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10132-1, Session 1

GPU-accelerated compressed-sensing (CS) image reconstruction in chest digital tomosynthesis (CDT) using CUDA programming

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A compressed-sensing (CS) technique has been rapidly applied in medical imaging field for retrieving volumetric data from highly under-sampled projections. Many algorithms of the CS techniques are based on a total-variation (TV) minimization because it can be well-suited in cone-beam geometry. In this study, we implemented the CS based image reconstruction strategy in our prototype chest digital tomosynthesis (CDT) R/F system. Due to the iterative nature of time consuming processes in solving a cost function, we took advantage of parallel computing using graphics processing units (GPU) by the compute unified device architecture (CUDA) programming to accelerate our algorithm. In order to evaluate the algorithmic performance, we also implemented conventional filtered back-projection (FBP) and simultaneous algebraic reconstruction technique (SART) with 10 iterations. The results indicated that the CS produced better contrast-to-noise ratios (CNRs) in the physical phantom images (Teflon region-of-interest) by factors of 3.91 and 1.93 than FBP and SART images, respectively. Also, the resulted human chest phantom images including lung nodules with different diameters were more clearly visible in the CS images. Our proposed CS reconstruction scheme could produce volumetric data in 198.24 sec, which could match the clinically feasible time (~ 3 min). Consequently, our results demonstrated that the proposed CS method showed a potential of additional dose reduction in digital tomosynthesis with reasonable image quality in a fast time.

10132-2, Session 1

Stationary intraoral tomosynthesis for dental imaging

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Despite recent advances in dental radiography, the diagnostic accuracies for some of the most common dental diseases have not improved significantly, and in some cases remain low. Intraoral x-ray is the most commonly used x-ray diagnostic tool in dental clinics. It suffers from the typical limitations of a 2D imaging modality including structure overlap. CBCT uses high radiation dose and suffers from image artifacts and relatively low resolution. The purpose of this study is to develop a stationary intraoral tomosynthesis (s-IOT) imaging device, and to evaluate its diagnostic accuracy for caries and root fracture detection.

An experimental s-IOT device was constructed using a linear CNT X-ray source array and a digital intraoral detector. Image reconstruction was performed using an iterative reconstruction algorithm. Studies were performed to optimize the imaging configuration. For evaluation of s-IOT's diagnostic accuracy, images were acquired of a dental quality assurance phantom (RMI 501A, Radiation Measurements, Inc.), and human specimens containing real and artificially induced caries and root fracture lesions. Standard radiographs and CT scans were acquired for each sample and used for comparison to reconstructed tomosynthesis slices. Tomosynthesis slices provided as much or more information than their 2D counterparts. Lesions obscured in 2D radiographs were clearly delineated using tomosynthesis.

Stationary intraoral tomosynthesis is not only feasible, it produces images that are superior to standard radiographs, with sufficient detail to possibly eliminate the need for CT in some applications. An optimized imaging system for full evaluation of this new modality is currently under development.

10132-3, Session 1

An atlas-based organ dose estimator for tomosynthesis and radiography

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The purpose of this study was to provide patient-specific organ dose estimation based on an atlas of human models for projection x-ray exams. The study utilized a library of 58 adult computational phantoms (age: 18-78 years, weight 52-117 kg) created based on CT data. The study modeled twenty-one tomosynthesis and radiography protocols using a validated Monte Carlo simulation package (PENELOPE). The field of view for each exam was calculated to include relevant organs per protocol. Positioning of patient anatomy was based on Merril's Atlas of Radiographic Positioning and Bontrager's Handbook of Radiographic Positioning. Energy deposited in each organ was binned to estimate normalized organ doses into a reference database. The database was used as the basis to devise a dose calculator for multiple operating systems to predict patient-specific organ dose values based on kVp, mAs, dose area product, and patient habitus for a given protocol. As an example of the utility of this tool, dose to a particular organ can be studied as a function of patient size. Results show that lung dose can vary from 0.36 mGy/mR to 0.51 mGy/mR for male patients ranging from 10% BMI to 90% BMI for a chest tomosynthesis protocol. The calculator developed in this work can provide a valuable tool to prospectively estimate patient-specific dose for a wide range of tomosynthesis and radiography protocols.

10132-4, Session 1

Lesion characterization in spectral photon-counting tomosynthesis

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Institute of Technology (Sweden); Klaus Erhard, Philips Research (Germany); Mats Danielsson, KTH Royal Institute of Technology (Sweden); Matthew Wallis, NIHR Cambridge Biomedical Research Ctr., Addenbrooke's Hospital (United Kingdom); Erik Fredenberg, Philips Health Systems (Sweden)

It has previously been shown that 2D spectral mammography can be used to discriminate between (likely benign) cystic and (potentially malignant) solid lesions in order to reduce unnecessary recalls. One limitation of the technique is, however, that the composition of overlapping tissue needs to be estimated from a region surrounding the lesion. We have investigated whether 3D information from spectral tomosynthesis can improve the estimation of overlapping tissue and potentially increase the specificity of spectral lesion characterization. A phantom experiment was designed to simulate a cyst and a tumor, where the tumor was overlaid with a structure that made it mimic a cyst. In 2D, the two targets appeared similar in composition (cystic), whereas spectral tomosynthesis revealed the exact compositional difference. An initial investigation of clinical data showed a similar improvement in measuring the composition. We conclude that spectral tomosynthesis improves lesion characterization compared to 2D spectral mammography, and has the potential to increase the specificity of screening mammography.

10132-5, Session 1

Pipeline for effective denoising of digital mammography and digital breast tomosynthesis

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Denoising can be used as a tool to enhance image quality and enforce the ALARA principle in X-ray medical imaging. The effectiveness of denoising techniques relies on the validity of the assumed noise model. In full-field digital mammography (FFDM), calibration steps such as the detector offset and flat-fielding can affect some assumptions made by most denoising techniques. Furthermore, quantum noise found in X ray images is signal-dependent and can only be treated by specific filters. In this work we propose a pipeline for FFDM image denoising, which considers the calibration steps and allows easy modeling of the noise statistics through variance-stabilizing transformations (VST). To evaluate the method, the improvement on the normalized root mean squared error (N-RMSE) was calculated as function of the mean pixel value. The performance of a state-of-the-art denoising method was tested with and without the proposed pipeline. Preliminary tests show that the pipeline improves denoising. When the pipeline is not used, bright pixels of the denoised image are under-filtered and dark pixels are over-smoothed due to the assumption of a signal-independent Gaussian model. The pipeline improves the performance of the filter in those regions in up to 25%.

10132-6, Session 2

Signal and noise characteristics of a CdTe-based photon counting detector: Cascaded systems analysis and experimental studies

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There are abundance of unknowns of the noise property of images generated by cadmium telluride (CdTe)-based photon counting detectors (PCDs). In this work, a theoretical model based on serial and parallel cascaded systems analysis was developed for CdTe-based photon counting detectors. The model incorporated the effects of k-fluorescence and reabsorption unique to CdTe, the anti-charge sharing process and the energy thresholding process, so that the transfer of noise from individual incident x-ray photon to the NPS in the output image of the PCDs could be analyzed. A CdTe-based PCD system (XC-FLITE X1, XCounter AB) was used to validate the cascaded model. Two x-ray radiation conditions were used for the measurement of the NPS, including a standard RQA-5 beam and a 40 kVp beam. Both theoretical predications and experimental results showed that the NPS of the CdTe-based PCD was almost flat. The white noise was primarily caused by the use of energy threshold which help to reject low energy signals. Such low signals, caused by k-fluorescence or charge sharing, were the primary origins of the correlated noise. In addition, the model predicted that higher energy threshold and the anti-charge sharing mechanism helped to boost the flatness of the NPS. It was also predicted that the output of the PCDs followed Poisson statistics. All predictions were further validated by the experimental studies.

10132-7, Session 2

SWAD: transient conductivity and pulse-height spectrum

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Photon counting detectors (PCDs) have the potential to improve x-ray imaging however, they are still hindered by high production cost and performance limitations. By using amorphous Selenium (a-Se) the cost of PCDs can be significantly reduced compared to currently used crystalline semiconductors and enable large area detector deposition. 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's multi-well, dual Frisch grid design creates separate non-avalanche interaction (bulk) and avalanche collection (well) regions, achieving nearly depth independent avalanche gain. Unipolar time-differential (UTD) charge sensing, combined with tunable avalanche gain in the wells allows for the fast timing necessary for photon counting and comparable performance to crystalline semiconductors. In the present work we propose a spatiotemporal charge transport model to simulate the signal formation in SWAD, which in combination with our previous Monte-Carlo modeling, can be used to generate pulse height spectrum from individual x-ray interactions. PHS analysis will allow us to characterize the photon counting performance of SWAD and optimize our design. Additionally, we present our initial time-of-flight measurement results, demonstrating successful UTD charge sensing in SWAD, which will be used to validate our charge transport model for signal detection.

10132-8, Session 2

Direct measurement of Lubberts effect in CsI:Tl scintillators using single x-ray photon imaging

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The imaging performance of an indirect flat panel detector (I-FPD) is fundamentally limited by that of its scintillator. The scintillator's

modulation transfer function (MTF) varies as a function of the depth of x-ray interaction in the layer, due to differences in the lateral spread of light before detection by the optical sensor. This variation degrades the spatial frequency-dependent detective quantum efficiency (DQE(f)) of I-FPDs, and is quantified by the Lubberts effect. The depth-dependent MTFs of various scintillators used in I-FPDs have been estimated using Monte Carlo simulations, but have never been measured directly. This work presents the first experimental measurements of the depth-dependent MTF of thallium-doped cesium iodide (CsI) scintillators with thickness ranging from 200 – 1000 μm. Light bursts from individual x-ray interactions occurring at known, fixed depths within CsI are imaged using an ultra-high-sensitivity II-EMCCD camera. X-ray interaction depth in CsI is localized using a micro-slit beam of parallel synchrotron radiation (32 keV), and varied by translation in 50 ± 1 μm depth intervals. Fourier analysis of the imaged light bursts is used to deduce the MTF versus x-ray interaction depth z. Measurements of MTF(z,f) are used to calculate CsI presampling MTF(f) with RQA-M 3, RQA5 and RQA9 beam qualities for comparison with conventional slanted edge measurements. Images of the depth-varying light bursts are also used to derive Lubberts function using analysis of their Fourier burst distributions.

10132-9, Session 2

Exploration of strategies for implementation of screen-printed mercuric iodide converters in direct detection AMFPIs for digital breast tomosynthesis

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Digital breast tomosynthesis (DBT) has become an increasingly important tool in the diagnosis of breast disease. For those DBT imaging systems based on active matrix, flat-panel imager (AMFPI) arrays, the incident radiation is detected directly or indirectly by means of a-Se or CsI:Tl, respectively. While all AMFPI DBT devices provide clinically useful volumetric information, their performance is limited by the relatively modest x-ray sensitivities of present converters compared to the electronic additive noise of the system. To address this constraint, we are pursuing the development of a screen-printed form of mercuric iodide (SP HgI2) which has demonstrated sensitivities three times greater than those of conventional a-Se and CsI:Tl converters (with prospects for further improvement) as well as impressive DQE and MTF performance under mammographic irradiation conditions. A converter offering such enhanced sensitivity would greatly improve signal-to-noise performance and facilitate quantum-limited imaging down to significantly lower exposures than present AMFPI DBT systems. However, before this novel converter material can be implemented practically, challenges associated with SP HgI2 must be addressed. Specifically, high levels of charge trapping (which lead to image lag as well as fall-off in DQE at higher exposures) and significant non-uniformity in pixel-to-pixel signal response need to be reduced – while maintaining low dark current and otherwise favorable DQE performance. In this presentation, novel strategies for overcoming these challenges, including incorporation of a Frisch grid structure into the converter material, will be described and results from initial calculational and empirical studies of these strategies will be reported.

10132-10, Session 2

Temporal imaging for accurate time, space and energy localization of photoelectric events in monolithic scintillators

Alain Iltis, Damavan Imaging (France); Hichem Snoussi, Univ. de Technologie Troyes (France); Luc Rodrigues, Ghislain Zeufack Tadonkeng, Damavan Imaging (France)

In this communication, we propose an original temporal imaging concept for accurate spatio-temporal localization of scintillation events within a monolithic scintillator and a digital Si-PM matrix. Jointly analyzing the light distribution and the arrival time distribution of the first detected photons, it was possible to better recognize a photoelectric event and to accurately localize it in space, time and energy. The rationale behind the temporal imaging concept is the use of the critical angle between the scintillator and the detector plane. In fact, the projected disc with diameter linearly proportional to the interaction depth is first filled by un-scattered photons. The scattered photons fill later the whole detector plane randomly. In this paper, we adapt this concept on a digital pixellized SiPM detector, which yields at least two distributions: (i) the light distribution, which contains the number of detected photons per pixel (photon counting) and (ii) the time distribution of the first detected photons. Combining the light distribution and the first arrival time distribution allows to spatially localize the scintillation event (X, Y, Z and T), by using a machine learning method.

In this paper, we propose also an original learning method to correct the estimation of the depth of interaction. We report experimental results corroborating the temporal imaging technique, using the temporal data provided by the Digital Philips Photon Counter device. Achieved Gamma interaction online localization precision (around 1x1x2 mm) in monolithic scintillators is very promising for accurate and online PET imaging.

10132-11, Session 2

Towards a high sensitivity small animal PET system based on CZT detectors

Shiva Abbaszadeh, Stanford Univ. (United States); Craig Levin, Stanford Health Care (United States)

Small animal positron emission tomography (PET) is a biological imaging technology that allows non-invasive interrogation of internal molecular and cellular processes and mechanisms of disease. New PET molecular probes with high specificity are under development to target, detect, visualize, and quantify subtle molecular and cellular processes associated with cancer, heart disease, and neurological disorders. However, the limited uptake of these targeted probes leads to significant reduction in signal. There is a need to advance the performance of small animal PET system technology to reach its full potential for molecular imaging. Our goal is to assemble a small animal PET system based on CZT detectors and to explore methods to enhance its photon sensitivity. In this work, we reconstruct an image from a phantom using a two-panel subsystem consisting of six CZT crystals in each panel. For image reconstruction, coincidence events with energy between 450 and 570 keV were included. We are developing an algorithm to improve sensitivity of the system by including multiple interaction events.

