ. de Montréal (Canada)

Even with recent hardware improvements, superpixel segmentation of large 3D medical images at interactive speed (<500 ms) remains a challenge. We will describe methods to achieve such performances using a GPU based hybrid framework implementing wavefront propagation and cellular automata resolution. Tasks will be scheduled in blocks (work units) and the impetus for this work will use a wavefront propagation, therefore allowing sparse scheduling. Because work units has been designed as spatially cohesive, the fast Thread Group Shared Memory can be used and reused through a Gauss-Seidel like acceleration. The work unit partitioning scheme will however vary on odd- and even-numbered iterations to reduce convergence barriers. Synchronization will be ensured by a 8-step 3D variant of the traditional Red Black Ordering scheme. An attack model and early termination will also be described and implemented as additional acceleration techniques. Using our hybrid framework and typical operating parameters, we were able to compute the superpixels of a high-resolution 512x512x512 aortic angioCT scan in 283 ms using a AMD R9 290X GPU. We achieved a 22.5X speed-up factor compared to the published reference GPU implementation.

9788-60, Session PS2
Liver recognition based on statistical shape model in CT images
Dehui Xiang, Xueqing Jiang, Fei Shi, Weifang Zhu, Xinjian Chen, Soochow Univ. (China)

In this paper, an automatic method is proposed to recognize the liver on clinical 3D CT images. The proposed method effectively use statistical shape model of the liver. Our approach consist of three main parts: (1) model training, in which shape variability is detected using principal component analysis from the manual annotation; (2) model localization, in which a fast Euclidean distance transformation based method is able to localize the liver in CT images; (3) model adaptation, the initial mesh is locally and iteratively deformed to the target boundary, which is constrained with region and surface constraints of the trained shape model. We validate our algorithm on a dataset which consists of 20 3D CT images obtained from different patients. The average ARVD was 8.99%, the average ASSD was 2.69mm, the average RMSD was 4.92mm, the average MSD was 28.841mm, and the average MSD was 13.31 %.

9788-61, Session PS2
Optimal target VOI size for accurate 4D coregistration of DCE-MRI
Brian J. Park M.D., Univ. of Pennsylvania (United States)

Dynamic contrast enhanced (DCE) MRI has emerged as a reliable and diagnostically useful functional imaging technique. DCE protocol typically lasts 3-15 minutes and results in a time series of N volumes. For automated analysis, it is important that volumes acquired at different times be spatially coregistered. We have recently introduced a novel 4D, or volume time series, coregistration tool based on a user-specified target volume of interest (VOI). However, the relationship between coregistration accuracy and target VOI size has not been investigated. In this study, coregistration accuracy was quantitatively measured using various sized target VOIs. Coregistration of 10 DCE-MRI mouse head image sets were performed with various sized VOIs targeting the mouse brain. Accuracy was quantified by measures based on the union and standard deviation of the coregistered volume time series. Coregistration accuracy was determined to improve rapidly as the size of the VOI increased and approached the approximate volume of the target (mouse brain). Further inflation of the VOI beyond the volume of the target (mouse brain) only marginally improved coregistration accuracy. The CPU time needed to accomplish coregistration is a linear function of N that varied gradually with VOI size. From the results of this study, we recommend the optimal size of the VOI to be slightly overinclusive, approximately by 5 voxels, of the target for computationally efficient and accurate coregistration.

9788-105, Session PS2
Automatic segmentation of canine retinal OCT using adaptive gradient enhancement and region growing
Yufan He, Tsinghua Univ. (China) and Univ. of Pennsylvania
In recent years, several studies have shown that the canine retina model offers important insight for our understanding of human retinal diseases. Several therapies developed to treat blindness in such models have already moved onto human clinical trials, with more currently under development [1]. Optical coherence tomography (OCT) offers a high resolution imaging modality for performing in-vivo analysis of the retinal layers. However, existing algorithms for automatically segmenting and analyzing such data have been mostly focused on the human retina. As a result, canine retinal images are often still being analyzed using manual segmentations, which is a slow and laborious task. In this work, we propose a method for automatically segmenting 5 boundaries in canine retinal OCT. The algorithm employs the position relationships between different layers to adaptively enhance the gradient map. A region growing algorithm is then used on the enhanced gradient maps to find the five boundaries separately. The automatic segmentation was compared against manual segmentations showing an average absolute error of 5.82 ± 4.02 microns.

9788-62, Session PS3
Effect of low-dose CT and iterative reconstruction on trabecular bone microstructure assessment
Felix K. Kopp, Thomas Baum, Radin A. Nasiruddin, Kai Mei, Eduardo G. Garcia, Rainer Burgkart, Ernst J. Rummeny M.D., Jan S. Bauer, Peter B. Noël, Technische Univ. München (Germany)

The trabecular bone microstructure is an important factor in the development of osteoporosis. It is well known that its deterioration is one effect when osteoporosis occurs. Previous research showed that the analysis of trabecular bone microstructure enables more precise diagnoses of osteoporosis than a sole measurement of the mineral density. Microstructure parameters are assessed on volumetric images of the bone acquired either with high-resolution magnetic resonance imaging, high-resolution peripheral quantitative computed tomography or high-resolution computed tomography (CT), with only CT being applicable to the spine, which is one of clinically most relevant fracture sites. However, due to the high radiation exposure for imaging the whole spine these measurements are not applicable in current clinical routine. In this work, twelve vertebrae from three different donors were scanned with standard and low radiation dose. Trabecular bone microstructure parameters were assessed for CT images reconstructed with statistical iterative reconstruction (SIR) and analytical filtered backprojection (FBP). The resulting slices were correlated to the biomechanically determined fracture load of each vertebra. Microstructure parameters assessed for low-dose data reconstructed with SIR significantly correlated with fracture loads as well as parameters assessed for normal-dose data reconstructed with FBP. However, regularization during SIR must be carefully chosen, because the ultra small trabecular microstructure has an appearance similar to image noise. Ideal results were achieved with low to zero regularization strength yielding microstructure parameters not significantly different from those assessed for normal-dose FBP data. Moreover, in comparison to other approaches, superior noise-resolution trade-offs can be found with the proposed methods.

9788-63, Session PS3
Linking bone microarchitecture to projections texture analysis
Erwan Freuchet, Florent Autrusseau, Univ. de Nantes (France); Yves Amouricq, Ctr. Hospitalier Univ. de Nantes (France); Jean-Pierre V. Guédon, Paul Pilet, Pierre Weiss, Univ. de Nantes (France)

Trabecular bone and its micro-architecture are of prime importance for health. This paper focuses onto the relationship between bone micro-architecture and the texture found on micro CT projections. From a small animal study, 6 mouses legs were studied by microCT at a resolution of 6µm. Softwares (NRecon and CtAn from Brucker, ImageJ, Mojette operator from IRCCyN) were used to perform the reconstructions and calculate bone micro-architecture parameters. The 3D reconstructions are only used as ground truth for their micro-architecture parameters. The study uses a set of 10 projections per volume. For each projection, a 512x512 ROI region of medial epiphysis was drawn. The Mojette transform of the ROI was performed for a set of Fary-Haros angles along (0,Pi). On the resulting 1D projections, a local entropy was computed giving the degree of isotropy or anisotropy. From this set of texture parameters around the ROI, we are able to characterize the texture. Finally, we have to rely these set of texture parameters to the 3D micro-architecture. This is the goal of building the atlas of ROIs in order to be able to guess the micro-architecture from only a small set of 2D projections.

9788-64, Session PS3
Segmentation of ribs in digital chest radiographs
Lin Cong, Shanghai United Imaging Healthcare Co., Ltd. (China); Wei Guo, Shenyang Aerospace Univ. (China); Qiang Li M.D., Shanghai Advanced Research Institute (China) and Shanghai United Imaging Healthcare Co., Ltd. (China)

Ribs and clavicles in posterior-anterior (PA) digital chest radiographs often overlap with lung abnormalities such as nodules, and cause missing of these abnormalities, it is therefore necessary to remove or reduce the ribs in chest radiographs. The purpose of this study was to develop a fully automated algorithm to segment ribs within lung area in digital radiography (DR) for removal of the ribs. The rib segmentation algorithm consists of three steps. Firstly, a radiograph was pre-processed for contrast adjustment and noise removal; second, generalized Hough transform was employed to localize the lower boundary of the ribs. In the third step, a novel bilateral dynamic programming algorithm was used to accurately segment the upper and lower boundaries of ribs simultaneously. The width of the ribs and the smoothness of the rib boundaries were incorporated in the cost function of the bilateral dynamic programming for obtaining consistent results for the upper and lower boundaries. Our database consisted of 93 DR images, including, respectively, 23 and 70 images acquired with a DR system from Shanghai United Imaging Healthcare Co. and from GE Healthcare Co. The rib localization algorithm achieved a sensitivity of 98.2% with 0.1 false positives per image. The accuracy of the detected ribs was further evaluated in 3 levels: “1”, good; “2”, fair; “3”, poor. The percentages of good, fair, and poor segmentation results were 91.1%, 7.2%, and 1.7%, respectively. Our algorithm can obtain good segmentation results for ribs in chest radiography and would be useful for rib reduction in our future study.

9788-65, Session PS3
Automatic construction of patient-specific biomechanical models of the spine from IVDS and vertebra segmentations
Isaac Castro-Mateos, José M. Pozo, The Univ. of Sheffield (United Kingdom); Áron Lazary, National Ctr. for Spinal Disorders (Hungary); Alejandro F. Frangi, The Univ. of Sheffield (United Kingdom)
Computational medicine aims at developing patient-specific models to help physicians in the diagnosis and treatment selection of patients. In the case of the spine, these models require the segmentation of the intervertebral discs (IVD) and vertebral body and the subsequent alignment of both structures. In the literature, there exists a vast selection of segmentation methods, but there is a lack of approaches to align both vertebral body and IVDs structures. This paper presents a method to merge these two structures by rigidly align the vertebral body in the MR image using the intervertebral disc location and the MR image intensities. This process employs a feature-based search technique to adapt the borders of the vertebral body taking into consideration to not overlap with IVDs. The process is extendible to other parts of the body, such as the knee. However, it is always necessary to align the bony structures over the soft tissues (IVDs, ligaments, muscles, etc.), since only the former has the same shape in both CT and MR images. Finally, a morphing registration based on B-splines is employed to map a volumetric mesh (template model for simulation) to the surface mesh segmentations.

Although results are still quite preliminary, they are also promising. Thus, this method is a step forward towards the automation of patient-specific models to perform simulations.

9788-68, Session PS4

Transcranial direct current stimulation transiently increases the blood-brain barrier solute permeability in vivo
Da Wi Shin, Niranjana Khadka, Jie Fan, Marom Bikson, Bingmei Fu, The City College of New York (United States)

Transcranial Direct Current Stimulation (tDCS) is a non-invasive electrical stimulation technique investigated for a broad range of medical and performance indications. Whereas prior studies have focused exclusively on direct neuron polarization, our hypothesis is that tDCS directly modulates endothelial cells leading to transient changes in blood-brain-barrier (BBB) permeability (P) that are highly meaningful for neuronal activity. For this, we developed state-of-the-art imaging and animal models to quantify P to various sized solutes after 20 min pretreatment of 1 mA tDCS. tDCS was administered using a constant current stimulator to deliver a 1mA current to the right frontal cortex of rat (approximately 2 mm posterior to bregma and 2 mm right to sagittal suture) to obtain similar physiological outcome as that in the human tDCS application studies. Sodium fluorescein (MW=376), or FITC-dextran (20K and 70K), in 1% BSA mammalian Ringer was injected into the rat (SD, 250-300g) cerebral circulation via the ipsilateral carotid artery by a syringe pump at a constant rate of ~3 μl/min. To determine P, Multiphoton microscopy was applied to take the images from the region of interest (ROI) with proper microvessels, which are 100-200 micron below the pia mater. It shows that the relative increase in P is about 8-fold for small solute, sodium fluorescein, ~35-fold for both intermediate-sized (Dex-20k) and large (Dex-70k) solutes, 10 min after tDCS treatment. All of the increased permeability returns to the control after 20 min. The results confirmed our hypothesis. Supported by NIH R21EB017510-01.

9788-67, Session PS4

Investigating changes in brain network properties in HIV-associated neurocognitive disease (HAND) using mutual connectivity analysis (MCA)
Anas Z. Abidin, Adora M. D’Souza, Mahesh B. Nagarajan, Axel Wismüller M.D., Univ. of Rochester Medical Ctr. (United States)

About 50% of subjects infected with HIV present deficits in cognitive domains, which are known collectively as HIV associated neurocognitive disorder (HAND). The underlying synaptodendritic damage can be captured using resting state functional MRI, as has been demonstrated by a few earlier studies. Such damage may induce topological changes of brain connectivity networks. We test this hypothesis by capturing the functional interdependence of 90 brain network nodes using a Mutual Connectivity Analysis (MCA) framework with non-linear time series modeling based on Generalized Radial Basis function (GRBF) neural networks. The network nodes are selected based on the regions defined in the Automated Anatomic Labeling (AAL) atlas. Each node is represented by the average time series of the voxels of that region. The resulting networks are then characterized using graph-theoretic measures that quantify various network topology properties at a global as well as at a local level. We tested for differences in these properties in network graphs obtained for 10 subjects (6 male and 4 female, 5 HIV+ and 5 HIV-). Global network properties captured some differences between these subject cohorts, though significant differences were seen only with the clustering coefficient measure. Local network properties, such as local efficiency and the degree of connections, captured significant differences in regions of the frontal lobe, precentral and cingulate cortex amongst a few others. These results suggest that our method can be used to effectively capture differences occurring in brain network connectivity properties revealed by resting-state functional MRI in neurological disease states, such as HAND.

9788-66, Session PS4

Three modality image registration of brain SPECT/CT and MR images for quantitative analysis of dopamine transporter imaging
Yuzuho Yamaguchi, Yuta Takeda, Takeshi Hara, Gifu Univ. (Japan); Xiangrong Zhou, Gifu Univ. (Japan); Masaki Matsusako, Yuki Tanaka, Kazuhiko Hosoya, Tsutomu Nihei, St. Luke’s International Hospital (Japan); Tetsuro Katafuchi, Hiroshi Fujita, Gifu Univ. (Japan)

Features in Parkinson’s disease (PD) are a degeneration and loss of the dopamine neurons in striatum. [123I]-FP-CIT can visualize the distribution by binding to the dopamine neurons. The radioactivated medicine is used for diagnosis of PD and Dementia with Lewy Bodies (DLB). The material can visualize activities in corpus striatum on SPECT images, but the location of the corpus striatum on SPECT images are often lost because of the low uptake. To realize a quantitative image analysis for the SPECT images, image registration technique to determine the region of corpus striatum on SPECT images are required to measure precise uptakes. In this study, we proposed an image fusion technique for SPECT and MR images by intervening CT image taken by SPECT/CT. We used 6 cases of SPECT/CT images and 4 cases of MR images taken by changing the direction of phantom materials. 16 of 24 patterns were registered within 5 pixels (1.3mm).

9788-69, Session PS4

Multimodal brain visualization from Stony Brook University
Saad Nadeem, Arie Kaufman, Stony Brook Univ. (United States)

Current connectivity diagrams of human brain image data are either overly complex or overly simplistic. In this work we introduce simple yet accurate interactive visual representations of multiple brain image structures and the connectivity among them. We map cortical surfaces extracted from human brain magnetic resonance image (MRI) data onto 2D surfaces that preserve shape (angle), extent (area), and spatial (neighborhood) information for 2D (circular disc or square) mapping or optimal angle preservation for 3D (spherical) mapping, split these surfaces into separate patches, and cluster functional and diffusion tractography MRI connections between pairs of these patches. The resulting visualizations are computationally easier to compute on and more visually intuitive to interact with than the original data, and facilitate simultaneous exploration of multiple data sets, modalities, and statistical maps.
9788-70, Session PS4

Comparative study of multimodal intra-subject image registration methods on a publicly available database

Mohammad Saleh Miri, Ali Ghayoor, Hans J. Johnson, Milan Sonka, The Univ. of Iowa (United States)

This work runs a comparative study between five manual and automated methods for intra-subject pair-wise registration of images from different modalities. The study includes a variety of inter-modal image registrations (MR-CT, PET-CT, PET-MR) utilizing different methods including two manual point-based techniques using rigid and similarity transformations, one automated point-based approach based on Iterative Closest Point (ICP) algorithm, and two automated intensity-based methods using the mutual information (MI) and the normalized MI. These techniques were applied for inter-modal registration of brain images of 9 subjects from a publicly available dataset, and the results were evaluated qualitatively via checkerboard images and quantitatively using root mean square error and MI criteria. In addition, for each inter-modal registration, a paired t-test was performed on the quantitative metrics in order to find any significant difference between the registration techniques.

9788-71, Session PS4

Automated tissue classification of pediatric brains from magnetic resonance images using age-specific atlases

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The goal of this project was to develop two age appropriate atlases (neonatal and 1 year old) that account for the rapid growth and maturational changes that occur during early development. Anatomical priors from each age group were initially created by manually correcting the resulting tissue maps generated using an expectation maximization (EM) algorithm based on an adult atlas. The EM algorithm classified each voxel into one of ten possible tissue types including several subcortical structures. To minimize the required manual corrections, the adult atlas was registered to the pediatric scans using a high-dimensional, symmetric image normalization (SyN) registration. To generate the age appropriate atlases, the subject images were then mapped to an age specific atlas space also using a SyN registration, and the resulting transformation was applied to the manually corrected tissue maps. Each tissue map was averaged in the age specific atlas space across subjects and blurred to generate the age appropriate anatomical priors. The resulting anatomical priors were then used by the EM algorithm to re-segment the initial training set as well as an independent testing set. Results from the adult and age specific anatomical priors were compared to the manually corrected results. The age appropriate atlas provided superior results as compared to the adult atlas. The age specific atlas can be incrementally improved by including additional subjects into the atlas thus incorporating additional anatomical variability into the anatomical priors. The image analysis pipeline used in this work was built using the open source software package BRAINSTools.

9788-72, Session PS4

Predicting human age using regional morphometry and inter-regional morphological similarity

Xunheng Wang, Lihua Li, Hangzhou Dianzi Univ. (China)

The goal of this project was to develop two age appropriate atlases (neonatal and 1 year old) that account for the rapid growth and maturational changes that occur during early development. Anatomical priors from each age group were initially created by manually correcting the resulting tissue maps generated using an expectation maximization (EM) algorithm based on an adult atlas. The EM algorithm classified each voxel into one of ten possible tissue types including several subcortical structures. To minimize the required manual corrections, the adult atlas was registered to the pediatric scans using a high-dimensional, symmetric image normalization (SyN) registration. To generate the age appropriate atlases, the subject images were then mapped to an age specific atlas space also using a SyN registration, and the resulting transformation was applied to the manually corrected tissue maps. Each tissue map was averaged in the age specific atlas space across subjects and blurred to generate the age appropriate anatomical priors. The resulting anatomical priors were then used by the EM algorithm to re-segment the initial training set as well as an independent testing set. Results from the adult and age specific anatomical priors were compared to the manually corrected results. The age appropriate atlas provided superior results as compared to the adult atlas. The age specific atlas can be incrementally improved by including additional subjects into the atlas thus incorporating additional anatomical variability into the anatomical priors. The image analysis pipeline used in this work was built using the open source software package BRAINSTools.

9788-73, Session PS4

Comparison of template registration methods for multi-site meta-analysis of brain morphometry

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Neuroimaging consortia such as ENIGMA can significantly improve power to discover factors that affect the human brain by pooling statistical inferences across cohorts to draw generalized conclusions from populations around the world. Voxelwise analyses such as tensor-based morphometry also allow an unbiased search for effects throughout the brain. Even so, such consortium based analyses have been limited by a lack of high-powered methods to harmonize voxelwise information across study populations and scanners. While the simplest approach may be to map all images to a single standard space, the benefits of cohort-specific templates have long been established. Here we studied methods to pool voxel-wise data across sites using templates customized for each cohort but providing a meaningful common space across all studies for voxelwise comparisons. As 3D MRI registrations and voxelwise statistical analyses are computationally burdensome, even when distributed across sites, we also considered the computational load. We created study-specific brain templates for four T1-weighted MRI datasets, and a common space from the four study-specific templates. We varied the registration methods and parameters required to register all templates to the common “metaspace”. We recorded computational times for the registration to the metaspace with each parameter set and assessed alignment accuracy using Dice overlap coefficients for anatomical labels transformed to each template space. Surprisingly, considerable computation time could be saved by using coarser registration parameters, without compromising final overlap.
An image registration pipeline for analysis of transynaptic tracing in mice

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Parkinson’s Disease (PD) is a movement disorder characterized by the loss of dopaminergic neurons in the substantia nigra pars compacta (SNc) and noradrenergic neurons in the locus coeruleus (LC). To further understand the effects of PD, the SNc and LC input neurons of mice can be transynaptically traced, imaged and counted. In the experiment, transgenic mice which express Cre in dopaminergic and noradrenergic neurons were created. A modified fluorescent rabies virus, missing a rabies glycoprotein (RG) necessary for its anterograde spread and pseudotyped with EnvA to restrict infection to cells with TVA receptors, was also generated. Helper viruses which express TVA and RG genes in the presence of Cre were injected into the mice. Thus when the mice were injected with the rabies virus several days later, only dopaminergic neurons and their input neurons were infected. These neurons and their inputs were then imaged using serial two-photon tomography. To determine the number of input neurons in specific brain regions, these images were transformed to a common space. This was done by first generating brain masks using morphological operators. The masks were then registered to the Allen Mouse Brain Atlas (ABA) using Large Deformation Diffeomorphic Metric Mapping (LDDMM), an algorithm specialized for calculating anatomically accurate transforms between images. The registration results were found to be sufficient for the purposes of this experiment. Future work may involve using additional information from subcortical structures to improve registration results.

Comparison of stroke infarction between CT perfusion and diffusion weighted imaging: preliminary results

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In this paper we present preliminary results of comparing between the stroke infarction core automatically segmented in both CT perfusion (based on time to peak parameter) and diffusion weighted imaging (DWI). For each patient, the two imaging volumes are automatically co-registered to a common frame of reference based on an acquired CT angiography image. The accuracy of image registration is measured by the overlap of the segmented brain from both images (CT perfusion and DWI), measured within their common field of view. Due to the limitations of the study, DWI was acquired as a follow up scan up to a week after initial CT based imaging.

However, we found that the segmented brain was still fairly highly overlapping (Jaccard indices of around 0.8) and the percentage of infarcted brain tissue from the two modalities were still fairly highly correlated (around 0.7). The results are promising with more data needed in future for clinical feasibility.

High-resolution in vivo Wistar rodent brain atlas based on T1 weighted image

Su Huang, Zhongkang Lu, Weimin Huang, Institute for Infocomm Research (Singapore); Boominathan Ramasamy, Sankar Seramani, Singapore Bioimaging Consortium (Singapore); Cuntai Guan, Institute for Infocomm Research (Singapore); Sakthivel Sekar, Kishore Bhakoo, Singapore Bioimaging Consortium (Singapore)

Image based atlases for rats brain have a significant impact on pre-clinical research. In this project we acquired T1-weighted images from Wistar rodent brains with fine 597m isotropical resolution for generation of the atlas template image. By applying post-process procedures using a semi-automatic brain extraction method, we delineated the brain tissues from source data. Furthermore, we applied a symmetric group-wise normalization method to generate an optimized template of T1 image of rodent brain, then aligned our template to the Waxholm Space. In addition, we defined several simple and explicit landmarks to correspond our template with the well known Paxinos stereotaxic reference system. Anchoring at the origin of the Waxholm Space, we applied piece-wise linear transformation method to map the voxels of the template into the brain space system in Paxinos’ stereotaxic coordinates to facilitate the labelling task. We also cross-referenced our data with both published rodent brain atlas and image atlases available online, methodologically labelling the template to produce a Wistar brain atlas identifying more than 130 structures. Particular attention was paid to the cortex and cerebellum, as these areas encompass the most researched aspects of brain functions. Moreover, we adopted the structure hierarchy and naming nomenclature common to various atlases, so that the names and hierarchy structure presented in the atlas are readily recognised for easy use. It is believed the atlas will present a useful tool in rodent brain functional and pharmaceutical studies.

Investigating the relationship between subjective drug craving and temporal dynamics of the default mode network, executive control network, and salience network in methamphetamine dependents using rsfMRI

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Resting state functional connectivity (rsFC) studies using fMRI have presented us with a great deal of knowledge about the spatiotemporal organization of the brain. The relationships between a number of resting state functional networks, namely the default mode network (DMN), salience network (SN) and executive control network (ECN) have been intensely studied in basic and clinical cognitive neuroscience. However, the assessment of rsFC has mostly been limited to the assumption of spatially and temporally stationary. In this study, sliding window correlation analysis and k-means clustering were exploited to examine the temporal dynamics of rsFC of these three networks in 24 abstinent methamphetamine dependents. Afterwards, using canonical correlation analysis (CCA) the possible relationship between the level of self reported craving and the temporal dynamics was examined. Results indicate that the rsFC transit between 6 discrete “FC states” in the meth dependents. CCA results show that higher levels of craving are associated with higher probability of transiting from state 4 to 6 (disappearance of positive FC DMN-ECN and appearance of negative FC DMN-SN) and staying in state 4 (positive FC DMN-ECN), lower probability of staying in state 2 (negative FC DMN-ECN), transiting from state 4 to 2 (change of positive FC DMN-ECN to negative...
FC), and transiting from state 3 to 5 (appearance of negative FC DMN-SN and positive FC DMN-ECN with the presence of negative FC SN-ECN). Quantitative measures of temporal dynamics in large-scale brain networks could bring new added values to increase potentials for applications of rsfMRI in addiction medicine.

9788-78, Session PS5

Functional connectivity analysis of resting-state fMRI networks in nicotine dependent patients

Aria Smith, Anahid Ehtemami, Daniel Fratte, Anke Meyer-Baese, Olmo Zavala-Romero, Florida State Univ. (United States)

This study evaluates the use of functional connectivity information of the brain to predict the mode of treatment in nicotine dependent patients. Functional connectivity of the brain is dynamic; it changes over time due to different causes such as learning, visual stimuli, quitting a habit. Functional connectivity analysis is useful in discovering and comparing patterns between functional magnetic resonance imaging (fMRI) scans of patients’ brains. In the resting state, the patient is asked to remain calm and do not any task to minimize the contribution of external stimuli. The study of resting-state fMRI networks have shown functionally connected brain regions that have a high level of activity during this state. In this project, the relationship between these functionally connected brain regions, identify nicotine dependent patients, who underwent a smoking cessation treatment, is evaluated. Our approach is on the comparison of the set of connections between fMRI scans before and after treatment. Support vector machines are used to classify patients that took a treatment and patients that took a placebo. Using the functional connectivity (CONN) toolbox, correlation matrices were obtained based on the functional connectivity between different regions of the brain. The experimental results show that there is inadequate predictive information to classify nicotine dependent patients using the SVM classifier. Other classification methods are suggested to be explored for better classify the nicotine dependent patients.

9788-79, Session PS6

FEM-based simulation of a fluorescence tomography experiment using anatomical MR images

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A hybrid system combining Fluorescence Molecular Tomography (FMT) and Magnetic Resonance Imaging (MRI) is attractive for preclinical imaging as it allows combining molecular information from FMT with anatomical reference from MRI. Such a system was previously developed and some successful biological applications have been described [1,2]. However, the first generation of FMT/MRI system suffers from limited spatial resolution and artifacts at the surface of reconstruction volume. Using a refined forward model based on finite element method (FEM) will help improving the reconstruction quality. Heterogeneity of tissues and irregular surface can be accurately described and taken into account by a well-segmented mesh, which is generated from anatomical MR images. Herein, we established simulation based on TOAST++ [3] to mimic an FMT experiment. MRI images were taken on a 9.4T MR scanner with a T1-weighted pulse sequence. The voxelized dataset was processed by iso2mesh [4] to yield a 3D-mesh. Four steps of FMT simulation includes: 1) Assignment of optical properties, 2) Specification of boundary conditions and generation of 3) Excitation and 4) Emission maps. Simulation using a slab phantom containing a fluorescence inclusion reveals realistic excitation and emission maps. The mesh introduced leads to a decrease of computational time by a factor of 95%. The efficiency and reliability will be further validated with phantom study and if successful the method will be used in solving inverse problem.

9788-80, Session PS6

Measuring skin penetration by confocal Raman microscopy (CRM): correlation to results from conventional experiments

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CRM is increasingly used for the detection of xenobiotics within the skin as it is capable of mapping the distribution of the active within the skin in microscale and can thereby visualize the distribution in more detail than most commonly used methods. To highlight this, we compared the results obtained with CRM to those from conventional experiments. Semisolid preparations that contained procaine HCl as a model drug and the penetration enhancers propylene glycol or polyoxyethylene-25-auryl ether were used as model formulations. Excised postauricular porcine skin was incubated in Franz diffusion cells with semisolid formulations that contained either enhancer. An enhancer free formulation was used as control. After the incubation, the skin was cleaned, frozen and sagittal cuts were made with a cryo-microtome. The cuts were examined with a confocal Raman microscope. The relative procaine amount that was delivered to the skin by the penetration enhancers was calculated and compared to the value that was obtained without enhancer. Penetration was visualized by color coded images. The CRM investigation revealed that propylene glycol did not enhance the penetration of procaine whereas POE-lauryl ether had a distinct enhancing effect on the amount of procaine in the epidermis. Results from conventional permeation and penetration experiments confirmed those results. Furthermore, the proposed CRM-methodology was proven to visualize the distribution of the drug within the skin and with respect to the skin constituents in microscale. Color coded images showed that procaine was predominantly located in the lipid rich domains in the skin.

9788-81, Session PS6

Modulation of fluorescence via ultrasound-switchable fluorescence for deep-tissue high-resolution imaging

Baohong Yuan, Jayanth Kandukuri, Bingbing Cheng, Shuai Yu, The Univ. of Texas at Arlington (United States); Venugopal Bandi, Univ. of North Texas (United States); Kytai T. Nguyen, Yi Hong, The Univ. of Texas at Arlington (United States); Francis D’Souza, Univ. of North Texas (United States)

In this experimental study, we first introduce a recently developed deep-tissue high-resolution imaging technique termed as ultrasound-switchable fluorescence (USF). A new approach of modulating ultrasound exposure time is adopted to increase the detectability of the USF signal. The control parameters of modulation of ultrasound such as 1) gating frequency -switching ultrasound ‘ON/OFF’ at desired frequency, 2) duty period -switching ultrasound ‘ON’ for desired duration, 3) Number of cycles in each burst (gating pulse train) 4) Initial long duration of ultrasound exposure and 5) driving power of HIFU can be varied to study its influence on the USF fluorescence signal quality and improve the detection sensitivity. The study was conducted using two types of USF contrast agents, which were synthesized by encapsulating NIR fluorophore ADPDCIA into pluronic nano-capsules and by encapsulating ICG into PNPAM nanoparticles. Additional experimental studies were undertaken, where USF system-1 with both the modulation of Ultrasonic exposure and modulation of excitation laser is compared with USF system-2 with just modulation of ultrasound exposure. USF system-1 showed higher sensitivity to USF phenomenon and improved SNR compared to USF system-2. All the instruments of the USF system are synchronized and the results were recorded simultaneously, using NI-Daq acquisition card, from output of photomultiplier tube (PMT), the lock-in amplifier LIA-1 (excitation laser modulation) and LIA-2 (ultrasound modulation). SNR calculated from maximum of the USF (PMT) output is less
9788-82, Session PS6

**Improve axial resolution of ultrasound-switchable fluorescence technique for deep-tissue high-resolution fluorescence imaging**

Baohong Yuan, Jayanth Kandukuri, Bingbing Cheng, Shuai Yu, The Univ. of Texas at Arlington (United States); Venugopal Bandi, Univ. of North Texas (United States); Kytai T. Nguyen, Yi Hong, The Univ. of Texas at Arlington (United States); Francis D’Souza, Univ. of North Texas (United States)

In the present experimental study, we introduce a recently developed deep tissue and high-resolution imaging technique termed as Ultrasound-switchable fluorescence (USF). This achieved by its high sensitivity and unique switching property of USF contrast agents. Two types of USF contrast agents were used to conduct the experiments, which are synthesized by encapsulating NIR fluorophore ADPDICA into pluronic nanocapsules and the other by encapsulating ICG into PNIPAM nanoparticles. Multi-color imaging was achieved by adopting both the contrast agents who have different emission wavelengths. High lateral resolution was also achieved which were governed by technical and physical limitations of the focused ultrasound transducer used but axial resolution was compromised. Therefore, a new modified USF system is adopted by incorporating dual High-Intensity focused ultrasound (HIFU) to improve the axial resolution of the previously adopted USF system is presented in this paper. By emphasizing on the overlap of induced temperatures profiles of the dual-HIFU, the experimental results obtained show that the axial resolution of the USF imaging can be significantly improved. In addition, multi-color multi-modality imaging can be performed by simultaneously undertaking USF imaging along with conventional ultrasound B-mode imaging thereby depicting capability of these dual imaging modalities to record molecular functional and structural information. Applying modified correlation algorithm to the respective USF signal of both contrast agents, SNR have been improved and, results have been presented and discussed.

9788-83, Session PS6

**Nanoscale donor-acceptor labelled liposome contrast agent for ultrasound modulated fluorescence tomography**

Qimei Zhang, Stephen P. Morgan, The Univ. of Nottingham (United Kingdom); Melissa L. Mather, Keele Univ. (United Kingdom)

Nanoscale liposomes incorporated with donor-acceptor fluorescence resonance energy transfer (FRET) pairs were investigated in the current work to push the fluorescence imaging technique of ultrasound modulated fluorescence tomography (USMFT) into deep tissue with high resolution. The lipophilic carbocyanine dyes DiIC18(5) (DiD) and DiIC18(7) (DiR) were used as FRET pair with DiD acting as the donor and DiR as the acceptor. The emission wavelength is located in the near-infrared window which is ideal for noninvasively tissue imaging. The labelled liposomes were injected through a light transparent Fluorinated Ethylene Propylene tube with 1 mm inner diameter buried at a depth of 1 cm in tissue-like phantom (reduced scattering coefficient: 1 mm⁻¹). The spectrums of the donor-acceptor labelled liposomes compared with donor-only liposomes and acceptor-only liposomes show significant decrease of donor emission and increase of acceptor emission, suggesting high FRET efficiency in the donor-acceptor labelled liposomes at equilibrium state. With application of ultrasound the distance of DiD and DiR was changed resulting as the changed FRET efficiency and thus modulated DiD and DiR emission intensity. Line scanning shows the resolution can be improved significantly compared with the case without influence of ultrasound. The important role FRET plays in enhancement of the emission modulation can be seen from the much greater contrast achieved with the DiD-DiR system as compared to the DiD only liposomes. These results indicate that donor-acceptor labelled nanoscale liposomes can be used as potential contrast agent for USMFT in deep tissue or for whole-body small animal.

9788-104, Session PS6

**3D registration of intravascular optical coherence tomography and cryo-image volumes for microscopic-resolution validation**

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High resolution, 100frames/sec intravascular optical coherence tomography (IVOCT) can distinguish plaque types, but further validation is needed, especially for automated plaque characterization. We developed experimental and 3D registration methods, to provide validation of IVOCT pullback volumes using microscopic, brightfield and fluorescent cryo-image volumes, with optional, exactly registered cryo-histology. The innovation was a method to match IVOCT pullback images, acquired in the catheter reference frame, to a true 3D cryo-image volume. Briefly, an 11-parameter, polynomial virtual catheter was initialized within the cryo-image volume, and perpendicular images were extracted, mimicking IVOCT image acquisition. Virtual catheter parameters were optimized to maximize cryo and IVOCT lumen overlap, resulting in accurately matched frames. Local minima were possible, but when we started within reasonable ranges, every one of 24 digital phantom cases converged to a good solution with a registration error of only ±1.34±2.65µm (signed distance). Registration was applied to 10 ex vivo cadaver coronary arteries (LADs), resulting in 10 registered cryo and IVOCT volumes yielding a total of 421 registered 2D-image pairs. Image overlays demonstrated high continuity between vascular and plaque features. Bland-Altman comparing cryo and IVOCT lumen area, showed 401 of 421 cases within 95% confidence interval. DICE coefficients were 0.905±0.011. Finally, visual assessment on 20 representative cases with easily identifiable features suggested all cases were within one frame of IVOCT (±200µm), eliminating significant misinterpretations introduced by 1mm errors in the literature. The method will provide 3D data for training of IVOCT plaque algorithms and can be used for validation of other intravascular imaging modalities.

9788-107, Session PS6

**High-sensitivity in vitro imaging for pancreatic cancer with GFP-Ferritin nanoprobes**

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Kwan Hyi Lee, Korea Institute of Science and Technology (Korea, Republic of) and Univ. of Science & Technology (Korea, Republic of)

There are a lot of researches about detection of biomarkers on cell membrane and therapies in the field of applied nanomedicine. However, there are difficulties in observation of the targeted biomarkers that exist in trace amount on the cell surface via fluorescent imaging. Therefore, we would like to demonstrate a highly sensitive detection of biomarkers by using GFP-Ferritin protein nanoparticles that is composed of 24 subunits of the genetically modified cancer molecular biomarker existing on the membrane of pancreatic cancer cells. We analyzed the successful production of GFP-Ferritin via dynamic light scattering (DLS), transmission electron microscopy (TEM), and quantum yield measurement. Moreover, we confirmed that compared to the existing conventional fluorophores, the usage of GFP-Ferritin significantly improved fluorescence intensity of the detected biomarker. Such biocompatible genetically modified GFP-Ferritin nanoparticles can be used widely in the field of biomedical application.

9788-84, Session PS7

Respiratory-gated electrical impedance tomography: a potential technique for quantifying stroke volume

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Telemonitoring is becoming increasingly important as the proportion of the population living with cardiovascular disease (CVD) increases. However, currently used health parameters in the suite of telemonitoring tools lack the sensitivity and specificity to accurately predict heart failure events, forcing physicians to play a reactive versus proactive role in patient care. A novel cardiac output (CO) monitoring device is proposed that leverages a custom smart phone application and a wearable electrical impedance tomography (EIT) system. The purpose of this work is to explore the potential of using respiratory-gated EIT to quantify stroke volume (SV) and assess its feasibility using real data from the PhysioNet database. Simulations were carried out using the 4D XCAT model to create anatomically realistic meshes and electrical conductivity profiles representing the human thorax and the intrathoracic tissue. A single 5-second period respiration cycle with chest/ lung expansion was modeled with end-diastole (ED) and end-systole (ES) heart volumes to evaluate how effective EIT-based conductivity changes represent clinically significant differences in stroke volume. After establishing a correlation between conductivity changes and SV, the applicability of the respiratory-gated EIT was refined using data from the PhysioNet database to estimate the number of useful end-diastole (ED) and end-systole (ES) heart events attained over a 3.3 minute period. The area associated with conductivity changes was found to correlate to SV with a correlation coefficient of 0.92. A window of 12.5% around peak exhalation was found to be the optimal phase of the respiratory cycle from which to record EIT data. Within this window, a mean of ~22 useable ED and ES were found with a standard deviation of 4.7 using 3.3 minutes of data for 20 patients.

9788-85, Session PS7

An efficient method for accurate segmentation of left ventricle in contrast-enhanced cardiac MRI images

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Segmentation of left ventricle (LV) in contrast-enhanced cardiac MRI images is a challenging task because of high variability in the image intensity. This variability is due to wash-in and wash-out of the contrast agent over time and poor contrast around the epicardium (outer wall) region. Current approaches for segmentation of the endocardium (inner wall) include application of a threshold within the region of interest, followed by refinement techniques like active contours. The limitation of these methods is under-segmentation of the inner wall because of gradual loss of contrast at the wall boundary. On the other hand, the challenge in outer wall segmentation is the lack of reliable boundaries because of poor contrast. Furthermore, high motion variability across time is the other challenging task. There are four main contributions in this paper to address the aforementioned issues. First, a seed image is selected using variance based approach on 4D time-frame images over which initial endocardium and epicardium is segmented. Secondly, we propose a patch based feature which overcomes the problem of gradual contrast loss for LV endocardium segmentation. Third, a novel method called as ‘Iterative-Edge-Refinement (IER)’ is used for epicardium segmentation. Fourth, a greedy search algorithm for propagating the initial contour segmented on seed-image across other time frame images was utilized. The proposed method was a tested in five contrast-enhanced cardiac MRI datasets (4D) having a total of 1097 images. The segmentation results show a good accuracy and correlation with the manual segmentation by an expert.

9788-86, Session PS7

Comparison of quantitative myocardial perfusion imaging CT to fluorescent microsphere-based flow from high-resolution cryo-images

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Myocardial perfusion imaging using CT (MPI-CT) has the potential to provide quantitative measures of myocardial blood flow (MBF) which can aid the diagnosis of coronary artery disease. We evaluated the quantitative accuracy of MPI-CT analysis approaches in a porcine model of balloon-induced LAD coronary artery ischemia guided by fractional flow reserve (FFR). We quantified MBF at baseline (FFR=1.0) and under moderate ischemia (FFR=0.7) using MPI-CT and compared to fluorescent microsphere-based MBF from high-resolution cryo-images. Dynamic, contrast-enhanced CT images were obtained using a spectral detector CT (Philips Healthcare). Projection-based mono-energetic images were reconstructed and processed to obtain MBF. Three MBF quantification approaches were evaluated: singular value decomposition (SVD) with fixed Tikhonov regularization (THSVD), SVD with regularization determined by the L-Curve criterion (LSVD), and Johnson-Wilson parameter estimation (JW). The three approaches over-estimated MBF as compared to microspheres, however relative blood flow corresponded well to FFR. At baseline, JW produced the most accurate MBF (LAD=110±4.6mL/min/100g, remote=114±5.4mL/min/100g). LAD=95±5.8, remote=103±3.1), whereas LSVD (LAD=121±9.9, remote=134±11.1) and THSVD (LAD=138±10.0, remote=150±12.6) had greater over-estimation. Under induced ischemia, MBF differences were more substantial but followed the same trends. We assessed tissue impulse response functions (IRFs) from each approach for sources of error. While JW was constrained to physiologic solutions, both LSVD and THSVD produced IRFs with non-physiologic properties due to noise. The L-curve provided adaptive regularization but did not eliminate non-physiologic IRF properties or optimize for MBF accuracy. These findings suggest that model-based MPI-CT approaches may be more appropriate for quantitative evaluation than model-independent deconvolution.
9788-87, Session PS7
Nonrigid 2D registration of fluoroscopic coronary artery image sequence with layered motion
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We present a new method for nonrigid registration of coronary artery models with layered motion information. 2D nonrigid registration method is proposed that brings layered motion information into correspondence with fluoroscopic angiograms. The registered model is overlaid on top of interventional angiograms to provide surgical assistance during image-guided chronic total occlusion procedures. The proposed methodology is divided into two parts: layered structures alignment and local nonrigid registration. In the first part, inpainting method is used to estimate a layered rigid transformation that aligns layered motion information. In the second part, a fully nonrigid registration method is implemented and used to compensate for any local shape discrepancy. Experimental evaluation conducted on a set of 5 fluoroscopic angiograms results in a reduced target registration error, which showed the effectiveness of the proposed method over single layered approach.

9788-88, Session PS7
Sensitivity evaluation of DSA-based parametric imaging using Doppler ultrasound in neurovascular phantoms
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To evaluate the relation between parametric imaging results obtained from Digital Subtraction Angiography (DSA) images and blood-flow velocity measured using Doppler ultrasound in patient-specific neurovascular phantoms. A silicone neurovascular phantom containing internal carotid artery, middle cerebral artery and anterior communicating artery was embedded in a tissue equivalent gel. The gel prevented movement of the vessels when blood mimicking fluid was pumped through it to obtain Colour Doppler images. The phantom was connected to a peristaltic pump, simulating physiological flow conditions. To obtain the parametric images, water was pumped through the phantom at various flow rates (100, 120 and 160 ml/min) and 10 ml contrast boluses were injected. DSA images were obtained at 10 frames/sec from the Toshiba C-arm and DSA image sequences were input into LabVIEW software to get parametric maps from time-density curves. The parametric maps were compared with velocities determined by Doppler ultrasound at the internal carotid artery. The velocities measured by the Doppler ultrasound were 38, 48 and 65 cm/s for flow rates of 100, 120 and 160 ml/min, respectively. For the 20% increase in flow rate, the percentage change of blood velocity measured by Doppler ultrasound was 26.3%. Correspondingly, there was a 20% decrease of Bolus Arrival Time (BAT) and 14.3% decrease of Mean Transit Time (MTT), showing strong inverse correlation with Doppler measured velocity. The parametric imaging parameters are quite sensitive to velocity changes and are well correlated to the velocities measured by Doppler ultrasound.

9788-89, Session PS7
Effect of beam hardening on transmural myocardial perfusion quantification in myocardial CT imaging
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The detection of subendocardial ischemia exhibiting an abnormal transmural perfusion gradient (TPG), may help identify ischemic conditions due to micro-vascular dysfunction. We evaluated the effect of beam hardening (BH) artifacts on TPG quantification using myocardial CT perfusion (CTP). We used a prototype spectral detector CT scanner (Philips Healthcare, Cleveland-OH) to acquire dynamic myocardial CTP scans in a porcine ischemia model with partial occlusion of the left anterior descending (LAD) coronary artery guided by FFR measurements. Conventional and 70keV projection-based mono-energetic images were reconstructed from the same projection data and used to compute myocardial blood flow (MBF) using the Johnson-Wilson model. Under moderate ischemia (FFR=0.7), we used three 5mm short axis slices and divided the myocardium into three LAD segments and three remote segments. For each slice and each segment, we characterized TPG as the mean "endo-to-epi" transmural flow ratio (TFR). BH-induced hyperenhancement on the ischemic anterior wall at 120kVp resulted in significantly lower mean TFR value as compared to the 70keV TFR value (0.29±0.01 vs. 0.55±0.01; p<1e-05). No significant difference was measured between mean 120kVp and mean 70keV TFR values on segments less or unaffected by BH. In the entire ischemic LAD territory, mean 120kVp endocardial flow was significantly reduced as compared to mean epicardial flow (15.80±10.98 vs. 40.85±23.44 ml/min/100g; p<1e-04). At 70keV, BH was effectively minimized resulting in mean endocardial MBF of 40.85±15.3407/ml/min/100g vs. 74.09±5.07ml/min/100g (p=0.0054) in the epicardium. We also found that BH effect in the conventional 120kVp images falsely resulted in lower MBF even under non-ischemic conditions.

9788-90, Session PS7
Investigating relationships between left atrial volume, symmetry, and sphericity
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Introduction: Left atrium (LA) remodeling is associated with atrial fibrillation (AF) progression and reduced success after catheter ablation. However, little is known about the relationships between changes in LA volume, symmetry and sphericity. As a precursor to evaluating clinical significance of specific LA shape metrics, we report on a computational geometric analysis in a pilot cohort evaluating the association between various LA shape metrics.

Materials and Methods: We included 17 patients (9 males, 62±8 years in age) presenting for ablation of paroxysmal (41%) or persistent (59%) AF. The LA in pre-interventional end-diastolic CT data were reconstructed and analyzed for regional volume, symmetry & sphericity using specialized software (QuantMD Surgery Explorer, QuantMD LLC). First, to quantify LA symmetry, a novel asymmetry index (ASI) was defined as the ratio between its anterior (LA-A) and posterior (LA-P) portions, based on a three-dimensional cutting plane dividing the LA volume (LAV) between the pulmonary vein ostia and the appendage and parallel to the posterior wall. Next, a patient-specific best-fit sphere was fitted to the LA using iterative closest point registration in order to quantify the average radius, AR, of the LA as well as its regional deviation from spherical shape. The mean deviation, S, from this best-fit sphere was finally utilized to compute LA Sphericity (LAS) as (1-CSV)100%, where CSV = AR/S. Regional deviation from spherical shape was additionally plotted as a color-map on the LA surface to visualize patient-specific LA similarity to an optimally sized spherical shape.

Results and Discussion: Patients had a preserved ejection fraction (55±8%) and a CHADS-VASc score of 2.1±1.5. LA dilatation (echocardiographic diameter LAD=43±6 mm, AR=31±4 mm, LAV=148±47 ml), ASI (64±6%) and LAS (88±2) changes were present. LAV correlated closely with all indexes.
CT guided diffuse optical tomography for breast cancer imaging

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Diffuse optical tomography (DOT) has attracted attentions during the last two decades due to its intrinsic sensitivity in sensing main chromophores of tissues such as blood, water, and lipid. However, DOT has not been clinically accepted yet due to its limitation in spatial resolution caused by strong optical scattering effect in tissues. Structural guidance provided by an anatomical imaging modality enhances the DOT imaging substantially. Here, we report a CT guided multispectral DOT imaging system for breast cancer detection. We have built a prototype DOT imaging system which consists of four lasers at wavelengths of 650, 715, 880, and 915 nm and an electron multiplier charge coupled device (EMCCD). The CT guided multispectral DOT reconstruction algorithms and concepts have been validated with numerical simulations and phantom experiments. The imaging setup parameters such as the measurement projection number and the effects of signal to noise ratio on the DOT reconstruction have been investigated. Our results indicate that an EMCCD camera with air cooling is good enough for the transmission mode DOT imaging. We have also found that measurements at six projections are sufficient for DOT to reconstruct the optical absorption targets when the CT guidance is applied. The EMCCD camera based system will make patients feel more comfortable than traditional compressed breast cancer detection system. Finally, our efforts and progress on the integration of the DOT imaging system inside a breast CT scanner will also be reported.

Microscopic validation of whole mouse micro-metastatic tumor imaging agents using cryo-imaging and sliding organ image registration

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We created a quantitative metastasis imaging, analysis platform consisting of software and multi-spectral cryo-imaging system suitable for evaluating emerging imaging agents targeting micro-metastatic tumor. We analyzed CREKA-Cy3 and CREKA-Gd in MRI, followed by cryo-imaging which repeatedly sectioned and tiled microscope images of the tissue block face, providing ana-tomical bright field and molecular fluorescence, enabling 3D microscopic imaging of the entire mouse with single metastatic cell sensitivity. To register MRI volumes to the cryo-bright field reference, we used our “standard” mutual information, non-rigid registration which proceeded: rigid, affine, and B-spline non-rigid 3D registration. In this report, we created two modified approaches: “mask” where we registered locally over a smaller rectangular solid, and “sliding organ”. Briefly, in “sliding organ”, we segmented the organ, registered the organ and body volumes, separately and combined results. Regularization parameters for each method were optimized in a grid search. Evaluations consisted of DICE, surface distance, and visual scoring of a checkerboard display. “Standard” worked well in all regions except near the kidney. Focusing on the kidney region, registration quality was “sliding organ” > “mask” > “standard”. All methods were reasonably robust with regards to regularization parameters. We optimized parameters on one mouse and found similar results in the training mouse as compared to three other test mice.

Improved diagnosis of tumor tissues with QUESPOWR MRI

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Introduction: The Quantification of Exchange as a function of Saturation Power On the Water Resonance (QUESPOWR) method is introduced as a simple way to detect tissues with fast exchanging labile protons with small chemical shifts. This method uses the OPARACHEE MRI pulse sequence1 to measure water signal as a function of RF power, and uses QUESPOWER linear fitting methods (that are similar to linear variations of QUES fitting methods)2 to estimate the average chemical exchange rate for each pixel. Simulations and phantom studies were used to evaluate QUESPOWR MRI. Demonstrations with an in vivo mouse model of mammary carcinoma showed that QUESPOWR MRI can detect tumor tissues with high sensitivity and specificity.

Methods and Results: Simulations were performed to determine the % water signal generated by OPARACHEE MRI over a range of RF powers for the WALTZ16 pulse train; this series of images is known as a QUESPOWR MRI (Fig. 1A). The simulations were performed for samples with large and small chemical shifts, and fast and slow chemical exchange rates. The water signal was renormalized and inverted to create a QUESPOWR plot that was similar to a QESP plot (Fig. 1B). The portion of this plot at high power was analyzed with HP-HW-QUEST MRI (Fig. 1C), which measured the chemical exchange rates used for initially simulating the % water signals.

Experimental phantoms of iopamidol (Isovue®) were prepared at 0-79 mM and pH 6.21 - 7.26. QUESPOWR MRI was acquired with RF powers of 0-25 T for the WALTZ16 pulse train. The % water signal (Fig. 1D) was renormalized and inverted (Fig. 1E) to create a QUESPOWR plot, and the linear HP-HW-QUEST method was fit to these results to measure chemical exchange rates (Fig. 1F). This experimental result confirmed simulated results.

Three mice with a subcutaneous MCF7 tumor were imaged with QUESPOWR MRI. The % water signals of two tissue regions (Fig. 1G) were renormalized and inverted to create a QUESPOWR plot (Fig. 1H), and HP-HW-QUEST was used to measure chemical exchange rates (Fig. 1I). The analysis was repeated on a pixelwise basis to create a parametric map of chemical exchange rates (Fig. 2). A linear variational Bayesian inference with an uninformative prior was used to avoid overfitting the results. The parametric map fit almost all pixels in the tumor and a few pixels in the bladder, but did not adequately fit pixels in non-fat, normal tissues. A patient with metastatic ovarian cancer was imaged using the QUESPOWR technique. QUESPOWR MRI was acquired with RF powers of 2.0, 2.5, 3.0, 3.5, 4.0, 4.5, 5.0 and 6.0 T. The analysis was repeated on a pixelwise basis to create a parametric map of chemical exchange rates (Fig. 2). A linear variational Bayesian inference with an uninformative prior was used to avoid overfitting the results. The parametric map fit almost all pixels in the tumor and a few pixels in the bladder, but did not adequately fit pixels in non-fat, normal tissues.

Discussion: Simulations and phantom studies showed that QUESPOWR MRI can detect endogenous species with small chemical shifts and slow chemical exchange rates. Importantly, the simulations and phantom studies showed that the HP-HW-QUEST analysis can only analyze QUESPOWR MRI that involve species with small chemical shifts and slow chemical exchange rates, such as endogenous biomolecules at low pH. Remarkably, the in vivo studies showed that HP-HW-QUEST analysis of QUESPOWR MRI is highly specific for pixels in the tumor that have low extracellular pH. Because QUESPOWR MRI is “blind” to tissues with neutral extracellular pH, this method has outstanding sensitivity and specificity for tumor diagnosis.
Computerized segmentation algorithm with personalized atlases of murine MRIs in a SV40 large T antigen mouse mammary cancer model

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Quantities of MRI data, much larger than can be analyzed by hand, are routinely generated in our lab. We aim to develop an automated image segmentation and registration pipeline to aid in analysis of data from our high-throughput 9.4 Tesla small animal MRI imaging center. T2-weighted MRIs were acquired over 4 time-points (up to 12 to 18 weeks) from twelve SV40 Large T-antigen mice for a total of 46 T2-weighted MRI volumes; each with a matrix size of 192x256, 61 slices, in plane resolution 0.1mm, and slice thickness 0.5 mm. These image sets were acquired with the goal of tracking and quantifying progression of mammary intraepithelial neoplasia (MIN) to invasive cancer in mice, believed to be similar to ductal carcinoma in situ (DCIS) in humans. Our segmentation algorithm takes a 2D seed-point drawn by the user at the center of an overlaid projection of the 4 co-registered volumes associated with each mouse. The level set then evolves in 3D using this single 2D seed. The contour evolution incorporates texture information, edge information, and a statistical shape model in a two step process. Volumetric DICE coefficients comparing the automatic with manual segmentations were computed and ranged between 0.75 and 0.58 for averages over the 4 life-cycle time points of the mice. Incorporation of these personalized atlases with intra and inter mouse registration is expected to locally and globally track the morphological and textural changes in the mammary tissue and associated lesions of these mice.

3D Segmentation of lung CT data with graph-cuts: analysis of parameter sensitivities

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Lung boundary image segmentation is important for many tasks including for example in development of radiation treatment plans for subjects with thoracic malignancies. In this paper, we describe a method and parameter settings for accurate 3D lung boundary segmentation based on graph-cuts from X-ray CT data. Even though previously several researchers have used graph-cuts for image segmentation [5], to date no systematic studies have been performed regarding the range of parameter that give accurate results. The energy function in the graph-cuts algorithm requires 3 suitable parameter settings: K, a large constant for assigning seed points, c, the similarity coefficient for n-links, and ?, the terminal coefficient for t-links. We analyzed the parameter sensitivity with four lung data sets from subjects with lung cancer using error metrics. Large values of K created artifacts on segmented images, and relatively much larger value of c than the value of ? influenced the balance between the boundary term and the data term in the energy function, leading to unacceptable segmentation results. For a range of parameter settings, we performed 3D image segmentation, and in each case compared the results with the expert-delineated lung boundaries. We used simple 6-neighborhood systems for n-link in 3D. The 3D image segmentation took 10 minutes for a 512x512x118 ~ 512x512x190 lung CT image volume. Our results indicate that the graph-cuts algorithm was more sensitive to the K and ? parameter settings than to the C parameter and furthermore that amongst the range of parameters tested, K=5 and ?=0.5 yielded good results.

The 3D edgerunner pipeline: a novel shape-based analysis for neoplasms characterization

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The characterization of tumors after being imaged is currently a qualitative process performed by skilled professionals. If we can aid their diagnosis by identifying quantifiable features associated with tumor classification we may avoid invasive procedures such as biopsies and enhance efficiency within their procedure. The aim of this paper is to describe the 3D EdgeRunner Pipeline which characterizes the shape of a tumor. Shape analysis is relevant as we know that malignant tumors tend to be more lobular and benign tumors tend to grow with symmetry. The method described considers the distance from each point on the edge of the tumor to the center and determines coordinates where these distances are rapidly changing (peaks) using a second derivative found by five point differentiation. The list of coordinates considered to be peaks can then be used as statistical data to compare tumors quantitatively or can be viewed on a color-coded 3D reconstruction to help visualize the tumor’s shape. We have found this process effectively captured the peaks on a selection of kidney tumors.

Application of probabilistic fiber-tracking method of MR imaging to measure impact of cranial irradiation on structural brain connectivity in children treated for medulloblastoma

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We apply a probabilistic fiber-tracking method for the extraction of fiber pathways to quantify myelin structural loss in connectivity due to irradiation as treatment for pediatric medulloblastoma. This pathway analysis created a structural connectome for comparison between baseline and post-radiation therapy scans and for comparison between standard and high dose irradiation. A paired-wise comparison of the connectivity between baseline and post-RT scans showed irradiation did have a significant detrimental impact on white matter integrity (decreased fractional anisotropy and bilateral decreased axial diffusivity, particularly in the Frontostriatal, Parietostriatal, and Basal Ganglia networks. Group comparisons of the change in the connectivity revealed that high-risk patients experienced greater changes in axial and radial diffusivity in the Frontostriatal and Parietostriatal networks compared to the standard-risk patients. Standard-risk patients were relatively stable across time while the high-risk subjects demonstrated significant decrease in diffusivity measures. This study on pediatric patients with medulloblastoma demonstrates the utility of this method to identify specific brain networks affected by radiation therapy.

Lung boundary image segmentation is currently a qualitative process performed by skilled professionals. If we can aid their diagnosis by identifying quantifiable features associated with tumor classification we may avoid invasive procedures such as biopsies and enhance efficiency within their procedure. The aim of this paper is to describe the 3D EdgeRunner Pipeline which characterizes the shape of a tumor. Shape analysis is relevant as we know that malignant tumors tend to be more lobular and benign tumors tend to grow with symmetry. The method described considers the distance from each point on the edge of the tumor to the center and determines coordinates where these distances are rapidly changing (peaks) using a second derivative found by five point differentiation. The list of coordinates considered to be peaks can then be used as statistical data to compare tumors quantitatively or can be viewed on a color-coded 3D reconstruction to help visualize the tumor’s shape. We have found this process effectively captured the peaks on a selection of kidney tumors.
Correlation between diffusion kurtosis and NODDI metrics in neonates and young children

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No Abstract Available

Multi-temporal MRI carpal bone volumes analysis by principal axes registration

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In this paper, a principal axes registration technique is presented, with the relevant application to segmented volumes. The segmentation method used herein is based on the graph theory and is a robust, unsupervised and parameters independent method. In this context, the registration is employed to compare multi-temporal volumes of carpal bones from MRI acquisitions. Starting from the study of the principal axes, the eigenvectors are used with respect to the reference axis along with the rotation of both volumes. Therefore, the volumes are shifted with respect to the center of gravity.

A quantitative evaluation of the results obtained is carried out by computing classical indices from the confusion matrix, with similarity measures. It is of great interest, within the medical field, the way a registration can be used to compare multi-temporal images, providing the physician with a tool, which allows a visual comparison of the evolution of the disease.

Within this framework, the present work is focused on the segmented volumes of carpal bones derived from Magnetic Resonance Imaging (MRI). The registration is applied on multi-temporal volumes, taking into consideration patients affected by rheumatic diseases.

A framework for incorporating DTI atlas builder registration into tract-based spatial statistics and a simulated comparison to standard TBSS

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Tract-based spatial statistics (TBSS) is a software pipeline widely employed in comparative analysis of the white matter integrity from diffusion tensor imaging (DTI) datasets. In this study, we seek to evaluate the relationship between different methods of atlas registration for use with TBSS and different measures of DTI (fractional anisotropy, FA, and axial diffusivity, AD). To do so, we have developed a novel tool that builds on an existing diffusion atlas building software, and integrated it into a new version of TBSS called DAB-TBSS (DTI Atlas Builder-Tract-Based Spatial Statistics) by using advanced registration offered in DTI Atlas Builder (UNC, NIRAL). To compare the effectiveness of these two versions of TBSS, we also propose a framework for simulating population differences for diffusion tensor imaging data, providing a more substantive means of empirically comparing DTI group analysis programs such as TBSS. In this study, we used 37 diffusion tensor imaging datasets and simulated group-wise changes by extending the principal tensor eigenvalue via Gaussian sampling in the ventral, middle, and dorsal corpus callosum. Our results indicate (1) that the most effective means of detecting differences between these DTI datasets is DAB-TBSS comparing AD (as opposed to FA), and (2) that, in contrast, standard TBSS reports a higher rate of false positives. Within the simulated changes investigated here, this study suggests that atlas building on AD as well as the use of DTI Atlas Builder enhances TBSS group based studies.

Hippocampus shape analysis for temporal lobe epilepsy detection in magnetic resonance imaging

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There are evidences in the literature that temporal lobe epilepsy (TLE) causes some lateralized atrophy and deformation on hippocampus and other substructures of the brain. Magnetic resonance imaging (MRI), due to high-contrast soft tissue imaging, is one of the most popular imaging modality being used in TLE diagnosis and treatment procedures. Using an algorithm to help clinicians for better and more effective shape deformations analysis could improve the diagnosis and treatment of the disease. In this project our purpose is to design, implement and test a classification algorithm for magnetic resonance (MR) images based on hippocampal asymmetry detection using shape- and size-based features and characteristics. Our method consisted of two main parts; (1) shape feature extraction, and (2) image classification. We tested 11 different shape and size features and selected four of them that detect the asymmetry in hippocampus significantly in a randomly selected subset of the dataset. Then we employed a support vector machine (SVM) classifier to classify the remaining images of the dataset to normal and epileptic images using our selected features. On a dataset of 25 images, 12 images were used for feature extraction and the rest 13 for classification. We measured accuracy, specificity and sensitivity of, respectively, 76%, 100%, and 70% for our algorithm. The preliminary results show that using shape and size features for detecting hippocampal asymmetry could be helpful in TLE diagnosis in MRI.

Multi-site study of diffusion metric variability: effects of site, vendor, field strength, and echo time on regions-of-interest and histogram-bin analyses

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It is now common for magnetic-resonance-imaging based multi-site trials to include diffusion-weighted imaging (DWI) as part of the protocol. It is also common for these sites to possess MR scanners of different manufacturers, different software and hardware, and different software licenses. These differences mean that scanners may not be able to acquire data with the same number of gradient amplitude values and number of available gradient directions. Variability can also occur in achievable b-values and minimum echo times. The challenge of a multi-site study then, is to create...
a common protocol by understanding and then minimizing the effects of
scanner variability and identifying reliable and accurate diffusion metrics.
This study describes the effect of site, scanner vendor, field strength,
and TE on two diffusion metrics: the first moment of the diffusion tensor
field (mean diffusivity, MD), and the fractional anisotropy (FA) using two
common analyses (region-of-interest and mean-bin value of whole brain
histograms). The goal of the study was to identify sources of variability in
diffusion-weighted imaging and their influence on commonly reported
metrics. The results demonstrate that the site, vendor, field strength, and
echo time all contribute to variability in FA and MD, though to different
extent. We conclude that characterization of the variability of DTI metrics
due to site, vendor, field strength, and echo time is a worthwhile step in
the construction of multi-center trials.

9788-30, Session 7

MPI as high-temporal resolution imaging technique for in vivo bolus tracking of Ferucarbotran in mouse model

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Purpose:
Magnetic particle imaging (MPI) is a new radiologic imaging method,
potentially capable of rapid 3D dynamic imaging of magnetic tracer. The
goal of this study was to follow and visualize the intravenously injected
nanoparticles in real time through cardiovascular system at MPI.

Material and Methods:
MPI scans of FVB mice (n=4) were carried out using a 3D imaging sequence
(1/T gradient strength, 10 mT drive-field strength, FOV 40x40x20 mm3).
After a first baseline control measurement a dynamic scan consisting of
100 000 repetitions (duration of about 35min and temporal resolution of
21.5ms per 3D volume) was performed. 50µl ferucarbotran (Resovist, Bayer
Schering Pharma AG) was injected into the tailvein via pump (5.7ml/h)
after the 13953th repetition. As MPI delivers no anatomic information,
MRI scans at 7T ClinScan (Bruker) were performed before and after MPI
examination using a T2-weighted 2D turbo spin echo sequence (FOV 32mm,
matrix 256x256, TR 1100ms, TE 28ms). The reconstruction was performed
on the MPI console (ParaVision 6.0/MPI, Bruker). Image fusion was done
using additional image processing software (Imalytics, Philips). The dynamic
information was extracted using self-written software using the Julia
programming environment.

Results:
The combined MR-MPI measurements were carried out successfully. No
dislocation of the mouse was observed. In the sagittal views it is clearly
visible how the tracer enters the vena cava inferior before it moves to the
heart and then into the liver. By co-registration with MRI the anatomical
regions were identified. Due to the frame rate of about 46 volumes
per second a signal modulation with the frequency of the heart beat is
detectable and a heart beat of 520bpm can be appreciated. Moreover
the bloodflow velocity of approximately 5cm/s in the vena cava can be
estimated.

Conclusions:
The high temporal resolution of MPI allows real-time imaging and bolus
tracking of intravenous injected nanoparticles and offers a tool to estimate
blood flow velocity. MRI was successful used for anatomical informations.

9788-31, Session 7

A dual energy CT study on vascular effects of gold nanoparticles in radiation therapy

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Jennifer L. West, Cristian T. Badea, Duke Univ. (United States)

Gold nanoparticles (AuNP) are emerging as promising agents for both
cancer therapy and CT imaging. AuNP are delivered to tumors via the
enhanced permeability and retention effect and they preferentially
accumulate in close proximity to the tumor blood vessels. AuNPs produce
low-energy, short-range photoelectrons during external beam radiation
therapy (RT), boosting dose. This work is focused on understanding how
tumor permeability is influenced by AuNP-augmented RT, and how this
knowledge can potentially improve the delivery of additional nanoparticle-
based chemotherapeutics. We use dual energy (DE) CT to detect
accumulation of AuNPs and increased vascular permeability to liposomal
iodine (i.e. a surrogate for chemotherapeutics with liposome encapsulation)
following RT. We use sarcoma tumors generated in LSL-KrasG12D; p53FL/
FL conditional mutant mice. A total of N=6 mice were injected with 20 mg
AuNP (0.1 ml/25 g mouse) immediately before RT (20 Gy) was delivered.
The control mice received no AuNP injection and 20 Gy RT (n=6), 10 Gy RT
(n=5), or no RT (n=6). A day post-RT, the mice were injected with liposomal
iodine (0.3 ml/25 mouse) and imaged with DE-CT two days later. The
results suggest that RT increases the permeability of tumor vasculature to
liposomal iodine and that the increase in permeability is dose-dependent.
AuNP-augmented RT (20 Gy) enables higher iodine accumulation than RT
(20 Gy) alone; however, this difference was not statistically significant.. We
hypothesize that the dose-response curve of vascular permeability after RT
is non-linear. We will test AuNP-augmented RT at lower doses to determine
the dose of maximum benefit.

9788-32, Session 7

Analysis of cardiac interventricular septum motion in different respiratory states

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The interaction between the left and right heart ventricles (LV and RV)
depends on load and pressure conditions that are affected by cardiac
contraction and respiration cycles. A novel MRI sequence, XD-GRASP,
allows the acquisition of multi-dimensional, respiration-sorted and cardiac-
synchronized free-breathing image data. In these data, effects of the
cardiac and respiratory cycles on the LV/RV interaction can be observed
independently. To enable the analysis of such data, we developed a
semi-automatic exploration workflow. After tracking a cross-sectional line
positioned over the heart, over all motion states, the septum and heart wall
border locations are detected by analyzing the grey-value profile under the
lines. These data are used to quantify septum motion, both in absolute units
and as a fraction of the heart size, to compare values for different subjects.
In addition to conventional visualization techniques, we used color maps
for intuitive exploration of the variable values for this multi-dimensional
data set. We acquired short-axis image data of nine healthy volunteers,
to analyze the position and the motion of the interventricular septum in
different breathing states and different cardiac cycle phases. The results
indicate a consistent range of normal septum motion values, and also
suggest that respiratory phase-dependent septum motion is greatest near
end-diastolic phases. These new methods are a promising tool to assess LV/
RV ventricle interaction and the effects of respiration on this interaction.

9788-33, Session 7

Comprehensive serial study of dynamic remodeling of atherosclerotic coronary arteries using intravascular ultrasound

Zhi Chen, Andreas Wahle, Ling Zhang, The Univ. of Iowa
Modern cardiac CT angiography (CCTA) is highly effective at identifying and assessing coronary blockages associated with CAD. The diagnostic value of CCTA. We have adapted this technique for application beyond the coronary arteries and present an assessment of its impact on image quality and coronary remodeling over the entire length of intravascular ultrasound (IVUS) imaged vessels. Serial measurements at baseline and 12-month follow-up are analyzed rather than static data obtained at a single time point. Every IVUS pullback is segmented automatically, and then reviewed and algorithmically refined by an expert using a computer-aided just-enough-interaction approach. Subsequently, pairs of serial IVUS pullbacks are registered automatically using 3D graph optimization approach. Based on plaque volume increases or decreases over time, pullback frames are divided into two groups – progression and regression. It is shown that plaque progression rates are constant within any level of stenosis while plaque regression rates are negatively correlated with percent stenosis indices ($p<0.01$, $R=0.31$). Moreover, for the progression group, adventitia area increases in direct relation with the baseline percent stenosis (PS) ($p=0.02$, $R=0.15$) when PS is less than 40%. Significance of such a correlation is not observed when percent stenosis exceeds 40%. Conversely, for the regression group, change of adventitia area is almost constant for percent stenosis <40%; but decreases in direct relation with baseline stenosis ($p<0.01$, $R=0.19$) when stenosis > 40%. This strongly suggests that lipid lowering treatment may effectively suppress plaque progression and accelerate plaque regression, especially for larger values of percent stenosis, and further accelerate the corresponding adventitia-remodeling process.

9788-34, Session 7

Motion correction for improving the accuracy of myocardial perfusion CT imaging

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Coronary Artery Disease (CAD) is the leading cause of death globally [1]. Modern cardiac CT angiography (CCTA) is highly effective at identifying and assessing coronary blockages associated with CAD. The diagnostic value of this anatomical information may be substantially increased in combination with a non-invasive, low-dose, quantitative measure of blood supply to the myocardium. While CT perfusion has shown promise of providing such indications of ischemia, artifacts due to motion, beam hardening, and other factors confound clinical findings and can limit quantitative accuracy. In this paper, we investigate the impact of applying the technology behind a novel motion correction algorithm to correct for motion in the myocardium. This motion compensation algorithm (originally designed to correct for the motion of the coronary arteries) has been shown to provide substantial improvements in both overall image quality and diagnostic accuracy of CCTA. We have adapted this technique for application beyond the coronary arteries and present an assessment of its impact on image quality and quantitative accuracy within the context of dual-energy CT perfusion imaging. We conclude that motion correction is a promising technique that can help to pave the way for routine clinical use of dual-energy CT perfusion. When combined, the anatomical information of CCTA and the hemodynamic information from dual-energy CT perfusion should facilitate better clinical decisions about which patients would benefit from treatments such as stent placement, drug therapy, or surgery and help other patients avoid the risks and costs associated with an unnecessary, invasive, coronary angiography procedure.
using a cross-validated area under the ROC curve (AUC). The AUC for receptor status alone was 0.59, while adding the PK parameters derived by the LRRM, NRRM, and Tofts resulted in AUCs of 0.82, 0.60, and 0.59 respectively. This suggests that the LRRM can be used to predict response to NAC in breast cancer.