10132-12, Session 3

Dependence of quantitative accuracy of CT perfusion imaging on system parameters: A four-dimensional cascaded systems analysis

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Deconvolution is one of the most popular methods to calculate 3D cerebral CT perfusion (CTP) maps from 4D dynamic CT source images. During deconvolution, the 4D space is squeezed into 3D space by removing the temporal dimension, and a prior knowledge is often used to suppress noise associated with the process. These additional complexities confound the understanding about deconvolution-based CTP imaging system and how its quantitative accuracy depends on parameters and sub-operations involved in the image formation process. Meanwhile, there has been a strong clinical need in answering this question, as physicians often rely heavily on the quantitative values of perfusion parameters to make diagnostic decisions, particularly during an emergency situation (e.g. diagnosis of acute ischemic stroke). The purpose of this work was to quantitatively relate the signal accuracy of perfusion parameters with CTP acquisition and postprocessing parameters. This goal was successfully achieved by developing a 4D cascaded systems model for deconvolution-based CTP imaging systems. Based on the model, the quantitative relationship between regularization strength, source image noise, arterial input function, and the signal accuracy of perfusion parameters was established. The model could potentially serve as a powerful to guide the technology developments and optimal clinical usage of deconvolution-based CT perfusion imaging.

10132-13, Session 3

Joint optimization of fluene field modulation and regularization in task-driven computed tomography

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Purpose: This work presents a task-driven joint optimization of fluence field modulation (FFM) and regularization in quadratic penalized-likelihood (PL) reconstruction. Conventional FFM strategies proposed for filtered-backprojection (FBP) are evaluated in the context of PL reconstruction for comparison.

Methods: We present a task-driven framework that leverages prior knowledge of the patient anatomy and imaging task to identify FFM and regularization. We adopted a maxi-min objective that ensures a minimum level of detectability index (d') across sample locations in the image volume. The FFM designs were parameterized by 2D Gaussian basis functions to reduce dimensionality of the optimization and basis function coefficients were estimated using the covariance matrix adaptation evolutionary strategy (CMA-ES) algorithm. The FFM was jointly optimized with both space-invariant and spatially-varying regularization strength (β) - the former via an exhaustive search through discrete values and the latter using an alternating optimization where β was exhaustively optimized locally and interpolated to form a spatially-varying map.

Results: The optimal FFM inverts as β increases, demonstrating the importance of a joint optimization. For the task and object investigated, the optimal FFM assigns more fluence through less attenuating views, counter to conventional FFM schemes proposed for FBP. The maxi-min objective homogenizes detectability throughout the image and achieves a higher minimum detectability than conventional FFM strategies.

Conclusions: The task-driven FFM designs found in this work are counter to conventional patterns for FBP and yield better performance in terms of the maxi-min objective, suggesting opportunities for improved image quality and/or dose reduction when model-based reconstructions are applied in conjunction with FFM.

10132-14, Session 3

Pushing the boundaries of diagnostic CT systems for high spatial resolution imaging tasks

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A model observer with a window model for spatial integration (WMSI) is developed in this work, in order to guide the optimal selection of scan mode and reconstruction kernel for high spatial resolution CT imaging tasks. Our proposal is based on an ideal model observer, with the difference that the spatial integration of the signal is limited by a sampling aperture or window model. This proposal is based on two assumptions about the human vision that were previously introduced by other authors: (i) the spatial integration of image information is limited to a window, and (ii) the observer generates a tailored discriminator for the signals in question using available information. The observer model dedicated for high spatial resolution tasks was compared with conventional observer models such as the ideal observer and the nonprewhitening observer. Human observer ROC experiments were performed to provide the needed reference. Finally, an in-vivo canine study was used to corroborate the conclusions drawn from this work.

The correlation between human observer performance and detectability values derived from conventional observer models was found to be extremely poor. The Spearman correlation coefficient in such cases ranged from 0.05 for the ideal observer to 0.30 for the NPWEi observer, with p-values of 0.904 and 0.428, respectively. The proposed WMSI observer showed an excellent agreement with the human observer data; the correlation coefficient between AUC and WMSI detectability index was found to be 0.88 with p-value of 0.003. The in-vivo study was consistent with the human and model observer data

10132-15, Session 3

Practical implementation of Channelized Hotelling Observers: effect of ROI size

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Fundamental to the development and application of channelized Hotelling observer (CHO) models is the selection of the region of interest (ROI) to evaluate. For assessment of medical imaging systems, reducing the ROI size can be advantageous. Smaller ROIs enable a greater concentration of interrogable objects in a single phantom image, thereby providing more information from a set of images and reducing the overall image acquisition burden. Additionally, smaller ROIs may promote better assessment of clinical patient images as different patient anatomies present different ROI constraints. To this end, we investigated the minimum ROI size that does not compromise the performance of the CHO model. In this study, we evaluated both simulated images and phantom CT images to identify the minimum ROI size that resulted in an accurate figure of merit (FOM) of the CHO's performance. More specifically, the minimum ROI size was evaluated as a function of the following: number of channels, spatial frequency and number of rotations of the Gabor filters, size and contrast of the object, and magnitude of the image noise. Results demonstrate that a minimum ROI size exists below which the CHO's performance is grossly inaccurate. The minimum ROI size is shown to increase with number of channels and be dictated by truncation of lower frequency filters. We developed a model to estimate the minimum ROI size as a parameterized function of the number of orientations and spatial frequencies of the Gabor filters, providing a guide for investigators to appropriately select parameters for model observer studies.

10132-16, Session 4

Task-driven orbit design and implementation on a robotic C-arm system for cone-beam CT

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Purpose: This work applies task-driven optimization to the design of non-circular orbits that maximize imaging performance for a particular imaging task. First implementation of task-driven imaging on a clinical robotic C-arm system is demonstrated, and a framework for orbit calculation is described and evaluated.

Methods: We implemented a task-driven imaging framework to optimize orbit parameters that maximize detectability index d'. This framework utilizes a specified Fourier domain task function and an analytical model for system spatial resolution and noise. Two experiments were conducted to test the framework. First, a simple task was considered consisting of frequencies lying entirely on the fz-axis (e.g., discrimination of structures oriented parallel to the central axial plane), and a "circle + arc" orbit was incorporated into the framework as a means to improve sampling of these frequencies, and thereby increase task-based detectability. The orbit was implemented on a robotic C-arm (Artis Zeego, Siemens Healthcare). A second task considered visualization of a cochlear implant simulated within a head phantom, with spatial frequency response emphasizing high-frequency content in the (fy,fz) plane of the cochlea. An optimal orbit was computed using the task-driven framework, and the resulting image was compared to that for a circular orbit.

Results: For the fz-axis task, the circle + arc orbit was shown to increase d' by a factor of 1.20, with an improvement of 0.71 mm in a 3D edge-spread measurement for edges located far from the central plane and a decrease in streak artifacts compared to a circular orbit. For the cochlear implant task, the resulting orbit favored complementary views of high tilt angles in a 360° orbit, and d' was increased by a factor of 1.83.

Conclusions: This work shows that a prospective definition of imaging task can be used to optimize source-detector orbit and improve imaging performance. The method was implemented for execution of non-circular, task-driven orbits on a clinical robotic C-arm system. The framework is sufficiently general to include both acquisition parameters (e.g., orbit, kV, and mA selection) and reconstruction parameters (e.g., a spatially varying regularizer).

10132-17, Session 4

Geometric calibration using line fiducials for cone-beam CT with general, non-circular source-detector trajectories

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Purpose: Traditional BB-based geometric calibration methods for cone-beam CT rely significantly on foreknowledge of the scan trajectory. This is a hindrance to the implementation of variable trajectory CBCT systems, normally requiring a dedicated calibration algorithm/phantom for every scan orbit of interest. A more flexible method of calibration is proposed here that accommodates various orbit types – including strongly noncircular trajectories – without software modification.

Methods: The proposed method uses a calibration phantom consisting of multiple radio-opaque wire segments. Geometric models relating the 3D line equations of the wires to the 2D line equations of their projections are used as the basis for system geometry estimation. This method was tested using a mobile C-arm CT system and comparisons were made to standard BB-based calibrations. Simulation studies were also conducted using a sinusoid-on-sphere orbit. Calibration performance was quantified in terms of PSF and back projection error, and visual image quality was assessed with respect to spatial resolution in trabecular bone in an anthropomorphic head phantom.

Results: The line fiducial calibration method performed equal to or better than BB-based calibrations in all metrics. For the sinusoidal scans, the method provided reliable calibration, validating its application to non-circular trajectories. Furthermore, the ability to improve image quality using non-circular orbits in conjunction with this calibration method was demonstrated.

Conclusion: The proposed method has been shown feasible for conventional circular CBCT scans and offers a promising tool for non-circular scan orbits that can improve image quality, reduce dose, and extend field of view.

10132-18, Session 4

Shading correction for cone-beam CT in radiotherapy: validation of dose calculation accuracy using clinical images

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Cone-beam CT (CBCT) images are routinely acquired to verify patient position in radiotherapy (RT), but are typically not calibrated in Hounsfield Units (HU) and feature non-uniformity due to X-ray scatter and detector persistence effects. This prevents direct use of CBCT for re-calculation of RT delivered dose. We previously developed a prior-image based correction method to restore HU values and improve uniformity of CBCT images. Here we validate the accuracy with which corrected CBCT can be used for dosimetric assessment of RT delivery, using CBCT images and RT plans for 45 patients including pelvis, lung and head sites. Dose distributions were calculated based on each patient's original RT plan and using CBCT image values for tissue heterogeneity correction. Clinically relevant dose metrics were calculated (e.g. median and minimum target dose, maximum organ at risk dose). Accuracy of CBCT based dose metrics was determined using an "override ratio" method where the ratio of the dose metric to that calculated on a bulk-density assigned version of the image is assumed to be constant for each patient, allowing comparison to "gold standard" CT. For pelvis and head images the proportion of dose errors >2% was reduced from 46% to 1.5% after applying shading correction. For lung images the proportion of dose errors >3% was reduced from 70% to 5%. Application of shading correction to CBCT images greatly improves their utility for dosimetric assessment of RT delivery, allowing high confidence that CBCT dose calculations are accurate within 2-3%.

10132-19, Session 4

Development and clinical translation of a cone-beam CT scanner for high-quality imaging of intracranial hemorrhage

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Purpose: Prompt, reliable detection of intracranial hemorrhage (ICH) is essential for treatment of stroke and traumatic brain injury, and would benefit from availability of imaging directly at the point-of-care. This work reports the performance evaluation of a clinical prototype of a cone-beam CT (CBCT) system for ICH imaging and introduces novel algorithms for model-based reconstruction with compensation for data truncation and patient motion.

Methods: The tradeoffs in dose and image quality were investigated as a function of analytical (FBP) and model-based iterative reconstruction (PWLS) algorithm parameters using phantoms with ICH-mimicking inserts. Image quality in clinical applications was evaluated in a human cadaver imaged with simulated ICH. Objects outside of the field of view (FOV), such as the head-holder, were found to introduce challenging truncation artifacts in PWLS that were mitigated with a novel multi-resolution reconstruction strategy. Following phantom and cadaver studies, the scanner was translated to a pilot clinical study. Initial clinical experience indicates the presence of motion in some patient scans, and an image-based motion estimation method that does not require fiducial tracking or prior patient

information was implemented and evaluated.

Results: The weighted CTDI for a nominal scan technique was 22.8 mGy. The high-resolution FBP reconstruction protocol achieved < 0.9 mm point spread function (PSF) full width at half maximum (FWHM). The PWLS soft-tissue reconstruction showed <1.2 mm PSF FWHM and lower noise than FBP at the same resolution. Effects of truncation in PWLS were mitigated with the multi-resolution approach, resulting in 60% reduction in root mean squared error compared to conventional PWLS. Cadaver images showed clear visualization of anatomical landmarks (ventricles and sulci), and ICH was conspicuous. The motion compensation method was shown in clinical studies to restore visibility of fine bone structures, such as the subtle fracture, cranial sutures, and the cochlea.

Conclusion: The imaging performance of the prototype suggests sufficient quality for ICH imaging. Ongoing clinical studies will provide assessment of the diagnosis utility of the CBCT system in realistic clinical scenarios at the point of care.

10132-20, Session 4

Lab-based X-ray nanoCT imaging

Mark Müller, Sebastian Allner, Simone Ferstl, Martin Dierolf, Technische Univ. München (Germany); Tomi Tuohima, Excillum AB (Sweden); Franz Pfeiffer, Technische Univ. München (Germany)

Due to the recent development of transmission X-ray tubes with very small focal spot sizes, laboratory-based CT imaging with submicron resolutions is nowadays possible.

We recently developed a novel nanoCT setup featuring a prototype nanofocus X-ray source and a single-photon counting detector. The system is based on mere geometrical magnification and can reach resolutions of 200 nm.

We present a study of soft tissue samples of various mice organs stained with standard histological stains such as eosin. The stains are modified and optimized in order to improve the contrast in X-ray imaging, while still offering the possibility for conventional histological examinations. This is achieved by various chemical methods, such as increasing the concentration of the stain in the sample, complexing elements with a higher effective nuclear charge Z compared to the original compound and replacing an element of the original compound by another element with higher Z.

We will show CT slices and renderings of different soft tissue samples with resolutions ranging from several microns down to 200 nm. The results clearly show that the X-ray contrast in the samples is considerably improved by our staining methods and detailed tissue substructures are visible that cannot be visualized without the staining. We will further present correlative data from electron and light microscopy to verify the X-ray data.

We believe that this study is an important step towards three-dimensional X-ray histology, which is expected to become a powerful tool in future histological and histopathological applications.