9788-37, Session 8

Hyperspectral imaging of neoplastic progression in a mouse model of oral carcinogenesis
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Early cancer detection could improve the survival and life quality of cancer patients. As an emerging modality, hyperspectral imaging (HSI) holds great potential for noninvasive early detection. In this paper, we explored the possibility of differentiating between premalignant lesions and healthy tongue tissues using hyperspectral imaging in a chemical induced oral cancer model. We proposed a novel classification algorithm for early cancer detection from hyperspectral images of ex vivo tongues. The method detected the dysplastic with an average area under the curve (AUC) of 0.89. The hyperspectral imaging and classification technique may provide a tool for early detection of oral cancer.

9788-38, Session 8

Superpixel-based spectral classification for the detection of head and neck cancer with hyperspectral imaging
Hyunkoo Chung, Emory Univ. School of Medicine (United States); Guolan Lu, Zhiqiang Tian, Dongsheng Wang, Georgia Z. Chen, Baowei Fei, Emory Univ. (United States)

Hyperspectral imaging (HSI) is a growing technology that acquires images at various wavelengths incorporating both spectral and spatial information. This technology may be able to provide quantitative information for cancer detection and diagnosis [1-2]. This paper proposes a superpixel-based spectral classification to distinguish regions of tumor and healthy tissue. The superpixel-based classification method obtains an average sensitivity of 0.96 and an average specificity of 0.79 based on the data from hyperspectral imaging experiments of 12 mice. Compared to a pixelwise classification, superpixel-based classification improves sensitivity, specificity, and computational cost. The image classification and hyperspectral imaging technology can have various applications in cancer research and management.

9788-39, Session 8

Quantitative evaluation of epigenetic modification in tumor with 18F-FAHA PET imaging
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Alteration in genetic expression is as important as gene mutations in cancer development and proliferation. Cellular epigenetic changes comprise modifications in genetic expression without altering DNA sequence. Histone deacetylase (HDAC), a gene regulator involved in epigenetic modifications by silencing tumor suppressor genes, can be a key to treatment of cancer by inhibiting HDAC. The efficacy of 18F-fluoroacetamido-L-hexanoic acid (18F-FAHA), an artificial HDAC substrate synthesized by us, was evaluated as imaging probe of HDAC activity in human tumor xenografts in immunocompromised host mice. Human breast and melanoma cell lines, MDA-MB-468 and MDA-MB-435 respectively, known to overexpress HDAC activity were xenograft into immunocompromised mice and HDAC was imaged using 18F-FAHA. The melanoma group were treated with SAHA, an approved therapeutically anticancer HDAC inhibitor, or DMSO as control vehicle. Tracer kinetic modelling and SUV were used to estimate HDAC activity in PET. 18F-FAHA was avidly taken up by the tumors with peak uptake at ~30 min post injection. Quantitative assessments showed great inter- and intra-variability in binding rate constant of the tracer indicative of variable HDAC activity. There was reduced whole body tracer uptake but not MDA-MB-435 growth which is consistent with results reported by Tang et al., 2014. Our preliminary study showed that this non-invasive PET imaging method has potential to identify patients for whom treatment with HDAC inhibitors are appropriate, to assess the effectiveness of that treatment as an early marker of target reduction, and also eliminate the need for invasive tissue biopsy to individualize treatment.

9788-40, Session 8

Respiration gating and block fitting improve pH measurements with acidoCEST-MRI in an ovarian orthotopic tumor model
Kyle Jones, Mark D. Pagel, Christine Howison, Edward Randtke, The Univ. of Arizona (United States)

We have developed a MRI method that can measure extracellular pH in tumor tissues, known as acidoCEST MRI. This method relies on the detection of Chemical Exchange Saturation Transfer (CEST) of iopamidol, an FDA-approved CT contrast agent that has two CEST signals. A log10 ratio of the two CEST signals is linearly correlated with pH, but independent of agent concentration, endogenous T1 relaxation time, and B1 inhomogeneity. Therefore, detecting both CEST effects of iopamidol during in vivo studies can be used to accurately measure the extracellular pH in tumor tissues. Past in vivo studies using acidoCEST-MRI have suffered from respiration artifacts in orthotopic and lung tumor models that have corrupted pH measurements. In addition, the non-linear fitting method used to analyze results is unreliable as it is subject to over-fitting especially with noisy CEST spectra. To improve the technique, we have recently developed a respiration gated CEST MRI pulse sequence that has greatly reduced motion artifacts, and we have included both a pre-scan and post scan to remove endogenous CEST effects. In addition, we fit the results by parameterizing the contrast of the exogenous agent with respect to pH via the Bloch equations modified for chemical exchange, which is less subject to over-fitting than the non-linear method. These advances in the acidoCEST MRI technique and analysis methods have made pH measurements more reliable, especially in areas of the body subject to respiratory motion.
A semi-automatic framework of measuring pulmonary arterial metrics at anatomic
airway locations using CT imaging

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Pulmonary vascular dysfunction has been implicated in smoking-related susceptibility to emphysema. With the growing interest in characterizing arterial morphology for early evaluation of the vascular role in pulmonary diseases, there is a growing need for the standardization of a framework for arterial morphological assessment at airway segmental levels. In this paper, we present a semi-automatic framework to segment pulmonary arteries at anatomic airway branches and measure their cross-sectional area (CSA). The method starts with user-specified endpoints of a target arterial segment through a custom-built graphical user interface. It automatically detects the centerline joining the endpoints, determines the local structure orientation and computes the CSA along the centerline after filtering out the adjacent pulmonary structures, such as airway walls or veins. Several new techniques are presented, including collision-impact based cost function for centerline detection, radial sample line based CSA computation, and outlier analysis of radial distance to subtract adjacent neighboring structures in CSA measurement. The method was applied to repeat-scan pulmonary multirow detector CT (MDCT) images from ten healthy subjects (age: 21-48 Yrs, mean: 28.5 Yrs; 7 female) at functional residual capacity (FRC). The reproducibility of computed arterial CSA from six airway segmental locations in upper, middle and lower lobes was analyzed. The overall repeat-scan intra-class correlation (ICC) of the computed CSA from all six airway regions in ten subjects was 95% with maximum ICC of 98% found at LB10 and RB4 regions.

Fat quantification and analysis of lung transplant patients on unenhanced chest CT images based on standardized anatomic space

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Chest fat estimation may be important for identifying high-risk lung transplant candidates. In this paper, an approach to chest fat quantification based on a recently formulated concept of standardized anatomic space (SAS) is presented. The goal of this paper is to seek answers to the following questions related to chest fat quantification on single slice versus whole volume CT, which have not been addressed in the literature. What level of correlation exists between total chest fat volume and fat areas measured on single abdominal and thigh slices? What is the anatomic location in the chest where maximal correlation of fat area with fat volume can be expected? Do the components of subcutaneous adipose tissue (SAT) and visceral adipose tissue (VAT) have the same area-to-volume correlational behavior or do they differ? How do these entities relate to body mass index (BMI)? The SAS approach includes two steps: calibration for the non-linearity existing in the anatomic locations of slices in different patients, and transformation which will map the patient slice locations to SAS. The optimal slice locations for SAT and VAT based on SAS are different (T8 for SAT and T7 for VAT), and are much more consistently determined than with the common linear mapping approach. Fat volume and area for SAT and VAT are correlated with correlation coefficients of 0.97 and 0.86, respectively. More optimal slices selected will generate higher correlation. There is no high correlation of chest fat volume with abdominal or thigh fat area or with BMI.

Patient-specific simulation of tidal breathing

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Patient-specific simulation of air flows in lungs is now straightforward, using segmented airways trees from CT scans as the basis for Computational Fluid Dynamics (CFD) simulations. These models however generally use static geometries, and do not account for the motion of the lungs, and their influence on important clinical indicators, such as airway resistance. This paper is concerned with the simulation of tidal breathing to include the dynamic motion of the lungs and the required analysis workflow, including segmentation, registration and simulation, based on CT scans at the two extremes of the breathing cycle, Total Lung Capacity (TLC) and Functional Residual Capacity (FRC). It describes how topologically consistent cleaned-up geometries are obtained at TLC and FRC, based on the use of a ‘skeleton’ of the network of airway branches, and then used to create a 3D computational mesh which morphs between TLC and FRC. It then describes results for a number of patient-specific cases, both healthy and asthmatic, at baseline conditions and during treatment follow-up, focussing on an important clinical indicator, the airway resistance. It also discusses the implications of the methodology, and the resolution of the CT scans and the subsequent segmentation. Finally it describes how the flow resistances can be reconstructed using simulation with static lung geometries, which are much easier to perform.

Preliminary study of visualizing membrane structures of spiculated pulmonary nodules in three-dimensional thoracic CT images

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Research results from the National Lung Screening Trial (NLST) revealed that screening for lung cancer with low-dose CT (LDCT) reduces lung cancer mortality in heavy smokers by 20% compared to radiography. While this study does show the efficacy of CT-based screening, radiologists often face the problem of estimating the malignant likelihoods of pulmonary nodules detected on LDCT screening for maximizing patient survival and for preserving lung function. Determination of factors predicting the cancer probability of pulmonary nodules detected on LDCT screening is an important preliminary step towards developing an accurate and practical model that can predict cancer probability and support clinical decision making. We focused on spiculation which is one of morphological characteristics associated with malignancy in three-dimensional thoracic CT scans and the subsequent segmentation. Finally it describes how the flow resistances can be reconstructed using simulation with static lung geometries, which are much easier to perform.
CT images. Needle-like structures can often be identified at the spiculated margin of nodule on CT images, but a spatial configuration of spiculation remains elusive. In this study, we present a visualization method to reveal a spatial configuration of spiculation of pulmonary nodules in three-dimensional thoracic CT images. Applying the method to an example of malignant nodule with the spiculated margins, the visualizing preliminary result of the spatial configuration reveals the presence of membrane structures of spiculation.

**9788-45, Session 9**

**Robust lung identification in MSCT via controlled flooding and shape constraints: dealing with anatomical and pathological specificity**

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Correct segmentation and labeling of lungs in thorax MSCT is a requirement in pulmonary/respiratory disease analysis as a basis for further processing or direct quantitative measures: lung texture classification, respiratory functional simulations, intrapulmonary vascular remodeling evaluation, detection of pleural effusion or subpleural opacities, are only few clinical applications related to this requirement. Whereas lung segmentation appears trivial for normal anatomico-pathological conditions, the presence of disease may complicate this task for fully-automated algorithms. The challenges come either from regional changes of lung texture opacity or from complex anatomic configurations (e.g., thin septum between lungs making difficult proper lung separation). They make difficult or even impossible the use of classic algorithms based on adaptive thresholding, 3-D connected component analysis and shape regularization. The objective of this work is to provide a robust segmentation approach of the pulmonary field, with individualized labeling of the lungs, able to overcome the mentioned limitations. The proposed approach relies on 3-D mathematical morphology and exploits the concept of controlled relief flooding (to identify contrasted lung areas) together with patient-specific shape properties for peripheral dense tissue detection. Tested on a database of 40 MSCT of pathological lungs, the proposed approach showed correct identification of lung areas with high sensitivity and specificity in locating peripheral dense opacities.

**9788-46, Session 10**

**Maturation index of developing human brain based on long- and short-range association fibers**

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From early childhood to adulthood, synaptogenesis and synaptic pruning continuous reshape the structural architecture and neural connection in developmental human brains. Disturbance of precisely balanced strengthening of certain axons and pruning of others may cause mental disorders such as autism and schizophrenia. To characterize this balance, we defined and measured a maturation index (MI) derived from the balance of long- and short-range association fibers and potentially sensitive to disease disruption. In the present study, diffusion MRI (dMRI) and TI weighted datasets of 21 healthy subjects 2-25 years were acquired. Brain cortex was parcellated into 68 gyral labels using T1 weighted images, then transformed into dMRI space to serve as the seed ROI for DTI-based tractography. Cortico-cortical association fiber initiated from each gyrus was categorized into long- and short-range based on the other end of fiber terminating in non-adjacent or adjacent gyri of the seed gyrus, respectively. The MI was defined as the ratio between number of long-range fiber and that of short-range fiber (long-short ratio). The developmental trajectory of the whole brain MI (i.e. global MI) follows a quadratic model with initial increases from 2 to 16 years followed by later decreases after 16 years. The trajectory of regional MI is heterogeneous among different cortical gyri reaching the peak earlier in primary somatosensory cortex and visual cortex while later in prefrontal cortex.

**9788-47, Session 10**

**Perfusion deficits and functional connectivity alterations in patients with post-traumatic stress disorder**

Yang Liu, Baojuan Li, Xi Zhang, Linchuan Zhang, Liang Li, Hongbing Lu, Fourth Military Medical Univ. (China)

To explore the alteration in cerebral blood flow (CBF) and functional connectivity between survivors with recent onset post-traumatic stress disorder (PTSD) and without PTSD, who survived from the same coal mine flood disaster. In this study, a processing pipeline using arterial spin labeling (ASL) sequence was proposed. Considering low spatial resolution of ASL sequence, a linear regression method was firstly used to correct the partial volume (PV) effect for better CBF estimation. Then the alterations of CBF between two groups were analyzed using both uncorrected and PV-corrected CBF maps. Based on altered CBF regions detected from the CBF analysis as seed regions, the functional connectivity abnormalities in PTSD patients was investigated. The CBF analysis using PV-corrected maps indicates CBF deficits in the bilateral frontal lobe, right superior frontal gyrus and right corpus callosum of PTSD patients, while only right corpus callosum was identified in uncorrected CBF analysis. Furthermore, the regional CBF of the right superior frontal gyrus exhibits significantly negative correlation with the symptom severity in PTSD patients. The resting-state functional connectivity indicates increased connectivity between left frontal lobe and right parietal lobe. These results indicate that PV-corrected CBF exhibits more subtle perfusion changes and may benefit further perfusion and connectivity analysis. The symptom-specific perfusion deficits and aberrant connectivity in above memories-related regions may be putative biomarkers for recent onset PTSD induced by a single prolonged trauma exposure and help predict the severity of PTSD.

**9788-48, Session 10**

**Monitoring fractional anisotropy in developing rabbit brain using MR diffusion tensor imaging at 3T**

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The aim of this study was to investigate the factional anisotropy (FA) in various regions of developing rabbit brain using magnetic resonance diffusion tensor imaging (MR DTI) at 3 T. A whole-body clinical MR imaging (MRI) scanner with a 15-channel high resolution knee coil was used. An echo-planar-imaging (EPI)-DTI pulse sequence was performed. Five 5 week-old New Zealand white (NZW) rabbits underwent MRI once per week for 24 weeks. After scanning, FA maps were obtained. ROIs (regions of interest) in the frontal lobe, parietal & temporal lobe, and occipital lobe were measured. FA changes with time were evaluated with a linear regression analysis. The results show that the FA values in all lobes of the brain
increased linearly with age. The ranking of FA values was FA(frontal lobe) > FA(parietal & temporal lobe) > FA(occipital lobe). There was significant difference (p < 0.05) among these lobes. FA values are associated with the nerve development and brain functions. The FA change rate could be a biomarker to monitor the brain development. Understanding the FA values of various lobes during brain development could provide helpful information to diagnose the abnormal syndrome earlier and have a better treatment and prognosis. This study established a brain MR-DTI protocol for rabbits to investigate the brain anatomy during development using clinical MRI. This technique can be further applied to the pre-clinical diagnosis, treatment, prognosis and follow-up of brain lesions.

9788-49, Session 10
A pilot DTI analysis in patients with recent onset post-traumatic stress disorder
Yang Liu, Liang Li, Baojuan Li, Xi Zhang, Hongbing Lu, Fourth Military Medical Univ. (China)

To explore the alteration in white matter between survivors with recent onset post-traumatic stress disorder (PTSD) and without PTSD, who survived from the same coal mine fire disaster, the diffusion tensor imaging (DTI) sequences were analyzed using DTI studio and statistical parametric mapping (SPM) packages in this paper. From DTI sequence, the fractional anisotropy (FA) describes the degree of anisotropy of a diffusion process, indicating the degree of anisotropy of the diffusing water along different axes of the image. The decrease of FA values usually represents tissue degeneration. Comparisons of FA calculated from DTI sequences of two groups (PTSD and non-PTSD) indicated that in the right caudate nucleus, right middle temporal gyrus, right fusiform gyrus, and right superior temporal gyrus, FA value of subjects with PTSD was obviously lower than those without PTSD, which indicates a possible relation of identified regions. It could be clearly observed that the three identified regions in the temporal lobes were associated with the left hemisphere. The FA change rate could be a biomarker to monitor the brain development. Understanding the FA values of various lobes during brain development could provide helpful information to diagnose the abnormal syndrome earlier and have a better treatment and prognosis. This study established a brain MR-DTI protocol for rabbits to investigate the brain anatomy during development using clinical MRI. This technique can be further applied to the pre-clinical diagnosis, treatment, prognosis and follow-up of brain lesions.

9788-50, Session 10
Quantification of traumatic meningeal injury using dynamic contrast enhanced (DEC) fluid attenuated inversion recovery (FLAIR) imaging
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Purpose: The aim of this work is to present a method to investigate the meningeal enhancement in Traumatic Meningeal Injury (TMI) by quantitative analysis of Dynamic Contrast Enhanced (DCE) Fluid Attenuated Inversion Recovery Imaging (FLAIR) MRI in patients with Traumatic Brain Injury (TBI).

Methods: Primary injury to the meninges and vasculature can be observed in the absence of conspicuous brain damage following minor head trauma (1). Meningeal enhancement is the result of extravasation of gadolinium contrast into space containing free fluid with a T1 relaxation time comparable to that of cerebrospinal fluid (2). However, the pathophysiology remains unclear. As part of an ongoing study of mild TBI, a total of eleven patients (TMI positive) presenting to a level II trauma center were imaged on a 3T MRI scanner within 96 hours of head injury. The evaluation included a single FLAIR scan prior to single-dose Gd-BOPTA injection, followed by four consecutive FLAIR scans spanning five minutes after injection (Fig. 1). In order to properly quantify the evolution in time of meningeal enhancement, post-contrast Dynamic FLAIR images were aligned with respect to the pre-contrast acquisition using rigid registration with mutual information metric and trilinear interpolation, and the median brain intensity in an upper axial slice was used to normalize the images. Regions of interest were selected to compare different estimations. A brain mask was obtained from the pre-contrast image, and used to identify the location of the cortical convexity. The mid-sagittal plane was computed to quantify enhancement in the falk. At every time point, the difference with respect to the pre-contrast image was computed, and the standard deviation of intensities was locally calculated in order to detect the most pronounced borders. Voxels with high local standard deviation around the cortex, and with a high deviation of intensities in time were retained to estimate the area of enhancement.

Results: Regions of enhancement varied among patients (Fig. 2). Evolution of meningeal enhancement in time is not significantly affected by image normalization (Fig. 3 and 4). When images are misaligned, the evolution of the enhancement in a region of interest strongly depends on their shapes and locations when the images are not co-registered and the regions of interest are manually delineated at every time point (Fig. 3a,b). When misalignment is not relevant, manual and automated methods provide comparable results (Fig. 4a,b). The median intensity in a selected region of interest exhibiting high enhancement was computed for each patient and normalized with respect to the correspondent value at the pre-contrast image, which showed maximum ratios close to 10 (Fig. 5). The slope between the two last points, typically at 3.5 and 5 minutes, was computed (Table 1). The method described above was used to estimate the area of the enhancement (Table 2). The number of enhanced voxels over the cortical convexity was normalized with respect to the total area of the mask boundary, while the number of enhanced voxels in the falk was normalized with respect to the total area of the mid-sagittal plane. Detected regions are shown in Fig. 6 to 11.

New or Breakthrough Work: Traumatic meningeal injury is a novel imaging marker of traumatic brain injury (TBI), which appears as enhancement of the dura on post-contrast T2 FLAIR MRI. TMI is suggested to occur with inflammation of the meninges. Several pro-inflammatory genes were previously implicated in this process. Accurate determination of enhancement patterns in the meninges of TMI patients is essential to properly investigate the pathogenesis of TMI and study correlations with patient conditions.

Conclusions: The present work presents a methodology to estimate the enhancement in the meninges of patients with traumatic brain injury. Accurate quantification based on image registration and normalization has the potential to better understand the mechanisms involved and evaluate the progression of the condition.

9788-51, Session 10
Multi-site study of diffusion metric variability: characterizing the effects of site, vendor, field strength, and echo time using the histogram distance
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MRI-based multi-site trials now routinely include some form of diffusion-weighted imaging (DWI) in their protocol. These studies can include data originating from scanners built by different vendors, each with their own set of unique protocol restrictions, including restrictions on the number of available gradient directions, whether an externally-generated list of gradient directions can be used, and restrictions on the echo time (TE). One challenge of multi-site studies is to create a common imaging protocol that will result in a reliable and accurate set of diffusion metrics. The present study describes the effect of site, scanner vendor, field strength, and TE on two common metrics: the first moment of the diffusion tensor field (mean diffusivity, MD), and the fractional anisotropy (FA). We have shown in earlier work that ROI metrics and the mean of MD and FA histograms are not sufficiently sensitive for use in site characterization. Here we use the distance between whole brain histograms of FA and MD to investigate within- and between-site effects. We concluded that the variability of DTI metrics due to site, vendor, field strength, and echo time could influence the results in multi-center trials and that histogram distance is sensitive metrics for each of these variables.
Connecting images to the electronic medical record: structured reporting, machine learning, and natural language processing (Keynote Presentation)
Curtis P. Langlotz M.D., Stanford Univ. Medical Ctr. (United States)

No Abstract Available

Patient-tailored multimodal neuroimaging, visualization and quantification of human intra-cerebral hemorrhage
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In traumatic brain injury (TBI) and intracerebral hemorrhage (ICH), the heterogeneity of lesion sizes and types necessitates a variety of imaging modalities to acquire a comprehensive perspective on injury extent. Although it is advantageous to combine imaging modalities and to leverage their complementary benefits, there are difficulties in integrating information across imaging types. Thus, it is important that efforts be dedicated to the creation and sustained refinement of resources for multimodal data integration. Here, we propose a novel approach to the integration of neuroimaging data acquired from human patients with TBI/ICH using various modalities; we also demonstrate the integrated use of multimodal magnetic resonance imaging (MRI) and diffusion tensor imaging (DTI) data for TBI analysis based on both visual observations and quantitative metrics. 3D models of healthy-appearing tissues and TBI-related pathology are generated, both of which are derived from multimodal imaging data. MRI volumes acquired using FLAIR, SWI, and T2 GRE are used to segment pathology. Healthy tissues are segmented using user-supervised tools, and results are visualized using a novel graphical approach called a ‘connectogram’, where brain connectivity information is depicted within a circle of radially aligned elements. Inter-region connectivity and its strength are represented by links of variable opacities drawn between regions, where opacity reflects the percentage longitudinal change in brain connectivity density. Our method for integrating, analyzing and visualizing structural brain changes due to TBI and ICH can promote knowledge extraction and enhance the understanding of mechanisms underlying recovery.

Radiogenomic analysis of breast cancer: dynamic contrast enhanced -MRI based features are associated with molecular subtypes
Shijian Wang, Ming Fan, Hangzhou Dianzi Univ. (China); Juan Zhang, Zhejiang Cancer Hospital (China); Bin Zheng, The Univ. of Oklahoma (United States); Xiaojia Wang, Zhejiang Cancer Hospital (China); Lihua Li, Hangzhou Dianzi Univ. (China)

Breast cancer is one of the most common malignant tumor with upgrading incidence in females. The key to decrease the mortality is early diagnosis and reasonable treatment. Molecular classification could provide better insights into patient-directed therapy and prognosis prediction of breast cancer. It is known that different molecular subtypes have different characteristics in magnetic resonance imaging (MRI) examination. Therefore, we speculated that imaging features can reflect molecular information in breast cancer. In this study, we investigated associations between dynamic contrasts enhanced-magnetic resonance imaging (DCE-MRI) features and molecular subtypes in breast cancer. Sixty patients with breast cancer were enrolled and the MRI images were pre-processed for noise reduction, registration and region segmentation. Sixty-five dimensional imaging features including statistical characteristics, morphology, textural and dynamic enhancement from DCE-MRI were semiautomatically extracted. The associations of imaging features and molecular subtypes were assessed by using statistical analyses, including univariate logistic regression and multivariate logistic regression. The results of multivariate regression showed that imaging features significantly associated with molecular subtypes of luminal A (p=0.00473), HER2-enriched (p=0.00277) and Basal like (p=0.0117), respectively. The results indicated that three molecular subtype are correlated with DCE-MRI features in breast cancer. Patients with a higher level of compactness or lower level of skewness in breast lesion are more likely to be luminal A subtype. Besides, the higher value of the dynamic enhancement at T1 time in normal side reflect higher possibility of HER2-enriched subtype in breast cancer.
9789-4, Session 1

Automatic lung nodule classification with radiomics approach
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Lung cancer is the first killer among the cancer deaths. Malignant lung nodules have extremely high mortality while benign nodules sometimes don’t need any treatment. Thus, the accuracy of diagnosis between benign or malignant nodules diagnosis is necessary. Of note, currently additional invasive biopsy or second CT scan in 3 months later may help radiologists to make a judgment. In this paper, we propose a novel CAD method to distinguish the benign and malignant lung cancer from CT images directly, which can not only improve the efficiency of tumor diagnosis but also greatly decrease the pain and risk of patients in biopsy process. Briefly, according to the state-of-the-art radiomics approach, 583 features were used for measurement of nodules’ intensity, shape, heterogeneity and information in multi-frequencies. Further, with Random Forest method, we distinguish the benign nodules from malignant nodules by analyzing all these features. Notably, our proposed scheme was tested on all 79 CT scans with diagnosis data available in The Cancer Imaging Archive (TCIA) that contained 127 nodules which were annotated by at least one of four radiologists participating in the project. Furthermore, this method achieved 82.7% accuracy in malignant primary lung nodules and benign nodules classification. We believe it would bring much value for routine lung cancer diagnosis in CT imaging and provide improvement in decision-support with much lower cost.

9789-5, Session 2

Development of a gestural interface with message hooking for manipulating medical images in the operating room
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In spite of technological advances and attempts being made to replace existing interfaces such as keyboards and mice in the operating room due to maintaining aseptic conditions, it is hard to find applications used in clinical practice. In our study, we developed a contactless interface based on hand gesture recognition for effectively controlling medical images in the operating room. An in-house program called GestureHook was developed for converting gestures into specific functions based on message hooking and set up in the operating room. This program allows users to control software in the operating room without any kind of modification of source codes. For clinical application and evaluation, this program was set up in the operating room to browse images of a rhinoplasty and genioplasty patient from three different programs: CT images from a PACS program, volume rendered images from a 3D PACS program and surgical planning photographs from a basic image viewing program. All three programs were seamlessly controlled by gestures and motions solely by the physician. In evaluation of the performance, we scanned through 96 images of a dynamic biliary CT study by gestures and compared the results with those of a mouse. Gesture based inputs significantly shortened time required to scan through images, 13.99±1.06 to 8.57±0.65 sec (p<0.001). In conclusion, we developed a message hooking program that detect gestures to control programs and applied it to the operating room. This program provided surgeons a new way to safely browse images during surgery.

9789-6, Session 2

3D printed cardiac phantom for procedural planning of a transcatheter native mitral valve replacement
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3D printing to create an anatomically accurate, functional flow loop phantom of a patient’s cardiac vasculature may be used to assist in the surgical planning of one of the first transcatheter native mitral valve replacement procedures. The CTA scans of a patient who was about to undergo the first minimally-invasive native mitral valve replacement procedure at the Gates Vascular Institute were acquired. A python scripting library, the Vascular Modeling Toolkit (VMTK) was used to segment the 3D geometry of the patient’s cardiac chambers and mitral valve with severe stenosis (calcific in nature). A stereolithographic mesh (STL) was generated and AutoDesk Meshmixer was used to turn the vascular outline into a functioning flow loop. A Stratasys Connex3 multi-material printer was used to fabricate the phantom with distinguishable material features.

Results: After examining the cardiac phantom, the interventional team optimized their transapical approach. The mitral valve stenosis and calcification was clearly visible, and the phantom could be used to size the valve which was to be implanted. Potentially offering a better method to do so than the typical CTA reconstruction.

Conclusion: With advances in image processing and 3D printing technology, it is possible to create life-like patient-specific phantoms which can act as a guide to the interventional team, allowing them to visualize their approach for a novel procedure. This technology proves to be particularly useful for generating insights into complex procedures.

9789-7, Session 2

Advanced 3D mesh manipulation in stereolithographic files and post-print processing for the manufacturing of patient-specific vascular flow phantoms
Ryan P. O’Hara, Arpita Chand, Sowmya Vidiyala, Toshiba Stroke and Vascular Research Ctr. (United States) and Univ. at Buffalo (United States); Stacie M. Arechavala, Univ. of Miami (United States) and Toshiba Stroke and Vascular Research Ctr. (United States); Stephen Rudin, Ciprian N. Ionita, Toshiba Stroke and Vascular Research Ctr. (United States) and Univ. at Buffalo (United States)

Complex vascular anatomies can cause the failure of image-guided endovascular procedures. 3D printed patient-specific vascular phantoms provide clinicians and medical device companies the ability to preemptively plan surgical treatments, test the likelihood of device success, and determine potential operative setbacks. This research aims to present advanced mesh-manipulation techniques using stereolithographic (STL) files segmented from medical data, and post-print surface optimization to
improve physiological vascular flow resistance. For phantom design, we
developed three mesh-manipulation techniques. The first method allows
outlet 3D mesh manipulations to merge superficial vessels into a single
junction, decreasing the number of flow outlets and making it feasible to
include smaller vessels. Next, we introduced Boolean operations to eliminate
the need to manually merge mesh layers and eliminate errors of mesh
self-intersections which previously occurred. Finally, we optimized support
addition to preserve the patient anatomical geometry. For post-print
surface optimization, we investigated various solutions and methods to
remove support material and smooth the inner vessel surface. Solutions of
chloroform and sodium hydroxide were used to process various phantoms
and hydraulic resistance was measured and compared with reported
literature values. New mesh-manipulation methods decrease phantom
design time by 30 – 80% and allow rapid development of accurate vascular
models. When compared with physiological hydraulic resistance, the
phantoms treated with sodium hydroxide decrease the hydraulic resistance
by almost two and half times versus the untreated phantoms. The methods
presented in this work could lead to shorter design time for patient-specific
phantoms and better physiological simulations. Supported partially by NIH
Grant R01EB002873.

9789-8, Session 2
A deep semantic mobile application for thyroid cytopathology
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Thyroid cytopathology is a branch of pathology that studies the diagnosis of
thyroid lesions and diseases at a cellular level. A pathologist views cell
images that may have high visual variance due to different anatomical
structures and pathological characteristics. To assist the physician with
identifying and searching through images, we propose a semantic mobile
application. Our system uses a custom thyroid ontology that can be
augmented with multimedia metadata extracted from images using machine
learning techniques. We demonstrate the benefits of our framework through
both quantitative and qualitative results.

9789-9, Session 2
Interconnecting smartphone, image analysis server, and case report forms in
clinical trials for automatic skin lesion tracking in clinical trials
Daniel Haak, Aliaa Doma, Alexander Gombert, Thomas Deserno, Uniklinik RWTH Aachen (Germany)

Today, subject’s medical data in controlled clinical trials is captured digitally
in electronic case report forms (eCRFs). For bed-side image integration, we
present a mobile application (App) that utilizes the smartphone-integrated camera. To ensure high image quality with this inexpensive
consumer hardware, color reference cards are placed in the camera’s field
of view next to the lesion. The cards are used for automatic calibration of
geometry, color, and contrast. In addition, a personalized barcode is read
from the cards that allows subject identification. For data integration, the
App is connected to an image analysis server that also holds the
barcode-study-subject relation. In a second system interconnection, web
services are used to connect the smartphone with OpenClinica, an open-
source, FDA-approved electronic data capture system in clinical trials.
Once the photographs have been securely stored on the server, they
are released automatically from the mobile device. The workflow of the
system is demonstrated by an ongoing clinical trial, in which photographic
documentation is frequently performed to measure the effect of wound
incision management systems. All 13 images, which have been collected in
the study so far, have been correctly identified and successfully integrated
into the corresponding subject’s eCRF. Using this system, manual steps for
the study personnel are reduced, and, therefore, errors, latency and costs
decreased. Our approach also increases data security and privacy.

9789-10, Session 3
Streamlining an interactive Bayesian-based diagnostic support tool alongside
traditional PACS system
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In radiology, diagnostic errors occur either through failure of detection or
incorrect interpretation. Errors are estimated to occur in 30-35% of all exams
and contribute to 40-54% of medical malpractice litigation. In this work, we
focus on reducing incorrect interpretation of known imaging features.
Existing literature categorizes cognitive biases leading a radiologist to
an incorrect diagnosis despite having correctly recognized the abnormal
imaging features: anchoring bias, framing effect, availability bias, and
posterior probability closure. Computational methods make a unique contribution
as they do not exhibit the same cognitive biases as a human. Bayesian
networks can formalize the diagnostic process. They modify pre-test
diagnostic probabilities using clinical and imaging features, arriving at a
post-test probability for each possible diagnosis.

To translate Bayesian networks to practice, we implemented an open-source
software tool. In our tool, the radiologist first selects a network of choice
(e.g. MRI for basal ganglia). Then, large, clearly labeled buttons displaying
salient imaging features are shown on the screen serving both as a checklist
and for input. As the radiologist inputs the value of a particular imaging
feature, the conditional probabilities of each possible diagnosis are updated.
The software presents its level of diagnostic discrimination using a pareto
distribution chart, updated with each additional imaging feature.
In addition to aiding clinical decision, the software also lays a foundation
for research in which Bayesian networks are trained using biopsy-proven
cases. It also contributes to radiology residency and fellowship education by
improving diagnostic accuracy when integrated with teaching cases.
sequences. Improvements to accurately characterizing such lesions are fundamental for all aspects of brain injury. Minimum intensity projection (minIP) reconstructions are routinely used to improve the visualization of microhemorrhages and, in particular, to help distinguish hemorrhage from vessels. The technique displays the minimum intensity in a given projection within a thick slab. Consequently, different connectivity patterns are easily revealed (see Figure 1). However, such reconstructions may not be accurate near the surface of the brain and close to the inner table of the skull because low intensity voxels beyond the surface project into the thick slab of the minIP, obscuring the edges of the brain. Existing algorithms for brain extraction can be used to mask the brain prior to assign high intensity value to any voxel outside the mask avoiding undesired projections from outer regions. However, variations in image intensity gradient across the brain boundary are commonly observed at some locations including, but not limited to, the frontal lobe and the inferior temporal lobes. Presence of pathology or hemorrhage due to traumatic brain injury (TBI) near the surface accentuates that variation. From the quantitative image analysis perspective, methods that rely on the intensity gradient field alone at the cerebral boundary to mask the brain usually fail to accurately preserve its volume. Consequently, either darker extracerebral regions are included in the mask, or tissue and vessels close to the surface are missed. Both scenarios have a negative impact on the ability to properly evaluate and follow up existing lesions and injuries from minIP reconstructions. In the former, lower intensity outer voxels projects onto adjacent slices obscuring brain tissue. In the latter, regions of clinical interest are missed. The proposed methodology automatically tunes the best edge detection parameter for an initial mask, and a second smaller mask is generated in such a way that the real boundary is contained within the rind of tissue between them. In order to properly determine what voxels were excluded from the smaller mask, an automatic classification of voxels within that rind is used. Morphological operations are later used to reclassify possible missed surface vessels (see Figure 2). The mean mask intensity is assigned to all voxels outside the mask.

Results: Twenty three isotropic SWI brain images (0.65 mm) were considered in this study. The dependence of the mask volume on the BSE’s edge detection parameter was analyzed within a typical range for brain SWI images where the volume remains roughly constant (see Figure 3). The highest volume corresponds to the smallest parameter within that interval, and was determined from the volume variation. Reliable masks were automatically found in twenty out of twenty three cases, and had to be manually adjusted in the three remaining cases. The mean brain volume was assigned to all voxels outside the mask. Minimum Intensity Projection reconstructions performed for different slab thickness showed a significant reduction of the mask volume for thicker slabs (see Figure 4). The ability to detect microhemorrhages strongly depends on their location (see Figure 5). Figure 6 shows a comparison at selected axial slices of a given subject between the magnitude SWI, the minIP computed with no mask, and the minIP computed with the mask.

New or Breakthrough Work: The proposed method represents a significant improvement in minIP visualization of SWI data, allowing for superior brain tissues to be assessed, surface venous anatomy to be visualized, and larger slab thickness applied. This has the potential to facilitate the detection of microhemorrhages, particularly in superficial cortex. Conclusions: Minimum intensity projection reconstructions from SWI are regularly used in the diagnosis, follow up, and outcome assessment of brain trauma because of their ability to better identify the extension and shape of vascular lesions such as hemorrhages and micro bleedings. However, such reconstructions are not accurate in or near the cerebral cortex because low intensity voxels beyond the surface projects into the thick slab affecting the calculation of the minimum intensity projection. The proposed method significantly improves minIP visualization of SWI data, and has the potential to facilitate the detection of microhemorrhages.

9789-13, Session 3

Lesion registration for longitudinal disease tracking using thin-plate splines deformation for multiple sclerosis eFolder

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We have designed and developed a multiple sclerosis eFolder system for patient data storage, image viewing, and automatic lesion quantification results stored in DICOM-SR format. The web-based system aims to be integrated in DICOM-compliant clinical and research environments to aid clinicians in patient treatments and data analysis. The system needs to quantify lesion volumes, identify and register lesion locations to track shifts in volume and quantity of lesions in a longitudinal study. In order to perform lesion registration, we have developed a brain warping and normalizing methodology using Thin-Plate Spines (TPS) deformation algorithm. Patients’ brain MR images are uploaded to the TPS-based warping module, and the images are warped to a set of reference images based on user-defined points. Lesion identification and contouring are completed by neuroradiologists, and lesion volume quantification is completed by the eFolder’s CAD program. The results display successful lesion regist

9789-14, Session 3

Altered effective connectivity within default mode network in major depression disorder

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Understanding the neural basis of Major Depressive Disorder (MDD) is important for the diagnosis and treatment of this mental disorder. The default mode network (DMN) is considered to be highly involved in the MDD. To identify the pattern of information flows in the DMN associated with the development of MDD, the effective connectivity within the DMN of the MDD patients and matched healthy controls was accessed by using a recently developed spectral dynamic causal modeling (sDCM).

Sixteen patients with MDD and sixteen matched healthy control (HC) subjects were included. All patients underwent psychometric tests and resting state fMRI scans before and after two months’ treatment, while the control group just underwent the psychometric tests and resting state fMRI once. Then the sDCM was used to estimate directed connections between four DMN nodes. The resulting patterns indicate that the efferent connections from the medial frontal cortex (MFC) to other nodes are
negative in the healthy control. For patients with MDD, none of these connections are negative before treatment but all become negative after two months’ treatment. These findings suggest that the MFC may play an important role for the inhibitory conditioning to the DMN, which is disrupted in the MDD patients. It also indicates that disrupted suppressive function of the MFC is a key alteration of the DMN in MDD patients, which can be effectively restored after treatment.

9789-15, Session 3
Segmentation of bone pixels from EROI Image using clustering method for bone age assessment
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The bone age of a human can be identified using carpal and epiphysis bones ossification, which is limited to teen age. The accurate age estimation depends on best separation of bone pixels and soft tissue pixels in the ROI image. The traditional approaches like canny, sobel, clustering, region growing and watershed can be applied, but these methods requires proper pre-processing and accurate initial seed point estimation to provide accurate results. Therefore this paper proposes new approach to segment the bone from soft tissue and background pixels. First pixels are enhanced using BPE and the edges are identified by HIPI. Later a K-Means clustering is applied for segmentation. The performance of the proposed approach has been evaluated and compared with the existing methods.

9789-16, Session 4
A case-based reasoning tool for breast cancer with data mining concepts and techniques
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Breast cancer is the second most common cancer in woman. Generally, it occurs in woman over the age of 50 but younger women are sometimes affected. Around one in nine of woman develops breast cancer in her life. Breast cancer can also develop in men, although this is rare [1]. The acquisition process of data deriving from screening operations is very complex and necessitates the creation of adequate models and requirement engineering tools. Traditional medical information systems such as: Hospital Information Systems (HIS), RIS (Radiological Information Systems) and PACS (Picture Archiving Information Systems) are not able to manage medical information providing from various sources and image modalities [2]. They have strict operation requirements and provide a little support for ad hoc queries or data analysis [3]. Data Mining can remediate to these problems. Indeed, Data Mining (DM) is defined as the process of “mining” or extracting information from a data set and transform it into an understandable structure for further use [4]. It has been proven that the application of Data Mining techniques in medicine are helpful in extracting medical knowledge for diagnosis, decision-making, screening, monitoring, therapy support and patient management record [5].

On the other hand, the medical diagnosis is based on the experts’ expertise (past experience). This experience is under form clinical cases. These cases are examples resulting from real situations.

Case-based reasoning (CBR) is the process of solving new problems based on the solutions of similar past problems [6]. This process is similar to their daily practice of experts. Case-based Reasoning is thus very appropriate to medical field.

Combining CBR to DM could be very benefit for improving patient’s diagnosis and her follow-up. CBR allows reusing past physician or radiologist experience to solve a new problem and Data Mining allows extracting relevant and focused information from large and scattered data sources [7].

In this paper, we propose to develop a CBR tool for managing breast cancer knowledge. This tool is under development. We have achieved the design of the tool and experiment it. The originality of this research work is its contribution to the medical and radiological field and the combination of the two approaches CBR and DM which allows better and flexible results.

9789-17, Session 4
Improving face image extraction by using deep learning technique
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The National Library of Medicine (NLM) has created a database of over a 750,000 research articles containing 2.3 million figure images which is searchable using the OPEN-I website. Many of these images are visible light photographs. In this paper, we focus on extracting images containing faces (“face images”) from these photographs. We first applied one of the most widely-used face detectors, a pre-trained Viola-Jones detector implemented in Matlab and OpenCV, to extract the face regions in our images. Although this Viola-Jones detector obtained high precision for a face detection database which contains face images acquired in unconstrained settings, the results for the NLM database included many false positives, which resulted in a very low precision. To improve this performance, we applied a deep learning technique, which reduced the number of false positives and as a result, the detection precision was improved significantly. (For example, the classification accuracy for identifying whether the face regions output by this Viola-Jones detector are true positives or not in a test set is about 96%) By combining these two techniques (Viola-Jones and deep learning) we were able to increase the system precision considerably, while avoiding the need to manually construct a large training set by manual delineation of the face regions.

9789-18, Session 4
Collection of sequential imaging events for research in breast cancer screening
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Due to the huge amount of research involving medical images, there is a widely accepted need for comprehensive collections of medical images, to be made available for research. This demand led to the design and implementation of a flexible image repository, which retrospectively collects images and data from multiple sites throughout the UK. The OPTIMAM Medical Image Database (OMI-DB)1.2 was created to provide a centralized, fully annotated dataset for research. The database contains both processed and unprocessed images, associated data, annotations and expert-determined ground truths. Collection has been ongoing for over three years, providing the opportunity to collect sequential imaging events. Extensive alterations to the identification, collection, processing and storage arms of the system have been undertaken to support the introduction of sequential events - including interval cancers. These updates to the collection systems allow the acquisition of many more images, but more importantly, allow one to build on the existing high-dimensional data stored in the OMI-DB. A research dataset of this scale, which includes original normal and subsequent malignant cases along with expert derived and clinical annotations, is currently unique. These data provide a powerful resource for future research and has initiated new research projects, amongst which, is the quantification of normal cases by applying a large number of quantitative imaging features, with a priori knowledge that eventually these cases develop a malignancy. This paper describes, extensions to the OMI-DB collection systems and tools and discusses the prospective applications of having such a rich dataset for future research applications.
9789-19, Session 4

**Mutual Information-based feature selection for radiomics**

Estanislaw Oubel, Hubert Beaumont, Median Technologies (France); Antoine Iannessi, Ctr. de lutte contre le cancer Antoine Lacassagne (France)

**Background:** The extraction and analysis of image features (radiomics) is a promising field in the precision medicine era, with applications to prognosis, prediction, and response to treatment quantification. In this work, we present a mutual information (MI) based method for quantifying reproducibility of features, a necessary step for qualification before inclusion in big data systems.

**Materials and Methods:** Ten patients with Non-Small Cell Lung Cancer (NSCLC) lesions were followed over time (7 time points in average) with Computed Tomography (CT). Five observers segmented lesions by using a semi-automatic method and 27 features describing shape and intensity distribution were extracted. Inter-observer reproducibility was assessed by computing the mutual information (MI) of the first derivative of feature values with respect to time, and the variability of global extrema.

**Results:** The highest MI values were obtained for volume-based features (VBF). Surface to volume ratio (SVR) and equivalent spherical diameter (ESD) presented statistically significant higher values of MI with respect to the rest of features. Within the same VBF group, SVR showed also a significantly lower variability of extremum. The correlation coefficient (CC) of feature values was unable to make a difference between features.

**Conclusions:** The proposed method allowed discriminating in a statistically significant manner two features (SoV and ESD) maximizing the MI between observers. This method better ranked VBF with respect to features computed from 2D measurements. The proposed method is a promising alternative for selecting features to be considered as surrogate biomarkers in a precision medicine context.

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9789-20, Session 4

**PACS-integrated electronic data capture of DICOM data in multi-centered clinical trials**

Daniel Haak, Charles-E. Page, Thomas Deserno, Uniklinik RWTH Aachen (Germany)

Providing eligibility, efficacy and security evaluation by quantitative and qualitative disease findings medical imaging has become increasingly important in clinical trials. Here, subject's data is today captured in electronic case reports forms (eCRFs), which are offered by electronic data capture (EDC) systems. However, integration of subject's medical image data into eCRFs is insufficiently supported, neither integration of subject's digital imaging and communications in medicine (DICOM) data, nor communication with picture archiving and communication systems (PACS), is supported. This aggravates the workflow of the study personnel, in special regarding studies with distributed data capture in multiple sites. Hence, in this work, a system architecture is presented, which connects an EDC system, a PACS and a DICOM viewer via the web access to DICOM objects (WADO) protocol. The architecture is implemented using the open source tools OpenClinica, DCM4CHEE and Weasis. The eCRF forms the primary endpoint for the study personnel, where subject's image data is stored and retrieved. Background communication with the PACS is completely hidden for the users. Data privacy and consistency is ensured by automatic de-identification and re-labelling of DICOM data with context information (e.g. study and subject identifiers), respectively. The system is exemplarily demonstrated in a clinical trial, where computer tomography (CT) data is de-critically captured from the subjects and centrally read by a chief radiologists to decide on inclusion of the subjects in the trial. Errors, latency and costs in the EDC workflow are reduced, while, a research database is implicitly built up in the background.

9789-21, Session 5

**Decentralizing radiology: preparing for the end of fee for service**

Steven C. Horii M.D., Tessa S. Cook M.D., Woojin Kim M.D., The Univ. of Pennsylvania Health System (United States)

Though the US Government has tried various means of reducing costs of healthcare, these costs have continued to rise. Though there is considerable debate about both the causes of these high costs and how to reduce them, one factor is the way in which healthcare providers are reimbursed. Most current providers are reimbursed on a fee for service basis. That is, practitioners are paid for doing examinations, consulting with patients, and performing procedures. In this model, doing more of these things results in greater reimbursement. As science and technology have provided improved diagnostic and treatment methods, the number and costs of these have generally increased. Some measure of control over utilization of expensive diagnostic and therapeutic techniques has been achieved through the requirement to document medical necessity before they are undertaken. An alternative to fee for service is accountable care. In this model, reimbursement is based not on numbers or complexity of things done for patients, but in demonstrating that diagnostic and treatment strategies result in measurable reductions in costs and improvements in quality and outcomes. This accountable care model will, among other things, require greater participation in patient care on the part of radiologists. One way of approaching this is to have radiologists in much closer proximity to both patients and the providers so that consultation with radiology becomes part of the workflow rather than activity that is parallel or serial but with a delay in time. This presentation will describe the practical approach to decentralization that we have undertaken and the informatics and workflow challenges it has posed.

9789-22, Session 5

**Toward an open-source semantic data infrastructure for integrating clinical and scientific data in cognition-guided surgery**

Andreas Fetzer, Jasmin Metzger, Deutsches Krebsforschungszentrum (Germany); Darko Katic, Karlsruher Institut für Technologie (Germany); Keno März, Deutsches Krebsforschungszentrum (Germany); Martin Wagner, Universitätsklinikum Heidelberg (Germany); Patrick Philipp, Karlsruher Institut für Technologie (Germany); Sandy Engelhardt, Deutsches Krebsforschungszentrum (Germany); Tobias Weller, Karlsruher Institut für Technologie (Germany); Sascha Zelzer, Alfred M. Franz, Deutsches Krebsforschungszentrum (Germany); Maria Maleshkova, Achim Rettinger, Stefanie Speidel, Karlsruher Institut für Technologie (Germany); IvO Wolf, Hochschule Mannheim (Germany); Hannes Kenngott, Beat Müller, Universitätsklinikum Heidelberg (Germany); Lena Maier-Hein, Hans-Peter Meinzner, Marco Nolden, Deutsches Krebsforschungszentrum (Germany)

In the surgical domain, individual clinical experience plays an important role in the treatment decision process. Keeping an overview of the large amount of diverse information available about the individual patient, ranging from anamnesis to diagnostic data as well as imaging and intraoperative sensors, while keeping up-to-date with the growing knowledge derived from clinical studies poses a big challenge to the surgeon. Our interdisciplinary and multi-institutional approach aims to create a cognitive surgical assistance system which utilizes these extensive clinical data sets as well as derived individual data like enhanced three-dimensional geometric descriptions of
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organs or biomechanical simulations in order to create individual treatment recommendations. A fundamental requirement of such a system is a flexible data storage that provides standardized access to users and applications. In this work we present a semantic data infrastructure that is capable of integrating these very heterogeneous data sources on the basis of a common knowledge representation. A combination of the XNAT imaging informatics platform with semantic web technologies and custom interfaces enables applications to access and semantically annotate data, perform semantic reasoning and eventually create individual treatment recommendations. Successful use cases from various projects show the applicability of the approach and of the system which is built completely using free technologies and will be made available to the community as an open source package.

9789-23, Session 5
A handheld computer-aided diagnosis system and simulated analysis
Ming Jian Su, Xuejun Zhang, Guangxi Univ. (China); Brent J. Liu, The Univ. of Southern California (United States); Kening Su, The First Affiliated Hospital of Guangxi Univ. of Chinese Medicine (China); Ryan Louie, The Univ. of Southern California (United States)

This paper proposes a Computer Aided Diagnosis (CAD) system deployment on cellphone and distributed cluster. A bottleneck of building a CAD system is the storage and process of mass pathology samples. Distributed computation on cluster may have ability to relieve this bottleneck. But the Hadoop architecture must refine to suit a large scale image classification, this is mainly because its file system HDFS is built to suit a big fragment record, our system workloads that manipulate primarily large numbers of small files. Thus, we develop our own module to combine mass image files to a dataset with key, value pairs, send datasets to Generic Data Handler Module in Hadoop, and prepare for the pattern recognition in the next step. Besides, using normal pattern matching algorithm on large scale image set will waste an unreasonable time. We apply a hierarchical processing algorithm to data pipeline based on MapReduce framework in order to make balance to the recognition accuracy and system cost. To promote the recognition accuracy, doctors manually figure out the lesion area by drawing on the screen, and upload the pattern to the server. Finally, we got 72% diagnosis hit rate by testing 100 skin illness. Our purpose is building a novel medical image dataset, collecting vast amounts of medical diagnosis evidence. Once the project is online, the participants are free to expand, we will eventually get a abundant sample dataset for learning. We believe it is a very promising technology and keep on improving the system in future work.

9789-24, Session 5
Performance management of high-performance computing for medical image processing in Amazon Web Services
Shunxing Bao, Stephen M. Damon, Bennett A. Landman, Aniruddha Gokhale, Vanderbilt Univ. (United States)

Adapting high performance cloud computing for medical image processing is a popular trend given the pressing needs of large studies. Amazon Web Services (AWS) provide reliable, on-demand, and inexpensive cloud computing services. Our research objective is to implement an affordable, scalable and easy-to-use AWS framework for the Java Image Science Toolkit (JIST). JIST is a plugin for Medical-Image Processing, Analysis, and Visualization (MIPAV) that provides a graphical pipeline implementation allowing users to quickly test and develop pipelines. JIST is DRMAA-compliant allowing it to run on portable batch system grids. However, as new processing methods are implemented and developed, memory may often be a bottleneck for not only lab computers, but possibly some local grids. Integrating JIST with the AWS cloud alleviates these possible restrictions and does not require the users to have deep knowledge of programming in Java. Workflow definition/management and cloud configurations are two key challenges in this research. Using a simple unified control panel, users have the ability to set the numbers of nodes and select from a variety of pre-configured AWS EC2 nodes with different numbers of processors and memory storage. Intuitively, we configured Amazon S3 storage to be mounted by every pay-for-use Amazon EC2 instances. Hence S3 storage is recognized as a shared cloud resource. The Amazon EC2 instances provide pre-installs of all necessary packages to run JIST. This work presents an implementation that easily facilitates the integration of JIST with AWS. We describe the theoretical cost/benefit formulae to decide between local serial execution versus cloud computing and apply this analysis to an empirical diffusion tensor imaging pipeline.

9789-32, Session 5
Mass classification in mammography with multi-agent based fusion of human and machine intelligence
Dongdong Xi, Ming Fan, Lihua Li, Hangzhou Dianzi Univ. (China); Juan Zhuang, Zhejiang Cancer Hospital (China); Yanna Shan, Hangzhou First People’s Hospital (China); Gang Dai, Zhejiang Cancer Hospital (China); Bin Zheng, Hangzhou Dianzi Univ. (China) and The Univ. of Oklahoma (United States)

Although the computer-aided diagnosis (CAD) system can be applied for classifying the breast masses, the effects of this method on improvement of the radiologist' accuracy for distinguishing malignant from benign lesions still remain unclear. This study provided a novel method to classify breast masses by integrating the intelligence of human and machine. In this research, 224 breast masses were selected in mammography from database of DDSM with Breast Imaging Reporting and Data System (BI-RADS) categories. Three observers (a senior and a junior radiologist, as well as a radiology resident) were employed to independently read and classify these masses utilizing the Positive Predictive Values (PPV) for each BI-RADS category. Meanwhile, a CAD system was also implemented for classification of these breast masses between malignant and benign. To combine the decisions from the radiologists and CAD, the fusion method of the Multi-Agent was provided.

Significant improvements are observed for the fusion system over solely radiologist or CAD. The area under the receiver operating characteristic curve (AUC) of the fusion system increased by 9.6%, 10.3% and 21% compared to that of radiologists with senior, junior and resident level, respectively. In addition, the AUC of this method based on the fusion of each radiologist and CAD are 3.5%, 3.6% and 3.3% higher than that of CAD alone. Finally, the fusion of the three radiologists with CAD achieved AUC value of 0.957, which was 5.6% larger compared to CAD. Our results indicated that the proposed fusion method has better performance than radiologist or CAD alone.

9789-25, Session PSMon
A cloud platform for remote diagnosis of breast cancer in mammography by fusion of machine and human intelligence
Guodong Jiang, Ming Fan, Lihua Li, Hangzhou Dianzi Univ. (China)

Mammography is the gold standard for breast cancer screening, reducing mortality by about 30%. The application of a computer-aided detection (CAD) system to assist a single radiologist is important to further improve mammographic sensitivity for breast cancer detection. In this study, a
design and realization of the prototype for remote diagnosis system in mammography based on cloud platform were proposed. To build this system, technologies were utilized including medical image information construction, cloud infrastructure and human-machine diagnosis model. Specifically, on one hand, web platform for remote diagnosis was established by JZEE web technology. Moreover, background design was realized through Hadoop open-source framework. On the other hand, storage system was set up with Hadoop distributed file system (HDFS) technology which enables users to easily develop and run on massive data application, and give full play to the advantages of cloud computing which is characterized by high efficiency, scalability and low cost. In addition, computer-aided diagnose system was realized through MapReduce frame. The diagnosis module in this system implemented the algorithms of fusion of machine and human intelligence. Specifically, we combined results of diagnoses from doctors’ experience and traditional CAD by using the man-machine intelligent fusion model based on Alpha-Integration and multi-agent algorithm. The applications on different levels of this system in the platform were also discussed. This diagnosis system will have great importance for the balanced health resource, lower medical expense and improvement of accuracy of diagnosis in basic medical institutes.

9789-26, Session PSMon
Semantic information extracting system for classification of radiological reports in radiology information system (RIS)
Liehang Shi, Tonghui Ling, Jianguo Zhang, Shanghai Institute of Technical Physics (China)

Abstract: Radiologists currently use a variety of terminologies and standards in most hospitals in China, and even there are multiple terminologies being used for different sections in one department. In this presentation, we introduce a medical semantic comprehension system (MedSCS) to extract semantic information about clinical findings and conclusion from free text radiology reports so that the reports can be classified correctly based on medical terms indexing standards such as Radlex or SONMED-CT. Our system (MedSCS) is based on both rule-based methods and statistics-based methods which improve the performance and the scalability of MedSCS. In order to evaluate the over all of the system and measure the accuracy of the outcomes, we developed computation methods to calculate the parameters of precision rate, recall rate, F-score and exact confidence interval.

Objectives: PACS and RIS have been widely used for imaging services in China hospitals and huge amount of images and related reports were being generated daily. But radiologists currently use a variety of terminologies and standards in most hospitals in China, and even there are multiple terminologies being used for different sections in one department. So, most radiological reports were not classified properly based on medical terms indexing standards such as Radlex or SONMED-CT. Our system (MedSCS) is based on both rule-based methods and statistics-based methods which improve the performance and the scalability of MedSCS. In this presentation, we present a new designed system (called MedSCS) which can perform semantic information extraction about clinical findings and conclusion from free text radiology reports so that the reports can be classified correctly based on medical terms indexing standards such as Radlex or SONMED-CT.

Methodology: Firstly, we design a structured disease information representation model (DIRM) based on SOMED-CT. Secondly, we develop a natural language process (NLP) engine to process the Chinese radiology reports, which adapts a combination of both rule-based method and statistics-based method to parse and analyze the content of free text radiology reports to extract the key information about clinical findings and conclusion embedded in the reports. Third, we map the extracted key words related to clinical findings and conclusion to a system to DIRM. In design of NLP for Chinese reports, a rule-based method was used which established a semantic corpus containing thousands of annotated words, and then designed a semantic analysis parser (SAP), by use of non-definite finite automata (NFA) technology and a set of successive grammars, to accomplish named entity recognition and relationship identification. Meanwhile, a statistics-based method was also used in NLP engine which collected over 1,000 reports with well-defined clinical findings and conclusion from clinical RIS, as training group to support our supervised machine learning approach by use of the pattern recognition method of hidden Markov model (HMM).

Results: We used another new 1,000 reports with unknown clinical findings and conclusions as the evaluation group to test the MedSCS. In order to evaluate the performance of MedSCS, we calculate the parameters of precision rate, recall rate, F-score and exact confidence interval. The MedSCS achieves F-scores of 0.80-0.95 for recognition of histology and anatomical sites, and obtains F-scores of 0.90-0.97 for identifying clinical terminologies such as disease name diagnosis. New Technologies and Results to be Presented: A combination of rule-based method and statistics-based method was used to parse and analyze the content of free text reports to extract the key information about clinical findings and conclusion embedded in the report. A structured disease information representation model (DIRM) was used visually to map the extracted key words related to clinical findings and conclusion to standardized terms indexing system such as SONMED-CT. Conclusions: In this presentation, we introduce a medical semantic comprehension system (MedSCS) to extract semantic information about clinical findings and conclusion from free text radiology reports of Chinese so that the reports can be classified correctly based on medical terms indexing standards such as Radlex or SONMED-CT. In order to evaluate the performance of MedSCS, we calculate the parameters of precision rate, recall rate, F-score and exact confidence interval with the results of F-scores of 0.80-0.95 for recognition of histology and anatomical sites, F-scores of 0.90-0.97 for identifying clinical terminologies such as disease name diagnosis. We discussed how to improve the design of MedSCS to achieve the better performance of semantic based search or content based retrieval in both radiology reports and images.

9789-27, Session PSMon
Multi-disciplinary data organization and visualization models for clinical and pre-clinical studies: A case study in the application of proton beam radiosurgery for treating spinal cord injury related pain
Sneha K. Verma, Brent J. Liu, The Univ. of Southern California (United States)

An increasing adoption of electronic medical records has made information more accessible to clinicians and researchers through dedicated systems such as HIS, RIS and PACS. The speed and the amount at which information are generated in a multi-institutional clinical study make the problem complicated compared to day-to-day hospital workflow. Often, increased access to the information does not translate into the efficient use of that information. Therefore it becomes crucial to establish models which can be used to organize and visualize multi-disciplinary data. Good visualization in turn makes it easy for clinical decision-makers to reach a conclusion within a small span of time in a clinical study involving multi-disciplinary data and multiple user groups who need access to the same data and presentation states based on the stage of the clinical trial or the task are crucial within the workflow. Therefore, in order to demonstrate the conceptual system design and system workflow, we will be presenting a clinical trial based on application of proton beam for radiosurgery which will utilize our proposed system. For demonstrating user role and visualization design purposes, we will be focusing on three different user groups which are researchers involved in patient enrollment and recruitment, clinicians involved in treatment and imaging review and lastly the principle investigators involved in monitoring progress of clinical study. Also datasets for each phase of the clinical study including preclinical and clinical data as it related to subject enrollment, subject recruitment (classifier), treatment (DICOM), imaging, and pathological analysis(protein staining ) of outcomes.
Building hybrid high-dimensional imaging database for content-based image search

Qinpei Sun, Jianyong Sun, Tonghui Ling, Mingqing Wang, Yuanjuan Yang, Jianguo Zhang, Shanghai Institute of Technical Physics (China)

Purposes:
In medical imaging informatics, content-based image retrieval (CBIR) techniques are employed to aid radiologists in the retrieval of images with similar image contents. CBIR uses visual contents, normally called as image features, to search images from large scale image databases according to users’ requests in the form of a query image. However, most of current CBIR systems require a distance computation of image character feature vectors to perform query, and the distance computations can be time consuming when the number of image character features grows large, and thus this limits the usability of the systems. In this presentation, we propose a novel framework which uses a hybrid high dimensional database to index the image character features and reports to improve the accuracy and retrieval speed of a CBIR in integrated RIS/PACS.

Methods:
The hybrid high dimensional database includes two parts, one of which is image character feature index database, and the other is report content index database. The character feature index database is built by using VA-Trie high-dimension index database, and the report content index database is built by using an inverted index database. The workflows of using this hybrid high dimensional database for CBIR indexing are: 1. An user draw ROIs and type the relevant symptoms or notes to query the VA-Trie high-dimension index database; 2. The semantic search engine uses the description or key words about the image in the reporting search GUI; 3. An image search engine extract the ROIs and calculate the image character features, and use these features as well as relevant symptoms or notes to query the VA-Trie high-dimension index database; 4. The related report retrieved from a RIS is parsed by using a Chinese Nature Language Processing module and their extracted key words are stored into the inverted database. The workflows of using this hybrid high dimensional database for image retrieval are: 1. An user draw ROIs on an input image (new image) and type the relevant symptoms or notes on the input image, at meanwhile, write short description or key words about the image in the reporting search GUI; 2. An image search engine extract the ROIs and calculate the image character features, and use these features as well as relevant symptoms or notes to query the VA-Trie high-dimension index database; 3. The related report retrieved from a RIS is parsed by using a Chinese Nature Language Processing module and their extracted key words are stored into the inverted database. The workflows of using this hybrid high dimensional database for image retrieval are:

Results:
We selected one hundred lung CT images with solid Solitary pulmonary nodules (SPNs) and ground glass obstacles (GGO), and one hundred CT images with liver nodules to test the performance of indexing and retrieval of this hybrid high dimensional imaging database for CBIR. The preliminary results showed that this new database is very positive to design a better performance of CBIR.

New Technologies and Results to be Presented:
This presentation presents a novel framework to design a better performance CBIR in integrated RIS/PACS environment. We take the radiology reports as high-level semantic descriptions of images and leverage them to navigate in large image database. So we combine text retrieval and CBIR techniques to improve the speed and accuracy of medical image retrieval process in CBIR.

Conclusions:
In this presentation, we give the design concept and propose an architecture to design hybrid high dimensional imaging database for CBIR in integrated RIS/PACS Environment. We selected one hundred lung CT images with SPNs and GGO, and one hundred CT images with liver nodules to test the performance of indexing and retrieval of this hybrid high dimensional imaging database for CBIR. The preliminary results showed that this new database is very positive to design a better performance of CBIR. We also discuss the applications and benefits of this design with traditional methods.

Comparing the role of shape and texture on staging hepatic fibrosis from medical imaging

Xuejun Zhang, Guangxi Univ. (China) and The Univ. of Southern California (United States); Ryan Louie, Brent J. Liu, The Univ. of Southern California (United States); Xin Gao, Suzhou Institute of Biomedical Engineering and Technology (China); Xiaomin Tan, Xianghe Qu, Guangxi Univ. (China); Liling Long, Guangxi Medical Univ. (China)

Background
Patients with chronic hepatitis or cirrhosis have a great risk of complications such as HCC and liver failure. In Guangxi province of China, death occurred by liver cancer rank 2 in male and 4 in female among mortality of organic cancers. Focusing on the stages of liver damage from normal liver to cancer, preventing the liver from turning the slight fibrosis into cirrhosis may significantly reduce the risk of cancer occurrence.

Fibrosis itself causes no symptoms but can lead to portal hypertension or cirrhosis. Therefore accurate assessment of the degree of fibrosis is an important issue in liver treatment. The most popular and accurate way to check fibrosis is liver biopsy. However it is invasive and the bleeding always continued for 2.5 minutes in average. In order to decrease the needs of painful biopsy, Non-invasive methods using CT, MR, Ultrasound device are proposed to obtain imaging findings of signs and structure of liver, But complex imaging findings on large medical image datasets leading to the needs of Computer-aided diagnosis (CAD). The purpose of this study is to investigate the role of shape and texture in the classification of hepatic fibrosis by selecting the optimal parameters for a better CAD system.

METHOD AND MATERIALS
120 patients are scanned by MDCT and all the cases are verified by needle biopsies as the gold standard of our experiment, ranging from 0(no fibrosis) to 5(cirrhosis).

In each equilibrium phase CT image, 10 surface shape features are extracted from a standardized profile of liver; while9 texture features calculated from gray level co-occurrence matrix (GLCM) are extracted within an ROI in liver. These two types of features are used as separated set of input vectors. Each combination of these input subsets is checked by using support vector machine (SVM) with leave-one-case-out method to differentiate fibrosis into two groups: normal or abnormal. The number of input items is selected from the combinations of 10 or 15 features exhaustively. Finally the best shape and texture features are mixed into an optimized number of inputs for fibrosis classification.

RESULTS
According to the accuracy rate (AR) calculated from each combination, the optimal number of texture features to classify liver fibrosis degree is from 4 to 7, while shape features is 2 to 5. The overall performance calculated by the average sum of maximum AR value of all 10/15 types number of features is 66.83% by texture, while 85.74% by shape features (Fig.1); respectively; among 15 texture features, mean gray value and entropy are in most common used, while the root mean square deviation of the profile and the maximum height of the profile irregularities are in top 2 ranks in shape features (Fig.2). AR value tends to decrease even though we combine most efficient 3 texture and 4 shape features, that reaches a performance of 80.3% in average. The irregularity of liver shape can demonstrate fibrotic grade efficiently and texture feature of CT image is not recommended to use with shape feature for interpretation of cirrhosis.

CONCLUSION
Comparing the accuracy of classification on two types of features, we should reveal that the accuracy rate of shape feature is considerably higher than texture feature. We can not improve the performance of CAD by combining texture into shape features.
Clinical experiences of collaborative imaging diagnosis in Shanghai District Healthcare Services
Kai Zhang, Tonghui Ling, Yuanyuan Yang, Jianyong Sun, Mingqing Wang, Jinaguo Zhang, Shanghai Institute of Technical Physics (China)

Purpose:
With the rapid growth of city populations, balancing healthcare supply and demand has become a serious issue. Most patients prefer to go to large hospitals to see doctors when they are sick, despite the high cost. This results in overloading the large hospitals and neglecting the smaller hospitals. To improve healthcare service quality, to balance healthcare resources between large and small hospitals, and to reduce costs, each district health administration has built iEHR system. We implemented solution for iEHR systems, based on the IHE XDS-I integration profile and installed the systems in more than 100 hospitals cross four districts in Shanghai city in last few years. Here, we give operational results of these systems in these four districts and evaluated the performance of the systems servicing the regional collaborative imaging diagnosis.

Methods and Materials:
We designed a method and implementation solution for iEHR systems, based on the IHE XDS-I integration profile, combined with the grid concept. This grid-based XDS-I image sharing system was used to provide collaborative diagnostic service. We extended the data models for XDS/ XDS-I transactions to meet the new requirements of regional collaborative imaging diagnosis with multiple service groups in each administrative district. In addition, we integrated the XDS-I based image sharing system with an existing EHR system to achieve iEHR systems in two districts of Shanghai. We installed the systems in more than 100 hospitals cross four districts in Shanghai city in last few years.

Results:
We implemented this new XDS-I Based Image Sharing Solution for Multiple Collaborative Imaging Diagnostic Centers in four districts of Shanghai city, which provides collaborative imaging diagnosis among 100 small and large hospitals. After installing and operating the systems for more than two years, we got the statistical results that almost 90% (84%?100%) of patients generated in small hospitals had been sent to large hospitals to see doctors when they are sick, despite the high cost. We improved healthcare service quality, to balance healthcare resources between large and small hospitals, and to reduce costs, each district health administration has built iEHR system. We implemented solution for iEHR systems, based on the IHE XDS-I integration profile and installed the systems in more than 100 hospitals cross four districts in Shanghai city in last few years. Here, we give operational results of these systems in these four districts and evaluated the performance of the systems servicing the regional collaborative imaging diagnosis.

Association between dynamic features of breast DCE-MR imaging and clinical response of neoadjuvant chemotherapy: a preliminary analysis
Lijuan Huang, Ming Fan, Hangzhou Dianzi University (China); Lihua Li, Hangzhou Dianzi Univ (China); Juan Zhang, Guoliang Shao, Zhejiang Cancer Hospital (China); Bin Zheng, Hangzhou Dianzi University (China) and University of Oklahoma (United States)

Neoadjuvant chemotherapy (NACT) is being used increasingly in the management of patients with breast cancer for systemically reducing the size of primary tumor before surgery in order to improve survival. The clinical response of patients to NACT is correlated with reduced or abolished of their primary tumor, which is important for treatment in the next stage. Recently, the dynamic contrast-enhanced magnetic resonance imaging (DCE-MRI) is used for evaluation of the response of patients to NACT. To measure this correlation, we extracted the dynamic features from the DCE-MRI and performed association analysis between these features and the clinical response to NACT. In this study, 59 patients are screened before NACT, of which 47 are complete or partial response, and 12 are no response. We segmented the breast areas depicted on each MR image by a computer-aided diagnosis (CAD) scheme, registered images acquired from the sequential MR image scan series, and calculated eighteen features extracted from DCE-MRI. We performed SVM with the 18 features for classification between patients of response and no response. Furthermore, 6 of the 18
features are selected to refine the classification by using Genetic Algorithm. The accuracy, sensitivity and specificity are 87%, 95.74% and 50%, respectively. The calculated area under a receiver operating characteristic (ROC) curve is 0.79±0.04. This study indicates that the features of DCE-MRI of breast cancer are associated with the response of NACT. Therefore, our method could be helpful for evaluation of NACT in treatment of breast cancer.
A Doppler ultrasound clutter filter that enables estimation of low velocity blood flow could considerably improve ultrasound as a tool for clinical diagnosis and monitoring, including the evaluation of vascular diseases and tumor perfusion. Conventional Doppler ultrasound is currently used for visualizing and estimating blood flow. However, conventional Doppler ultrasound is limited by frame rate and tissue clutter caused by involuntary movement of the patient or sonographer. Spectral broadening of the clutter due to tissue motion limits ultrasound's ability to detect blood flow less than about 5mm/s at an 8MHz center frequency. We propose a clutter filtering technique that may increase the sensitivity of Doppler measurements to at least as low as 2mm/s. The proposed filter uses an adaptive demodulation scheme that decreases the bandwidth of the clutter. To test the performance of the adaptive demodulation method at removing sonographer hand motion, six volunteer subjects acquired data from a basic quality assurance phantom. Additionally, to test initial in vivo feasibility, an arterial occlusion study was performed to assess the efficiency of the proposed filter at preserving signals from blood velocities 2mm/s or greater. The hand motion study resulted in average bandwidths of 384Hz, which was decreased to 44Hz at -60 dB at 2cm using our approach. The in vivo power Doppler study resulted in 27.8dB and 10.2dB dynamic ranges between the lowest and highest blood flow time points for the proposed filter and conventional 50Hz high pass filter, respectively.