10132-21, Session 5

High quality high spatial resolution functional classifcation in low dose dynamic CT perfusion using singular value decomposition (SVD) and k-means clustering

Francesco Pisana, Deutsches Krebsforschungszentrum (Germany); Thomas Henzler, Stefan Schoenberg, Institute of Clinical Radiology and Nuclear Medicine, Ruprecht-Karls-Univ. Heidelberg (Germany); Ernst Klotz, Bernhard Schmidt, Siemens AG (Germany); Marc Kachelrieß, Deutsches Krebsforschungszentrum (Germany)

Dynamic CT perfusion acquisitions are intrinsically high-dose examinations, due to repeated scanning. To keep radiation dose under control, relatively noisy images are acquired. Such images can be assumed to be temporally correlated and decorrelating transforms, like singular value thresholding (SVT), can be used to reduce temporal noise and compress data. SVT shows limitations for high frequency signals, like vessels. We aim at defining a more robust patient-specific decorrelating transform.

In our approach, the temporal dimension is first exploited to cluster all voxels into different classes via k-means clustering. After that, cluster-specific temporal profiles are obtained, which are then shrunk and delayed to obtain an over-complete set. The singular vectors of this set are finally considered to obtain the new orthonormal basis functions. The original dataset is projected onto the first few of these functions, in a similar fashion as SVT. We named our method k-means-derived singular value thresholding (KM-SVT).

Results were tested on a digital phantom and on one clinical case. When compared to the SVT, the KM-SVT performed significantly better for vessels' signal restoration. Deviation from the ground truth was, on an average, reduced by 13.8%, while CNR was improved by 50% for the phantom and 19% for the clinical case, suggesting that 40% of dose reduction might be possible.

In conclusion, the KM-SVT is able to compress the useful information with a similar or lower error compared to the SVT while image quality is improved.

10132-22, Session 5

Limits on estimating attenuation from ultra-low dose CT sinograms

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In the ultra-low-dose (ULD) CT regime it is possible to use statistically-principled iterative image reconstruction methods when using a standard data processing stream (i.e. the non-positivity correction and log-transform etc.) to reduce bias and variance. Commonly, CT Iterative reconstruction methods are designed and efficient estimators for only normally distributed post-log data. Our goal is to understand the statistical distribution of ULDCT data with different non-positivity correction methods and evaluate the limits of where attenuation estimation is possible. We used phantom measurement and calibrated simulations to reveal how the noise distribution deviate from normal assumption under the ULD CT flux environment. In summary, our results indicate that there are three general regimes: (1) Diagnostic CT, where post-log data are well modeled by normal distribution. (2) Low-dose CT, where normal distribution remains a reasonable approximation and statistically-principled (post-log) methods that assume a normal distribution have an advantage. (3) An ULD regime that is photon-starved and the normal approximation is no longer effective. In all cases we observed that there is a fundamental limit to the maximum level of estimation of attenuation from ULD CT data when using a standard data processing stream. This limit depends on the photon fluence and electronic noise interacting with the non-positivity correction and log-transform.

10132-23, Session 5

Polyenergetic known-component reconstruction without prior shape models

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Purpose: Previous work has demonstrated that structural models of surgical tools and implants can be integrated into model-based CT reconstruction to greatly reduce metal artifacts and improve image quality. This work extends a polyenergetic formulation of known-component reconstruction (Poly-KCR) by removing the requirement that a physical model (e.g. CAD drawing) be known a priori.

Methods: We adopt a single-threshold segmentation technique to build a shape model of metal components in a patient scan based on initial filtered-backprojection (FBP) reconstructions. These shape models are used as inputs to Poly-KCR, a formulation of known-component reconstruction that does not require a prior knowledge of beam quality or component material composition. An investigation of performance as a function of segmentation thresholds is performed in simulation studies, and qualitative comparisons to Poly-KCR with an a priori shape model are made using physical CBCT data of an implanted cadaver.

Results: In both simulation and physical data studies we find that the proposed approach can remove most of the blooming and streak artifacts around the component permitting visualization of the surrounding soft-tissues. In simulation studies, we find that imaging performance generally follows segmentation accuracy; however, slight underestimation of the size of the implant appears to be an advantage.

Conclusion: This work shows that it is possible to perform known-component reconstruction without prior knowledge of the known component. In conjunction with the Poly-KCR technique, very little needs to be known about the metal implant and system beforehand, which will allow more widespread application in real patient studies.

10132-24, Session 5

Practical Interior tomography with small region piecewise model prior

Ryosuke Ueda, Takuya Nemoto, Hiroyuki Kudo, Univ. of Tsukuba (Japan)

Interior CT is one of the reconstruction method from incomplete projection data. In the method, the X-ray passes through only the Region-of-Interest. Hence, the method has various advantages, e.g., the reduction of radiation doze and the inspection of the Region-of-Interest (ROI) of large size target. These are highly expected to be implemented in practical application.
For a long time, the approximate solution has been studied because the Interior CT has not the unique solution. Recently, it has been proved that the unique solution for Interior CT problem can be obtained if we have a priori knowledge for the ROI. However, the priors shown in previous studies have problems for practical application, e.g., difficulty to know the true prior and the image degradation due to patchy artifacts. This paper proposes more practical prior, which assumes piecewise constant or piecewise polynomial inner the ROI. Unlike the previous piecewise prior models, the proposed prior needs just a small region inner the ROI. The piecewise prior models are implemented by total variation (TV). We also propose the method without identifying optimal layout of the prior region. In the method, the prior region is placed as band-like shape near the ROI boundary. Using the proposed method and Compressed Sensing based technique, we can reconstruct the reasonable image stably. The experimental results and the reduction of the patchy artifacts compared with previous method are presented.

10132-25, Session 5

SparseCT: Interrupted-beam acquisition and sparse reconstruction for radiation dose reduction

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State-of-the-art low-dose CT methods reduce the x-ray tube current and use iterative reconstruction methods to denoise the resulting images. However, there are compromises between denoising and image quality, and in typical clinical practice, only moderate dose reductions up to 30-40% are accepted. An alternative approach is to reduce the number of full-tube-current x-ray projections and use compressed sensing to reconstruct the undersampled data. This idea was recognized in the early days of compressed sensing and proposals for CT dose reduction appeared soon afterwards. However, no practical means of undersampling has yet been demonstrated in the challenging environment of a rapidly rotating CT gantry. In this work, we propose a moving multislit collimator as a practical incoherent undersampling scheme for compressed sensing CT and evaluate its application for radiation dose reduction. The proposed collimator is composed of narrow slits and moves linearly along the slice dimension (z), to interrupt the incident beam in different slices for each x-ray tube angle (?). The reduced projection dataset is then reconstructed using a sparsity-based approach, where 3D image gradients are employed to enforce sparsity. The effects of the collimator slits on the beam profile were measured and represented as a continuous slice profile, which was included in the reconstruction algorithm. SparseCT was tested using retrospective undersampling and compared against commercial current-reduction techniques on phantoms and in vivo studies. Initial results suggest that SparseCT may enable higher performance than current-reduction, particularly for high dose reduction factors. The design of the proposed collimator is currently underway

10132-26, Session 5

Localized and efficient cardiac CT reconstruction

Darin P. Clark, Cristian T. Badea, Duke Univ. School of Medicine (United States)

The superiority of iterative reconstruction techniques over classic analytical ones is well documented in a variety of CT imaging applications where radiation dose and sampling time are limiting factors. However, by definition, the iterative nature of advanced reconstruction techniques is accompanied by a substantial increase in data processing time, greatly slowing the progress of the state-of-the-art. This problem is further exacerbated in temporal and spectral CT reconstruction problems where the gap between the amount of data acquired and the amount of data to be reconstructed is exaggerated within the framework of compressive sensing. Two keys to overcoming this barrier include (1) advancements in cost-efficient parallel-computing technology and (2) advancements in data efficient reconstruction strategies which operate at a lower dimensionality than the data to be reconstructed. In this work, we propose a novel, two-stage strategy for 4D cardiac CT reconstruction which leverages these two keys by (1) exploiting massively parallel GPU computing hardware and by (2) reconstructing temporal contrast on a limited spatial domain. Combining GPU computing with reconstruction on a limited domain provides further synergistic benefits by reducing the problem size such that it fits entirely within the memory constraints of the GPU. Following a review of the proposed algorithm, we demonstrate its application to the 4D MOBY mouse phantom, providing a preliminary account of the algorithm’s potential. For the conference paper we will further develop our GPU code for improved efficiency, and we will apply it to in vivo mouse data acquired with our micro-CT scanner.

10132-27, Session 6

Driving CT developments the last mile: case examples of successful and somewhat less successful translations into clinical practice *(Keynote Presentation)*

Aaron Sodickson, Brigham and Women’s Hospital (United States)

No Abstract Available

10132-28, Session 6

Dose comparison between CTDI and the AAPM Report No. 111 methodology in adult, adolescent, and child head phantoms

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The standard computed tomography dose index (CTDI) metric underestimates scatter radiation in cone beam computed tomography (CBCT); therefore, the American Association of Physicists in Medicine (AAPM) Task Group 111 proposed a new dosimetry methodology to measure equilibrium dose at the center of a phantom (z = 0) using a 2-cm thimble ionization chamber. In this study, we implement the CTDI and AAPM method with a thimble chamber on adult, adolescent, and child head phantoms using the Toshiba Aquilion One CBCT and compare the results to the CTDI measured with a pencil chamber. Following the AAPM protocol, the equilibrium doses (Deq) normalized to 100 mAs at phantom center, periphery, and by the CTDIw equation are 20.13 ± 0.19, 21.53 ± 0.48, and 20.93 ± 0.40 mGy for adult; 21.55 ± 0.40, 21.14 ± 0.43, and 21.08 ± 0.45 mGy for adolescent; and 24.58 ± 0.40, 24.92 ± 0.85, and 24.77 ± 0.72 mGy for child, respectively. The CTDIw,100mm, which measured 17.70, 19.86, and 22.43 mGy for adult, adolescent and child respectively, is about 10% lower than the corresponding Deq. The extended AAPM method proposed by Deman et al., which estimates dose profile at other planes (z ≠ 0), has demonstrated consistency between theory and measurements for all phantoms. Using adult and pediatric head phantoms, we have emphasized the practical aspects of CBCT dosimetry including relative convenience of the CTDI method and accuracy of the AAPM method, but also proposed a method to approximate Deq for different sized patients.

10132-29, Session 6

Skin dose mapping for non-uniform x-ray fields using a backscatter point spread function

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Beam shaping devices like ROI attenuators and compensation filters modulate the intensity distribution of the x-ray beam incident on the patient. This results in a spatial variation of skin dose due to the variation of primary radiation and also a variation in backscattered radiation from the patient. To determine the backscatter component, backscatter point spread functions (PSF) are generated using EGS Monte-Carlo software. For this study, PSF's were determined by simulating a 1 mm beam incident on the lateral surface of an anthropomorphic head phantom and a 20 cm thick PMMA block phantom. The backscatter PSF for the head phantom is curve fit with a Gaussian function and for the PMMA phantom with a Lorentzian function after being normalized to the primary dose intensity (PSFn). PSFn is convolved with the primary dose distribution to generate the scatter dose distribution, which is added to the primary to obtain the total dose distribution. The backscatter convolution technique is incorporated in the dose tracking system (DTS), which tracks skin dose during fluoroscopic procedures and provides a color map of the dose distribution on a 3D patient graphic model. A convolution technique is developed for the backscatter dose determination for the non-uniformly spaced graphic-model surface vertices. A Gafchromic film validation was performed for shaped x-ray beams generated with an ROI attenuator and with two compensation filters inserted into the field. The total dose distribution calculated by the backscatter convolution technique closely agreed with that measured with the film.

10132-30, Session 7

Effect of spatio-energy correlation in PCD due to charge sharing, scatter and secondary photons

Paurakh L. Rajbhandary, Scott S. Hsieh, Norbert J. Pelc, Stanford Univ. (United States)

Charge sharing, scatter and fluorescence events in photon counting detector (PCD) can result in multi-counting of a single incident photon in neighboring pixels. This causes energy distortion in a single pixel and correlation across energy bins in neighboring pixels (spatio-energy correlation). If a "macro-pixel" is formed by combining multiple small pixels it will exhibit correlations across energy bins. Charge sharing and fluorescence escape are dependent on pixel size and detector material. Accurately modeling these effect can be crucial for detector design and for model based correction. This study derives an accurate model for the multi-counting events and investigates its effect in virtual non-contrast and effective monoenergetic imaging applications. 1 mm2 square macro-pixels formed by binning 4x4 250x250 m2, 2x2 500 m2 or a single 1 mm2 CdTe PCD detectors with the same flux were simulated. Pulse pile-up was ignored. Mean and covariance matrix of measured photon counts is derived analytically using pre-computed spatio-energy response functions (SERF) estimated from Monte Carlo simulation. Based on Cramér-Rao Bound, a macro-pixel with 250x250 μm2 sub-pixels shows ~2.2 times worse variance than a single 1 mm2 pixel for spectral imaging, while its penalty for conventional imaging is <10% compared to a single 1 mm2 pixel.

10132-31, Session 7

Improving material separation of high-flux whole-body photon counting computed tomography by K-edge pre-filtration

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Photon counting detectors in computed tomography (CT) allow for measuring the energy of the incident x-ray photons within certain energy windows. This information can be used to enhance contrast or reconstruct CT images of different material bases. Compared to energy integrating CT-detectors, pixel dimensions have to be smaller to limit the negative effect of pulse pile-up at high X-ray flux. Unfortunately, reducing the pixel size leads to increased K-escape and charge sharing effects. As a consequence, an incident X-ray photon may create more than one detector signal, and with deteriorated energy information. In earlier simulations studies it has been shown that these limitations can be mitigated by optimizing the X-ray spectrum by K-edge pre-filtration. In the current study, we have used a prototype CT scanner with high-flux capable photon counting detector for experiments, in which for the first time a pre-patient hafnium filter was installed. Our measurement results demonstrate substantial improvement of the material decomposition capability at comparable dose levels. The results are in agreement with the predictions provided by simulations.