Estimation of the velocity of the popliteal vein using transverse oscillation

Thor Bechgaard M.D., Kristoffer L. Hansen M.D., Andreas H. Brandt M.D., Rigshospitalet (Denmark); Simon Holbek, Technical Univ. of Denmark (Denmark); Charlotte Strandberg M.D., Niels Bækgaard M.D., Gentofte Hospital (Denmark); Jørgen A. Jensen, Technical Univ. of Denmark (Denmark); Michael B. Nielsen M.D., Rigshospitalet (Denmark)

Varicose veins are a common condition affecting about 20% of the adult population and are mainly caused by venous valve incompetence in the veins of the lower extremities. Evaluation of the venous flow in the lower extremities is currently performed with color Doppler ultrasound. Velocity estimates measured with spectral Doppler (SD) ultrasound are rarely used in a clinical setting for evaluating venous insufficiency because of inadequate reproducibility mainly caused by the angle dependency of the estimate, even though it has been shown that velocities are of importance on characterizing the disease. Transverse Oscillation (TO) is a novel angle independent ultrasound method, which has been implemented on a commercial scanner. The aim of the study was to evaluate whether TO perform equal to SD for recording velocities in the veins of the lower extremities. Four volunteers were recruited for the study. Each volunteer had ten measurements of the peak antegrade blood velocity in the popliteal vein obtained with SD and TO. The flow was provoked and standardized with a cuff compression-decompression system placed around the lower leg. The mean peak velocity in the popliteal vein of the four volunteers was 151.51 cm/s for SD and 105.94 cm/s for TO (p <0.001). The mean of the standard deviations of the peak velocities were 17.01 cm/s for SD and 13.11 cm/s for TO (p <0.005). Thus the study indicates that TO estimates lower peak velocity with improved standard deviation when compared to SD and may provide quantitative measures for the evaluation of veins.
beamformed and processed offline. A transverse oscillation (TO) velocity estimator was used to estimate the 3-D vector flow along a line originating from the center of the transducer. The estimated velocities in the lateral and axial direction were close to zero as expected. In the transverse direction a characteristic parabolic velocity profile was estimated with a peak velocity of 0.48 m/s ± 0.02 m/s in reference to the expected 0.54 m/s. The results presented are the first angle-independent 3-D vector flow estimates obtained with a row-column array, and, in addition, demonstrates that the CMUT technology is feasible for flow estimation.

9790-5, Session 1

Fast myocardial strain estimation from 3D ultrasound through elastic image registration with analytic regularization

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Image registration techniques using free-form deformation models have shown promising results for 3D myocardial strain estimation from ultrasound. However, the use of this technique has mostly been limited to research institutes due to the high computational demand, which is primarily a convergence of the computational load of the regularization term ensuring spatially smooth cardiac strain estimates. Indeed, this term typically requires evaluating derivatives of the transformation field numerically in each voxel of the image during every iteration of the optimization process. In this paper, we replace this time-consuming step with a closed-form solution directly associated with the transformation field resulting in a speed-up factor of ~10-6000, for a typical 3D B-mode image of 250^3 and 500^3 voxels, depending upon the size and the parametrization of the transformation field. The performance of the numeric and the analytic solutions were contrasted by computing tracking and strain accuracy on two realistic synthetic 3D cardiac ultrasound sequences, mimicking two ischemic motion patterns. Mean and standard deviation of the displacement errors over the cardiac cycle for the numeric and analytic solutions were 0.68±0.40 mm and 0.75±0.43 mm respectively. Correlations for the radial, longitudinal and circumferential strain components at end-systole were 0.89, 0.83 and 0.95 versus 0.90, 0.88 and 0.92 for the numeric and the analytic regularization respectively. The analytic regularizer matched the performance of the numeric solution as no statistically significant differences (p>0.05) were found when expressed in terms of bias or limits-of-agreement.

9790-6, Session 2

Breast tumour visualization using 3D quantitative ultrasound spectroscopy

Mehrdad J. Gangeh, Univ. of Toronto (Canada); Abdul Raheem, Sunnybrook Research Institute (Canada); Hadi Tadayyon, Univ. of Toronto (Canada); Simon Liu, Farnoosh Hadizad, Sunnybrook Research Institute (Canada); Gregory J. Czarnota, Sunnybrook Health Sciences Ctr. (Canada)

Breast cancer is one of the most common cancer types accounting for 29% of all cancer cases. Early detection and treatment has a crucial impact on improving the survival of affected patients. Ultrasound (US) is non-ionizing, portable, inexpensive, and real-time imaging modality for screening and quantifying breast cancer. Due to these attractive attributes, the last decade has witnessed many studies on using quantitative ultrasound (QUS) methods in tissue characterization. However, these studies have mainly been limited to 2-D QUS methods using hand-held US (HHUS) scanners. With the availability of automated breast ultrasound (ABUS) technology, this study is the first to develop 3-D QUS methods for the ABUS visualization of breast tumours. Using an ABUS system, unlike the manual 2-D HHUS device, the whole patient’s breast was scanned in an automated manner. The acquired frames were subsequently examined and a region of interest (ROI) was selected in each frame where tumour was identified. Standard 2-D QUS methods were used to compute spectral and backscatter coefficient (BSC) parametric maps on the selected ROIs. Next, the computed 2-D parameters were mapped to a Cartesian 3-D space, interpolated, and rendered to provide a transparent color-coded visualization of the entire breast tumour. Such 3-D visualization can potentially be used for further analysis of the breast tumour in terms of their size and extension. Moreover, the 3-D volumetric scans can be used for tissue characterization and the categorization of breast tumours as benign or malignant by quantifying the computed parametric maps over the whole tumour volume.

9790-7, Session 2

Spatial smoothing coherence factor for ultrasound computed tomography

Cuijuan Lou, Mengling Xu, Ming Yue Ding, Ming Yuchi, Huazhong Univ. of Science and Technology (China)

In recent years, many research studies have been carried out on ultrasound computed tomography (USCT) for its application prospect in early diagnosis of breast cancer. This paper applies four kinds of coherence-factor-like beamforming methods to improve the image quality of synthetic aperture focusing method for USCT, including the coherence-factor (CF), the phase coherence factor (PCF), the sign coherence factor (SCF) and the spatial smoothing coherence factor (SSCF) (proposed in our previous work). The performance of these methods were tested with simulated raw data which were generated by the ultrasound simulation software PZFlex 2014. The simulated phantom was set to be water of 4cm diameter with three nylon objects of different diameters inside. The ring-type transducer had 72 elements with a center frequency of 1MHZ. The results show that all the methods can reveal the biggest nylon circle with the radius of 2.5mm. However only can CF and SSCF efficiently eliminate the clutter. In addition, SSCF can provide a more homogenous image inside the circle. None of these methods can reveal the two smaller nylon circles with the radius of 0.75mm and 0.25mm. This may due to the small number of elements.

9790-8, Session 2

Analysis of patient movement during 3D USCT data acquisition

Nicole V. Ruiter, Torsten Hopp, Michael Zapf, Ernst Kretzek, Hartmut E. Gemmeke, Karlsruher Institut für Technologie (Germany)

Ultrasound Computer Tomography (USCT) is a promising candidate for sensitive imaging of breast cancer. In our first clinical study with a full 3D USCT system patient data was acquired over six minutes for one breast. In this paper the patient movement was analyzed qualitatively and as far as possible corrected in the resulting images. The movement was tracked using ten successive reflectivity reconstructions of full breast volumes acquired during 10s intervals at different aperture positions which were separated by 40s intervals. The average sum of all movement distances was 4.86 mm (STD ± 1.90 mm, max. 8.81 mm, min. 2.72 mm), and the mean distance between initial position and final position was 2.16 mm (STD ± 1.90 mm, max. 8.81 mm, min. 2.72 mm), and the mean distance between initial position and final position was 2.16 mm (STD ± 1.90 mm, max. 8.81 mm, min. 2.72 mm). The tracked movement was used to reconstruct registered volumes by summing successive images, which were transformed accordingly. The contrast of these images increases and additional image content becomes visible.
Both numerical and *in vivo* examples of waveform tomography for breast imaging were presented. We successfully tested our 3D USCT system in a pilot study and are currently conducting a comparative clinical study with 200 patients. Through the integration of our reconstruction methods and software, we achieved a comprehensive workflow including a dedicated DICOM viewer for interactive assessment of fused USCT images. We showed a significant positive correlation between average sound speed in the breast and density estimated from segmented MRIs. Despite the small patient collective, the results for visual comparison and breast density correlation are promising and will be further evaluated in our ongoing study.

Ultrasound breast imaging using frequency domain reverse time migration

Olivier Roy, Delphinus Medical Technologies, Inc. (United States); Mohammad Akbar Hosain Zuberi, Gerhard Pratt, Western Univ. (Canada); Neb Duric, Delphinus Medical Technologies, Inc. (United States)

No Abstract Available

Automatic short axis orientation of the left ventricle in 3D ultrasound recordings

João Pedrosoa, Brecht Heyde, Piet Claus, Jan D’hooge, Lab. on Cardiovascular Imaging and Dynamics (Belgium)

The recent advent of three-dimensional echocardiography has led to an increased interest from the scientific community in left ventricle segmentation frameworks for cardiac function. An automatic orientation of the segmented left ventricular mesh is an important step to obtain a point-to-point correspondence between the mesh and the cardiac anatomy. Furthermore, this would allow for automatic division of the left ventricle into the standard 17 segments, and, thus, fully automatic per-segment analysis, e.g., regional strain assessment. In this work, a method for fully automatic short axis orientation of the segmented left ventricle is presented. The proposed framework aims at detecting the inferior right ventricular insertion point using not only the image intensity information but also the detection of the surrounding structures, namely the right ventricular and right atrial cavities. Twenty-seven three-dimensional echocardiographic images were used to validate this framework by comparison to manual annotation of the inferior right ventricular insertion point. A mean absolute error of 4.6° and standard deviation of 3.49° were found. The mean error was -3.33° which indicates that the automatic detection is biased towards the septal side of the insertion point. The average computation time for this method was 666ms in a non-optimized MATLAB environment, which may potentiate real-time application. In conclusion, a successful method for automatic orientation of the segmented left ventricle is proposed.
The Autoprogressive algorithm has been successfully used to estimate to “teach” artificial neural networks the stress-strain relationship of tissues.

Surface force and volumetric displacement data gathered regarding the stress field, by building an empirical model directly from such as unknown boundary conditions and simplifying assumptions.

Specificity and thus diagnostic potential; however, the inverse problem is ill-posed when using imaging modalities.

Mapping mechanical parameters to the imaged region may increase tissue stiffness, but ambiguities and artifacts limit its diagnostic value.

Strain images provide a map of the relative deformation or strain of tissues, which is in turn reduced visual enhancement. The contrast enhancement retention time varies according to the frequency and power level of the ultrasound wave, as well as the contrast agent used.

The primary objective of this study was to investigate and identify the most appropriate image acquisition parameters that render optimal contrast effect for two intravenous contrast agents, Optison™ and Definity™. Several controlled in vitro experiments were conducted using an experimental apparatus that featured a perfused tissue-emulating phantom. A continuous flow of contrast agent was imaged using ultrasound at different frequencies and power levels, while a pulse wave Doppler device was used to monitor the concentration of the contrast agent solution. The contrast effect was determined based on the image intensity inside the flow pipe mimicking the blood-pool relative to the intensity of the surrounding phantom tissue. To identify the combination of parameters that yielded optimal visualization for each contrast agent tested, the contrast effect was assessed at different microbubble concentrations and different ultrasound imaging frequencies and transmit power levels.

Registration of multiple 3D ultrasound sectors in order to provide an extended field of view is important for the appreciation of larger anatomical structures at high spatial and temporal resolution. In this paper, we present a method for fully automatic spatio-temporal registration between two partially overlapping 3D ultrasound sequences. The temporal alignment is solved by aligning the normalized cross correlation-over-time curves of the sequences. For the spatial alignment, corresponding 3D Scale Invariant Feature Transform (SIFT) features are extracted from all frames of both sequences independently of the temporal alignment. A rigid transform is then calculated by least squares minimization in combination with random sample consensus. The method is applied to 16 echocardiographic sequences of the left and right ventricles and evaluated against manually annotated temporal events and spatial anatomical landmarks. The mean distances between manually identified landmarks in the left and right ventricles after automatic registration were (mean ± SD) 4.3 ± 1.2 mm compared to a ground truth error of 2.8 ± 0.6 mm with manual registration.

For the temporal alignment, the absolute errors in valvular event times were 14.4 ± 11.6 ms for Aortic Valve (AV) opening, 18.6 ± 16.0 ms for AV closing, and 34.6 ± 26.4 ms for mitral valve opening, compared to a mean inter-frame time of 29 ms.

Biomechanical properties of tissues can provide information regarding the health status of tissues. Typically, normal tissues are softer than surrounding healthy tissue. Quasi-static ultrasonic elasticity imaging provides a way to image these mechanical properties for detecting and diagnosing diseased states. Strain images provide a map of the relative tissue stiffness, but ambiguities and artifacts limit its diagnostic value.

Mapping mechanical parameters to the imaged region may increase specificity and thus diagnostic potential; however, the inverse problem is ill-posed when using imaging modalities. The Autopregressive algorithm has been successfully used to estimate ocular pressure and corneal stiffness, in vivo. We are expanding its use to any tissues imaged ultrasonically. We show that using force-displacement data recorded by the ultrasound probe, and estimated displacements at a few points in the imaged region, we can estimate the full stress and strain fields while assuming only conservation laws, from which elastic modulus images are computed. This method is a fundamentally new approach to medical elasticity imaging that for the first time provides three stress and three strain tensor images from one set of observation data.

Robust spatio-temporal registration of 4D cardiac ultrasound sequences

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A new approach to ultrasonic elasticity imaging

Cameron Hoerig, Jamshid Ghaboussi, Michael F. Insana, Univ. of Illinois at Urbana-Champaign (United States)

Development of 3D ultrasound needle guidance for high-dose-rate interstitial brachytherapy of gynaecological cancers

Jessica R. Rodgers, David Tessier, Robarts Research Institute (Canada) and Western Univ. (Canada); David D’Souza, London Regional Cancer Program (Canada); Eric Leung, Odette Cancer Ctr. (Canada) and Sunnybrook Health Sciences Ctr. (Canada); George Hajdok, London Regional Cancer Program (Canada); Aaron Fenster, Robarts Research Institute (Canada) and Western Univ. (Canada)

High-dose-rate (HDR) interstitial brachytherapy is often included in standard-of-care for gynaecological cancers. Needles are currently inserted through a perineal template without any standard real-time imaging modality to assist needle guidance, causing physicians to rely on pre-operative imaging, clinical examination, and experience. While two-dimensional (2D) ultrasound (US) is sometimes used for real-time guidance, visualization of needle placement and depth is difficult and subject to variability and inaccuracy in 2D images. The close proximity to critical organs, in particular the rectum and bladder, can lead to serious complications. We have developed a three-dimensional (3D) transrectal US system and are investigating its use for intra-operative visualization of needle positions used in HDR gynaecological brachytherapy. As a proof-
of concept, two patients were imaged with post-insertion 3D US and x-ray CT. Using software developed in our laboratory, manual rigid registration of the two modalities was performed based on the perineal template’s vaginal cylinder. The needle tip and a second point along the needle path were identified for each needle visible in US. The difference between modalities in the needle trajectory and needle tip position was calculated for each identified needle. Based on the preliminary results, 3D transrectal US shows potential for the development of a 3D US-based needle guidance system for interstitial gynaecological brachytherapy.

9790-18, Session 4
Non-invasive ultrasound method for measuring large range pressure changes in deep-positioned vessels
Jacob B. Olesen, Carlos A. Villagomez-Hoyos, Technical Univ. of Denmark (Denmark); Marie S. Traberg, Technical Univ. of Denmark (Denmark); Jørgen A. Jensen, Technical Univ. of Denmark (Denmark)

This abstract proposes a new non-invasive method for measuring pressure changes in deep-tissue vessels using vector velocity ultrasound data. The large penetration depth is ensured by acquiring data using a phased array transducer. Vascular pressure changes are then calculated from 2-D angle-independent vector fields using a model based on the Navier-Stokes equations. Experimental scans are performed on a fabricated flow phantom having a constriction of 36% at a depth of 100 mm. Scans are carried out using a phased array transducer connected to the experimental scanner, SARUS. 2-D fields of angle-independent vector velocities are acquired using directional synthetic aperture vector flow imaging. The obtained results are evaluated by comparison to a 3-D numerical simulation model with equivalent geometry as the designed phantom. The study showed pressure drops across the constricted phantom varying from -40 Pa to 15 Pa with a standard deviation of 32%, and a bias of 25% found relative to the peak simulated pressure drop. This preliminary study shows that pressure can be estimated non-invasively to a depth that enables cardiac scans, and thereby, the possibility of detecting the pressure drops across the mitral valve.

9790-19, Session 4
Automatic real-time detection of pleura and B-lines (comet-tail artifacts) on in-vivo ultrasound lung scans
Ramin Moshavegh, Technical Univ. of Denmark (Denmark); Kristoffer Lindskov Hansen M.D., Hasse Møller Sørensen M.D., Rigshospitalet (Denmark); Martin C. Hemmansen Sr., Technical Univ. of Denmark (Denmark); Michael B. Nielsen M.D., Rigshospitalet (Denmark); Jørgen A Jensen Jr., Technical Univ. of Denmark (Denmark)

In ultrasound an intimate mixture of air and water can characterize the lung. The change in their balance can be the sign of the pulmonary diseases. Interactions of water and air in lung ultrasound scans generate a variety of artifacts, and therefore, the lung ultrasound is rather based on analysing these artifacts than pure visualization of the lung structures. One of the most commonly used artifacts for diagnosing the pulmonary edema is a vertical artifact called “comet tail” or B-line, which is increased in number when edema is present.

This paper presents a novel automatic real-time method for detection of pleura and the B-lines (comet-tail artifacts) in lung ultrasound scans. The B-lines appear as laser-like vertical beams, which arise from the pleural line and spreads down without fading to the edge of the screen. The Pleural line is first segmented using graphs, the upper-pleural region is excluded from the scan, the Hilbert transform of the remaining region is computed, a cumulative frequency histogram is generated and a zone of influence of strong signals in the image is calculated, and finally the B-line artifacts are identified on the scan plain. The method can be used as the basis of a method of qualitatively characterizing the distribution of b-lines by computing features for individual and the collection of b-lines on the scan.

9790-20, Session 5
Sub-msV breast XACT scanner: concept and design
Shanshan Tang, Liqiang Ren, Pratik Samant, Jian Chen, Hong Liu, Liangzhong Xiang, The Univ. of Oklahoma (United States)

Excessive exposure to radiation increases the risk of cancer. We present the concept and design of a new imaging paradigm, X-ray induced acoustic computed tomography (XACT). Applying this innovative technology to breast imaging, an X-ray exposure can generate a 3D acoustic image, which dramatically reduces the radiation dose to patients when compared to breast CT and/or breast tomosynthesis. A theoretical model is developed to analyze the sensitivity of XACT as compared with conventional mammography. A noise equivalent pressure model is used for calculating the minimal radiation dose in XACT imaging. Furthermore, an XACT imaging system with an X-ray pulse duration of 60 nanoseconds is designed to evaluate the X-ray induced acoustic signal generation. Theoretical analysis shows that the X-ray induced acoustic signal has 100% relative sensitivity to the X-ray absorption (given that the percentage change in the X-ray absorption coefficient yields the same percentage change in the acoustic signal amplitude), but not to X-ray scattering. The final detection sensitivity is primarily limited by the thermal noise. The implication of 60 nanosecond pulsed X-rays results in an increase in the conversion efficiency by over 3 orders of magnitude, compared to our previous XACT imaging system in which a 5 microseconds pulsed X-ray was used. The radiation dose can be reduced by a factor of 100 compared with the newly FDA approved breast CT. Therefore, with the proposed innovative technology, one can potentially reduce radiation dose to patient in 3D breast imaging as compared with current x-ray modalities.

9790-21, Session 5
An evolutionary Bayesian search scheme for ultrasound modulated optical tomography
Mamatha Venugopal, Debasis Roy, Ram Mohan Vasu, Indian Institute of Science (India)

Ultrasound modulated optical tomography (UMOT) combines high optical contrast with high ultrasound resolution to image soft tissues. A focussed ultrasound beam introduced to a specific region of interest (ROI) in the object modulates the mean position of the scattering centres locally. This in turn modulates the overall decay of the specific intensity of an incident coherent light beam as it passes through the insonified region. The inverse problem of UMOT aims to recover the mean-squared displacements of the scattering centres from the measured amplitude autocorrelation of light. We propose an evolutionary Bayesian search scheme to invert the measurements through repeated solves of the correlation diffusion equation so as to drive the resultant measurement-prediction misfit to a zero-mean Brownian process. The discretized parameter vector evolves as a stochastic process with respect to an iteration variable and follows a recursive prediction-update algorithm. The conventional multiplicative-weight-based Bayesian update schemes suffer from sample degeneracy and are consequently ill-equipped to solve large dimensional problems in imaging. The key idea of this work is to incorporate a derivative-free additive correction to the predicted parameter process via a gain term that is functionally analogous to the weights. The numerical results for simulated data indicate that the proposed scheme substantively improves the
reconstruction accuracy vis-à-vis a popularly adopted regularized Gauss-Newton approach. The advantage of a derivative-free scheme is particularly highlighted in cases characterized by low sensitivity of measurements to variations in the parameters. Moreover, the proposed scheme circumvents the tedious Jacobian calculations involved in a Gauss-Newton approach.

9790-22, Session 5

Monte Carlo investigation of the dosimetric effect of the Autoscan ultrasound probe for guidance of radiotherapy

Michael Martyn, National Univ. of Ireland, Galway (Ireland); Tuathan O’Shea, The Institute of Cancer Research (United Kingdom) and The Royal Marsden NHS Foundation Trust (United Kingdom); Emma J. Harris, The Institute of Cancer Research (United Kingdom) and The Royal Marsden NHS Foundation Trust (United Kingdom); Jeffrey C. Bamber, The Institute of Cancer Research (United Kingdom) and The Royal Marsden NHS Foundation Trust (United Kingdom); Mark J. Foley, National Univ. of Ireland, Galway (Ireland)

The aim of this study was to quantify the dosimetric effect of the AutoscanTM ultrasound probe, which is a 3D trans-perineal probe used for real-time tissue tracking during the delivery of radiotherapy. The Monte Carlo software packages BEAMnrc and DOSXYZnrc were used to simulate the delivery of radiation beams at varying distances from (0 - 5 mm), but not directly through the AutoscanTM probe. Perineal surface doses as a function of distance from the radiation field edge could be considered in this way.

An anthropomorphic phantom, with and without the AutoscanTM probe placed in contact with its surface, was CT imaged (0.75 mm slice width, 140 kVp); the probe and phantom were positioned to mimic a trans-perineal imaging configuration. CT datasets were used for relative dose calculation in simulations of a 7-field plan delivered to the phantom. Perineal surface doses delivered to the phantom, with and without the probe in place, were compared directly.

The presence of the AutoscanTM probe resulted in consistently higher perineal surface dose values. However, this increase in surface dose fell-off rapidly as probe-to-radiation field edge distance increased; less than 1% at distances greater than 5 mm. Using CT image data from three patient volunteers, a typical probe-to-radiation field edge distance was calculated to be 27 mm. Our results therefore indicate that the presence of the AutoscanTM probe does not adversely affect a typical patient treatment, since the dosimetric effect of the probe is minimal when the probe-to-radiation field edge distance is greater than 5 mm.

9790-23, Session 5

Signal processing for enhanced tumor perfusion detection

MinWoo Kim, Univ. of Illinois at Urbana-Champaign (United States); Craig K. Abbey, Univ. of California, Santa Barbara (United States); Michael F. Insana, Univ. of Illinois at Urbana-Champaign (United States)

Enhanced blood perfusion in a tissue mass is an indication of neo-vascularity and a sign of a potential malignancy. Ultrasonic pulsed-Doppler imaging is a preferred modality for noninvasive monitoring of blood flow. However, the weak blood echoes and the slow, disorganized flow of perfusion make it difficult to detect using standard methods without the expense and risk of contrast enhancement. Our approach to enhancing perfusion detection without contrast media exploits ideal-observer techniques. A classifier is developed to discriminate among flow conditions using differences between echo covariances obtained under different flow conditions. We use adaptive methods that involve estimating the covariance matrix from slow-time echo samples obtained during a pulsed-Doppler acquisition. Principal components analysis (PCA) is first applied reducing the dimensionality of the recorded signals by isolating the blood perfusion signal and improving covariance matrix estimates with fewer training samples. To validate the technique, we estimated perfusion-detection performance using a phantom composed of a dialysis cartridge infused with tissue-mimicking blood. ROC analysis applied to the experimental results show that the ideal-observer detector can perform significantly better than standard pulsed-Doppler methods.

9790-24, Session 5

Frequency-shift low-pass filtering and least mean square adaptive filtering for ultrasound imaging

Shanshan Wang, Chunyu Li, Ming Yue Ding, Ming Yuchi, Huazhong Univ. of Science and Technology (China)

This paper investigates a method based on frequency-shift low-pass filtering (FSLF) and least mean-square adaptive filtering (LMSAF) for ultrasound image quality enhancement. FSLF is used for processing the ultrasound signal in the frequency domain, while LMSAF in the time domain. Firstly, FSLF shifts the center frequency of the focused signal to zero. Then the real and imaginary part of the complex data are filtered respectively by finite impulse response (FIR) low-pass filter. Thus the information around the center frequency are retained while the undesired ones, especially background noises are filtered. Secondly, LMSAF multiplies the signals with an automatically adjusted weight vector to further eliminate the noises and artifacts. Through the combination of the two filters, the ultrasound image is expected to have less noises and artifacts and higher resolution, and contrast. The proposed method was verified with the RF data of the CIRS phantom 055A captured by SonixTouch DAQ system. Experimental results show that the background noises and artifacts can be efficiently restrained, the wire object has a higher resolution and the contrast ratio (CR) can be enhanced for about 12dB to 15dB at different image depth comparing to delay-and-sum (DAS).

9790-25, Session 6

Enhanced ultrasound, ultrasound tomography for volume limb imaging and prosthetic fitting (Keynote Presentation)

Brian W. Anthony, Massachusetts Institute of Technology (United States)

Ultrasound imaging methods hold the potential to deliver low-cost, high-resolution, operator-independent and non-ionizing imaging systems – such systems couple appropriate algorithms with imaging devices and techniques. The increasing demands on general practitioners motivate us to develop more usable and productive diagnostic imaging equipment. Ultrasound, specifically freehand ultrasound, is a low cost and safe medical imaging technique. It doesn’t expose a patient to ionizing radiation. Its safety and versatility make it very well suited for the increasing demands on general practitioners, or for providing improved medical care in rural regions or the developing world. However it typically suffers from sonographer variability; we will discuss techniques to address user variability.

As with any medical imaging technique, methods are developed for imaging specific regions of the body; ultrasound is typically used to image soft tissues of the body. Ultrasound methods have been developed for applications involving pre-natal health, cardiac imaging, detection of breast cancer and therapeutic uses, however, ultrasound systems for 3-D imaging and quantification of hard tissues like bone in vivo are currently non-
existential. We will discuss our work to combine cylindrical scanning systems with state of the art inversion algorithms to deliver ultrasound systems for imaging and quantifying limbs in 3-D in vivo. Such systems have the potential to track the progression of bone health at a low cost and without radiation exposure, as well as, improve prosthetic socket fitting. Current methods of prosthetic socket fabrication remain subjective and ineffective at creating an interface to the human body that is both comfortable and functional. Though there has been recent success using methods like magnetic resonance imaging and biomechanical modeling, a low-cost, streamlined, and quantitative process for prosthetic cup design and fabrication has not been fully demonstrated. Medical ultrasonography may inform the design process of prosthetic sockets in a more objective manner. This talk presents the results of progress in this area.

9790-26, Session 6

**3D optical imagery for motion compensation in a limb ultrasound system**

Bryan J. Ranger, Micha Feigin, Xiang Zhang, Al Mireault, Ramesh Raskar, Hugh M. Herr, Brian W. Anthony, Massachusetts Institute of Technology (United States)

Conventional processes for prosthetic socket fabrication are heavily subjective, often resulting in an interface to the human body that is neither comfortable nor completely functional. With nearly 100% of amputees reporting that they experience discomfort with the wearing of their prosthetic limb, designing an effective interface to the body can significantly affect quality of life and future health outcomes. Active research in computer aided design, medical imaging, and biomechanical tissue modeling as it relates to prosthetic socket design has demonstrated an interest in moving toward more quantifiable processes that are still individualized for each patient.

In this work, medical ultrasonography, which has substantial potential to expand its clinical applications, is being pursued to acquire data that may quantify and improve the design process and fabrication of prosthetic sockets while greatly reducing cost compared to an MRI-based system. This paper presents a prototype limb imaging system that uses a medical ultrasound probe, mounted to a mechanical positioning system and submerged in a water bath. This is combined with three-dimensional optical imaging for motion compensation. Images are collected circumferentially around the limb and combined into cross-sectional imaged slices, resulting in a compounded image that shows tissue distributions and anatomical boundaries comparable to magnetic resonance imaging. Here, we present preliminary results as we move toward full volumetric imaging of residual limbs for prosthetic socket design. This demonstrates a novel multi-modal approach to residual limb imaging.

9790-27, Session 6

**Quantitative head ultrasound measurements to determine thresholds for preterm neonates requiring interventional therapies following intraventricular hemorrhage**

Jessica Kishimoto, Aaron Fenster, Robarts Research Institute (Canada); Fatemeh Salehi, Western Univ. (Canada); Walter Romano, David S. C. Lee, St. Thomas Elgin General Hospital (Canada); Sandrine de Ribaupierre, Western Univ. (Canada)

Dilation of the cerebral ventricles is a common condition in preterm neonates with intraventricular hemorrhage (IVH). This post hemorrhagic ventricle dilation (PHVD) can lead to lifelong neurological impairment through ischemic injury due to increased intracranial pressure and without treatment, can lead to death. Clinically, 2D ultrasound (US) through the fontanelles (‘soft spots’) of the patients are serially acquired to monitor the progression of the ventricle dilation. These images are used to determine when interventional therapies such as needle aspiration of the built up cerebrospinal fluid (CSF) (‘ventricle tap’, VT) might be indicated for a patient; however, quantitative measurements of the growth of the ventricles are often not performed. There is no consensus on when a neonate with PHVD should have an intervention and often interventions are performed after the potential for brain damage is quite high.

Previously we have developed and validated a 3D US system to monitor the progression of ventricle volumes (VV) in IVH patients. We will describe the potential utility of quantitative 2D and 3D US to monitor and manage PHVD in neonates. Specifically, we will look to determine image-based measurement thresholds for patients who will require VT in comparison to patients with PHVD who resolve without intervention. Additionally, since many patients who have an initial VT will require subsequent interventions, we look at the potential for US to determine which PHVD patients will require additional VT after the initial one has been performed.

9790-28, Session 6

**Development and evaluation of a novel VEGFR2-targeted nanoscale ultrasound contrast agents**

Houqiang Yu, Chunfang Li, Huazhong Univ. of Science and Technology (China); Xiaoling He, China Univ. of Geosciences (China); Giping Zhou, Mingyue Ding, Huazhong Univ. of Science and Technology (China)

Nanoscaled ultrasound contrast agents are promising for extra-vascular targeted ultrasonic imaging and therapy. The study concentrated on three aims; 1) to measure the fundamental characterizations and stability; 2) to evaluate the contrast enhancement abilities in normal Wistar rats liver ultrasound image; 3) to investigate the tumor targeting contrast imaging of nude mice.

9790-29, Session 7

**A pseudo non-linear method for fast simulations of ultrasonic reverberation**

Brett C. Byram, Jasmine Shu, Vanderbilt Univ. (United States)

There is growing evidence that reverberation is a primary mechanism of clinical image degradation. This has led to a number of new approaches to suppress reverberation, including our recently proposed model-based algorithm. The algorithm can work well, but it must be trained to reject clutter, while preserving the signal of interest. One way to do this is to use simulated data, but current simulation methods that include multipath scattering are slow and do not readily allow separation of clutter and signal. Here, we propose a more convenient pseudo non-linear simulation method that utilizes existing linear simulation tools like Field II or FOCUS. The approach functions by linearly simulating scattered wavefronts at shallow depths, and then time-shifting these wavefronts to deeper depths. The simulation only requires specification of the first and last scatterers encountered by a multiply reflected wave and a third point that establishes the arrival time of the reverberation. To maintain appropriate 2D correlation, this set of three points is fixed for the entire simulation and is shifted as with a normal linear simulation scattering field. The algorithm was implemented using Field II. We show example images and we compute first order speckle statistics as a function of scatterer density. We also perform ex vivo measures of reverberation where we find that the average speckle SNR is 1.73, which we can simulate with 2 reverberation scatterers per resolution cell. Finally, the van Cittert Zernike curve was calculated for the simulated clutter and shown to match empirical and theoretical observations.
A beamforming method for plane wave Doppler imaging of high flow velocities

Omar Mansour, Tamie L. Poepping, James C. Lacefield, Robarts Research Institute (Canada)

Plane wave imaging (PWI) has been a focus of research in the past few years and is desirable for its ability to achieve high frame rates, allowing the capture of fast dynamic events, and continuous Doppler data. Multiple low resolution image (LRI) frames from different plane wave tilt angles are compounded to form a single high resolution image (HRI) frame, thereby reducing the frame rate. Compounding is a low pass mean filter that causes attenuation and aliasing to signals with high Doppler shifts. On the other hand, the lateral beam profile and hence the quality of the HRI frames is improved by increasing the number of compounded frames. Hence, a tradeoff exists between the Doppler limits and beam profile. In this paper, we present a method that eliminates this tradeoff and produces high resolution images without the use of compounding and its side effects. The method suppresses the out-of-cell (off-focus or clutter) signal by spreading its spectrum, while keeping the spectrum of the in-cell (in-focus) signal intact. The spreading is achieved by using a random sequence of tilt angles, as opposed to a linear sweep, as is traditionally done. Experiments were performed using a carotid vessel phantom with constant flow. The new method more accurately measures the parabolic flow profile of the vessel and specially outperforms conventional PWI Doppler at higher flow velocities. Therefore, the spread spectrum method eliminates the tradeoff between beam profile and the maximum Doppler limit.

Detection of and compensation for blocked elements using large coherent apertures: ex vivo studies

Marko Jakovljevic, Nick Bottenus, Lily Kuo, Shalki Kumar, Gregg E. Trahey, Duke Univ. (United States)

When imaging with ultrasound through the chest wall, it is not uncommon for parts of the array to get blocked by ribs, which can limit the acoustic window and significantly impede visualization of the structures of interest. With the development of large-aperture, high-element-count, 2-D arrays and their potential use in transthoracic imaging, detecting and compensating for the blocked elements is becoming increasingly important.

We synthesized large coherent 2-D apertures and used them to image a point target through excised samples of canine chest wall. Blocked elements are detected based on low amplitude of their signals. As a part of compensation, blocked elements are turned off on Tx and Rx, and point-target images are created using: coherent summation of the remaining channels, compounding of intercostal subapertures, and adaptive weighting of the available Tx/Rx channel-pairs to recover the desired k-space response.

To evaluate the methods, we compare the point-spread functions (PSFs) and near-field clutter levels for the transcostal and control acquisitions. Notably, applying k-space compensation to the sparse aperture data created from the control acquisition reduces side lobes by 8.3 dB. When applied to the transcostal data, the same method reduces side lobes by only 1 dB, likely due to significant phase aberration and clutter. For the transcostal acquisition, turning off blocked elements and applying uniform weighting results in maximum clutter reduction of 5 dB on average, while the PSF stays intact. Compounding reduces clutter by about 3 dB while the k-space compensation increases clutter magnitude to the non-compensated levels.

Real-time 3D image reconstruction of a 24x24 row-column addressing array: from raw data to image

Chunyu Li, Jiali Yang, Xu Li, Xiaoli Zhong, Junjie Song, Ming Yue Ding, Ming Yuchi, Huazhong Univ. of Science and Technology (China)

This paper presents a work of real-time 3-D image reconstruction for a 7.5-MHz, 24x24 row-column addressing array transducer. The transducer works with a predesigned transmit/receive module. After the raw data are captured by the NI PXie data acquisition (DAQ) module, the following processing procedures are performed: delay and sum (DAS), base-line calibration, envelope detection, logarithm compression, down-sampling, gray scale mapping and 3-D display. These procedures are optimized for obtaining real-time 3-D images (24fps). Fixed-point focusing scheme is applied in delay and sum (DAS) to obtain line data from channel data. Zero-phase high-pass filter is used to calibrate the base-line shift of echo. The classical Hilbert transform is applied to detect the envelopes of echo. Logarithm compression is implemented to enlarge the weak signals and narrow the gap between strong signals. Down-sampling reduces the amount of data to improve the processing speed. Linear grey scale mapping is introduced that the weakest signal is mapped to 0 and the strongest signal 255. The 3-D real-time images are displayed with multi-planar mode, which shows three orthogonal sections (vertical section, coronal section, transverse section). A trigger signal is sent from the transmit/receive module to the DAQ module at the start of each volume data generation to ensure synchronization between these two modules. All procedures, include data acquisition (DAQ), signal processing and image display, are programmed on the platform of LabVIEW. 675MB raw echo data are acquired in one minute to generate 24x24x48, 27fps 3-D images. The experiment on the strong reflection object (aluminum slice) shows the feasibility of the whole process from raw data to 3-D real-time images.

Synthetic aperture volumetric ultrasound imaging using 2D row-column addressed transducer array

Hamed Bouzari, Thomas L. Christiansen, Technical Univ. of Denmark (Denmark); Christopher Beers, Sound Technology, Inc. (United States); Matthias B. Stuart, Technical Univ. of Denmark (Denmark); Svetoslav I. Nikolov, BK Ultrasound (Denmark); Jørgen A. Jensen, Technical Univ. of Denmark (Denmark)

Synthetic aperture (SA) technique can be used for achieving real-time volumetric ultrasound imaging using 2-D row-column addressed transducers. A fully addressed NxN 2-D array has N^2 elements which, have to be addressed individually. This results in a vast amount of interconnections and offers a great challenge in acquiring and processing the large amount of data. Therefore, reducing the number of interconnections by row-column addressing the 2-D array is of great importance, as it effectively reduces the number of elements from N^2 to 2N. Larger aperture sizes are realizable with these kind of arrays and therefore a better spatial resolution and deeper penetration depth are achievable. This paper investigates the volumetric imaging performance of a 3 MHz 64x64 in-house prototyped piezoelectric 2-D row-column addressed transducer using SA imaging.

Utilizing single element transmit events, a volume rate of 90 Hz down to 14 cm depth was achieved. Data were obtained using an experimental scanner (SARUS) with 70 MHz sampling frequency. Three phantoms were volumetrically imaged to assess the imaging performance of the transducer. A Signal to noise ratio (SNR) of 32 dB was measured on the beamformed images of the tissue mimicking phantom and the penetration depth was...
Advanced optimization of the synthetic aperture imaging quality for fast ultrasound imaging

Ramin Moshavegh, Jonas Jensen Sr., Carlos A. Villagomez Hoyos, Matthias B. Stuart, Martin C. Hemmson Sr., Jørgen A. Jensen, Technical Univ. of Denmark (Denmark)

Synthetic Aperture (SA) imaging produces high-quality images and velocity estimates of both slow and fast flow at high frame rates. However, grating lobe artifacts appear both in the transmission and the reception. These affect the image quality and the frame rate. Therefore optimization of parameters affecting the image quality of SA is of great importance.

This paper proposes an advanced procedure for optimizing the parameters essential for acquiring the optimal image quality while generating high resolution images in Synthetic aperture imaging. Optimization of the image quality is mainly performed based on measures such as F-number, number of emissions and the aperture size. They are considered to be the most contributing acquisition factors in the quality of the high resolution images in SA. The performance of the synthetic aperture is measured in terms of full-width at half maximum (FWHM) and the cystic resolution(CTR). The results of the study showed that imaging with only 32 emissions with a maximum sweep angle of 22 degrees yields a very good image quality compared with using high number of emissions. Therefore the number of emissions and the maximum sweep angle in the SA can be optimized to reach a reasonably good performance, and to increase the frame rate by lowering the required number of emissions.

Analog gradient beamformer for a portable ultrasound scanner

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The development of a low-cost hand-held ultrasound scanner is of primary importance for the large-scale distribution of diagnostic imaging in underdeveloped countries. To maximize the battery life, limitations on the complexity and power consumption of the circuit must be imposed, while the image quality needs to be preserved.

This paper investigates whether a compact gradient beamformer architecture for a Synthetic Aperture Sequential Beamforming (SASB) hand-held wireless probe can maintain the image quality. The system integrates the delay values in successive steps, and uses simple analog all-pass shifting networks yielding an ultra-compact low-power architecture. Furthermore, manually segmenting three-dimensional (3D) ultrasound images in their entirety is very time-consuming and impractical. In this paper, an automated method is proposed to segment 3D ultrasound image into major tissue components, which include fatty tissues, fibro-glandular tissues, cyst or tumor, for the purpose of assisting breast cancer diagnosis. The proposed automated method was employed on a database of 19 human cases. Experiment results proved that our proposed method not only correctly distinguish the fat and nonfat tissues, but also performed well in classifying cysts or tumors. Density assessment comparison between the automated method and manual segmentation demonstrated good consistency. Thus, our proposed method provides a potential approach to help correct ultrasound images for assisting breast cancer diagnosis.

Automated 3D ultrasound image segmentation for assistant diagnosis of breast cancer

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Segmentation an ultrasound image into functional tissues is of great importance for clinical breast cancer diagnosis. Many studies are found to segment masses only while few are found to segment all major tissues. Differences and inconsistencies in ultrasound interpretation call for an automated segmentation method to make results operator-independent. Furthermore, manually segmenting three-dimensional (3D) ultrasound images in their entirety is very time-consuming and impractical. In this paper, an automated method is proposed to segment 3D ultrasound image into major tissue components, which include fatty tissues, fibro-glandular tissues, cyst or tumor, for the purpose of assisting breast cancer diagnosis. The proposed automated method was employed on a database of 19 human cases. Experiment results proved that our proposed method not only correctly distinguish the fat and nonfat tissues, but also performed well in classifying cysts or tumors. Density assessment comparison between the automated method and manual segmentation demonstrated good consistency. Thus, our proposed method provides a potential approach to help correct ultrasound images for assisting breast cancer diagnosis.

Development of estimation system of knee extension strength using image features in ultrasound images of rectus femoris

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The measurement of knee extension strength using the dynamometer is one of the most direct and quantitative methods. This study aims to develop a system for measuring the knee extension strength using ultrasound images of the rectus femoris muscles obtained with non-invasive ultrasonic diagnostic equipment. First, we extract the muscle area from the ultrasound images and determine the image features, such as the thickness of the muscle. We combine these features and physical features, such as the patient’s height, and build a regression model of the knee extension strength from the training data. We have developed a system for estimating the knee extension strength by applying the regression model to the features obtained from the test data. Using the test data of 168 cases, the correlation coefficient value between the measured values and estimated values was 0.82. This result suggests that this system can estimate knee extension strength with high accuracy.
**9790-38, Session PS1**

**Precise reconstruction of fast moving cardiac valve in high frame rate synthetic transmit aperture ultrasound imaging**

Kazuki Takahashi, Yuki Tabata, Masayuki Fukuzawa, Kyoto Institute of Technology (Japan); Yoshihito Kitsunezuka, Saiseikai Hyogo-ken Hospital (Japan)

To diagnose heart valve incompetence, which is one of the most serious cardiac dysfunctions, it is essential to obtain high spatial and temporal resolution images of fast-moving valves. Ultrasound synthetic transmit aperture (STA) imaging has the potential to achieve high spatial resolution by synthesizing the pre-beamformed images through multiple transmissions. However, when the target is moving, the deteriorated coherence among the transmission events causes serious target deformation. We propose a high frame rate STA imaging (fast STA) which utilizes reduced number of transmission events in one image. Fast STA is better for reconstructing moving targets because it can quickly produce one image. Thus, it is expected to suppress deformation although it may have deteriorated spatial resolution. In this study, we quantitatively evaluated the minimized deformation and deteriorated spatial resolution to determine the feasibility of fast STA in the diagnosis of the valve incompetence. We modeled a radically moving valve at the maximum speed of 0.5 m/s. The simulated channel RF data of the valve phantom was processed by offline beamforming programs. We compared B-mode images for SRT (single received-line in a transmission), STA, and fast STA. The results show that a 4 times faster STA gives a distinguished performance when reconstructing the shape of the moving valve. The accuracy of the valve location is 53%, and this is an improvement of 72% compared with the SRT and STA methods. In spite of some decreased resolution, the improved performance of shape reconstruction can provide more precise diagnostic information on cardiovascular diseases.

**9790-39, Session PS1**

**Effect of echo artifacts on characterization of pulsatile tissues in neonatal cranial ultrasonic movies**

Kazuki Takahashi, Yuki Tabata, Masayuki Fukuzawa, Kyoto Institute of Technology (Japan); Yoshihito Kitsunezuka, Saiseikai Hyogo-ken Hospital (Japan)

Effect of echo artifacts on characterization of pulsatile tissues has been examined in neonatal cranial ultrasonic movies by characterizing pulsatile intensities with different regions of interests (ROIs). The pulsatile tissue, which is a key point in pediatric diagnosis of brain tissue, was detected from a heartbeat-frequency component in Fourier transform of a time-variation of 64 samples of echo intensity at each pixel in a movie fragment. The pulsatile-intensity average was evaluated in two ROIs: common fan-shape including the outside of subject cranium with several echo artifacts such as multiple reflection and individual cranial-shape to exclude such artifacts. The pulsatile area was also evaluated as the number of pixels where the pulsatile intensity exceeds a proper threshold. There was significant difference between two ROIs not only in the pulsatile-intensity average but also in the pulsatile area, which confirms that the echo artifacts give considerable effects on statistics of pulsatile tissues. The pulsatile-intensity average in the cranial-shape ROI exhibited similar tendency in the pulsatile area. It effects on statistics of pulsatile tissues. The pulsatile-intensity average in the pulsatile area, which confirms that the echo artifacts give considerable difference between two ROIs not only in the pulsatile-intensity average but also in the pulsatile area, which confirms that the echo artifacts give considerable effects on statistics of pulsatile tissues. The pulsatile-intensity average in the cranial-shape ROI exhibited similar tendency in the pulsatile area. It suggests its potential of a characterization measure of pulsatile tissues because it was neither affected by echo artifacts nor evaluated without any parameter optimization such as threshold.

**9790-40, Session PS1**

**Determining cardiac fiber orientation using FSL and registered ultrasound/DTI volumes**

James Dormer, Emory Univ. (United States); Xulei Qin, Emory Univ (United States); Ming Shen, Silun Wang, Xiaodong Zhang, Rong Jiang, Mary B. Wagner, Baowei Fei, Emory Univ. (United States)

Accurate extraction of cardiac fiber orientation from diffusion tensor imaging is an important tool for determining heart structure and function. However, the acquisition of diffusion images is costly and time consuming. By comparison, cardiac ultrasound imaging is rapid and relatively inexpensive, but it lacks the capability to directly measure fiber orientations. In order to create a detailed heart model from ultrasound data, a three-dimensional (3D) diffusion tensor imaging (DTI) with known fiber orientations can be registered to an ultrasound volume through a geometric mask. After registration, the cardiac orientations from the template DTI can be mapped to the heart using a deformable transformation field. This process depends heavily on accurate fiber orientation extraction from the DTI. In this study, we use the FMRIB Software Library (FSL) to determine cardiac fiber orientations in diffusion weighted images. For the registration between ultrasound and MRI volumes, we achieved an average Dice similarity coefficient (DSC) of 82.3±4.7%. For the estimation of fiber orientations from the proposed method, we achieved an accuracy error (AAE) of 27.1±13.8° as compared to the direct measurements from DTI. This work provides a new approach to generate cardiac fiber orientation that may be used for many cardiac applications.

**9790-41, Session PS2**

**Ultrasound transmission attenuation tomography with two parallel transducer arrays**

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Ultrasound attenuation of breast tumors is related to their types and pathological states, and can be used to detect and characterize breast cancer. Particularly, ultrasound scattering attenuation can infer the margin properties of breast tumors. Ultrasound attenuation tomography quantitatively reconstructs the attenuation properties of the breast. Our synthetic-aperture breast ultrasound tomography system with two parallel transducer arrays records both ultrasound reflection and transmission signals. We develop an ultrasound attenuation tomography method using ultrasound energy-scaled amplitude decays of ultrasound transmission signals and conduct ultrasound attenuation tomography using a known velocity model. We apply our ultrasound transmission attenuation tomography method to a breast phantom dataset, and compare the ultrasound attenuation tomography results with conventional B-mode ultrasound images obtained using reflection signals. We show that ultrasound attenuation tomography complements and even outperforms B-mode images in identifying breast lesions.

**9790-42, Session PS2**

**Image reconstruction for robot assisted ultrasound tomography**

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An investigation of several ray-based methods of reconstruction that can be used with robot-assisted ultrasound (US) tomography setup is presented.
In robot-assisted setup, an expert moves the US probe to the location of interest and a robotic arm aligns with it a second probe automatically. The two aligned probes can then transmit/receive US signals which can be used for tomographic reconstruction. Here, we focus on reconstruction of speed of sound in phantoms. We show that the limited data provided by two aligned probes can reconstruct pixel-wise images which distinguish between different speeds of sound in various simulation evaluations and also in an experiment with two aligned probes with a millimeter-range inaccuracy. US tomography has been so far used for breast imaging and has shown efficacy in cancer diagnosis. Combining the results of this investigation with the developed robot assisted US tomography setup, we envision feasibility of this setup for tomographic imaging in more applications and for other organs such as the kidney, liver, or prostate. There are multiple other configurations and methods of reconstruction that can be explored and this paper opens the window to this area, and is a first step toward tomographic reconstruction for robot assisted US tomography.

9790-43, Session PS2

Phase aberration correction by multi-stencils fast marching method using sound speed image in ultrasound computed tomography

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Reflection image from ultrasound computed tomography (USCT) system can be obtained by synthetic aperture techniques, however its quality is decreased by phase aberration caused by inhomogeneous media. Therefore, phase aberration correction is important to improve image quality. Previous studies tried to correct phase aberration using sound speed image, but straight sound ray was assumed and refraction wasn’t considered. In this study, multi-stencils fast marching method (MSFMM) is employed for phase correction. The MSFMM is an accurate and fast solution of Eikonal equation which considers the refraction. The proposed method includes two steps. First, the MSFMM is used to compute sound propagation time from each element to each image grid using sound speed image of USCT. Second, synthetic aperture techniques are employed to obtain reflection image using the computed propagation time. To evaluate the proposed method, both numerical simulation and phantom experiment were conducted. With regard to numerical simulation, both quantitative and qualitative comparisons between reflection images with and without phase aberration correction were given. For the quantitative comparison, PSF diameters in reflection images of a two layers structure with point targets were presented. For the qualitative comparison, reflection images of simple circle and complex breast models were shown. In respect to phantom experiment, a piece of breast phantom with artificial glandular structure inside was scanned by USCT prototype, and its reflection images with and without phase correction were compared. In this study, a phase aberration correction method by MSFMM are proposed for reflection image of the USCT.

9790-44, Session PS2

Using ultrasound tomography to identify the distributions of density throughout the breast

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Women with high breast density are at increased risk of developing breast cancer. Breast density has usually been defined using mammography as the ratio of fibroglandular tissue to total breast area. Ultrasound tomography (UST) is an emerging modality that can also be used to measure breast density. UST creates tomographic sound speed images of the patient’s breast which is useful as sound speed is directly proportional to tissue density. Furthermore, the volumetric and quantitative information contained in the sound speed images can be used to describe the distribution of breast density. The work presented here measures the UST sound speed density distributions of 165 women with negative screening mammography. Frequency distributions of the sound speed voxel information were examined for each patient. In a preliminary analysis, the UST sound speed distributions were averaged across patients and grouped by various patient and density-related factors (e.g., age, body mass index, menopausal status, average mammographic breast density). It was found that differences in the distribution of density could be easily visualized for different patient groupings. Furthermore, findings suggest that the shape of the distributions may be used to identify participants with varying amounts of dense and non-dense tissue.

9790-45, Session PS3

Automated kidney morphology measurements from ultrasound images using texture and edge analysis

Harisharan Ravishankar, Pavan Annangi, GE Global Research (India); Justin Lanning, Michael Washburn, GE Healthcare (United States)

In a typical ultrasound scan, a sonographer measures kidney morphology manually to assess renal abnormalities. The caliper placements and volume measurements are time consuming and an automated solution will help to improve accuracy, repeatability and throughput. In this work, we propose an automated kidney morphology measurement solution from Ultrasound scans. The problem is challenging due to wide variability in kidney shape, size, texture, weak contrast of the boundaries and presence of strong edges like diaphragm & fat layers. We present a two-step algorithm that exploits edge and texture information in combination with anatomical cues. First, we use edge analysis to approximately localize kidney by searching the edge map with predefined templates. In the second step, we propose a machine learning framework using popular texture features and ensemble classifier methods to refine the localization step and accurately estimate kidney morphology. We have trained our algorithms on 45 images and tested the performance on 45 unseen cases. The performance against ground truth is measured by computing Dice overlap with ground truth kidney ROIs and % error in major and minor axis measurements of kidney. From our experiments, we found out that Haar features & Gradient boosting classifier combination gave the best results, with successful kidney localization in 83% of the cases. Further, successful morphology measurements were achieved in 80% of the cases. Incorporating edge based localization step helped to reduce computational complexity by 4x times while preserving the performance, thereby making it feasible to deploy on commercial scanners and enable clinical usage.

9790-46, Session PS3

Automated kidney detection for 3D ultrasound using scan line searching

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Ultrasound (US) as fast and non-expensive imaging modality is used for the examination of various anatomies, e.g. the kidneys. One important task for subsequent tracking or automated computer-aided diagnosis is the automatic identification of the kidney region. US as imaging modality without an a priori known orientation and location of the transducer makes the implementation of automatic methods challenging. We propose an automatic method for the detection of the kidney in 3D US images. This novel technique analyses the US image data along virtual scan lines. Characteristic texture changes when entering and leaving the symmetric tissue stripes of the renal cortex and the renal pelvis are searched for. A following accumulation of all cortex candidates along a second image axis results in a 2D candidate heat map from where the kidney location is extracted in two steps. First, the strongest candidate and its counterpart on the other side of the heat map gap that is caused by the renal pelvis are extracted. This is followed by renal cortex sizes analysis as well as heat map intensity ranking. In contrast to other methods that use a 3D shape which is moved through the data set in order to detect characteristic kidney patterns our method is simpler and therefore faster. And compared to simple threshold-based methods that rely on identifying the renal pelvis as smallest bright compact region the scan line approach is more reliable. An evaluation performed on 61 3D US data sets revealed that in 55 cases the kidney was correctly identified.

9790-47, Session PS3
US-Cut: interactive algorithm for rapid detection and segmentation of liver tumors in ultrasound acquisitions
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Ultrasound (US) is the most commonly used liver imaging modality worldwide. It plays an important role in follow-up of cancer patients with liver metastases. We present an interactive segmentation approach for liver tumors in US acquisitions. Due to the low image quality and the low contrast between the tumors and the surrounding tissue in US images, the segmentation is very challenging. Thus, the clinical practice still relies on manual measurement and outlining of the tumors in the US images. We target this problem by applying an interactive segmentation algorithm to the US data, allowing the user to get real-time feedback of the segmentation results. The algorithm has been developed and tested hand-in-hand by physicians and computer scientists to make sure a future practical usage in a clinical setting is feasible. To cover typical acquisitions from the clinical routine, the approach has been evaluated with dozens of datasets where the tumors are hyperechoic (brighter), hypoechoic (darker) or isoechoic (similar) in comparison to the surrounding liver tissue. Due to the interactive real-time behavior of the approach, it was possible even in difficult cases to find satisfying segmentations of the tumors within seconds and without parameter settings, and the average tumor deviation was only 1.4mm compared with manual measurements. However, the long term goal is to ease the volumetric acquisition of liver tumors in order to evaluate for treatment response. Additional aim is the registration of intraoperative US images via the interactive segmentations to the patient's pre-interventional CT acquisitions.

9790-48, Session PS3
Delimitation of the lung region with distributed ultrasound transducers
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One technique used to infer and monitor patient’s respiratory conditions is the electrical impedance tomography (EIT). This provides images with information about lung function. Nevertheless, an important problem is that it does not provide anatomical details in border regions of several organs. To contribute to a clinical solution, our approach uses several ultrasound transducers distributed around the chest, in order to delimit organs of interest such as the lung and to improve the reconstruction quality of the EIT.

Using a Matlab Toolbox (k-wave), the ultrasound propagation phenomenon in a homogeneous medium without patient (Reference) and with thoracic models were simulated, separately (fig1). After pulse emission by a transducer (TR), all received signals were compared considering the two sets of signals (fig2). If the energy relation between parts of the signals (Eq.3) does not exceed an empirical threshold (20% in this study), a partial mask is generated between the transmitter and the receptor. This process was repeated until all 128 transducers are considered as TR-emitters: The 128 transducers (150kHz) are uniformly distributed (fig4). Each one generates a set of 127 signals. Figure_5 shows examples of masks that limit the highest contrast materials and the objects that change impedance. A simple approach was presented to delimit high contrast organs with ultrasound transducers distributed around the patient. This approach allows other lower contrast objects to become invisible by varying the threshold limit.

The investigation, based on numerical simulations of ultrasonic propagation, has shown promising results in the delimitation of the lung region.

9790-49, Session PS3
Rotation elastogram: a novel method to visualize local rigid-body rotation under quasi-static compression
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During manual palpation of breast masses, the perception of its stiffness and slipperiness are two commonly used information by the physician. In order to reliably and quantitatively obtain this information several non-invasive elastography techniques have been developed that seek to provide an image of the underlying mechanical properties, mostly stiffness-related. Very few approaches have visualized the “slip” at the lesion-background boundary that only occurs for a loosely-bonded benign lesion, and none have yet demonstrated the direct visualization of rigid body rotation. It has been shown that axial-shear strain distribution provides information about underlying slip. One such feature, referred to as “fill-in” was interpreted as a surrogate of the rotation undergone by an asymmetrically-oriented-loosely bonded-benign-lesion under quasi-static compression. However, imaging the rotation itself has not been addressed. In order to accomplish this, the quality of lateral displacement estimation needs to be improved. In this simulation study, we utilize spatial compounding approach and assess the feasibility to obtain good quality rotation elastogram. The angular axial and lateral displacement estimates were obtained at different sonification angles from a phantom containing an elliptical inclusion oriented at 450, subjected to 1% compression from the top. A multilevel 2D-block matching algorithm was used for displacement tracking and 2D-least square compounding of angular axial and lateral displacement estimates was employed. By varying the maximum steering angle and incremental angle the improvement in the lateral motion tracking accuracy and its effect on quality of rotational elastogram was evaluated. Results demonstrate significantly improved rotation elastogram using this technique.

9790-50, Session PS3
Dynamic programing on a tree for ultrasound elastography
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Paul Martineau, McGill Univ. Health Ctr. (Canada); Hassan Rivaz, Concordia Univ. (Canada)

Ultrasound Elastography is an emerging imaging technique that allows estimation of the mechanical characteristics of tissue, and similar to ultrasound imaging is easy-to-use, convenient and safe. Two issues that need to be addressed before widespread clinical use of elastography in clinical environments are real time constraints and deteriorating effects of signal decorrelation between pre- and post-compression images. A method based on dynamic programming (DP) has been introduced and further improved by using Analytical Minimization (AM). An integer displacement field would be first calculated for a single RF-line (the seedline) and it would be refined and then propagated laterally through the image by using AM. However, in case of large signal decorrelation, the DP solution may be incorrect. In this paper we have proposed a novel solution to this problem by solving DP on a tree instead of a single RF-line. Formulation of DP on a tree allows exploiting significantly more information, and as such, is more robust and accurate. Our results on phantom and in-vivo patient data show that DP on tree significantly outperforms traditional DP in ultrasound elastography.

9790-51, Session PS3

Image based temporal alignment of echocardiographic sequences

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Temporal alignment of echocardiographic sequences allows for a fair comparison between multiple cardiac sequences by showing frames at corresponding time points in the cardiac cycle. Spatial registration of echo volumes in order to combine several acquisitions, either to enhance image quality or to form larger field of view also requires the volumes to be captured at corresponding time points. Image-based temporal alignment methods utilize the information that is already available in the sequence, without the need for additional measurements or apparatus. In this study, three different image-based temporal alignment methods were implemented and compared. The first method is an implementation of dynamic time warping (DTW). The second one is a spline-based method that optimizes the similarity between temporal characteristic curves of the cardiac cycle using 1D cubic B-spline. The third method is based on the spline-based method with piecewise modification. The methods were tested on an in vivo dataset of 12 echo sequence pairs in which mitral valve opening (MVO) time was manually annotated. The computation times of all methods were in the same order of magnitude and all methods resulted in average MVO timing errors less than the average inter-frame time.

9790-52, Session PS3

Quantitative viscoelastic imaging using ARFI

Yassin Labyed, Seungsoo Kim, Stephen J. Rosenzweig, Liexiang Fan, Siemens Healthcare (United States)

We present a model-free method for quantitative viscoelastic imaging (QVI). In QVI, shear wave particle velocity data is analyzed to estimate the frequency-dependent complex wave number, from which images of several viscoelastic parameters can be obtained. QVI utilizes the time-domain Fourier transform of the shear wave particle velocity to obtain 1D spectra at multiple lateral locations. At each temporal frequency, linear frequency is performed to determine the slope of the logarithm of the spectra as a function of lateral position. The resulting slope gives the complex wave number. The simulation results show that the viscoelastic parameters estimated with QVI are in agreement with the true values.

9790-53, Session PS3

Comparison of ultrasound B-mode, strain imaging, acoustic radiation force impulse displacement and shear wave velocity imaging using real time clinical breast images

Kavitha Manickam, Ramasubba Reddy Machireddy, Indian Institute of Technology Madras (India); Bagyam Raghavan, Apollo Specialty Hospital (India)

It has been observed that many pathological process increase the elastic modulus of soft tissue compared to normal. In order to image tissue stiffness using ultrasound, a mechanical compression is applied to tissues of interest and local tissue deformation is measured. Based on the mechanical excitation, ultrasound stiffness imaging methods are classified as compression or strain imaging which is based on external compression and Acoustic Radiation Force Impulse (ARFI) imaging which is based on force generated by focused ultrasound. When ultrasound is focused on tissue, shear wave is generated in lateral direction and shear wave velocity is proportional to stiffness of tissues. The work presented in this paper investigates strain elastography and ARFI imaging in clinical cancer diagnostics using real time patient data. Ultrasound B-mode imaging, strain imaging, ARFI displacement and ARFI shear wave velocity imaging were conducted on 50 patients (31 benign and 23 malignant categories) using Siemens S2000 machine. True modulus contrast values were calculated from the measured shear wave velocities. For ultrasound B-mode, ARFI displacement imaging and strain imaging, observed image contrast and CNR were calculated for benign and malignant cancers. Observed contrast values were compared based on the true modulus contrast values calculated from shear wave velocity imaging. In addition to that, student unpaired t-test was conducted for all the four techniques and box plots are presented. Results show that, strain imaging is better for malignant cancers whereas ARFI imaging is superior than strain imaging and B-mode for benign lesions representations.

9790-54, Session PS3

Differential diagnosis of thyroid nodules with virtual touch tissue imaging of ARFI elastography

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The aim of this study was to evaluate the diagnostic performance of virtual touch tissue imaging (VTI) based on ARFI elastography technique for differentiating malignant from benign thyroid nodules. One hundred pathologically proven thyroid nodules (80 benign, 20 malignant) in 76 participants were recruited in this study. The likelihood of malignancy in the light of VTI features was scored on the basis of a six-point scale by one experienced sonologist who was blinded to pathological results. In addition, the mean gray value within the thyroid nodule (mGVTN) derived from VTI image was measured for quantitative analysis. Receiver-operating characteristic curve (ROC) analyses were performed to assess the diagnostic performance of VTI score and mGVTN. The more frequently malignant
Compressed sensing (CS) or compressive sampling allows much lower sampling frequency than the Nyquist sampling frequency. We previously proposed a novel beamforming technique, named compressive sensing ultrasound imaging (CSUI) to overcome this contradiction. Simulations and phantom experiments show that CSUI can achieve comparable or higher lateral resolution than STA, as well as a contrast-to-noise ratio (CNR) comparable to that of the conventional focused mode. Moreover, CSUI has a unique advantage in that it can achieve higher frame rates than STA, which enables us to track moving objects in real time. Another benefit of CSUI is the ability to change the focus and sector size at runtime, which makes it suitable for applications such as needle tracking and therapy monitoring.


doi:10.1117/12.2107141

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New platform for evaluating medical imaging

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9790-56, Session PS4

Speed of sound estimation with active PZT element for thermal monitoring therapy: feasibility study

Johns Hopkins Univ. (United States)

9790-55, Session PS4

Ultrasound-guided needle tracking systems are frequently used in image-guided medical procedures. Ultrasound guided needle tracking systems can be a common tool in such procedures as prostate biopsy, breast biopsy, and bone biopsy. In particular, ultrasound needle tracking can be used for image-guided neuronavigation and tumor ablation therapy. Neuronavigation and tumor ablation therapy are commonly used in the treatment of brain tumors and lung tumors, respectively. In this study, we developed a new ultrasound needle tracking system that is based on the active PZT element for thermal monitoring during needle ablation. The system consists of an ultrasound needle, an active PZT element, and a temperature sensor. The ultrasound needle is inserted into the tissue, and the active PZT element is used to generate sound waves that propagate through the tissue and are detected by the temperature sensor. The temperature sensor is used to measure the temperature of the tissue, and the temperature data is used to estimate the speed of sound in the tissue.


doi:10.1117/12.2107141

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Compressed sensing for high performance ultrasound imaging

9790-58, Session PS5

Selective differencing for nonlinear ultrasound imaging

Jen-Liang Lu, Jason W. Fleischer, Princeton Univ. (United States)

9790-57, Session PS5

Selective differencing for nonlinear ultrasound imaging

Jen-Liang Lu, Jason W. Fleischer, Princeton Univ. (United States)

Compressed sensing (CS) or compressive sampling allows much lower sampling frequency than the Nyquist sampling frequency. We previously proposed a novel beamforming technique, named compressive sensing ultrasound imaging (CSUI) to overcome this contradiction. Simulations and phantom experiments show that CSUI can achieve comparable or higher lateral resolution than STA, as well as a contrast-to-noise ratio (CNR) comparable to that of the conventional focused mode. Moreover, CSUI has a unique advantage in that it can achieve higher frame rates than STA, which enables us to track moving objects in real time. Another benefit of CSUI is the ability to change the focus and sector size at runtime, which makes it suitable for applications such as needle tracking and therapy monitoring.
9790-59, Session PS5

Endocavity ultrasound, fiber-guided photoacoustic, and quasi-static elasticity imaging

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Background and Significance: A hybrid imaging modality, capable visualizing structural, functional, and cellular an molecular characteristics of tissue could be extremely helpful in more accurate and early stage detection of diseases such as cancer. Ultrasound imaging, with its unique advantages such as being non-ionizing and real time and capable of imaging deep lying tissue structures is the first line imaging for many clinical applications. Therefore, development of hybrid imaging modalities, built around ultrasound imaging could become a useful clinical tool. In this study, we investigate the development of a hybrid, multimodal endocavity ultrasound, Photoacoustic, and elasticity imaging (ENUPEI) system.

Materials and Methods: Our developed endocavity ultrasound, photoacoustic, and elasticity imaging system was built around a fully digital and programmable US scanner (Verasonics Vantage 128) equipped with a transvaginal ultrasound transducer (ATL C9-5). Photoacoustic light source consisted of an optical parametric oscillator (OPO) pumped with a pulsed Nd:YAG (SpectraPhysics Quanta-Ray PRO 270) capable of generating high energy pulsed (8-12 ns) within a wide range of spectrum (400-2500 nm). The OPO output was coupled to a custom-built fiber bundle, made out of 19 multimode hard polymer clad optical fiber with core diameter of 1000 μm (Thorlabs FT1000EMT). A 3D printed mechanical holder was designed for holding the fibers with a pre-calculated bending and positioning in order to maximize the light penetration, uniformity, and in order to deliver maximum light to the elevational focus of the ultrasound transducer. Quasi-static elasticity measurements were performed through applying a slight compressive force to produce strain (tissue deformation) and measurement of axially induced strain via well-known cross-correlation technique. A MATLAB-based user interface was developed to process and provide overlaid ultrasound/photoacoustic/elasticity images.

Results and Discussions: The utility of the developed hybrid imaging probe was tested through a set of tissue mimicking phantom experiments. Tissue mimicking phantoms made out of gelatin (with different concentration) were utilized in ultrasound/elasticity measurements. Photoacoustic tissue mimicking phantoms were made out of gelatin background with optical absorber inclusions (mixture of gelatin with optical absorbers such as ink, or blood) at different depths ranging from 5mm to 20 mm. The results indicated the ability of developed imaging system to provide co-registered ultrasound, photoacoustic, and elasticity images. Future studies are planned to further evaluate the ability of the developed multimodal imaging system.

Conclusions: An integrated ultrasound, photoacoustic, and quasi-static elasticity imaging system, suitable for multiple applications such as imaging female pelvic organs is developed and its functionality was tested through a set of tissue-mimicking phantom experiments.

9790-61, Session PS6

Towards predictive diagnosis and management of rotator cuff disease: using curvelet transform for edge detection and segmentation of tissue

Vipul Pai Raikar, David M. Kwiatkowski, Clemson Univ. (United States)

Degradation and injury of the rotator cuff is one of the most common diseases of the shoulder among the general population. In orthopedic injuries, rotator cuff disease is second only to back pain in terms of overall reduced quality of life for patients. Clinically, this disease is managed via pain and activity assessment and diagnostic imaging using ultrasound and MRI. Ultrasound has been shown to have good accuracy for identification and measurement of rotator cuff tears. In our previous work, we have developed novel, real-time techniques to biomechanically assess the condition of the rotator cuff based on Musculoskeletal Ultrasound. Of the rotator cuff tissues, supraspinatus is the first that sees degradation and is the most commonly affected. In our work one of the challenges lies in effectively segmenting and characterizing the supraspinatus. We are exploring the possibility of using curvelet transform for improving tissue segmentation techniques in ultrasound. Curvelets have been shown to give optimal multi-scale representation of edges in images. They are designed to represent edges and singularities along curves in images which makes them an attractive proposition for use in ultrasound segmentation. In this work, we present preliminary results of using curvelet transforms for automatic edge and feature extraction for the supraspinatus.

9790-62, Session PS6

Classification of motor intent in transradial amputees using sonomyography and spatio-temporal image analysis

Harishwaran Hariharan, Nima Aklaghi, Alex Baker, Jana Kosecka, Huzefa Rangwala, Siddhartha Sikdar, George Mason Univ. (United States)

In spite of major advances in biomechanical design of upper extremity prosthetics, there has been a significant lag in the integration of intuitive control and dexterity in such prosthetics. Conventional myoelectric control strategies typically utilize electromyography (EMG) signal amplitude sensed from forearm muscles. EMG has limited specificity in resolving deep muscle activity and poor signal-to-noise ratio. We present an ultrasound image sequence classification method that capitalizes on local space-time behavior. Ultrasound images of the forearm muscles were obtained from a trans-radial amputee and analyzed to extract spatiotemporal features describing muscle activity. For every image location, based on a response function; short time and space limited cuboidal sequences are extracted and assigned an optical flow behavior label. The image space is clustered based on the location of cuboids and features calculated from the cuboids in each cluster. Using sequences of known motions, we extract feature vectors that describe said motion. A k-nearest neighbor classifier is designed for classification experiments. Using the leave-one-out cross validation on image sequences for an amputee subject, we demonstrate that the classifier is able to discern three important hand motions with an accuracy of 93.33% accuracy, 80-100% precision and 91-100% recall rate. We anticipate
9790-63, Session PS6

**Single element ultrasonic imaging of limb geometry: an in-vivo study with comparison to MRI**

Xiang Zhang, Brian W. Anthony, Massachusetts Institute of Technology (United States)

Despite advancements in medical imaging, current prosthetic fitting methods remain subjective, operator dependent, and non-repeatable. The current plaster casting method relies on prosthetist experience and tactile feel of the limb to design the prosthetic socket. Often times, multiple fitting iterations are required to achieve an acceptable fit. Use of improper socket fittings can lead to painful pathologies including neuromas, inflammation, soft tissue calcification, and pressure sores, often forcing the wearer to into a wheelchair and reducing mobility and quality of life. Computer software along with MRI/CT imaging has already been explored to aid the socket design process. In this paper, we explore the use of ultrasound instead of MRI/CT to accurately obtain the underlying limb geometry to assist the prosthetic socket design process. Using a single element ultrasound system, multiple patients’ proximal limbs were imaged using L2, and 5MHz single element transducers. Each ultrasound transducer was calibrated to ensure acoustic exposure within the limits defined by the FDA. To validate image quality, each patient was also imaged in an MRI. Fiducial markers visible in both MRI and ultrasound was used to compare the same limb cross-sectional image for each patient. After applying a migration algorithm, B-mode ultrasound cross-sections showed sufficient high image resolution to characterize the skin and bone boundaries along with the underlying tissue structures.