10132-32, Session 7

Nanoparticle imaging probes for molecular imaging with computed tomography and application to cancer imaging

Ryan K. Roeder, Univ. of Notre Dame (United States)

Precision imaging is needed to realize precision medicine in cancer detection and treatment. Molecular imaging offers the ability to target and identify tumors, associated abnormalities, and specific cell populations with overexpressed receptors (e.g., HER2). Nuclear imaging and radionuclide probes provide high sensitivity but subject the patient to a high radiation dose and provide limited spatiotemporal information, requiring combined computed tomography (CT) for anatomic imaging. Therefore, nanoparticle contrast agents have been designed for enabling molecular imaging and improving detection in CT alone. Core-shell nanoparticles provide a powerful platform for designing tailored probes. The composition of the core is chosen for enabling strong X-ray contrast, multi-agent imaging with photon-counting spectral CT, and multimodal imaging. A silica shell is used for protective, biocompatible encapsulation of the core composition, volume-loading fluorophores or radionuclides for multimodal imaging, and facile surface functionalization with antibodies or small molecules for targeted delivery. Bisphosphonate functionalized Au nanoparticles were demonstrated to enhance sensitivity and specificity for the detection of breast microcalcifications by conventional radiography and CT in both normal and dense mammary tissue using murine models. Moreover, photon-counting spectral CT enabled quantitative material decomposition of the Au and calcium signals. Multi-agent (k-edge) imaging and quantitative molecular imaging with spectral CT was demonstrated using current clinical agents (iodine and BaSO4) and a proposed spectral library of contrast agents (Gd2O3, HfO2, and Au). Immunoconjugated Au@SiO2 nanoparticles enabled highly-specific targeting of HER2+ breast cancer cells, as well as CD133+ ovarian cancer stem cells, and are being investigated in tumor models.

10132-33, Session 7

Ultra-high spatial resolution, multi-energy CT using photon counting detector technology

Shuai Leng, Mayo Clinic (United States); Ralf Gutjahr, Siemens Healthineers (Germany); Andrea Ferrero, Mayo Clinic (United States); Steffen Kappler, André Henning, Siemens Healthineers (Germany); Ahmed Halaweish, Siemens Healthineers (United States); Wei Zhou, Juan Cardona Montoya , Cynthia H. McCollough, Mayo Clinic (United States)

Two ultra-high-resolution (UHR) imaging modes, each with two energy thresholds, were implemented on a research, whole-body photon-counting-detector (PCD) CT scanner, referred to as sharp and UHR. The UHR mode has a pixel size of 0.25 mm at iso-center for both energy thresholds, with a collimation of 32 x 0.25 mm. The sharp mode has a 0.25 mm pixel for the low-energy threshold and a 0.5 mm for the high-energy threshold, with a collimation of 48 x 0.25 mm. Kidney stones with mixed mineral composition and lung nodules with different shapes were scanned using both modes, and with the standard imaging mode, referred to as macro mode (0.5 mm pixel and 32 x 0.5 mm collimation). Evaluation and comparison of the three modes focused on the ability to accurately delineate anatomic structures using the high-spatial resolution capability and the ability to quantify stone composition using the multi-energy capability. The low-energy threshold images of the sharp and UHR modes showed better shape and texture information due to the achieved higher spatial resolution, although noise was also higher. No noticeable benefit was shown in multi-energy analysis using UHR compared to standard resolution (macro mode) when standard doses were used. This was due to excessive noise in the higher resolution images. However, UHR scans at higher dose showed improvement in multi-energy analysis over macro mode with regular dose. To fully take advantage of the higher spatial resolution in multi-energy analysis, either increased radiation dose, or application of noise reduction techniques, is needed.

10132-34, Session 8

Low signal correction scheme for low dose CBCT: The good, the bad, and the ugly

Daniel Gomez-Cardona, Ran Zhang, Ke Li, Juan Pablo Cruz-Bastida, Guang-Hong Chen, Univ. of Wisconsin School of Medicine and Public Health (United States)

Flat panel detector based C-arm Cone-beam CT (CBCT) systems have been widely introduced to image-guided interventions and radiation therapy, naturally assuring to perform low dose imaging to reduce unnecessary exposure, not only to the patient, but also to the medical staff during the interventional procedures. When the exposure level is reduced, the overall noise magnitude increases and noise streaks appear in the final reconstructed image due to photon starvation caused by highly attenuating regions of the human anatomy. Several approaches, from simple to highly complex have been proposed for multi-detector CT applications in an attempt to mitigate the overall noise and artifacts caused by low photon counts at the detector. Some involve: apodizing the ramp kernel used before backprojection, using an adaptive trimmed filter based on local flux information, employing penalized-likelihood approaches for sinogram smoothing, and incorporating statistical models into the so-called model based iterative reconstruction framework. This work presents a simple yet powerful scheme for low signal correction in low dose CBCT, by the implementation of local anisotropic diffusion filtration of the sinogram data in the raw measurements domain before the logarithmic operation is performed. The advantages and potential challenges of the method are investigated. It was found that the proposed scheme reduces overall noise magnitude and most importantly, mitigates noise streaks efficiently without sacrificing spatial resolution. Yet, caution must be taken since, in some cases, spurious information from very noisy data may cause artifactual features on the final image when low signal correction is performed.

10132-35, Session 8

High-resolution cone-beam CT of the extremities with a CMOS detector: task-based optimization of scintillator thickness

Qian Cao, Michael Brehler, Alejandro Sisniega, Joseph W. Stayman, Johns Hopkins Univ. (United States); John Yorkston, Carestream Health, Inc. (United States); Jeffrey H. Siewerdsen, Wojciech Zbijewski, Johns Hopkins Univ. (United States)

Purpose: CMOS x-ray detectors offer small pixel sizes and low electronic noise that may support the development of novel high-resolution imaging applications of cone-beam CT (CBCT). We investigate the effects of CsI scintillator thickness on the performance of CMOS detectors in high resolution imaging tasks, in particular in quantitative imaging of bone microstructure in extremity CBCT.

Methods: A scintillator thickness-dependent cascaded systems model of CMOS x-ray detectors was developed. Detectability in low-, high- and ultra-high resolution imaging tasks (Gaussian with FWHM of ~250 ?m, ~80 ?m and ~40 ?m, respectively) was studied as a function of scintillator thickness using the theoretical model. Experimental studies were performed on a CBCT test bench equipped with DALSA Xineos3030 CMOS detectors (99 ?m pixels) with CsI scintillator thicknesses of 400 ?m and 700 ?m, and a 0.3 FS compact rotating anode x-ray source. The evaluation involved a radiographic resolution gauge (0.6-5.0 lp/mm), a 127 ?m tungsten wire for assessment of 3D resolution, a contrast phantom with tissue-mimicking

inserts, and an excised fragment of human tibia for visual assessment of fine trabecular detail.

Results: Experimental studies show ~35% improvement in the frequency of 50% MTF modulation when using the 400 μm scintillator compared to the standard nominal CsI thickness of 700 μm. Even though the high-frequency DQE of the two detectors is comparable, theoretical studies show a 14% to 28% increase in detectability index (d'2) of high- and ultra-high resolution tasks, respectively, for the detector with 400 μm CsI compared to 700 μm CsI. Experiments confirm the theoretical findings, showing improvements with the adoption of 400 μm panel in the visibility of the radiographic pattern (2x improvement in peak-to-through distance at 4.6 lp/mm) and a 12.5% decrease in the FWHM of the tungsten wire. Reconstructions of the tibial plateau reveal enhanced visibility of trabecular structures with the CMOS detector with 400 μm scinitllator.

Conclusion: Applications on CMOS detectors in high resolution CBCT imaging of trabecular bone will benefit from using a thinner scintillator than the current standard in general radiography. The results support the translation of the CMOS sensor with 400 μm CsI onto the clinical prototype of CMOS-based extremity CBCT.

10132-36, Session 8

Integration of prior CT into CBCT reconstruction for improved image quality via reconstruction of difference: first patient studies

Hao Zhang, Grace J. Gang, Junghoon Lee, John W. Wong, Joseph W. Stayman, Johns Hopkins Univ. (United States)

Purpose: There are many clinical situations where diagnostic CT is used for an initial diagnosis or treatment planning, followed by one or more CBCT scans that are part of an image-guided intervention. Because the high-quality diagnostic CT scan is a rich source of patient-specific anatomical knowledge, this provides an opportunity to incorporate the prior CT image into subsequent CBCT reconstruction for improved image quality. We propose a penalized-likelihood method called reconstruction of difference (RoD), to directly reconstruct differences between the CBCT scan and the CT prior. In this work, we demonstrate the efficacy of RoD with clinical patient datasets.

Methods: We introduce a data processing workflow using the RoD framework to reconstruct anatomical changes between the prior CT and current CBCT. This workflow includes processing steps to account for non-anatomical differences between the two scans including 1) scatter correction for CBCT datasets due to increased scatter fractions in CBCT data; 2) histogram matching for attenuation variations between CT and CBCT; and 3) registration for different patient positioning. CBCT projection data and CT planning volumes for two radiotherapy patients – one abdominal study and one head-and-neck study – were investigated.

Results: In comparisons between the proposed RoD framework and more traditional FDK and penalized-likelihood reconstructions, we find a significant improvement in image quality when prior CT information is incorporated into the reconstruction. RoD is able to provide additional low-contrast details while correctly incorporating actual physical changes in patient anatomy.

Conclusions: The proposed framework provides an opportunity to either improve image quality or relax data fidelity constraints for CBCT imaging when prior CT studies of the same patient are available. Possible clinical targets include CBCT image-guided radiotherapy and CBCT image-guided surgeries.

10132-37, Session 8

Brain perfusion imaging using a reconstruction of difference approach for cone-beam computed tomography

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

Purpose: To improve the timely detection and treatment of ischemic stroke, recent efforts include the development of cone-beam CT (CBCT) systems for perfusion imaging and new approaches to estimate perfusion parameters despite slow rotation speeds compared to multi-detector CT (MDCT) systems. This work describes development of brain perfusion CBCT systems using a reconstruction of difference (RoD) approach to enable perfusion imaging on a newly developed CBCT head scanner prototype.

Methods: A new reconstruction approach using RoD with a penalized-likelihood framework was developed to directly control image properties of an enhancement difference image. A digital perfusion simulation was developed to give a realistic representation of brain anatomy, artifacts, noise, scanner limitations, and dynamic properties. This simulation includes a digital brain phantom, time-attenuation curves and noise parameters, a novel forward projection method for computational efficiency, and perfusion parameters calculation.

Results: Our results show the feasibility of estimating perfusion parameters from a set of images reconstructed from short arc length scans as low as 60 degrees. The RoD framework significantly reduces noise and time-varying artifacts from inconsistent projections. Proper regularization and the use of overlapping reconstructed arcs can potentially further decrease bias and increase temporal resolution respectively.

Conclusions: A digital brain perfusion simulation with a RoD approach has been developed and supports the feasibility of using a CBCT head scanner for perfusion imaging. Future work will include testing with data acquired using a 3D-printed perfusion phantom currently under development and translation to preclinical and clinical studies.

10132-38, Session 8

Deformable known component model-based reconstruction for coronary CT angiography

Xiaoxuan Zhang, Steven W. Tilley II, Shiyu Xu, Aswin J. Mathews, Johns Hopkins Univ. (United States); Elliot R. McVeigh, Univ. of California, San Diego (United States); Joseph W. Stayman, Johns Hopkins Univ. (United States)

Purpose: Atherosclerosis detection remains challenging in coronary CT angiography for patients with cardiac implants. Pacing electrodes of a pacemaker or lead components of a defibrillator can create substantial blooming and streak artifacts in the heart region, severely hindering the visualization of a plaque of interest. We present a novel reconstruction method that incorporates a deformable model for metal leads to eliminate metal artifacts and improve anatomy visualization even near the boundary of the component.

Methods: The proposed reconstruction method, referred as Poly-dKCR, includes a novel parameterization of the component that integrates deformation, a 3D-2D preregistration process that estimates component shape and position, and a polyenergetic forward model for x-ray propagation through the component where the spectral properties are jointly estimated. The methodology was tested on physical data of a cardiac phantom acquired on a CBCT testbench. The phantom included a simulated vessel, a metal wire emulating a pacing lead, and a small Teflon sphere attached to the vessel wall, mimicking a calcified plaque. The proposed method was also compared to the traditional FBP reconstruction.

Results: While metal artifacts were sufficiently strong in standard FBP reconstructions to nearly obscure the small Teflon target (within 2 mm of the metal wire), the Poly-dKCR approach significantly improved the visibility of this feature. The attenuation of the Teflon bead improved to 0.0408 mm-1 with Poly-dKCR from 0.0195 mm-1 with FBP – much closer to the expected 0.0414 mm-1.

Conclusion: The proposed method has the potential to improve plaque visualization in coronary CT angiography in the presence of wire-shaped metal components.

10132-39, Session 9

Improving image quality in laboratory x-ray phase-contrast imaging

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Grating-based X-ray phase-contrast (gbPC) is known to provide significant benefits for biomedical imaging. To investigate these benefits, a high-sensitivity gbPC micro-CT setup for small (~5cm) biological samples has been constructed. Unfortunately, high differential-phase sensitivity is accompanied with an increased magnitude of data processing artifacts, limiting the quality of tomographic reconstructions. Most importantly, processing of phase-stepping data with incorrect stepping positions can introduce artifacts resembling Moiré fringes to the projections. Additionally, tomogram resolution is limited by the focal spot size of the X-ray source.