9790-64, Session PS6

**Towards ultrasound travel time tomography for quantifying human limb geometry and material properties**

Jonathan R. Fincke, Micha Feigin, Germán A. Prieto, Xiang Zhang, Brian W. Anthony, Massachusetts Institute of Technology (United States)

Sound speed inversions made using simulated time of flight data from a numerical limb-mimicking phantom comprised of soft tissue and a bone inclusion demonstrate that wave front tracking forward modeling combined with L1 regularization could lead to accurate estimates of bone sound speed. Ultrasonic tomographic imaging of limbs has the potential to impact prosthetic socket fitting, as well as detect and track muscular dystrophy diseases, osteoporosis and bone fractures at low cost and without radiation exposure. Research in ultrasound tomography of bones has increased in the last 10 years, however, methods delivering clinically useful sound speed inversions are lacking. Inversions for the sound speed of the numerical phantoms using L1, L2 and Laplacian regularizations are compared for ray trace and wave front forward models. The simulations are based on a custom-made cylindrically-scanning tomographic medical ultrasound system (0.5 – 5 MHz) consisting of two acoustic transducers capable of collecting pulse echo and travel time measurements over the entire 360° aperture.

9790-65, Session PS7

**Observations of liver cancer cells in scanning probe acoustic microscope: a preliminary study**

Xiaohui Chen, Xiaoyue Fang, Huazhong Univ. of Science and Technology (China); Qing Xi, Tianjin Medical Univ. (China); Hua Guo, Tianjin Medical Univ. Cancer Institute and Hospital (China); Ning Zhang, Tianjin Medical Univ. (China); Ming Yue Ding, Huazhong Univ. of Science and Technology (China)

Scanning probe acoustic microscope (SPAM) can be used to acquire the morphology image as well as the non-destructive internal structures. However, the observations of the morphology image as well as the internal structures acoustic image of liver cancer cells in SPAM are few. In this paper, we cultured 4 different types of liver cancer cells on the silicon wafer and coverslip to observe their morphology images as well as acoustic images, and made a preliminary study of the 4 types of cells. First, the 4 types of cells were cultured with DMEM supplemented with 10% fetal bovine serum (FBS), in a humidified atmosphere of 5% CO2 at 37°C. Then, the morphology images of the 4 types of cells were observed in optical microscope and collected, which were cultured on the silicon wafer and overslip, respectively. Furthermore, after the 8 types of cells specimens (hereinafter referred to as the silicon specimens and coverslip specimens) rapid drying, a series of morphology images and acoustic images were collected. Finally, we made a preliminary study of the differences of these 4 types of liver cancer cells with SPAM. The experimental measurement results showed that the long axis of single liver cancer cell is about 5.28µm, while the short one is about 2.85µm, which are reasonable with theoretical expectation. In addition, some cellular pseudopodium were observed in the morphology images of the coverslip specimens while no such cellular pseudopodium were appeared in the morphology images of the silicon specimens, which concluded that the living liver cancer cells were less likely to grow on the silicon wafer. This research has a great significance in the visual morphology and internal information studies of different types of liver cancer cells. SPAM provides a rapid and sensitive visual method for studying the morphology and internal structures of the cancer cells. The proposed method can be also used to obtain the morphology and internal information in both solid and soft material wafers, such as silicon and cells, with the resolution of nanometer scale.

9790-66, Session PS7

**A preliminary evaluation work on a 3D ultrasound imaging system for 2D array transducer**

Xiaoli Zhong, Xu Li, Jiali Yang, Chunyu Li, Junjie Song, Ming Yue Ding, Ming Yuchi, Huazhong Univ. of Science and Technology (China)

This paper presents a preliminary evaluation work on a pre-designed 3-D ultrasound imaging system. The system mainly consists of four parts, a 7.5MHz, 24x24 2-D array transducer, the transmit/receive circuit, power supply and data acquisition and real-time imaging module. The row-column addressing scheme is adopted for the transducer fabrication, which greatly reduces the number of active channels needed to acquire a 3-D volume. The array area of the transducer is 4.6mm by 4.6mm. The detailed description of the whole system can be found in our former work. Four kinds of tests were carried out to evaluate the imaging performances, including the penetration depth range, axial and lateral resolutions, positioning accuracy and 3-D imaging frame rate. The strong reflection metal objects in water were selected for imaging due to the low signal-to-noise ratio of the transducer. The experimental results showed that the imaging penetration depth range was from 1.7cm to 6.2cm, the axial and lateral resolutions were 0.32mm and 1.37mm respectively, the imaging speed was 27 frames per second and
the positioning accuracy was 26%. The distances between the transducer and the test object, the thickness of aluminum and the seam width of the aluminum sheet used to test lateral resolution were all measured by a calibrated micrometer.

9790-67, Session PS7

A new post-phase rotation based dynamic receive beamforming architecture for smartphone-based wireless ultrasound imaging

Minsuk Park, Jeeun Kang, Gunho Lee, Mln Kim, Tai Kyong Song, Sogang Univ. (Korea, Republic of)

In this paper, an effective post-phase rotation-based dynamic receive beamforming (PRBF-POST) method is presented for wireless US imaging device integrating US probe system and commercial smart device (e.g., smartphone, tablet, etc.). In conventional, the frame rate of conventional PRBF (PRBF-CON) method suffers from the large amount of calculations for the bifurcated processing paths of in-phase and quadrature signal components as the number of channel increase. Otherwise, the proposed PRBF-POST method can preserve the frame rate regardless of the number of channels by firstly aggregating the baseband IQ data along the channels whose phase quantization levels are identical ahead of phase rotation and summation procedures on a smart device. To evaluate the performance of the proposed PRBF-POST method, the point-spread functions of PRBF-CON and PRBF-POST methods were compared each other. Also, the frame rate of each PRBF method was measured 20-times to calculate the average frame rate and its standard deviation. As a result, the PRBF-CON and PRBF-POST methods indicates identical beamforming performance in the Field-II simulation (correlation coefficient = 1). Also, the proposed PRBF-POST method indicates the consistent frame rate for varying number of channels (i.e., 44.25, 44.32, and 44.35 fps for 16, 64, and 128 channels, respectively), while the PRBF-CON method shows the decrease of frame rate as the number of channel increase (39.73, 13.19, and 3.8 fps). These results indicate that the proposed PRBF-POST method can be more advantageous for implementing the wireless US imaging system than the PRBF-CON method.

9790-68, Session PS7

High-resolution synthetic-aperture ultrasound imaging with minimum variance beamforming and spiking deconvolution

Junseob Shin, Lianjie Huang, Los Alamos National Lab. (United States)

Minimum variance beamforming (MVBF) is an adaptive beamforming technique. It aims to improve the lateral resolution by computing and applying signal-dependent apodization rather than predetermined apodization as typically done in conventional delay-and-sum (DAS) beamforming. Although studies have shown that the improvement in lateral resolution associated with MVBF is significant, the axial resolution remains unaffected. In this work, we combine MVBF and spiking deconvolution to improve both lateral and axial resolutions in synthetic-aperture ultrasound imaging. We implement our new method and evaluate its performance using Field II simulation and experimental datasets from a tissue mimicking phantom. Our results show that the new method yields improved axial and lateral resolutions as well as image contrast.

9790-69, Session PS7

In vivo visualization of robotically implemented Synthetic-Tracked Aperture UltraSound (STrAtUS) imaging system using curvilinear array

Haichong K. Zhang, Fereshteh Aalamifar, Johns Hopkins Univ. (United States); Gregg E. Trahey, Duke Univ. (United States); Emad M. Doctor, Johns Hopkins Univ. (United States)

Synthetic aperture is a technique to utilize a wide aperture for transmit and receive focusing. The limitation of synthetic aperture is that the maximum available aperture size is limited by the physical size of ultrasound probe. In addition, a wide aperture probe is not realistic to be used because each element has its angle sensitivity limitation. We propose Synthetic-Tracked Aperture UltraSound (STrAtUS) imaging system to address those issues. In this approach, we extend the idea of synthetic aperture to the outsize the array width. While the ultrasound probe is moved using a robot arm, the position is tracked real-time, and data from each pose will be synthesized to construct a high resolution image. In previous studies, we have demonstrated the feasibility of the system through phantom experiments. However, it is needed to test the system to the in-vivo target to investigate the tolerance in presence of various factors such as motion artifacts. In this work, we build a StAtUS imaging system with continuous data collection capability considering the practical clinical implementation. A curvilinear array is used instead of a linear array to utilize the capability of capturing wider angle. We scanned a human wrist submerged in the water tank, and the image quality improved as the aperture extended. The result indicates the practical feasibility of StAtUS imaging system, and the technique can be potentially applied to the wide range of human body.

9790-70, Session PS7

Hadamard-encoded synthetic transmit aperture imaging with a reduced number of receiving channels

Ying Li, Ping Gong, Michael C. Kolios, Yuan Xu, Ryerson Univ. (Canada)

Synthetic transmit aperture imaging (STA) has been widely studied in ultrasound imaging. When the number of receiving channels is large, the system cost will be high due to the receive electronics required for each element. Therefore, it is desirable to reduce the number of receiving channels while keeping a large number of transmit-channels to ensure adequate SNR. However, a reduced number of receiving channels in the standard STA will lead to reduced image quality. We propose a novel technique designed to maintain image quality with a reduced number of receiving channels. In standard STA, the signal received at i-th receiver and transmitted by j-th transmitter is equivalent to the signal received at the j-th receiver and transmitted by the i-th transmitter ($S_{ij} = S_{ji}$). To lower the number of receiving channels, we utilized this symmetry property of the signal with the encoded measurement data to solve for the equivalent data in traditional STA. The Hadamard matrix was used to encode this transmission process. The receiving elements were also combined to reduce the number of receiving channels. We compared the different ways to combine the receivers in terms of the ultrasound image quality. In the decoding process, we applied the pseudoinverse to decode for the equivalent data in the traditional STA. After decoding, ultrasound images were reconstructed using the standard image reconstruction method in STA.

The image quality using the new method was comparable with the standard STA for the tested phantom. The reconstruction results showed better contrast compared to the regular-selected sparse array.
Higher-frame-rate ultrasound imaging with reduced cross-talk by combining a synthetic aperture and spatial coded excitation

Chizue Ishihara, Teiichiro Ikeda, Hiroshi Masuzawa, Hitachi, Ltd. (Japan)

In recent clinical practice of ultrasound imaging, the importance of advanced applications such as three-dimensional imaging is steadily growing. These advanced ultrasound imaging techniques must acquire more scan data while attaining a frame rate of B-mode image equivalent to that of conventional imaging. Thus, to support both the advanced applications and high-definition images, it will be necessary to develop a B-mode imaging technique that achieves higher-frame-rate while maintaining high image quality. Simultaneous multiple transmission (SMT) is one way to increase frame rate, since it can construct multiple scan lines simultaneously. However, SMT has an inherent issue, called “cross-talk artifacts,” which appear between the multiple transmitted pulses. Accordingly, a novel method for increasing frame rate while significantly reducing the cross-talk artifacts affecting SMT is proposed. This method utilizes a synthetic aperture and spatial coded pulses to reduce the cross-talk. In particular, two coded transmission beams are simultaneously excited during beam steering in lateral direction. To reduce the cross-talk, a decoding operation is carried out by using receive signals beamformed in a region where the excited beam and the previous excited beam overlap. Finally, cross-talk is further reduced by coherently synthesizing the cross-talk-reduced receive signals. The method was evaluated by using a simulated phantom image under the assumption of imaging with a sector probe. The evaluation results confirm that the method achieves twice the frame rate while perfectly maintaining image resolution (100.1%) and reducing the cross-talk artifact from -37 dB to less than -54 dB.
Current challenges in digital pathology
(Keynote Presentation)

Kenneth J. Bloom, Clarient, Inc. (United States)

Digital Pathology is an enabling technology that holds the promise to transform anatomic pathology into an objective science, but major hurdles still exist. The regulatory landscape of WSI (whole slide imaging) is still evolving. In the United States, the US Food and Drug Administration has indicated that WSI systems are class III medical devices and thus will require premarket approval. Several vendors are in the process of obtaining approval to use these systems for primary diagnosis, but the value of digital pathology extends far beyond replacing the microscope. Once untethered from the microscope pathologists will be able to utilize the full power of the next generation of tools and techniques waiting to be developed. Multiplexing, machine learning, quantitative image analysis, interpreting spatial relationships and integration with other large data sets are but a few of the applications waiting to be perfected. I will discuss the current challenges in digital pathology, where and how I believe basic research will be most effective and future trends in pathology.

Automated robust registration of grossly misregistered whole-slide images with varying stains

Geert J. S. Litjens, Hamamatsu TIGA Ctr. (Germany) and Steinbeis-Transferzentrum Medizinische Systembiologie (Germany); Kai Safferling, Niels Grabe, Hamamatsu TIGA Ctr. (Germany) and Nationales Centrum für Tumorerkrankungen Heidelberg (Germany) and Steinbeis-Transferzentrum Medizinische Systembiologie (Germany)

Cancer diagnosis and pharmaceutical research increasingly depend on the accurate quantification of cancer biomarkers. Identification of biomarkers is usually performed through immunohistochemical staining of cancer sections on glass slides. However, combination of multiple biomarkers from a wide variety of immunohistochemically stained slides is a tedious process in traditional histopathology due to the switching of glass slides and re-identification of regions of interest by pathologists. Digital pathology now allows us to apply image registration algorithms to digitized whole slides to align the differing immunohistochemical stains automatically. However, registration algorithms need to be robust to changes in color due to differing stains and severe changes in tissue content between slides. In this work we developed a robust registration methodology to allow for fast coarse alignment of multiple immunohistochemical stains to the base hematoxylin and eosin stained image. We applied HSD color model conversion to obtain a less stain color dependent representation of the whole-slide images. Subsequently, optical density thresholding and connected component analysis were used to identify the relevant regions for registration. Template matching using normalized mutual information was applied to provide initial translation and rotation parameters, after which a cost function-driven affine registration was performed. The algorithm was validated using 40 slides from 10 prostate cancer patients, with landmark registration error as a metric. Median landmark registration error was around 180 microns, which indicates performance is adequate for practical application. None of the registrations failed, indicating the robustness of the algorithm.

Model coupling for predicting a developmental patterning process

Bülent Yener, Rensselaer Polytechnic Institute (United States); Nimit Dhulekar, The MathWorks, Inc. (United States); Basak Oztag, American Science and Engineering, Inc. (United States)

Physics-based-theoretical models have been used to predict developmental patterning processes such as branching morphogenesis for over half a century. While such techniques are quite successful in understanding the patterning processes in organs such as the lung and the kidney, they are unable to accurately model the processes in other organs such as the submandibular salivary gland. One possible reason is the detachment of these models from data that describe the underlying biological process. This hypothesis coupled with the increasing availability of high quality data has made discrete, data-driven models attractive alternatives. These models are based on extracting features from data to describe the patterns and their time evolving multivariate statistics. These discrete models have low computational complexity and comparable or better accuracy than the continuous models.

This paper presents a case study for coupling continuous-physics-based and discrete-empirical-models to address the prediction of cleft formation during the early stages of branching morphogenesis in mouse submandibular salivary glands (SMG). Given a time-lapse movie of a growing SMG, first we build a descriptive model that captures the underlying biological process and quantifies this ground truth. Tissue-scale (global) morphological features are used to characterize the biological ground truth. Second, we formulate a predictive model using the level-set method that simulates branching morphogenesis. This model successfully predicts the topological evolution, however, it is blind to the cellular organization, and cell-to-cell interactions occurring inside a gland; information that is available in the image data. Our primary objective via this study is to couple the continuous level set model with a discrete graph theory model that captures the cellular organization but ignores the forces that determine the evolution of the gland surface, i.e. formation of clefts and buds. We compared the prediction accuracy of our model to an on-lattice Monte-Carlo simulation model which has been used extensively for modeling morphogenesis and organogenesis. The results demonstrate that the coupled model yields comparable simulations of gland growth to that of the Monte-Carlo simulation model with a significantly lower computational complexity.

Classification of breast cancer stroma as a tool for prognosis

Sara Reis, Univ. College London (United Kingdom); Patrycja Gazinska, King’s College London (United Kingdom); John H. Hipwell, Thomy Mertzamidou, Univ. College London (United Kingdom); Kalnisha Naidoo, The Institute of Cancer Research (United Kingdom); Sarah Pinder, King’s College London (United Kingdom); David J. Hawkes, Univ. College London (United Kingdom)

Routine pathologic reporting of invasive breast cancer (IBC) includes the assessment of histological grade, which is a composite, semi-quantitative score of tubule formation, nuclear pleomorphism, mitosis and nucleic activity in the malignant epithelium. It has been shown that the tumour microenvironment plays a crucial role in regulating tumour progression by a number of different mechanisms, such as the remodeling of collagen fibers in tumour-associated stroma. It is still unclear, however, if these stromal...
changes are of benefit to the host or the tumour. We hypothesise that stromal maturity is an important reflection of tumor biology, and thus can be used to predict prognosis. Furthermore, these stromal features could help us interpret the radiological signal and relate it to changes that occur at the microscopic level. Variations in the stroma may cause detectable changes in water mobility (diffusion MRI) and mechanical properties (Shear-Wave Elastography). This in turn could enhance the ability of non-invasive pre-operative imaging to predict progression and treatment outcome.

The aim of this study is to develop a texture analysis methodology, which will automatically classify stromal regions from images of hematoxylin and eosin-stained (H&E) sections into two categories: mature and immature. The hypothesis is that stromal maturity could be used as a predictor of survival and also as a means to better understand the relationship between the radiological imaging signal and the underlying tissue microstructure. We present our initial results for 103 regions-of-interest from a dataset of 39 patients with invasive breast cancer.

9791-5, Session 2

**Automated tubule nuclei quantification on ER+ breast cancer images: Comparison with Oncotype DX risk categories**

David E. Romo-Bucheli, Univ. Nacional de Colombia (Colombia); Andrew Janowczyk, Case Western Reserve Univ. (United States); Eduardo Romero Castro, Univ. Nacional de Colombia (Colombia); Hannah L. Gilmore M.D., Univ. Hospitals Case Medical Ctr. (United States); Anant Madabhushi, Case Western Reserve Univ. (United States)

Early stage estrogen receptor positive (ER+) breast cancer (BCa) treatment is based on the presumed aggressiveness and likelihood of recurrence. Currently, genetic assays such as Oncotype DX (ODX) are used to assign cancer recurrence risk scores for informing clinical treatment decisions (i.e., hormonal therapy with/without adjuvant chemotherapy). Unfortunately, these genetic tests are expensive, tissue destructive, and require off-site processing. As such, alternative methods for predicting BCa recurrence risk, leveraging existing histologic workflows, are highly desirable. Previous work has shown that high risk ODX scores are correlated with high scores derived from BCa grading schemes. A major component of these schemes, and the focus of this work, is the quantification of tubule formation. We present a deep learning based algorithm for discriminating between tubule and non-tubule nuclei in BCa whole slide images (WSI). The performance of our approach was evaluated on a set of 61 high power fields. Using a 5-fold cross-validation, the mean precision and recall measures were 0.72 and 0.56 respectively. Next, on a selection of at most 50 high power fields from each of 54 WSI, we computed the ratio of the number of tubule to non-tubule nuclei per image. Our results show that for the low risk ODX category, our mean tubule nuclei ratio was significantly larger than in high ODX samples ($p = 0.042$), indicating that our approach has discriminating potential between these two classes.

9791-6, Session 2

**Computer-assisted bladder cancer grading: α-shapes for color space decomposition**

Muhammad Khalid Khan Niazi, Anil V. Parwani M.D., The Ohio State Univ. Medical Ctr. (United States); Metin N. Gurcan, The Ohio State Univ. Wexner Medical Ctr. (United States)

According to American Cancer Society, we are expecting around 74,000 new cases of bladder cancer during 2015 in the US. To facilitate the bladder cancer diagnosis, we present an automatic method to differentiate carcinoma in situ (CIS) from normal/reactive cases from hematoxylin and eosin (H&E) stained images of bladder. The method automatically determines the color deconvolution matrix by utilizing the α-shapes of the color distribution in the RGB color space. Then, variations in the boundary of transitional epithelium are quantified, and sizes of nuclei in the transitional epithelium are measured. We also compute the surrogate to nuclear to cytoplasmic ratio by computing the shortest distance between the boundary of transitional epithelium and nuclei borders. Nuclei homogeneity is measured by computing the kurtosis of the nuclei size histogram. The results show that 30 (88.2%) out of 34 images were correctly classified by the proposed method, indicating that these novel features are good markers to differentiate CIS from normal/reactive bladder.

9791-7, Session 2

**Multi-instance multi-label learning for whole slide breast histopathology**

Caner Mercan, Bilkent Univ. (Turkey); Ezgi Mercan, Univ. of Washington (United States); Selim Aksoy, Bilkent Univ. (Turkey); Linda G. Shapiro, Univ. of Washington (United States); Donald L. Weaver, The Univ. of Vermont (United States); Joann G. Elmore, Univ. of Washington (United States)

Digitization of full biopsy slides using the whole slide imaging technology has provided new opportunities for understanding the diagnostic process of pathologists and developing more accurate computer aided diagnosis systems. However, the whole slide images also provide two new challenges to image analysis algorithms. The first one is the need for simultaneous localization and classification of malignant areas in these large images as different parts of the image may have different levels of diagnostic relevance. The second challenge is the uncertainty regarding the correspondence between the particular image areas and the diagnostic labels typically provided by the pathologists at the slide level. In this paper, we exploit a data set that consists of recorded actions of pathologists while they were interpreting whole slide images of breast biopsies to find solutions to these challenges. First, we extract candidate regions of interest (ROI) from the logs of pathologists’ image screenings based on different actions corresponding to zoom events, panning motions, and fixations. Then, we model these ROIs using color and texture features. Next, we represent each slide as a bag of instances corresponding to the collection of candidate ROIs and a set of labels extracted from the forms that the pathologists filled according to what they saw during their screenings. Finally, we build multi-class slide-level and ROI-level classifiers using five different multi-instance multi-label learning algorithms, and evaluate their performances under different scenarios corresponding to screenings by multiple pathologists. Preliminary experiments showed promising results regarding the localization of diagnostically important ROIs and classification of whole slides.

9791-8, Session 2

**Intraoperative neuropathology of glioma recurrence: cell detection and classification**

Fazly S. Abas, The Ohio State Univ. (United States) and Multimedia Univ. (Malaysia); Hamza N. Gokozan, Univ. Hospitals of Cleveland (United States); Behiye Goksel, Jose J. Otero, Metin N. Gurcan, The Ohio State Univ. (United States)

Intraoperative neuropathology of glioma recurrence represents significant visual challenges to pathologists as they carry significant clinical implications. For example, rendering a diagnosis of recurrent glioma can help the surgeon decide to perform more aggressive resection if surgically appropriate. In addition, the success of recent clinical trials for intraoperative
administration of therapies, such as inoculation with oncolytic viruses, may suggest that refinement of the intraoperative diagnosis during neurosurgery is an up and coming need of pathologists. Typically, these diagnoses require rapid/STAT processing lasting only 20-30 minutes from receipt from neurosurgery. Thus, only dyes, such as hematoxylin and eosin (H&E), can be implemented in this time frame. The visual challenge lies in the fact that these patients have undergone chemotherapy and radiation, both of which induce cytological atypia in astrocytes, and pathologists are unable to implement helpful biomarkers in their diagnoses. Therefore, aid in distinction between astrocytes cytologically atypical due to treatment versus infiltrating recurrent neoplastic astrocytes is needed. A classification of neoplastic versus non-neoplastic astrocytes is good starting point. This paper presents a method to detect cells in H&E stained digitized slides of intraoperative cytologic preparations. This is done with the long term goal of providing a better neuropathological computer-aided consultation via characterization of cells into reactive gliosis versus recurrent glioma. The method uses a combination of the 'hue' component of the HSV color space and 'luminance' component of the CIE L*a*b* color space to create an enhanced image that suppresses the background while revealing cells on an image. A composite image is formed based on the morphological closing of the hue-luminance combined image. Using a fusion of both geometrical and textural feature extraction (based on Discrete Wavelet Frames), it is shown that cells can be classified into neoplastic and non-neoplastic cells. The proposed method demonstrates a strong consensus between the computer’s cell detection markings with those of the pathologists’. Experiments on 48 images from 6 patients resulted in F1 score as high as 85.5%, 86.6% and 85.4% for Reader 1, Reader 2 and the reader consensus, respectively. Cell classification results revealed a high classification rate (94% and 93.4%) for both Reader 1 and Reader 2 using the binary classification tree while support vector machine classifier recorded true positive rates of 87.3% and 86.2%, respectively for these two readers.

9791-9, Session 2

Preliminary evaluation of a fully-automated quantitative framework for characterizing general breast tissue histology via color histogram and color texture analysis

Brad M. Keller, Univ. of Pennsylvania School of Medicine (United States); Aimilia Gastounioti, Univ. of Pennsylvania (United States); Rebecca C. Batiste, Despina Kontos, Michael D. Feldman, Univ. of Pennsylvania School of Medicine (United States)

Visual characterization of histologic specimens is known to suffer from intra- and inter-observer variability. To help address this, we developed an automated framework for characterizing digitized histology specimens based on a novel application of color histogram and color texture analysis. We perform a preliminary evaluation of this framework using a set of 73 trichrome-stained, digitized slides of normal breast tissue which were visually assessed by an expert pathologist in terms of the percentage of collagenous stroma, stromal collagen density, duct-lobular unit density and the presence of elastosis. For each slide, our algorithm automatically segments the tissue region based on the lightness channel in CIE-LAB colorspace. Within each tissue region, a color histogram feature vector is extracted using a common color palette for trichrome images generated with a previously described method. Then, using a whole-slide, lattice-based methodology, color texture maps are generated using a set of color co-occurrence matrix statistics: contrast, correlation, energy and entropy. The extracted features sets are compared to the visually assessed tissue characteristics. Overall, the extracted texture features have high correlations to both the percentage of collagenous stroma (r=0.95, p<0.001) and duct-lobular unit density (r=0.71, p<0.001) seen in the tissue samples, and several individual features were associated with either collagen density and/or the presence of elastosis (p=0.05). This suggests that the proposed framework has promise as a means to quantitatively extract descriptors reflecting tissue-level characteristics and thus could be useful in detecting and characterizing histological processes in digitized histology specimens.

9791-10, Session 3

Hotspot detection in pancreatic neuroendocrine tumors: Density approximation by $\alpha$-shape maps

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Accurate hotspot detection is crucial for grading of neuroendocrine tumors of the digestive system. At the moment, most pathologists manually identify the hotspots, a practice which is tedious and irreproducible. To better help pathologists, we present an automatic method to detect all potential hotspots in neuroendocrine tumors of the digestive system. The method starts by segmenting all Ki-67 positive nuclei by utilizing entropy based thresholding, followed by detection of centroids for all Ki-67 positive nuclei. Approximate geodesic distance among the nuclei is approximated by these centroids. Based on the geodesic distance, we compute two maps: an amoeba map and a weighted amoeba map, which are later combined to generate the heatmap. The segmentation of heat map results in the hotspots. The method was trained using three whole slide images of neuroendocrine tumors. The testing was performed on a set of 9 whole slide images which was evaluated by two expert pathologists. The method obtained an accuracy of 92.6%. The results show that $\alpha$-shape maps are good representative of how humans define hotspots.

9791-11, Session 3

Adaptive local thresholding for robust nucleus segmentation using shape prior

Shawn Wang, Chukka Srinivas, Christophe Chefd’huiel, Ventana Medical Systems, Inc. (United States)

This paper describes a novel local thresholding method for nucleus segmentation. First, a Canny type edge detection method is used for initial edge detection, which, although quite robust, still produces a fair amount of noise edge segments. Then, tensor voting is applied on the initial edge pixels with a non-symmetric tensor voting field, which is designed to encode the prior information about nucleus size and shape, and intensity spatial distribution. Tensor analysis is then performed to generate the saliency image and further the saliency edge. Next, the whole image is divide into blocks, foreground pixels and background pixels are sampled for each saliency edge pixel along the gradient direction, based on which saliency weighted foreground histogram and and background histogram are created. Finally, the two histograms are used to generate a threshold for the image block by minimizing the pixel classification error, which is then used to generate the threshold for each pixel through interpolation. The effective use of prior information, combined with several robust techniques, leads to a far more robust foreground detection and nucleus segmentation, which has been demonstrated via tests.

9791-12, Session 3

Non-uniform object counting method in large-format pyramid images applied to CD31 vessel counting in whole-mount digital pathology sections

Mayan Murray, Melissa L. Hill, Kela Liu, James G. Mainprize, Sunnybrook Research Institute (Canada); Martin J. Yaffe, Sunnybrook Research Institute (Canada) and Univ. of Toronto (Canada)
Whole-mount pathology imaging has the potential to revolutionize clinical practice by preserving context lost when tissue is cut to fit onto conventional slides. Whole-mount digital images range from 4GB to greater than 50GB, which makes concurrent processing infeasible. Block-processing is a method commonly used to divide the image into smaller blocks and process them individually. This approach is useful for certain tasks, but leads to over-counting objects which lie on the seams between blocks. This issue is exaggerated as the block size decreases. In this work we apply a novel technique to enumerate vessels, a clinical task that would benefit from automation in whole-mount images.

Whole-mount sections of rabbit VX2 tumours were digitized. A color threshold was applied to segment the brown CD31-DAB stained vessels. Two distinct phases of block-processing applied this vessel enumeration to the entire whole-mount image. The first (whole-processing) phase used a basic grid and only counted objects that did not intersect the block’s borders. The second (seam-processing) phase used a shifted grid to ensure that all blocks captured the block-seam regions from the original grid. Only objects touching this seam-intersection were counted.

For validation, segmented vessels were randomly embedded into a whole-mount sized image. The technique was tested on the image using 24 different block-widths. Results indicated that the error reaches a minimum at a block-width equal to the maximum vessel length, with no improvement as the block-width increases further.

Object-density maps showed very good correlation between the vessel-dense regions and the pathologist outlined tumour regions.

**9791-13, Session 3**

**Segmentation of vessel structures in serial whole slide sections using region-based context features**

Michael Schwier, Horst K. Hahn, Fraunhofer MEVIS (Germany); Uta Dahmen, Friedrich-Schiller-Univ. Jena (Germany); Olaf Dirsch, Chemnitz Central Hospital (Germany)

We present a method for the automatic segmentation of vascular structures in stacks of serial sections. It was initially motivated within the Virtual Liver Network research project that aims at creating a multi-scale virtual model of the liver. For this the vascular systems of several murine livers under different conditions need to be analyzed. To get high detailed datasets, stacks of serial sections of the whole organs are prepared. Due to the huge amount of image data an automatic approach for segmenting the vessels is required.

After registering the slides with an established method we use a set of Random Forest classifiers to distinguish vessels from tissue. Instead of a pixel-wise approach we perform the classification on small regions. This allows us to use more meaningful features. Besides basic intensity and texture features we introduce the concept of context features, which allow the classifiers to also consider the neighborhood of a region. Classification is performed in two stages. In the second stage the previous classification result of a region and its neighbors is used to refine the decision for a particular region.

The context features and two stage classification process make our method very successful. It can handle different stainings and also detect vessels in which residue like blood cells remained. The specificity on all tested stainings reaches 99% for pure tissue. Only in the direct vicinity of vessels the specificity goes down to 95% - 88%. Depending on the staining we reach sensitivity rates between 93% and 98%.

**9791-14, Session 3**

**Automated quantification of glomeruli features in renal pathology**

Brandon Ginley, Univ. at Buffalo (United States); Piyush Tripathi, Feng Chen, Washington Univ. in St. Louis (United States); Edwin Anand, John E Tomaszewski M.D., Pinaki Sarder, Univ. at Buffalo (United States)

Glomeruli are small intertwined groups of capillaries located at the beginning of a nephron. They filter blood during urine formation. A glomerulus of a patient with nephrotic syndrome often depicts variable sized glomerular volume, increased mesangial cellularity, and a change in lumen content compared to the glomerulus from a healthy patient. Existing clinical practice for quantifying these features from needle biopsy samples of renal tissues relies on time-intensive manual examination of these features, and such procedure might increase time till diagnosis and/or lead to reduced precision of the diagnostic process. To address this issue, we have developed an automated method to quantitatively estimate the pathologically relevant glomeruli features from hematoxylin and eosin (H&E) stained renal biopsy images. Our method first automatically extracts the glomeruli using information from the red component intensity of the H&E image. From each glomerulus image, we then quantify the Bowman’s space, glomerular tuft, and lumenal areas using the green component intensity image, and the nuclei density using the red component intensity image. To perform the segmentation, we use a variety of morphological processing operations. Average computation time of feature extraction for a typical H&E image, containing ~30 glomeruli and imaged by a digital whole-slide scanner at 40X magnification, is ~8 sec using an Intel(R) Core(TM) i7-4790 CPU. Using images from murine renal tissue samples, automatic computation of the features was reproducibly demonstrated for 3 sets of such images and for >350 glomeruli images. The proposed method holds immense potential to enhance early clinical determination of nephrotic syndrome and aiding in making correct treatment decisions.

**9791-15, Session 4**

**Differentiation of arterioles from venules in mouse histology images using machine learning**

Sachi Elkerton, Yiwen Xu, J. Geoffrey Pickering, Aaron D. Ward, Western Univ. (Canada)

Analysis and morphological comparison of arteriolar and venular networks are essential to our understanding of multiple diseases affecting every organ system. We have developed and evaluated the first fully automatic software system for differentiation of arterioles from venules on high-resolution digital histology images of the mouse hind limb immunostained for smooth muscle ?-actin. Classifiers trained on texture and morphologic features by supervised machine learning provided excellent classification accuracy for differentiation of arterioles and venules, achieving an area under the receiver operating characteristic curve of 0.89 and balanced false-positive and false-negative rates. Feature selection was consistent across cross-validation iterations, and a small set of three features was required to achieve the reported performance, suggesting good generalizability of the system. This system eliminates the need for laborious manual classification of the hundreds of microvessels occurring in a typical sample, and paves the way for high-throughput analysis the arteriolar and venular networks in the mouse.

**9791-16, Session 4**

**Lymphoma diagnosis in histopathology using a multi-stage visual learning approach**

Noel Codella, IBM Thomas J. Watson Research Ctr. (United States); Mehdi Moradi, IBM Research - Almaden (United States); Matt Matasar, Memorial Sloan-Kettering Cancer Ctr. (United States); Tanveer F. Syeda-Mahmood, IBM Research - Almaden (United States); John R. Smith, IBM
A structure-based approach for colon gland segmentation in digital pathology

Bassem Ben Cheikh, UPMC Sorbonne Univ. (France); Philippe Bertheau, Univ. Paris Diderot (France) and Hôpital Saint-Louis (France); Daniel Racoceanu, UPMC Sorbonne Univ. (France) and INSERM (France)

The morphology of intestinal glands is an important and significant indicator of the level of the severity of an inflammatory bowel disease and has also been used routinely by pathologists to evaluate the malignancy and the prognosis of colorectal cancers such as adenocarcinomas. The extraction of meaningful features describing the morphology of glands relies on an accurate segmentation method. In this paper, we propose an advanced technique based on mathematical morphology that characterizes the spatial positioning of cells for intestinal gland segmentation in histopathological images. According to their composition, glands can be divided into two categories: hollow glands and closed glands. Hollow glands are composed of lumen and/or goblet cells’ cytoplasm, or filled with abscess in some advanced stages of the disease. While closed glands are composed of bunches of cells clustered together and can also be filled with necrotic debris. Given this scheme, an efficient characterization of the spatial distribution of cells is sufficient to carry out the segmentation. In this approach, hollow glands are first identified as regions empty of nuclei and surrounded by thick layers of epithelial cells, then closed glands are identified by detecting populous regions. First, cell nuclei are identified by color classification, after color normalization. Then, advanced morphological operators are applied to nuclei objects in order to interpret their spatial distribution to identify candidates for glands’ central regions and epithelial layers, that are combined later to extract the glandular structures. The method was tested on two different datasets composed of 81 images and containing 2079 intestinal glands in total.