Here we present a set of algorithms to minimize artifacts, increase resolution and improve visual impression of projections and tomograms from the examined setup. Two algorithms for artifact reduction were examined: Firstly, a correction algorithm exploiting correlations of the artifacts and differential-phase data was developed and tested. Artifacts could be reliably removed without compromising image data. Secondly, a new algorithm for flat-field selection was implemented and shown to exclude flat-fields with strong artifacts. Both procedures successfully improved image quality of projections and tomograms. Deconvolution of all projections of a CT scan can minimize blurring introduced by the finite size of the X-ray source focal spot. Application of the Richardson-Lucy deconvolution algorithm to gbPC-CT projections was shown to improve the resolution of phase-contrast tomograms. Additionally, nearest-neighbor interpolation of projections was shown to improve the visual impression of very small features in phase-contrast tomograms. In conclusion, we achieved an increase in image resolution and quality for the investigated setup, which leads to an improved detection of very small sample features, thereby maximizing the setup's utility.

10132-40, Session 9

First experience with x-ray dark-field radiography for human chest imaging

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Purpose: To evaluate the performance of an experimental X-ray dark-field radiography system for chest imaging in humans and to compare with conventional diagnostic imaging. Materials and Methods: The study was institutional review board (IRB) approved. A single human cadaver (52 years, female, height: 173 cm, weight: 84 kg, chest circumference: 97 cm) was imaged within 24 hours post mortem on the experimental x-ray dark-field system. In addition, the cadaver was imaged on a clinical CT system to obtain a reference scan. The grating-based dark-field radiography setup was equipped with a set of three gratings to enable grating-based dark-field contrast x-ray imaging. The prototype operates at an acceleration voltage of up to 70 kVp and with a field-of-view large enough for clinical chest x-ray (>35 x 35 cm2). Results: It was feasible to extract x-ray dark-field signal of the whole human thorax, clearly demonstrating that human x-ray dark-field chest radiography is feasible. Lung tissue produced strong scattering, reflected in a pronounced x-ray dark-field signal. The ribcage and the backbone are less prominent than the lung but are also distinguishable. Finally, the soft tissue is not present in the dark-field radiography. The regions of the lungs affected by edema, as verified by CT, showed less dark-field signal compared to healthy lung tissue. Conclusion: Our results reveal the current status of translating dark-field imaging from a micro (small animal) scale to a macro (patient) scale. The performance of the experimental x-ray dark-field radiography setup offers, for the first time, obtaining multi-contrast chest x-ray images (attenuation and dark-field signal) from a human cadaver.

10132-41, Session 9

A resolution-enhancing image reconstruction method for few-view differential phase-contrast tomography

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It is well-known that properly designed iterative image reconstruction methods for few-view data can facilitate reductions in imaging doses and data-acquisition times in tomographic imaging. The ability to do so is particularly important for emerging modalities such as di?erential X-ray phase-contrast tomography (D-XPCT). An important application of D-XPCT is high-resolution imaging of biomedical samples. However, reconstructing high resolution D-XPCT images from few-view tomographic measurements remains a challenging task that has not been systematically explored in the literature. In recent years, the use of sparsity-promoting regularization has proven to be useful for few-view image reconstruction. However, choosing the optimal sparsifying operator for a particular object remains challenging in practice. As opposed to the conventional approach of keeping a statistically motivated data fidelity term fixed and attempting to determine an e?ective choice for regularization term, in this work, an alternative choice for the data fidelity term is proposed. A non-conventional (filtered) objective function is investigated for use in few-view D-XPCT image reconstruction. It is demonstrated that the resulting iterative algorithm can mitigate the high-frequency information loss caused by data incompleteness and produce images that have better preserved high spatial frequency content, as opposed to those produced by use of a conventional penalized least squares (PLS) estimator. The proposed algorithm is investigated by use of experimental data produced by an edge illumination XPCT imager.

10132-42, Session 9

A joint-reconstruction approach for single-shot edge illumination x-ray phase-contrast tomography

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Edge illumination X-ray phase-contrast tomography (EIXPCT) is an emerging imaging technique that seeks to circumvent the limitations of previous benchtop implementations of X-ray phase-contrast tomography. The goal of EIXPCT is to produce images that separately depict the spatially variant X-ray refractive index and absorption distributions within an object. As with grating- or analyzer-based methods, conventional image reconstruction methods for EIXPCT require that two or more images are acquired at each tomographic view angle. This requirement leads to increased data-acquisition times and radiation doses, which can hinder in vivo applications. To circumvent this, a joint reconstruction (JR) approach is proposed that concurrently produces estimates of the refractive index and absorption distributions from a tomographic data set containing only a single image per tomographic view angle. The JR reconstruction method solves a non-linear optimization problem by use of a novel iterative gradient-based algorithm. The JR method is validated and investigated by use of both computer-simulated and experimental EIXPCT data.

10132-43, Session 9

Design of a sensitive grating-based phase contrast mammography prototype

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Grating-based phase contrast mammography can help facilitate breast cancer diagnosis, as several research works have demonstrated. To translate this technique to the clinics, it has to be adapted to cover a large field of view within a limited exposure time and with a clinically acceptable radiation dose. This indicates that a straightforward approach would be to install a grating interferometer (GI) into a commercial mammography device. We developed a wave propagation based optimization method to select the most convenient GI designs in terms of phase and dark-field sensitivities for the Philips Microdose Mammography (PMM) setup. The phase sensitivity was defined as the minimum detectable breast tissue electron density gradient, whereas the dark-field sensitivity was defined as its corresponding signal-to-noise Ratio (SNR). To be able to derive sample-dependent sensitivity metrics, a visibility reduction model for breast tissue was formulated, based on previous research works on the dark-field signal and utilizing available Ultra-Small-Angle X-ray Scattering (USAXS) data and the outcomes of measurements on formalin-fixed breast tissue specimens carried out in tube-based grating interferometers. The results of this optimization indicate the optimal scenarios for each metric are different and fundamentally depend on the noise behavior of the signals and the visibility reduction trend with respect to the system autocorrelation length. In addition, since the inter-grating distance is constrained by the space available between the breast support and the detector, the best way we have to improve sensitivity is to count on a small G2 pitch.

10132-44, Session 9

Theoretical and experimental investigation of potential bias in signal estimation for grating-based x-ray multi-contrast imaging

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In grating based multi-contrast x-ray imaging, signals of three contrast mechanisms: absorption contrast, differential phase contrast (DPC) and dark-field contrast can be estimated from a single data acquisition with several phase steps. The extracted signals, N0 (related to absorption), N1 (related to dark-field) and φ (related to DPC) may be intrinsically biased. In this work, the biases of the extracted N0,N1 and φ from the well-known least square fitting method were theoretically derived. Furthermore, experimental data acquired from a benchtop grating-based x-ray multi-contrast data acquisition system equipped with a photon counting detector was used to validate the derived theoretical formulae for the signal bias of all three contrast mechanisms. The theoretical predictions were in good agreement with the experimental results. The bias of the absorption contrast is precisely zero. The signal bias for N1 (dark-field contrast) is inversely proportional to the number of phase steps and to the average fringe visibility of the grating interferometer. The bias of φ is related to several parameters, including the total exposure, the fringe visibility produced by the interferometer system and φ. The larger the exposure and fringe visibility, the smaller the bias of φ.

10132-45, Session 10

Estimating basis line-integrals in spectral distortion-modeled photon counting CT: K-edge imaging using dictionary learning-based x-ray transmittance modeling

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Photon counting detector (PCD) provides spectral information for estimating basis line-integrals; however, the recorded spectrum is distorted from spectral response effect (SRE). One of the conventional approaches to compensate for the SRE is to incorporate the SRE model in the forward imaging process. For this purpose, we recently developed a three-step algorithm as a (~1,000) fast alternative to maximum likelihood (ML) estimator based on the modeling of x-ray transmittance with low-order polynomials. However, it is limited on the case when K-edge is absent due to the smoothness property of the low-order polynomials. In this paper, we propose a dictionary learning-based x-ray transmittance modeling to address this limitation. More specifically, we design a dictionary which consists of several energy-dependent bases to model an unknown x-ray transmittance by training the dictionary based on various known x-ray transmittance as a training data. We show that the number of bases in the dictionary can be as large as the number of energy bins and that the modeling error is relatively small considering a practical number of energy bins. Once the dictionary is trained, the three-step algorithm can be derived as follows: estimating the unknown coefficients of the dictionary, estimating basis line-integrals, and then correcting for a bias. We validate the proposed method with various simulation studies for K-edge imaging with gadolinium contrast agent, and show that both bias and computational time are substantially reduced compared to those of the ML estimator.

10132-46, Session 10

Spectral CT metal artifact reduction with an optimization-based reconstruction algorithm

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Metal objects cause artifacts in computed tomography (CT) images. This work investigated the feasibility of a spectral CT method to reduce metal artifacts. Spectral CT acquisition combined with optimization-based reconstruction is proposed to reduce artifacts by modeling the physical effects that cause metal artifacts and by providing the flexibility to selectively remove corrupted spectral measurements in the spectral-sinogram space. The proposed 'one-step' spectral CT image reconstruction (OSSCIR) algorithm directly estimates the basis material maps while enforcing convex constraints. The incorporation of constraints on the reconstructed basis material maps is expected to mitigate undersampling effects that occur when corrupted data is excluded from reconstruction. The feasibility of the OSSCIR algorithm to reduce metal artifacts was investigated through simulations of a pelvis phantom and experiments on a bench-top photon counting CT system. The OSSCIR algorithm was investigated with and without the use of a third basis material representing metal. The effects of excluding data corrupted by metal were also investigated. The results demonstrated that the proposed OSSCIR algorithm reduced metal artifacts and improved CT number accuracy. For example, CT number error in a bright shading artifact region was reduced from 403 HU in the reference filtered backprojection reconstruction to 33 HU using the proposed algorithm in simulation. In the dark shading regions, the error was reduced from 1141 HU to 25 HU. Of the investigated approaches, decomposing the data into three basis material maps and excluding the corrupted data demonstrated the greatest reduction in metal artifacts.

10132-47, Session 10

A multi-step method for material decomposition in spectral CT

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A multi-step algorithmic method of material decomposition is proposed for spectral CT where the problem is formulated as series of simpler decomposition rather than solved simultaneously. The method is a variation of material decomposition strategy where the solution provides maps of the volume fractions of each of the constituents. A simple domain of three materials; water, hydroxyapatite and iodine was explored. The results showed an improvement in accuracy over a similar method where the volume fractions of the materials were found simultaneously. In the multi-step approach, the problem is reformulated in each step thereby improving flexibility of choice of energy bins and choice of best suitable energy model at each step. This approach offers several possibilities when separating mixtures of low and high attenuating materials. Complete work will include detailed analysis of this approach and experimental data with more complex mixtures.

10132-48, Session 10

Resolution improvement in x-ray imaging with an energy-resolving detector

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In x-ray imaging, improving spatial resolution is an important goal, but developing detectors with smaller pixels is technically challenging. We demonstrate a technique for improving the spatial resolution by utilizing the fact that linear attenuation coefficients of all substances within the human body can be expressed, to a good approximation, as a linear combination of two basis functions, or three if there is iodine contrast present in the image. When the x rays pass an interface parallel to the beam direction, the exponential attenuation law makes the linear attenuation coefficient measured by the detector a nonlinear combination of the linear attenuation coefficients on each side of the interface. This so-called nonlinear partial volume effect causes the spectral response to be dependent on the steepness of interfaces in the imaged volume.

In his work, we show how this effect can be used to improve the spatial resolution in spectral projection x-ray imaging and quantify the achievable resolution improvement. We simulate x-ray transmission imaging of sharp and gradual changes in the projected path length of iodine contrast with an energy-resolving photon-counting detector and demonstrate that the slope of the transition can be determined from the registered spectrum. By simulating an ideal step transition, we study the improvement in the edge-spread function and, by differentiation, the point-spread function.

The results show that the method is able to improve spatial resolution when imaging interfaces of highly attenuating objects.

10132-49, Session 10

Classification of breast microcalcifications using spectral mammography

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Purpose: To investigate the potential of spectral mammography to distinguish between type I calcifications, consisting of calcium oxalate dihydrate or weddellite compounds that are more often associated with benign lesions, and type II calcifications containing hydroxyapatite which are predominantly associated with malignant tumors.

Methods: Using a ray tracing algorithm, we simulated the total number of x-ray photons recorded by the detector at one pixel from a single pencil-beam projection through a breast of 50/50 (adipose/glandular) tissues with inserted microcalcifications of different types and sizes. Material decomposition using two energy bins was then applied to characterize the simulated calcifications into hydroxyapatite and weddellite using maximum-likelihood estimation, taking into account the polychromatic source, the detector response function and the energy dependent attenuation.

Results: Simulation tests were carried out for different doses and calcification sizes for multiple realizations. The results were summarized using receiver operating characteristic (ROC) analysis with the area under the curve (AUC) taken as an overall indicator of discrimination performance and showing high AUC values up to 0.99.

Conclusion: Our simulation results obtained for a uniform breast imaging phantom indicate that spectral mammography using two energy bins has the potential to be used as a non-invasive method for discrimination between type I and type II microcalcifications to improve early breast cancer diagnosis and reduce the number of unnecessary breast biopsies.

10132-50, Session 11

MLAA-based RF surface coil attenuation estimation in hybrid PET/MR imaging

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Attenuation correction (AC) for both patient and hardware attenuation of the 511 keV annihilation photons is required for accurate PET quantification. In hybrid PET/MR imaging, AC for stationary hardware components such as patient table and MR head coil is performed using CT-derived attenuation templates. AC for flexible hardware components such as MR

radiofrequency (RF) surface coils is more challenging. Registration-based approaches, aligning scaled CT-based attenuation templates with the current patient position, have been proposed but are not used in clinical routine. Ignoring RF coil attenuation has been shown to result in local activity underestimation values of up to 15 %. We propose to employ the maximum-likelihood reconstruction of attenuation and activity (MLAA) algorithm to obtain an estimate of the RF coil attenuation. Starting with an initial attenuation map not including the RF coil, the attenuation update of MLAA is applied outside the body outline only, allowing to estimate RF coil attenuation without changing the patient attenuation map. The proposed method is investigated using phantom and patient data acquired with a Siemens Biograph mMR. For the phantom data, average activity underestimation compared to the ground truth was reduced from -5.0 % to -0.7 % when using the proposed method. Patient data revealed an average activity underestimation of -7.8 % for the abdominal region and -5.3 % for the thoracic region when ignoring RF coil attenuation.

10132-51, Session 11

Nonlinear PET parametric image reconstruction with MRI information using kernel method

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Positron Emission Tomography (PET) is a functional imaging modality widely used in oncology, cardiology, and neurology. It is highly sensitive, but suffers from relatively poor spatial resolution, as compared with anatomical imaging modalities, such as magnetic resonance imaging (MRI). With the recent development of combined PET/MR systems, we can improve the PET image quality by incorporating MR information. Previously kernel learning based on MR information has been successfully embedded into static PET reconstruction and direct Patlak reconstruction. Here we extend this method to direct reconstruction of nonlinear parameters in a compartment model by using the alternating direction of multiplier method (ADMM) algorithm. Preliminary studies show that the proposed method can produce superior parametric images compared with existing methods.

10132-52, Session 11

Fast and accurate Monte-Carlo based system response modeling for a digital whole-body PET

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Recently, we have developed a digital whole-body PET scanner based on SiPMs and multi-voltage threshold (MVT) digitizers. To mitigate the impact of resolution degrading factors, an accurate system response is calculated by Monte Carlo methods, which is computationally expensive. To address the problem, we improve the method of using symmetries by simulating a small axial wedge region. A basic subset of system matrix were firstly calculated from the simulation region by performing symmetries based on events. The remaining system matrix were calculated by performing symmetries based on the basic subset generated above. This approach takes full advantage of intrinsic symmetries in the cylindrical PET system without significantly increasing the computation cost of symmetries. A total of 4224 symmetries are exploited in this work. It took 17 days to generate the system maxtrix on 160 cores of Xeon 2.5 GHz. Both simulation and experimental data are used to evaluate the accuracy of system response modeling. The simulation studies show the full-width-half-maximum of a line source are 2.1 mm and 3.8 mm at the center of FOV and 200 mm off the center of FOV. Experimental results show the 2.4 mm rods in the Derenzo phantom image can be well distinguished.

10132-53, Session 11

Improved attenuation correction for respiratory gated PET/CT with extended-duration cine CT: a simulation study

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Due to the wide variability of intra-patient respiratory motion patterns, traditional short-duration cine CT used in respiratory gated PET/CT may be insufficient to match the PET scan data, resulting in suboptimal attenuation correction that eventually compromises the PET quantitative accuracy. Thus, extending the duration of cine CT can be beneficial to address this data mismatch issue. In this work, we propose to use long-duration cine CT for respiratory gated PET/CT, whose cine acquisition time is ten times as long as the traditional short-duration cine CT. We compare the proposed long-duration cine CT with the traditional short-duration cine CT through numerous phantom simulations with 11 respiratory traces measured during patient PET/CT scans. We evaluate the performance of different methods by calculating the root-mean-square-error values between the phase-gated cine CT images and the corresponding phase-gated PET attenuation images. Experimental results show that, the long-duration cine CT reduces the error of mismatch between PET and CT images by 42.5% on average, ranging from 14.5% to 70.0%, as compared to the traditional short-duration cine CT. The long-duration cine CT also reduces the misalignment and mismatch between adjacent slices in phase-gated CT images. The improvement on motion matching between PET and CT by extending the cine duration depends on the patient, with potentially greater benefits for patients with irregular breathing patterns or larger diaphragm movements.

10132-54, Session 11

Estimation of posterior image variance with sparsity-based object priors with application to MRI

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Point estimates, such as the maximum a posteriori (MAP) estimate, are commonly computed in image reconstruction tasks. However, such point estimates provide no information about the range of highly probable solutions or uncertainty in the computed estimate. Bayesian inference methods that seek to compute the posterior probability distribution function (PDF) of the object can achieve exactly these things, but are generally too computationally burdensome to be applied to medical image reconstruction problems. Moreover, sampling methods, such as the Monte Carlo Markov Chain (MCMC) method, require considerable expertise to run in a proper way. In this work, a computationally-efficient variational Bayesian inference approach is investigated for use in computing the posterior image variance. The posterior variance map provides valuable information that reveals how noise level, data-acquisition parameters, and specification of the object prior will affect the reliability of a reconstructed MAP image estimate. The methodology assumes that the object prior is described by a Laplacian distribution, which corresponds to use of an l1-norm-based penalty in the associated MAP estimator. The method is investigated by use of computer-simulated and clinical magnetic resonance imaging (MRI) data.

10132-55, Session 11

Affordable CZT SPECT with dose-time minimization

James W. Hugg, Brian W. Harris, Kromek (United States); Ian Radley, Kromek (United Kingdom)

PURPOSE

Pixelated CdZnTe (CZT) detector arrays are used in molecular imaging applications that can enable precision medicine, including small-animal SPECT, cardiac SPECT, molecular breast imaging (MBI), and general purpose SPECT. The interplay of gamma camera, collimator, gantry motion, and image reconstruction determines image quality and dose-time-FOV tradeoffs. Both dose and exam time can be minimized without compromising diagnostic content.

METHODS

Integration of pixelated CZT detectors with advanced ASICs and readout electronics improves system performance. Because historically CZT was expensive, the first clinical applications were limited to small FOV. Radiation doses were initially high and exam times long. Advances have significantly improved efficiency of CZT-based molecular imaging systems and the cost has steadily declined. We have built a general purpose SPECT system using our 40 cm x 53 cm CZT gamma camera with 2 mm pixel pitch and characterized system performance.

RESULTS

Compared to NaI scintillator gamma cameras: intrinsic spatial resolution improved from 3.8 mm to 2.0 mm; energy resolution improved from 9.8% to <4 % at 140 keV; maximum count rate is >1.5 times higher; non-detection camera edges are reduced ~3-fold. Scattered photons are greatly reduced in the photopeak energy window; image contrast is improved; and the optimal FOV is increased to the entire camera area.

CONCLUSION

Continual improvements in CZT detector arrays for molecular imaging, coupled with optimal collimator and image reconstruction, result in minimized dose and exam time. With CZT cost improving, affordable whole-body CZT general purpose SPECT is expected to enable precision medicine applications.

10132-78, Session PS1

Cone-beam CT image contrast and attenuation-map linearity improvement (CALI) for brain stereotactic radiosurgery procedures

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A Contrast and Attenuation–map (CT-number) Linearity Improvement (CALI) framework is proposed for cone-beam CT (CBCT) images used for brain stereotactic radiosurgery (SRS). The proposed framework is used together with our high spatial resolution iterative reconstruction algorithm and is tailored for the Leksell Gamma Knife ICON (Elekta, Stockholm, Sweden). The incorporated CBCT system in ICON facilitates frameless SRS planning and treatment delivery. The ICON employs a half-cone geometry to accommodate the existing treatment couch. This geometry increases the amount of artifacts and together with other physical imperfections causes image inhomogeneity and contrast reduction. Our proposed framework includes a preprocessing step, involving a shading and beam-hardening artifact correction, and a post-processing step to correct the dome/capping artifact caused by the spatial variations in x-ray energy generated by bowtie-filter. Our shading correction algorithm relies solely on the acquired projection images (i.e. no prior information required) and utilizes filtered-back-projection (FBP) reconstructed images to generate a segmented bone and soft-tissue map. Ideal projections are estimated from the segmented images and a smoothed version of the difference between the ideal and measured projections is used in correction. The proposed beam-hardening and dome artifact corrections are segmentation free. The CALI was tested on CatPhan, as well as patient images acquired on the ICON system. The resulting clinical brain images show substantial improvements in soft contrast visibility, revealing structures such as ventricles and lesions which were otherwise undetectable in FBP-reconstructed images. The linearity of the reconstructed attenuation-map was also improved, resulting in more accurate CT#.

10132-79, Session PS1

Dual energy approach for cone beam artifacts correction

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Cone beam computed tomography systems generate 3D volumetric images, which provide morphological information compared to radiography and tomosynthesis systems. However, reconstructed images by FDK algorithm contain cone beam artifacts when a cone angle is large. To reduce the cone beam artifacts, two-pass algorithm has been proposed. The two-pass algorithm considers the cone beam artifacts are mainly caused by high density materials, and proposes an effective method to estimate the error images (i.e., cone beam artifacts images) by high density materials. While this approach is simple and effective with a moderate cone angle (i.e., 5 ~ 7 degrees), the correction performance is degraded as the cone angle increases. In this work, we propose a new method to reduce cone beam artifacts using a dual energy technique. The basic idea of the proposed method is to estimate the error images generated by high density materials more reliably. To do this, projection data of the high density materials are extracted from dual energy CT projection data using a material decomposition technique, and then reconstructed by iterative reconstruction using total-variation regularization. The reconstructed high density materials are used to estimate the error images (i.e., cone beam artifacts images) from the original FDK images. The performance of the proposed method is compared with the two-pass algorithm using root mean square errors. The results show that the proposed method reduces the cone beam artifacts more effectively, especially with a large cone angle.

10132-80, Session PS1

A patch-based CBCT scatter artifact correction using prior CT

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We have developed a novel patch-based cone beam CT (CBCT) artifact correction method based on prior CT images. First, we used the image registration to align the planning CT with the CBCT to reduce the geometry difference between the two images. Then, we brought the planning CT-based prior information into the Bayesian deconvolution framework to perform the CBCT scatter artifact correction based on patch-wise nonlocal mean strategy. We evaluated the proposed correction method using a Catphan phantom with multiple inserts based on contrast-to-noise ratios (CNR) and signal-to-noise ratios (SNR), and the image spatial nonuniformity (ISN). All values of CNR, SNR and ISN in the corrected CBCT image were much closer to those in the planning CT images. The results demonstrated that the proposed CT-guided correction method could significantly reduce scatter artifacts and improve the image quality. This method has great potential to correct CBCT images allowing its use in adaptive radiotherapy.

10132-81, Session PS1

Shading correction algorithm for cone-beam CT in radiotherapy: extensive clinical validation of image quality improvement

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A shading correction algorithm for the improvement of cone-beam CT (CBCT) images (Phys. Med. Biol. 53 5719–33) has been further developed, optimised and validated extensively using a large number of clinical images. Additional processing steps have been added to allow the robust correction of lung images. A prototype stand-alone application has been developed which is fully automatic and can produce enhanced (shading-corrected) CBCT image volumes in around 6 seconds.

The algorithm has been validated using 135 clinical CBCT images of patients undergoing radiotherapy treatment of the pelvis, lungs and head & neck. An automated technique has been developed to efficiently analyse the large number of clinical images. Small regions of similar tissue (for example fat tissue) are automatically identified using CT images. The regions on the corresponding CBCT image are analysed to ensure that they do not contain pixels representing multiple types of tissue. The mean value of all selected pixels and the non-uniformity, defined as the standard deviation of the mean values in each small region, are calculated and compared for raw and corrected CBCT images.

Analysis of fat regions in pelvis images shows a median absolute difference in mean pixel value of 135.6 HU in raw CBCT images, which is reduced to 2.0 HU after the application of the shading correction algorithm. The median absolute difference in non-uniformity of fat tissue pixels is reduced from 45.6 in raw CBCT images to 7.1 in shading-corrected CBCT images. Similar results are obtained in the analysis of lung and head & neck images.

10132-82, Session PS1

A biomechanical modeling guided simultaneous motion estimation and image reconstruction technique (SMEIR-Bio) for 4D-CBCT reconstruction

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Four-dimensional (4D) cone-beam computed tomography (CBCT) enables motion tracking of anatomical structures and removes artifacts introduced by motion. However, the imaging time/dose of 4D-CBCT is substantially longer/higher than traditional 3D-CBCT. We previously developed a simultaneous motion estimation and image reconstruction (SMEIR) algorithm, to reconstruct high-quality 4D-CBCT from limited number of projections to reduce the imaging time/dose. However, the accuracy of SMEIR is limited in reconstructing low-contrast regions with fine structure details. In this study, we incorporate biomechanical modeling into the SMEIR algorithm (SMEIR-Bio), to improve the reconstruction accuracy at low-contrast regions with fine details. The efficacy of SMEIR-Bio is evaluated using a lung patient case and compared to that of the original SMEIR algorithm. Qualitative and quantitative comparisons showed that SMEIR-Bio greatly enhances the accuracy of reconstructed 4D-CBCT volume in low-contrast regions, which can potentially benefit multiple clinical applications including treatment outcome analysis.

10132-83, Session PS1

4D DSA reconstruction using tomosynthesis projections

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We investigate the use of tomosynthesis in 4D DSA to improve the accuracy of reconstructed vessel time-attenuation curves (TACs). It is hypothesized that a narrow-angle tomosynthesis dataset for each time point can be exploited to reduce artifacts caused by vessel overlap in individual projections. 4D DSA reconstructs time-resolved 3D angiographic volumes from a typical 3D DSA scan consisting of mask and iodine-enhanced C-arm rotations. Tomosynthesis projections are obtained either from a conventional C-arm rotation, or from a scanning-beam digital x-ray (SBDX) system. In the proposed method, rays of the tomosynthesis dataset which pass through multiple vessels can be ignored, allowing the non-overlapped rays to impart temporal information to the 4D DSA. The technique was tested in simulated scans of 2 to 4 mm diameter vessels separated by 2 to 5 cm, with TACs following either early or late enhancement. Uncorrected overlap artifact magnitudes were 2-21% in early enhancement TACs. Tomosynthesis reduced the artifact magnitude in TACs to <2% for vessel separations ≥ 3 cm and tomographic angles ≥ 6°. Smaller tomographic angle, smaller vessel separation and larger vessel diameter reduced the fraction of non-overlapped rays available for reconstruction. Use of tomosynthesis projections in 4D DSA can reduce TAC artifacts caused by vessel overlap, assuming a sufficient fraction of non-overlapped rays available in each time frame. SBDX can provide a tomosynthesis scan for each frame period in a rotational acquisition, whereas a standard C-arm geometry requires the grouping of multiple frames.