Miniature objective lens for array microscopy digital pathology: evaluation and improvement

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A miniature objective designed for digital detection of Mycobacterium tuberculosis (MTB) was evaluated for diagnostic accuracy. The objective was designed for array microscopy, but fabricated and evaluated at this stage of development as a single objective. The counts and diagnoses of patient samples were directly compared for digital detection and standard microscopy. The results were found to be correlated and highly concordant. This evaluation led to insights in the role played by key system parameters. We found that some of the more demanding design parameters could be relaxed in order to improve other qualities of the optical system, namely higher signal to noise ratio, longer working distance, and longer depth of focus. These insights and a new optical design taking advantage of these insights are presented.

1. INTRODUCTION

Previous work has shown that a high NA microscope objective can be designed and fabricated using all-plastic elements built with self-aligning material. This objective was built as a test objective with a prescription optimized for an array microscope to be used for digital detection of Mycobacterium tuberculosis (MTB) according to minimum requirements for sputum smear microscopy set out by the World Health Organization (WHO) [1]. The objective was evaluated by comparing counts and diagnoses of clinical samples using standard fluorescence sputum smear microscopy (FSSM) and digital fluorescent images obtained with this microscope objective. The results were correlated and highly concordant, which shows that this approach to detection of MTB [2], however there were some drawbacks to the objective design. When tested with clinical samples, the miniature objective was found to have a lower than desirable signal to noise ration, leading to lengthy integration times. The array would also fit into a more compact system if the back working distance could be shortened. Finally, the ease of use of the instrument would also be improved with a longer depth of focus and front working distance. The evaluation of this miniature objective revealed some changes that could be made to the lens design requirements in order to improve on all three of these design parameters.

2. REVIEW OF LENS DESIGN PARAMETERS

As described in earlier work, the system parameters were determined according to WHO recommendations for sputum smear microscopy, the best available sensors at the time the system was designed, available plastic material, prior research on fluorescence sputum smear microscopy [1]. The WHO recommendations were supplemented with analysis of first order optical properties. Nyquist sampling determined system magnification, and a complex relationship between clear aperture diameter and total area imaged, shown in Figure 1, guided the choice of clear aperture, lens pitch, and field of view. Reasonable manufacturing limitations were also considered when determining the proper constraints of the lens design. The complete set of lens design parameters are shown in Table 2. In addition to the parameters listed in this table, the design was driven to be diffraction limited (Strehl ratio of 0.8 or higher) across the entire field of view.

Since evaluating the test lens, the magnification and the diffraction limited performance requirement have been found to be of less importance than first thought. They do, however, have a substantial impact on the lens signal to noise ratio, working distances, and depth of focus.

3. IMPROVING LENS DESIGN PARAMETERS

One of the improvements sought can be addressed directly by looking at the magnification. The photon flux at the sensor is inversely proportional to M2. In the course of preparing digital images for examination in our prior work, we found that the images needed to be down-sampled by a factor of 4 in order to keep the file sizes manageable for desktop image viewing software. This means that a magnification of 16x could be used instead of a magnification of 65x. Decreasing magnification by a factor of 4 would increase photon flux, and therefore signal to noise, by a factor of 16. The magnification is a also major factor in the relationship between clear aperture diameter and field of view. So reducing this magnification can open up wide new areas in the design space, which can enable longer working distances.

The other system parameter that was found to be of less importance than first thought was the image quality of the lens. We can draw this conclusion from the fact that the images were anti-aliased (i.e. - low-pass filtered) prior
to down-sampling. Some image quality is also lost by imaging with Acridine, peak excitation 647 nm, instead of the design wavelength of 516 nm. By determining the effect of these operations on the contrast of the image, we can find a less restrictive criterion for image contrast at the reduced magnification of 16x. With the contrast requirement lowered, we can trade excess contrast for depth of focus.

4. RESULTS
The results that will be shown in this paper are the effective contrast obtained during anti-aliasing and down-sampling of the 63x images obtained during evaluation of the miniature objective. The relationship between field of view, lens pitch / clear aperture, and total area imaged will be recalculated for a smaller magnification. Based on this new analysis, a new combination of field of view and clear aperture will be chosen. A new design will be presented for a miniature objective meeting these specifications. It’s theoretical performance will be compared to the original design.

5. CONCLUSIONS
A miniature objective has been tested and found to be a suitable lens for digital FSSM, enabling diagnostic results that are accurate and highly concordant with standard FSSM. In the course of evaluating this lens, it was found that key system design parameters can be relaxed. These relaxed requirements will open up the design space to solutions that will have a higher signal to noise ratio, a longer working distance, and a longer depth of focus.

6. REFERENCES

9791-20, Session 4
Quantitative diagnosis of tongue cancer from histological images in an animal model
Guolan Lu, Xulei Qin, Dongsheng Wang, Susan Muller M.D., Hongzheng Zhang, Amy Y. Chen, Georgia Z. Chen, Baowei Fei, Emory Univ. (United States)

We present a computer aided approach for tongue cancer diagnosis using histological images. A chemically-induced oral cancer mouse model was used to capture the progression of oral lesions. Tongue tissue dissected from euthanized mice was sent for histological processing. Representative areas of hematoxylin and eosin (H&E) stained tissue from tongue sections were captured for classification of tumor and non-tumor classes. The image set used in this paper consisted of 214 color images (114 tumor and 100 normal tissue samples), and a total of 753 color, texture, morphometry and topology features were extracted from histological images. The combination of image features from epithelium tissue and its constituent nuclei and cytoplasm has improved the classification results. An average sensitivity of 96.5% and specificity of 82% from five-fold cross validation has been achieved for cancer diagnosis. The next step of this research is to apply this approach to human tissue and to aid in the diagnosis of tongue cancer.

9791-25, Session 4
Evaluating stability of histomorphometric features across scanner and staining variations: predicting biochemical recurrence from prostate cancer whole slide images
Patrick Leo, George Lee, Anant Madabhushi, Case Western Reserve Univ. (United States)

Quantitative histomorphometry (QH) is the process of computerized extraction of features from digitized slide images. Typically these features are used in machine learning classifiers to predict disease behavior and outcome. Successful robust classifiers require features that both discriminate between classes of interest and are stable across data from multiple sites. Feature stability may be compromised by variation in slide staining and scanning procedures. In this paper we present two new measures, Preparation-induced Instability Score (PI) and Latent Instability Score (LI), to quantify feature instability across and within datasets respectively. Dividing PI by LI gives a ratio for how often a feature is different between datasets from different sites versus what would be expected from random chance. Using this ratio we quantify feature vulnerability to preparation variation. Since our goal is to identify stable QH features we evaluate these features in a use case involving prostate cancer. Specifically we examine QH features which may predict biochemical recurrence from whole slide images. We present evidence from 80 patients across four sites that QH features can vary significantly. Using our method we found that five feature families (graph, shape, co-occurring gland tensors, gland sub-graphs, texture) were different between datasets in 19.3% to 55.6% of comparisons while the values expected due to random chance would be 4.3% to 4.4%. Our results appear to suggest that evaluation of QH features across multiple sites needs to be undertaken to assess robustness and class discriminability alone should not represent the benchmark for digital pathology feature selection.

9791-21, Session 5
Multi-scale learning based segmentation of glands in digital colorectal pathology images
Yi Gao, Stony Brook Univ. (United States); William Liu, Buckingham Browne & Nichols School (United States); Shipra Arjun, Liangjia Zhu, Vadim Ratner, Tahsin Kurc, Joel H. Saltz M.D., Allen R. Tannenbaum, Stony Brook Univ. (United States)

Digital histopathological images provide detailed spatial information of the tissue at micrometer resolution. Among the available contents in the pathology images, meso-scale information, such as the gland morphology, texture, and distribution, are useful diagnostic features. In this work, focusing on the colon-rectal cancer tissue samples, we propose a multi-scale learning based segmentation scheme for the glands in the colon-rectal digital pathology slides. The algorithm learns the gland and non-gland textures from a set of training images in various scales through a sparse dictionary representation. After the learning step, the dictionaries are used collectively to perform the classification and segmentation for the new image.

9791-22, Session 5
3D morphological measurement of whole slide histological vasculature reconstructions
Yiwen Xu, J. Geoffrey Pickering, The Univ. of Western
Properties of the microvasculature that contribute to tissue perfusion can be assessed using immunohistochemistry on 2D histology sections. However, the vasculature is inherently 3D and the ability to measure and visualize the vessel wall components in 3D will aid in detecting focal pathologies. Our objectives were (1) to develop a method for 3D measurement and visualization of microvasculature in 3D, (2) to compare the normal and regenerated post-ischemia mouse hind limb microvasculature, and (3) to compare the 2D and 3D vessel morphology measures. Vessels were stained for smooth muscle using 3,3'-Diaminobenzidine (DAB) immunostain for both normal (n = 6 mice) and regenerated vasculature (n = 5 mice). 2D vessel segmentations were reconstructed into 3D using landmark based registration. No substantial bias was found in the 2D measurements relative to 3D, but larger differences were observed for individual vessels oriented non-orthogonally to the plane of sectioning. A larger value of area, perimeter, and vessel wall thickness was found in the normal vasculature as compared to the regenerated vasculature, for both the 2D and 3D measurements (p < 0.01). Aggregated 2D measurements are sufficient for identifying morphological differences between groups of mice; however, one must interpret individual 2D measurements with caution if the vessel centerline direction is unknown. Visualization of 3D measurements permits the detection of localized vessel morphology aberrations that are not revealed by 2D measurements. With vascular measure visualization methodologies in 3D, we are now capable of locating focal pathologies on a whole slide level.

High-resolution single pixel imaging: Pushing toward a real time hyperspectral imaging system

Joseph A. Peller, Didier Dréau, Faramarz Farahi, Susan R. Trammell, The Univ. of North Carolina at Charlotte (United States)

Pancreatic cancer is the fourth leading cause of cancer death in the United States. Most pancreatic cancer patients will die within the first year of diagnosis, and just 6% survive five years. Currently, surgery is the only treatment that offers a chance of cure for pancreatic cancer. However, accurately identifying tumor margins in real-time is a significant difficulty during surgery and contributes to the low 5-year survival rate. We are developing a single-pixel hyperspectral imaging system based on compressive sensing for real-time tumor margin detection to facilitate more effective removal of diseased tissue. Our spectral imaging system uses autofluorescent emission from NAD(P)H (475 nm) as well as reflectance spectroscopy near 550 nm as diagnostics for differentiating between healthy and diseased tissue. In this study, we demonstrate the ability of our imaging system to discriminate between healthy and damaged porcine skin tissue. Ex vivo porcine skin samples (n=5) were imaged using our hyperspectral system. The tissue samples were then thermally damaged using a 1850 nm Thulium fiber laser and re-imaged after laser irradiation. The damaged regions were clearly visible in the spectral imaging. Margins of the damaged regions were determined based on the NAD(P)H emission seen in the spectral images and reflectance spectroscopy. Margins determined via imaging are compared to those determined by histology and found to be in good agreement.
characterizing tumor vessel and cellular organization. We determine a multifunctional immunomarker cocktail in order to quantify morphological and physiological vasculature changes after tumor irradiation. Using Type-I/IV collagen, Rat Endothelial Cell Antibody Glucose 1R, antibodies, we assessed vessel length, diameter, tortuosity, density, blood volume, number of branching points, inter-vessel distances, spatial distribution maps and hypoxia regions. Ki67, pH2AX and DAPI staining allowed the measurements of cell density, necrosis index, proliferative index, radiation-induced DNA damages and micronuclei, infiltration index. To validate the algorithms, F98 glioma bearing rats were irradiated by synchrotron X-rays and culled at different times after exposure. The cross-analysis of these different histological morphometric parameters led to the description of the cellular and vascular biological events occurring after irradiation. The results showed that the radiation regimen induced a progressive remodelling of the vascular network, i.e., significant changes in vessel spatial distribution, increases in vessel diameter, tortuosity inter-distances and hypoxia regions. This was correlated with an increase of the size of the necrotic core and the proliferative surviving tumor cells were redistributed at the tumor margins where vessel density increased, mainly through co-optation of normal vessels. Whole slide measurements (X20 magnification) were performed in less than one hour on a standard PC allowing the quantification of more than 4.10^6 cells or vessels.

9791-27, Session PSWed

Deciphering protein signatures using color, morphological, and topological analysis of immunohistochemically stained human tissues

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Images of tissue specimens enable evidence-based study of disease susceptibility and stratification. Moreover, novel staining technologies empower the evidencing of molecular expression patterns by multicolor visualization, thus enabling personalized disease treatment and prevention. However, translating molecular expression imaging into direct health benefits has been slow. Two major factors contribute to that. At one side, disease susceptibility and progression is a complex, multifactorial molecular process. Diseases, such as cancer, exhibit cellular heterogeneity, impeding the differentiation between diverse stages or types of cell formations. On the other hand, the relative quantification of the stained tissue selected features is ambiguous, tedious and thus time consuming, prone to clerical error, leading to intra- and inter-observer variability and low throughput. Image analysis of digital histopathology images is a fast-developing and exciting area of disease research that aims to address the above limitations.

Protein expression images, like from immunohistochemistry assays, provide significant information regarding disease progression and treatment selection. However, tissue morphology may have different molecular signatures due to genetics and other parameters. By analyzing images solely based on the staining intensity significant information may be missed. We have developed computational techniques which extract cellular staining response along with morphological and topological features that define unique molecular signatures, per protein and disease stage. Initial results show the prevalence of the tumor suppressor protein PTEN in the early stages of the oncogene-encoded protein ERG at more aggressive stages of the studied disease, and the improvement in pathogenesis prediction when using both.

9791-28, Session PSWed

A machine learning approach to quantifying noise in medical images

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As advances in medical imaging technology are resulting in significant growth of biomedical image data, new techniques are needed to automate the process of identifying images of low quality. Automation is needed because it is very time consuming for a domain expert such as a medical practitioner or a biologist to manually separate good images from bad ones. While there are plenty of de-noising algorithms in the literature, their focus is on designing filters which are necessary but not sufficient for determining how useful an image is to a domain expert.

Thus a computational tool is needed to assign a score to each image based on its perceived quality. In this paper, we introduce a machine learning-based score and call it the Quality of Image (QoI) score. The QoI score is computed by combining the confidence values of two popular classification techniques—support vector machines (SVMs) and Naïve Bayes classifiers.

We test our technique on clinical image data obtained from cancerous tissue samples. We used 747 tissue samples that are stained by four different markers (abbreviated as CK15, pck26, E_cad and Vimentin) leading to a total of 2,988 images. The results show that images can be classified as good (high QoI), bad (low QoI) or ugly (Intermediate QoI) based on their QoI scores. Our automated labeling is in agreement with the domain experts with a bi-modal classification accuracy of 94%, on average. Furthermore, ugly images can be recovered and forwarded for further post-processing.

9791-29, Session PSWed

Pathological Gleason prediction through gland ring morphometry in immunofluorescent prostate cancer images

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The Gleason score is the most common architectural and morphological assessment of prostate cancer severity and prognosis. There have been numerous quantitative techniques developed to approximate and duplicate the Gleason scoring system. Most of these approaches have been developed in standard H&E brightfield microscopy. Immunofluorescence (IF) image analysis of tissue pathology has recently been proven to be extremely valuable and robust in developing prognostic assessments of disease, particularly in prostate cancer. There have been significant advances in the literature in quantitative biomarker expression as well as characterization of glandular architectures in discrete gland rings. In this work we leverage a new method of segmenting gland rings in IF images for predicting the pathological Gleason; both the clinical and the image specific grade, which may not necessarily be the same. We combine these measures with nuclear specific characteristics as assessed by the MST algorithm. Our individual features correlate well univariately with the Gleason grades, and in a multivariate setting have an accuracy of 85% in predicting the Gleason grade. Additionally, these features correlate strongly with clinical progression outcomes (CI of 0.89), significantly outperforming the clinical Gleason grades (CI of 0.78). This work presents the first assessment of morphological gland unit features from IF images for predicting the Gleason grade.

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9791-30, Session PSWed

Color-texture based extreme learning machines for tissue tumor classification

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One of the pre-requisites to diagnosis and grading of a disease is the identification and classification of relevant histological features. Visual assessments by pathologists determine tumor versus non-tumor tissues, in which a computer-aided diagnostic system needs to mimic visual classification by identifying observed features like textures. Computer-aided diagnostic systems could enhance research output and efficiency in identifying the pathology type (normal, non-tumor or tumor) of a tissue pattern from scanned and archived slide images. In this paper, a computational method in terms of color-texture based extreme learning machines (ELM) is proposed for automatic tissue tumor classification. The approach consists of two steps: (1) color and texture features are extracted from the regions-of-interest (ROIs) of the individual cores de-arrayed from tissue microarrays (TMAs); (2) ELM is applied to the extracted features to classify the ROIs into non-tumor or tumor categories. The proposed approach is tested on 90 images from a kidney TMA, which leads to 91.7% classification accuracy.

9791-31, Session PSWed

Cell nuclei attributed relational graphs for efficient representation and classification of gastric cancer in digital histopathology

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This paper describes a novel graph-based method for efficient representation and subsequent classification in histological whole slide images of gastric cancer. Her2/neu immunohistochemically stained and haematoxylin and eosin stained histological sections of gastric carcinoma are digitized. Immunohistochemical staining is used in practice by pathologists to determine extent of malignancy, however, it is more laborious to visually discriminate the corresponding malignancy levels in the more commonly used H&E stain, and this study attempts to solve this problem using a computer-based method. Cell nuclei are first isolated at high magnification using an automatic nuclei segmentation strategy, followed by construction of cell nuclei attributed relational graphs of the tissue regions. These graphs represent tissue architecture comprehensively, as they contain information about cell nuclei morphology as vertex attributes, along with knowledge of neighborhood in the form of edge linking and edge attributes. Global graph characteristics are derived and used in an ensemble learning approach to discriminate between the three type of malignancy levels, namely, Her2/neu positive tumor, Her2/neu negative tumor and non tumor. Performance is compared with state-of-the-art methods including three texture feature groups (Haralick, Gabor and Local Binary Patterns), intensity-based features and Voronoi diagram and Delaunay triangulations. Combining low-level information with graph-based approach results in best classification rate of 84.31%. Hence, the proposed method provides a promising way for automatic classification of tumor in histopathological images of gastric carcinoma based on Her2/neu immunohistochemistry.

9791-32, Session PSWed

Mixture of online learners for cancer stem cell detection in CD133 colored microscopic images

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In this article the goal is to identify “cancer stem cells” in CD133 dyed microscopic images. Cancer stem cells appear as brown regions in CD133 dyed images. We use various image feature sets to characterize cancer stem cells. Feature parameters include region covariance features, region co-difference features, and color values of pixels. We divide CD133 dyed images into overlapping small blocks, whose size are roughly equal to the size of a nucleus of a cell. In each block we extract feature vectors using the region covariance, co-difference and average color values. We train five Support Vector Machines (SVM) using the above feature vectors. We used RBF kernel in which the parameters of the RBF kernel are obtained by 10-fold cross validation. The first SVM is trained using the region covariance features, the second SVM is trained using the region co-difference features, the third SVM is trained using the color pixel values, the fourth one is trained by using YCbCr color mean values of small image blocks, and the cosine of the color vector angle and the fifth SVM is trained by Red-Green and Red-Blue mean ratios and the cosine of the color vector angle. Additionally, we trained two Neural Networks (NN). The first NN is trained using the region covariance features and the second one is trained using the region co-difference features. Initially, results of individual SVMs and NNs are linearly combined to reach a final decision. Each block is classified as a cancer stem cell or not. The result is displayed to the user. The user provides feedback to the system by correcting incorrectly marked image blocks. The online adaptation system takes the feedback from the user and updates the weights of the individual SVMs and NNs using a gradient descent-type algorithm. The adaptive algorithm is similar to the well-known normalized Least-Mean-Square (LMS) adaptive filtering algorithm.

9791-33, Session PSWed

Automatic extraction of a novel imaging biomarker from fluorescence microscopic imaging of TRA-8/DR5 oligomers to predict TRA-8 therapeutic efficacy in breast and pancreatic cancer mouse models

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The goal of this study was to extract a reliable imaging biomarker from fluorescence microscopic imaging of TRA-8/DR5 oligomer to predict TRA-8 therapeutic efficacy in human breast and pancreatic cancer mouse models. Two breast (2LMP, SUM159) and two pancreatic (MIA PaCa-2, PANC1) cancer cell lines were used. 105 cells per cell line were placed in a culture dish, and treated with Cy5.5 labeled TRA-8 overnight in vitro. Three fluorescence microphotographs (20x) were acquired from randomly selected areas, and about 300 cells were analyzed per cell line. 2-dimensional (2D) fluorescence signal distribution of Cy5.5-TRA-8 on each cell was measured. Gaussian curve fitting to the distribution was determined by the least square regression method, and the coefficient of determination (R2) of the fitting was found. Peak amplitude and full width at half maximum (FWHM) of the best fitting Gaussian curve were retrieved. A novel image biomarker was extracted by correlating the combination of R2 value, peak amplitude, and FWHM with the percentage of tumor growth inhibition (%TGI) at a week of
Identification of leukocyte infiltration in hematoxylin-eosin stained breast cancer samples: texture-based classification of tissue morphologies

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The spatial profile of immune cells in the tumor microenvironment (TME) of breast cancer can reveal clinically important information. Despite the heterogeneity of tumor-infiltrating leukocytes, it has been shown that the degree of infiltration assessed by simple evaluation of hematoxylin-eosin (H&E) stained samples can have prognostic and possibly predictive value. However, quantification of the infiltrating leukocytes in H&E is currently dependent on visual scoring by an expert.

Digital pathology and computer vision tools provide solutions for automated characterization of the components of the TME. Moreover, texture-based methods have successfully been applied to discriminate between different tissue morphologies and cell phenotypes. In this study, we evaluate whether a texture-based tissue morphology classification can be utilized to identify leukocyte infiltration in H&E-stained breast cancer tumors.

In the training set (n=116) a 3-fold cross-validation resulted in 98% accuracy and an area under the receiver-operating characteristic curve (AUC) of 0.98. In test set (n=204), we achieved an accuracy of 96% and AUC of 0.996 to label cropped tissue regions correctly into leukocyte-rich and leukocyte-poor categories. Image datasets were annotated from 35 patients operated for primary breast cancer and cut stained consecutively with H&E and the pan-leukocyte CD45 marker to confirm the infiltration regions.

The obtained results demonstrate strong discrimination between leukocyte-rich and leukocyte-poor tissue morphologies with texture-based image analysis approach. The proposed method can provide a quantitative measurement of the degree of immune cell infiltration and applied to digitally scanned H&E-stained breast cancer samples for diagnostic support purposes.

Nucleus Segmentation in Histology Images with Hierarchical Multilevel Thresholding

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Automatic segmentation of histopathology images is a crucial step to decrease the cost of medical diagnosis for diseases such as cancer. In this paper, we present a new unsupervised method to segment histopathology images. Color deconvolution and image reconstructions are used for the image preprocessing. The segmentation step consists of multilevel thresholds, followed by morphological operations. The only parameter used in the method is the minimum region size which can be set according to the resolution of the image. Hence, the proposed method does not need any training set or parameter learning, and because it does not use any priori information on cell features, it is not biased in favor of any tissue. The method was evaluated on a dataset consisting of diverse tissues including breast, liver, gastric mucosa and bone marrow and it outperforms the results of four other recent methods on the same dataset in terms of F-measure, with precision and recall of 0.929 and 0.886 respectively.

Quantification of tumor morphology via 3D histology: Application to oral cavity cancers

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Traditional histopathology quantifies disease through the study of glass slides, i.e. two-dimensional samples that are representative of the overall process. We propose that 3D reconstruction can enhance our understanding of histopathologic interpretations. For example, a risk model for oral cavity cancer (OCC) stratifies patients into low-, intermediate-, and high-risk for locoregional disease-free survival; classification is based on study of hematoxylin and eosin (H&E) stained tissues sampled from the resection specimens. Worst Pattern of Invasion (WPOI) is an important component of this model, representing specific architecture at the interface between cancer and non-cancer. Classification of WPOI is based solely on 2D views of complex 3D structures. It is possible that important diagnostic information is revealed in a fully 3D model. Therefore, we introduce a framework for visualizing tissue architecture and morphology in 3D from serial sections of histopathology. This framework can be used to enhance predictive models for diseases where severity is determined by 3D biological structure. In this study, serial H&E-stained OCC resections are obtained from 7 patients exhibiting WPOI-3 (nonaggressive) through WPOI-5 (aggressive). A supervised classifier automatically generates a map of tumor regions on each slide, which are then co-registered using an elastic deformation algorithm. A smooth 3D model of the tumor region is generated from the registered maps, which is suitable for quantitative tumor interface morphology feature extraction. We report our preliminary results using this system and suggest further enhancements to traditional histology scoring mechanisms that take spatial architecture into consideration.

Designing an automated classification method using latent support vector machine algorithms as a predictive tool for prostate cancer lesions

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Prostate-Specific Antigen (PSA) screening has led to over-detection/over-treatment of organ confined prostate cancers. Current diagnostic methods are based on PSA level, clinical stage and Gleason Score since a reliable predictive assay of biological behavior of the disease are still lacking. Recently researchers started using quantification of DNA ploidy from biopsy results for prediction. Many image based predictive methods have been introduced and most of them require extra human expert interaction/extra classifiers to select high quality nuclei or determine if they belong to specific anatomical areas. Here we propose a method based on Latent Support Vector Machine (LSVM) that reduces the need for extra classifiers or human interaction. We modeled some of the intermediate nucleus properties (e.g. segmented nucleus quality, anatomical location and dependence to cluster nuclei) as latent variables. By optimizing our scoring function toward the accuracy of the prediction we outperformed the existing methods that use the same amount of human interactions and training materials. We tested this algorithm on our dataset (Tissue MicroArray, TMA, image of 33 patients)
and compared our results with one of our recent predictive methods which uses human expert to select high quality nuclei from anatomically relevant areas (with 83% prediction accuracy). Our proposed method reached 81% accuracy which is close the accuracy of the method that uses the human experts. By extensive validation of our work we hope to eventually add a reliable, cost effective and accurate prediction tool to the routine clinical procedure.

9791-38, Session PSWed

Automatic cell detection and segmentation from H&E stained pathology slides using colorspace decorrelation stretching

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Purpose: automatic cell segmentation plays an important role in reliable diagnosis and prognosis of patients. Most of the state-of-the-art cell detection and segmentation techniques focus on complicated methods to subtract foreground cells from the background. In this study, we propose a preprocessing method which leads to a better detection and segmentation results compared to a well-known state-of-the-art work. Method: We transform the original red-green-blue (RGB) space into a new space defined by the top eigenvectors of the RGB space. Stretching is done by manipulating the contrast of each pixel value to equalize the color variances. New pixel values are then inverse transformed to the original RGB space. This altered RGB image is then used to segment cells. Result: The validation of our method with a well-known state-of-the-art technique revealed a statistically significant improvement on an identical validation set. We achieved a mean F1-score of 0.901. Conclusion: Preprocessing steps to decorrelate colorspaces may improve cell segmentation performances.

9791-39, Session PSWed

Deep learning-based gland quantification in digitized tissue samples from patients with colorectal cancer: associations with clinical data and outcome

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The aim of this study is to design an automated method to detect and segment glands in digitized images of colorectal cancer of different histological grades. Intermediate and high-grade cancer is especially challenging for segmentation due to the big variation in glandular morphology. Here we adapt deep learning techniques to generate a hierarchical representation of morphological features in colorectal cancer tissue samples and correlate the extracted features with clinical parameters from 643 patients. We utilize digitized image dataset consisting of hematoxylin and eosin (H&E) stained slides of a variety of histological grades, ground truth annotations done by expert pathologists and clinicalpathological characterization of the patients. Initial experiments demonstrate sensible segmentation performance of our deep neural network architecture on a small set including 70 images of 480 ?m x 324 ?m size each (0.62?m/pixel). Our model achieved a performance of 0.86 as measured with F1-score for object detection and 192 in Hausdorff distance measure of shape similarity. According to the initial results the proposed method will be extended and trained on a bigger set of images with clinical information to allow for automated analysis of colorectal cancer morphology. Integrated analysis of image data and clinical information from retrospective cohorts enables assessment of the clinical relevance of the detected glandular features and validation of the proposed deep learning-based diagnostic support method.

9791-40, Session PSWed

High-definition infrared imaging of colon sections for improved automated histology

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Fourier Transform Infrared imaging (FT-IR) is widely used to develop stainless stains in biological specimens for identification of diseases. In colorectal cancer, the disease originates from the epithelial cells lining the colon or rectum, invades the thin layer of muscle in the gastrointestinal tract known as lamina muscularis mucosae, followed by invasion in the submucosa and eventually muscularis propria. Minia changes need to be identified in epithelium as it begins to mutate before the disease has spread further. This can be done by utilizing infrared spectroscopy which probes biochemical changes in tissue much before they are visible through chemical staining. However, due to intricate organization of colon crypts, it was previously difficult to separate epithelial cells from goblet cells by conventional FT-IR imaging that offered low spatial resolution. To address this, we imaged colon biopsy samples by high definition infrared imaging microscopy and tested its viability in accurate differentiation of different histological classes in anonymized colon biopsy samples collected from patients. The spatial resolution was almost 5 times higher than previously used FT-IR imaging instruments. We observed that the images obtained by this method showed more clear resolution of classes as compared to low magnification mode and this detection also correlated well hematoxylin and eosin (H&E) stained serial section. These results indicate that through high definition infrared imaging, it is possible to resolve more classes and consequently produce digital stains closer to conventional chemical stains, and the resolution advantage offered here can enable probing of epithelial cells to determine predisposition to colorectal cancer.

9791-41, Session PSWed

Hierarchical nucleus segmentation in digital pathology images

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Extracting nuclei is one of the most actively studied topic in the digital pathology researches. Most of the studies directly search the nuclei (or seeds for the nuclei) from the finest resolution available. While the richest information has been utilized by such approaches, it is sometimes difficult to address the heterogeneity of nuclei in different tissues. In this work, we propose a hierarchical approach which starts from the lower resolution level and adaptively adjusts the parameters while progressing into finer and finer resolution. The algorithm is tested on brain and lung cancer images from The Cancer Genome Atlas dataset.
A four class model for digital breast histopathology using high-definition Fourier transform infrared (FT-IR) spectroscopic imaging

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High-definition (HD) Fourier transform infrared (FT-IR) spectroscopic imaging enables chemistry-based visualization of tissue constituents, label free extraction of biochemical information and is a potentially useful platform to conduct digital pathology. This methodology, along with fast and efficient data analysis, can enable both quantitative and automated pathology. In this manuscript, we demonstrate a combination of HD FT-IR spectroscopic imaging of breast tissue microarrays (TMAs) with data analysis algorithms. The samples comprise various disease states. i.e. hyperplasia, dysplasia, malignant and normal. We identify various cell types which would act as biomarkers for breast cancer detection and differentiate between them using statistical pattern recognition tools i.e. random forest and Bayesian algorithms. Feature optimization is integrally carried out for the random forest algorithm. This has helped in both reducing the computation time and removal of redundant features in the classification model. We achieved an order of magnitude reduction in the number of features with comparable prediction accuracy to that of the original feature set. Together, the demonstration of histology and selection of features paves the way for future applications in more complex models and rapid data acquisition.

The role of imaging based prostate biopsy morphology in a data fusion paradigm for transducing prognostic predictions

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A major focus area for precision medicine is in managing the treatment of newly diagnosed prostate cancer patients. For patients with a positive biopsy, clinicians aim to develop an individualized treatment plan based on a mechanistic understanding of the disease factors unique to each patient. Recently, there has been a movement towards a multi-modal view of the cancer through the fusion of quantitative information from multiple sources. Simultaneously, there have been significant advances in machine learning methods for medical prognostics which integrate a multitude of predictive factors to develop an individualized risk assessment and prognosis for patients. An emerging area of research is in semi-supervised approaches which transduce the appropriate survival time for censored patients. Our group has developed a method to examine biological specimens in cellular detail using synchrotron microCT. The imaging method can achieve [0.743 um x 0.743 um x 0.743 um] isotropic resolution of tissue specimens, allowing for individual cell types to be visualized in the context of the entire organism. The tool enables the high-throughput imaging and analysis of model organisms, allowing for the rapid characterization of tissue architecture and cellular morphology from every organ system. This characterization is critical for proposed and ongoing “phenome” projects that aim to phenotype whole model organism mutants and diseased tissues from larger organisms including humans.

With the envisioned collection of hundreds to thousands of images for a phenome project, it is important to develop quantitative image analysis tools for the automated scoring of organism phenotypes across organ systems. Here we present a first step towards that goal, showing the use of support vector machines (SVM) to detect and segment retinal cell nuclei in synchrotron microCT images of wild-type and mutant zebrafish. The zebrafish mutant studied provides a model for the study of mutant phenotypes that include apoptosis as a cellular pathophysiological process. After segmentation of the nuclei, we compute the average cell nuclei morphology of both wild-type and mutant organisms and show that SVMs can be used to capture phenotypic differences in these images. The long-term goal of this work is to allow cellular and tissue morphology to be characterized quantitatively for many organ systems, at the level of the whole-organism.

Automatic choroid cells segmentation and counting in fluorescence microscopic image

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In this paper, we proposed a method to automatically segment and count the rhesus choroid-retinal vascular endothelial cells (RF/6A) in fluorescence microscopic images which is based on shape classification, bottleneck detection and accelerated Dijkstra algorithm. The proposed method includes four main steps. First, a thresholding filter and morphological operation were applied to reduce the noise. Second, a shape classifier was used to decide whether a connected component is to be segmented. In this step, the AdaBoost classifier was applied with a set of shape features. Third, the bottleneck positions were found based on the contours of the connected components. Finally, the cells segmentation and counting were completed based on the accelerated Dijkstra algorithm with the gradient information between the bottleneck positions. The proposed method was tested on 20 fluorescence microscopic cell images. The results show the feasibility and efficiency of the proposed method.

Classification of human carcinoma cells using hyperspectral imagery

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Automatic recognition of cancerous cell groups is an important task for accurate decision making in medical diagnosis of cancer types. With the advances of recent imaging and microscopy technologies, human cell morphology can be identified in order to manually find out possible cancerous structures. However, this work is time consuming and costly. Therefore, automatic classification methods are desired.

In this study, the cell lines obtained for different cancer diseases are investigated to devise an efficient method for categorizing cancer types. Our dataset is composed of 14 different groups of cancerous cell lines. Although spatial features like morphology and texture are robust descriptors for discriminating healthy and unhealthy cells, it is sometimes hard to discriminate between cancerous classes due to their irregular structures. In this research, we employ both spatial and HSI spectral features in order to highlight inter-class variance between cell lines. We utilize a hyperspectral imaging (HSI) system mounted to a microscopy device in order to evaluate the contribution of HSI to classification of human carcinoma cells.

9791-47, Session PSWed

High-definition Fourier transform infrared spectroscopic imaging of prostate tissue
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Histopathology forms the gold standard for cancer diagnosis and therapy, and generally relies on manual examination of microscopic structural morphology within tissue. Fourier-Transform Infrared (FT-IR) imaging is an emerging vibrational spectroscopic imaging technique, especially in a high-definition (HD) format, that provides the spatial specificity of microscopy at magnifications used in pathology. IR absorption by tissue creates a strong signal where the spectrum at each pixel is a quantitative “fingerprint” of the molecular composition of the sample. Here we show that this fingerprint enables direct digital pathology without the need for stains or dyes. An assessment of the potential of HD imaging to improve pathology is presented.

9791-48, Session PSWed

A generic nuclei detection method for histopathological breast images
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The detection of cell nuclei plays a key role in various histopathological image analysis problems. Typical applications are the detection of lymphocytic infiltrates or the quantification of PR-positive cells. Considering the high variability of these tasks, we propose a novel generic and trainable nuclei detection approach. Adaptation to specific nuclei detection tasks is done by providing training samples. Besides the training, the method is almost parameter free, which makes it easy to use also for users unaware of any implementation details.

A trainable deconvolution and classification algorithm is used to map each image pixel to a probability value for the presence of a nucleus. This algorithm is trained with pixel samples of representative nuclei and non-nuclei regions and, therefore, enables an intuitive and quick adaption of the algorithm to the specific applications. The resulting probability image is processed by an optimized region merging step in order to identify the nuclei positions.

We have tested our method on 4 datasets with different stains and different types of nuclei to detect. The 43 images comprised more than 12000 nuclei in total. On these datasets, an f1-measure between 0.83 and 0.93 was obtained. The average execution time of the algorithm was 5.54s per Megapixel using a single thread.