10132-84, Session PS1

Estimating 3D local noise power spectrum from a few FDK-reconstructed cone-beam CT scans

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The Noise Power Spectrum (NPS) is a major image quality metric that is useful in system characterization, optimization and in template design for model observers. CT noise is nonstationary. A faithful estimation of the local NPS for CT usually requires many repeated scans. We have previously developed a radial NPS method to estimate the 2D local NPS from a few FBP-reconstructed CT scans utilizing a polar separability: a 2D CT NPS can be factored into products of a 1D angular and a 1D radial function in polar coordinates . In this work we extend the 2D approach to estimate the 3D local NPS for FDK-reconstructed cone-beam CT (CBCT), since the CBCT NPS has similar property. The 3D NPS can be factored into a 1D angular function and a 2D radial planar function in cylindrical coordinates. The 2D radial planar function is a Kronecker tensor product determined by the FDK reconstruction filters. The 1D angular function is determined by the object structure and x-ray dose. We evaluated the accuracy of the proposed 3D local radial NPS method compared to the traditional local NPS estimates using simulated CBCT data. The results showed that the 3D radial local NPS method with only 2 to 6 scans yielded very small mean squared error relative to the reference truth compared to the traditional NPS method. Further evaluation of the proposed 3D local NPS method will be conducted using real phantom data and on improvement of detectability when used by a pre-whitening model observer.

10132-85, Session PS1

Motion vector field upsampling for improved 4D cone-beam CT motion compensation of the thorax

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To improve the accuracy of motion vector fields (MVFs) required for respiratory motion compensated (MoCo) CT image reconstruction without increasing the computational complexity of the MVF estimation approach, we propose a MVF upsampling method that is able to reduce the motion blurring in reconstructed 4D images. While respiratory gating improves the temporal resolution, it leads to sparse view sampling artifacts. MoCo image reconstruction has the potential to remove all motion artifacts while simultaneously making use of 100% of the rawdata. However the MVF accuracy is still below the temporal resolution of the CBCT data acquisition. Increasing the number of motion bins would increase reconstruction time and amplify sparse view artifacts, but not necessarily the accuracy of MVF. Therefore we propose a new method to upsample estimated MVFs and use those for MoCo. To estimate the MVFs, a modified version of the Demons algorithm is used. Our proposed method is able to interpolate the original MVFs up to a factor that each projection has its own individual MVF. To validate the method we use an artificially deformed clinical CT scan, with a breathing pattern of a real patient, and patient data acquired with a TrueBeam 4D CBCT system (Varian Medical Systems). We evaluate our method for different numbers of respiratory bins, each again with different upsampling factors. Employing our upsampling method, motion blurring in the reconstructed 4D images, induced by irregular breathing and the limited temporal resolution of phase–correlated images, is substantially reduced.

10132-86, Session PS1

Automated framework for estimation of lung tumor locations in kV-CBCT images for tumor-based patient positioning in stereotactic lung body radiotherapy

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Recently, image-guided radiotherapy (IGRT) systems using kilovolt cone-beam computed tomography (kV-CBCT) images have become more common for highly accurate patient positioning in stereotactic lung body radiotherapy (SLBRT). However, current IGRT procedures are based on bone structures and subjective correction. Therefore, the aim of this study was to evaluate the proposed framework for automated estimation of lung tumor locations in kV-CBCT images for tumor-based patient positioning in SLBRT. Forty clinical cases including solid, pure ground-glass opacity (GGO), mixed GGO, solitary, and non-solitary types of tumors, were employed. The proposed framework consisted of four steps: (1) determination of a searching region for detection of a tumor location in a kV-CBCT image, (2) extraction of a tumor template from a planning CT image, (3) preprocessing for enhancement of a tumor region (edge enhancement by Sobel filter, tumor enhancement by blob structure enhancement (BSE) filter), and (4) estimation of a tumor location based on a template matching technique. The location errors in original, edge enhancement, and tumor enhancement images were 1.2 ± 0.7 mm, 5.5 ± 10.1 mm and 2.7 ± 4.4 mm, respectively. The location errors in original images for solid, pure GGO, mixed GGO, solitary, and non-solitary types of tumors were 1.0 ± 1.0 mm, 1.3 ± 0.9 mm, 0.4 ± 0.9 mm, 0.9 ± 0.9 mm and 1.1 ± 1.2 mm, respectively. The results suggested that the proposed framework was robust to automatically estimate several types of tumor locations in kV-CBCT images for tumor-based patient positioning in SLBRT.

10132-88, Session PS2

Comparative study of bowtie and patient scatter in diagnostic CT

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A fast, GPU accelerated Monte Carlo engine for simulating relevant photon interaction processes over the diagnostic energy range in third-generation CT systems was developed to study the relative contributions of bowtie and object scatter to the total scatter reaching an imaging detector. Primary and scattered projections for an elliptical water phantom (major axis set to 300mm) with muscle and fat inserts were simulated for a typical diagnostic CT system as a function of varying anti-scatter grid (ASG) configurations. The ASG design space explored grid orientation, i.e. septa either a) parallel or b) parallel and perpendicular to the axis of rotation, as well as septa height. The septa material was Tungsten. The resulting projections were reconstructed and the scatter induced image degradation was quantified using common CT image metrics (such as Hounsfield Unit (HU) inaccuracy and loss in contrast), along with qualitative review of image artifacts. Results indicate object scatter dominates total scatter in the detector channels under the shadow of the imaged object with the bowtie scatter fraction progressively increasing towards the edges of the object projection. Object scatter was shown to be the driving factor behind HU inaccuracy and contrast reduction in images while shading artifacts and elevated loss in HU accuracy at the object boundary were largely attributed to bowtie scatter. Because the impact of bowtie scatter could not be sufficiently mitigated with a large grid ratio ASG, algorithmic correction may be necessary to further mitigate these artifacts.

10132-89, Session PS2

A deterministic integral spherical harmonics method for scatter simulation in computed tomography

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Scatter is an important problem in computed tomography especially with the increase of X-ray illumination coverage in one single view. Poor scatter correction results in CT HU number inaccuracy, degrades low contrast detectability, and introduces artifacts. Hardware method can be used to handle scatter problem. However, it requires the scatter simulation tool for optimizing hardware design and improving scatter correction. Although Monte Carlo (MC) method can perform precise scatter simulation, simulated noise due to its statistical nature affects the simulation results. In this abstract, a deterministic scatter simulation method with radiative transfer equation (RTE) is proposed. Compared to MC method, the deterministic RTE method is free from statistical noise. Popular numerical methods with differential RTE are not used and a novel iterative integral formula is developed. Spherical harmonics expansion and first scatter distributed source (FSDS) method efficiently avoid ray effects arising from discrete ordinate method. Compared to MC method, 1.5% average relative error of SPR (scatter primary ratio) shows the accuracy of the proposed method.

10132-90, Session PS2

Optimal sinogram sampling with temporally offset pixels in continuous rotation CT

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Development in the CT field makes increasingly high gantry rotation speeds and higher spatial resolution of the detectors possible; with this, the requirement for sufficient angular sampling increases. Insufficient angular sampling in CT leads to aliasing which destroys the reconstructed images by introducing streak-like artifacts from sharp edges. Several approaches for oversampling in CT, such as flying focal-spot (FFS) and quarter detector offset (QDO), have been developed in order to decrease the risk of aliasing. Both the number of samples and the grid on which the sinogram is sampled determine the risk for aliasing.

Hexagonal sampling in 2D achieves optimal tiling of the Fourier spectra, thus reducing the risk for aliasing. This is particularly effective for a CT sinogram since the ‘bowtie’ shaped spectral support makes it suitable for tiling without spectral overlap. In theory, hexagonal sampling of the sinogram can reduce the angular sampling requirement by a factor of two.

In this paper, we will show that hexagonal sampling of the sinogram transform can be achieved in continuous rotation CT by introducing a temporal offset between the measurements acquired by adjacent pixels. The clinical benefit of the temporally offset pixels (TOP) method will be evaluated by simulation and post processing high-resolution CT data.

Since the method is easy to implement and does not require any major modifications to the imaging system, we believe that the approach can have high practical impact for high-resolution CT imaging and become as useful as flying focal-spot and quarter detector offset is today.

10132-91, Session PS2

Beam hardening correction using length linearization

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Computed tomography (CT) has been used to obtain 3D data from an object or patient. However, most of CT uses polychromatic energy and that results in beam hardening artifact. Therefore many methods for correcting beam hardening were proposed. Linearization method and post reconstruction method are main category of beam hardening correction method. Especially empirical approaches were commonly used at linearization method; however, empirical methods do not guarantee the linearity of projection data because it uses reconstructed image to decide linearity. Therefore, corrected images are not monochromatic CT images because we could not specify the energy. Proposed method use linearization method as a basic concept. However, we had considered about the relationship between path length and projection data and then found a way to specify the energy of corrected images because proposed method linearizes the projection data fundamentally. The result shows that we could make a monochromatic image with single scan in contrast with dual energy approach. Moreover, calculation time for making corrected sinogram was very short. Therefore, this method can be used practically and can be used to obtain multi contrast CT image.

10132-92, Session PS2

Fast frame rate rodent cardiac x-ray imaging using scintillator lens coupled to CMOS camera

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Micro-CT systems for small animal imaging play a critical role for monitoring disease progression and therapy evaluation. In this work, an in-house built micro-CT system equipped with a X-ray scintillator lens coupled to a commercial CMOS camera was used to test the feasibility of its application to Digital Subtraction Angiography (DSA). Literature has reported such studies being done with clinical X-ray tubes that can be pulsed rapidly or with rotating gantry systems, thus increasing the cost and infrastructural requirements. The X-ray micro-CT has a 50kVp X-ray tube (Source Ray inc.), rotary stage and a scintillator(CsI:Tl,Hamamatsu inc, Japan) lens coupled to a CMOS camera (model Blackfly, PointGrey, USA). The CMOS camera can acquire up to 33fps enabling a sampling time 30ms. A preliminary study was done by acquiring projection images of capillary tubes (1.12mm diameter) filled with iodinated contrast agents of varying concentrations at 2 different frame rates- 2 and 33fps. The CNR of 2 was obtained inside the capillary tube at the lowest Iodine concentration of 21.87 mg-I/ml and CNR=7 for 350 mg-I/ml at 33fps. In-vivo studies on mice will be performed to further demonstrate feasibility.

10132-93, Session PS2

Low-dose, 4D myocardial perfusion with x-ray micro-CT

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X-ray CT is widely used, both clinically and pre-clinically, for fast, high-resolution, anatomic imaging; however, compelling opportunities exist to expand its use in functional imaging applications. For instance, temporally-resolved CT data can detail cardiac motion and blood flow dynamics for one-stop cardiovascular CT imaging procedures. In previous work, we demonstrated efficient, low-dose projection acquisition and reconstruction strategies for cardiac micro-CT imaging and for multiple-injection micro-CT perfusion imaging. Here, we extend this previous work by proposing a reconstruction algorithm that uses an alternative formulation of rank-sparse kernel regression for the assessment of both myocardial perfusion and cardiac functional metrics from a single set of projections. We test the algorithm in simulations using a modified version of the MOBY mouse phantom which contains realistic perfusion and cardiac dynamics. The proposed algorithm reduced the reconstruction error by 63% relative to unregularized, algebraic reconstruction. We have also performed in vivo micro-CT experiments and reconstructed 8 cardiac phases and 6 perfusion time points using the proposed algorithm. The results confirm our ability to simultaneously solve for cardiac temporal motion and perfusion dynamics. In future work, we will investigate the incorporation of gamma-variate priors to improve the robustness with which perfusion information can be recovered.

10132-94, Session PS2

An investigation of low-dose 3D scout scans for computed tomography

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Purpose: Commonly 2D scouts or topograms are used prior to CT scan acquisition. However, low-dose 3D scouts could potentially provide additional information for more effective patient positioning and selection of acquisition protocols. We propose using model-based iterative reconstruction to reconstruct low exposure tomographic data to maintain image quality in both low-dose 3D scouts and reprojected topograms based on those 3D scouts.

Methods: We performed tomographic acquisitions on a CBCT test-bench using a range of exposure settings from 16.6 to 231.9 total mAs. Both an anthropomorphic phantom and a 32 cm CTDI phantom were scanned. The penalized-likelihood reconstructions were made using Matlab and CUDA libraries and reconstruction parameters were tuned to determine the best regularization strength and delta parameter. RMS error between reconstructions and the highest exposure reconstruction were computed, and CTDIW values were computed for each exposure setting. RMS error for reprojected topograms were also computed.

Results: We find that we are able to produce low-dose (0.417 mGy) 3D scouts that show high-contrast and large anatomical features while maintaining the ability to produce traditional topograms.

Conclusions: We demonstrated that iterative reconstruction can mitigate noise in very low exposure CT acquisitions to enable 3D CT scout. Such additional 3D information may lead to improved protocols for patient positioning and acquisition refinements as well as a number of advanced dose reduction strategies that require localization of anatomical features and quantities that are not provided by simple 2D topograms.

10132-95, Session PS2

Adaptability index: quantifying CT tube current modulation performance from dose and quality informatics

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The balance between risk and benefit in modern CT scanners is governed by the automatic adaptation mechanisms that adjust x-ray flux for accommodating patient size to achieve certain image noise values. The effectiveness of this adaptation is an important aspect of CT performance and should ideally be characterized in the context of real patient cases. Objective of this study was to characterize CT performance with an index that includes image-noise and radiation-dose across a clinical patient population.

The study included 1526 examinations performed by three scanners, from two vendors, used for two clinical protocols (abdominopelvic and chest). The dose-patient size and noise-patient size dependencies were linearized, and a 3D-fit was performed for each protocol and each scanner with a planar function. In the fit residual plots the Root Mean Square Error (RMSE) values were estimated as a metric of CT adaptability across the patient population.

The RMSE values were between 0.0344 HU^1/2 and 0.0215 HU^1/2: different scanners offer varying degrees of reproducibility of noise and dose across the population. This analysis could be performed with phantoms, but phantom data would only provide information concerning specific exposure parameters for a scan: instead, a general population comparison is a way to obtain new information related to the relevant clinical adaptability of scanner models.

A theoretical relationship between image noise, CTDIvol and patient size was determined based on real patient data. This relationship may provide a new index related to the scanners' adaptability concerning image quality and radiation dose across a patient population.

10132-96, Session PS2

Experimental evaluation of dual multiple aperture devices for fluence field modulated x-ray computed tomography

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Acquisition of CT images with comparable diagnostic power can potentially be achieved with lower radiation exposure than the current standard of care through the adoption of hardware-based fluence-field modulation (e.g. dynamic bowtie filters). While modern CT scanners employ elements such as static bowtie filters and tube-current modulation, such solutions are limited in the fluence patterns that they can achieve, and thus are limited in their ability to adapt to broad classes of patient morphology. Fluence-field modulation also enables new applications such as region-of-interest imaging, task specific imaging, reducing measurement noise or improving image quality. The work presented in this paper leverages a novel fluence modulation strategy that uses "Multiple Aperture Devices" (MADs) which are, in essence, binary filters, blocking or passing x-rays on a fine scale. Utilizing two MAD devices in series provides the capability of generating a large number of fluence patterns via small relative motions between the MAD filters. We present the first experimental evaluation of fluence-field modulation using a dual-MAD system, and demonstrate the efficacy of this technique with a characterization of achievable fluence patterns and an investigation of experimental projection data

10132-97, Session PS2

Estimation of non-solid lung nodule volume with screening and sub-screening CT protocols: effect of reconstruction algorithm and measurement method

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Non-solid pulmonary nodules are regions of translucent tissue (sometimes referred to as ground-glass opacity) without solid components other than vessels. The surveillance of non-solid nodules with CT is primarily the modality of choice to assess stability for three or more years, with change in size being the primary factor to monitor. Since volume extracted from CT is being examined as a quantitative biomarker of lung nodule size, it is important to examine factors affecting the performance of volumetric CT for this task. Most specifically, the effect of reconstruction algorithms (RA) and measurement methods in the context of screening and sub-screening CT protocols has been an under-examined area of research. In this phantom study we assessed volumetric CT with two different measurement methods (model-based and segmentation-based) for nodules with radio-densities of both nonsolid (-800HU and -630HU) and solid (-10HU) nodules, sizes of 5mm and 10mm, and two shapes (spherical and spiculated). Imaging protocols included CTDIvol typical of screening (1.7mGy) and sub-screening (0.6mGy) scans and different types of RA (filter-back projection and both statistical and model-based iterative algorithms). Results showed that radiodensity was the factor contributing most to overall error based on ANOVA. RA and measurement method did not substantially affect the accuracy of measurements; however, measurement method affected repeatability with repeatability coefficients ranging from 3-5% for the model-based estimator to 20-30% across RAs for the segmentation–based method. The findings of the study can be valuable for developing standardized protocols and performance claims for non-solid nodules.

10132-98, Session PS2

Novel method to calibrate CT scanners with a conic probe body

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The assessment of the geometry of a CT scanner and calibrating its misalignments is a task that must be performed regularly. Many methods developed for the estimation of geometric parameters of CT scanners are based on observation of projections of space points and solving model equations that contain the geometric parameters as unknowns. Since the solution of these equations depends non-linearly on measurement errors, it is advisable to reduce the magnitude of those errors as much as possible. A common object utilized for the calibration is a spherical ball the center of which plays the role of a space point. The identification of the projection of the ball's center in the image is non-trivial task concerning the analysis of the grey value image of the ball and the geometry of its shadow. Therefore the utilization of a ball for the calibration can cause significant measurements error. In order to avoid the described difficulties related to the usage of the ball, we propose to utilize instead a solid conic body the apex of which can be considered as a space point. Accuracy in the straightness of the line segments forming the conical surface is the only requirement imposed on the cone; its tip may be blunt. Using the new approach we could exemplarily estimate that misalignment of a detector that may cause severe artefacts in the reconstruction. Although the applied estimating routine is sensible to measurement errors the obtained result is very accurate owing to the small magnitude of the errors.

10132-99, Session PS3

ROI model-based iterative reconstruction (MBIR) via a coupled dictionary learning

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Model based iterative reconstruction (MBIR) algorithms have shown significant improvement in CT image quality by increasing resolution as well as reducing noise and artifacts. In diagnostic protocols, radiologists often need the high-resolution reconstruction of a limited region of interest (ROI). This ROI reconstruction is complicated for MBIR which should reconstruct an image in a full field of view (FOV) given full sinogram measurements. Multi-resolution approaches are widely used for this ROI reconstruction of MBIR, in which the image with a full FOV is reconstructed in a low-resolution and the forward projection of non-ROI is subtracted from the original sinogram measurements for high-resolution ROI reconstruction. However, a low-resolution reconstruction of a full FOV can be susceptible to streaking and blurring artifacts and these can be propagated into the following high-resolution ROI reconstruction. To tackle this challenge, we use a coupled dictionary representation model between low- and high-resolution training dataset for artifact removal and super resolution of a low-resolution full FOV reconstruction. Experimental results on phantom data show that the restored full FOV reconstruction via a coupled dictionary learning significantly improve the image quality of high-resolution ROI reconstruction for MBIR.

10132-100, Session PS3

Accelerating separable footprint (SF) forward and back projection on GPU

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Statistical image reconstruction (SIR) methods for X-ray CT can improve image quality and reduce radiation dosages over conventional reconstruction methods, such as filtered back projection (FBP). However, SIR methods require much longer computation time. Most SIR methods require one forward projection and one back projection in each iteration. These operations are the primary computational bottleneck in SIR methods, especially in 3D image reconstruction. Accelerating forward and back projection is crucial to fast implementation of SIR methods. The separable footprint (SF) forward and back projection technique simplifies the calculation of intersecting volumes of image voxels and finite-size beams in a way that is both accurate and efficient for parallel implementation. We propose a new method to accelerate the SF forward and back projection on GPU with NVIDIA's CUDA environment. For the forward projection, we parallelize over all detector cells. For the back projection, we parallelize over all 3D image voxels. The simulation results show that the proposed method is faster than the acceleration method of the SF projectors proposed by Wu and Fessler. We further accelerate the proposed method using multiple GPUs. The results show that the computation time is reduced approximately proportional to the number of GPUs.

10132-101, Session PS3

A new approach to solving the prior image constrained compressed sensing (PICCS) with applications in CT image reconstruction

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Reduce does exposure in computed tomography (CT) scan has been received much attention in recent years. It is reasonable to reduce the number of projections for reducing does. However, conventional CT image reconstruction methods will lead to streaking artifact due to few-view data. Inspired by the theory of compressive sensing, the total variation minimization method was widely studied in the CT image reconstruction from few-view and limited-angle data. It takes full advantage of the sparsity in the image gradient magnitude.

In this paper, we develop a new iterative algorithm for image reconstruction based on the prior image constrained compressed sensing (PICCS) minimization. The main idea of our approach is to reformulate the original optimization problem as an unconstrained optimization problem with the sum of two convex functions. Then we derive the iterative algorithm by use of the primal dual proximity method.

The prior image is reconstructed by a conventional analytic algorithm such as filtered backprojection (FBP) or from a dynamic CT image sequences. We demonstrate the performance of the proposed iterative algorithm in a quite few-view projection data with just 3 percent of the reconstructed image size. The numerical simulation results show that the proposed reconstruction algorithm outperforms the commonly used total variation minimization method.

10132-102, Session PS3

Computer Simulation of Low-dose CT with Clinical Lung Image Database: a preliminary study

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Large samples of raw low-dose CT (LDCT) projections on lungs are needed for evaluating or designing novel and effective reconstruction algorithms suitable for lung LDCT imaging. However, there exists radiation risk when getting them from clinical scanning. To avoid the problem, a new strategy for producing large samples of lung LDCT projections with computer simulations is proposed in this paper. In the simulation, clinical images from the publicly available medical image database-the Lung Image Database Consortium(LIDC) and Image Database Resource Initiative (IDRI) database (LIDC/IDRI) are used as the projected object to form the noise-free sinogram. Then by adding a Poisson distributed quantum noise plus Gaussian distributed electronic noise to the projected transmission data calculated from the noise-free sinogram, different noise levels of LDCT projections are obtained. At last the LDCT projections are used for evaluating two reconstruction strategies. One is the conventional filtered back projection (FBP) algorithm and the other is FBP reconstruction from the filtered sinogram with penalized weighted least square criterion (PWLS-FBP). Images reconstructed with the LDCT simulations have shown that the PWLS-FBP algorithm performs better than the FBP algorithm in reducing streaking artifacts and preserving resolution. Preliminary results indicate that the feasibility of the proposed lung LDCT simulation strategy for helping to determine advanced reconstruction algorithms.

10132-103, Session PS3

Reconstruction of four-dimensional computed tomography images during treatment time using electronic portal imaging device images based on a dynamic 2D/3D registration

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The goal of our study was to develop a computational framework for reconstruction of four-dimensional computed tomography (4D-CT) images during treatment time using electronic portal imaging device (EPID) images based on a dynamic 2D/3D registration. The 4D-CT images during treatment time ("treatment" 4D-CT images) were reconstructed by performing an affine transformation-based dynamic 2D/3D registration between clinical portal dose images (PDIs) derived from the EPID images with planning CT images through planning PDIs for all frames. Elements of the affine transformation matrices (transformation parameters) were optimized using a Levenberg-Marquardt (LM) algorithm so that the planning PDIs could be similar to the clinical PDIs for all frames. Initial transformation parameters in each frame should be determined for finding optimum transformation parameters in the LM algorithm. In this study, the optimum transformation parameters in a frame employed as the initial transformation parameters for optimizing the transformation parameter in the consecutive frame. Gamma pass rates (3 mm/3%) were calculated for evaluating a similarity of the dose distributions between the clinical PDIs and "treatment" PDIs, which were calculated from "treatment" 4D-CT images, for all frames. The framework was applied to eight lung cancer patients who were treated with stereotactic body radiation therapy (SBRT). A mean of the average gamma pass rates between the clinical PDIs and the "treatment" PDIs for all frames was 98.3±1.2% for eight cases. In conclusion, the proposed framework makes it possible to dynamically monitor patients' movement during treatment time.

10132-104, Session PS3

Deep learning methods to guide CT image reconstruction and reduce metal artifacts

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A common application of deep learning is image classification, in which an artificial neural network is trained with labeled images to later categorize new images based on learned features. In this study, a neural network is employed to monitor the image quality of computed tomography (CT) images during the iterative reconstruction process and decide when a sufficiently high quality result is obtained. For traditional iterative CT reconstruction, multiple stopping rules have been proposed, including a fixed threshold of error or similarity, a maximum number of iterations, and an analysis of the L-curve. With deep learning, the iteration can be stopped as judged by an intelligent numerical observer – the neural network. The neural network consists of two convolutional layers, each followed by a pooling/subsampling layer. The fully connected layers activate the neurons and a softmax loss layer computes the loss function to determine image quality scores, which quantifies how well the reconstructed image compared with the ground truth based on structure, contrast, and luminance. After training, the neural network was successfully applied to guide new SART reconstructions. The reconstruction is stopped when the softmax loss falls below 0.5, indicating that the network has judged the image quality to be sufficiently similar to training images reconstructed with several hundred iterations. Deep learning is also used to predict high resolution images based on a low resolution input.

10132-105, Session PS3

Choosing anisotropic voxel dimensions in optimization-based image reconstruction for limited angle CT

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Resolution of reconstructions in limited angle X-ray computed tomography (CT) is inherently anisotropic due to the limited angular range of acquired projections. This justifies the use of anisotropic voxels in limited angle image reconstruction. For analytic reconstruction algorithms, this only changes the intervals at which the reconstruction is sampled, but for optimization-based image reconstruction, changing the voxel dimensions redefines the reconstruction optimization problem and can have pronounced effects on the reconstructed image. In this work we investigate the choice of anisotropic voxel dimensions in optimization-based image reconstruction for limited angle CT. In particular, a 2D simulation study is performed to assess the optimal choice of pixel dimension in the longitudinal direction — the direction of lowest resolution. It is demonstrated that as this pixel dimension is decreased, deterioration of system matrix conditioning can lead to severe distortion in reconstructions performed with low regularization strength. This conditioning issue occurs at approximately the point where the number of pixels is equal to the number of measurements. While the distortion can be mitigated by increasing regularization, our results suggest that there are structures which are only resolvable by using even smaller voxel sizes.

10132-106, Session PS3

A data-driven regularization strategy for statistical CT reconstruction

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There is an unmet need for CT image reconstruction algorithms that reliably provide diagnostic image quality at reduced radiation dose. Toward this end, we integrate a state-of-the-art statistical reconstruction algorithm, ordered subsets, and separable quadratic surrogates (OS-SQS) accelerated with Nesterov's method, with our own data-driven regularization strategy using the split Bregman method. The regularization enforces intensity-gradient sparsity by minimizing bilateral total variation through the application of bilateral filtration. Adding to the advantages of statistical reconstruction, our implementation of bilateral filtration dynamically varies the regularization strength based on the noise level algorithmically measured within the data, accommodating variations in patient size and photon flux. We refer to this modified form of OS-SQS as OS-SQS with bilateral filtration (OS-SQS-BF), and we apply it to reconstruct clinical, helical CT data provided to us as part of the Low Dose CT Grand Challenge. Specifically, we evaluate OS-SQS-BF for quarter-dose statistical reconstruction and compare its performance with both quarter-dose and full-dose filtered backprojection reconstruction. In this abstract, we show preliminary results for both the American College of Radiology (ACR) phantom and an abdominal CT scan. Our algorithm reduces noise by approximately 52% relative to filtered backprojection in the ACR phantom while maintaining contrast and spatial-resolution performance relative to commercial filtered backprojection. The quarter-dose scan for the abdominal data set confirmed the identification of 3 liver lesions when using OS-SQS-BF. For the full conference paper, we will provide a quantitative account of the noise and resolution properties of our proposed algorithm for additional training sets used in the Low Dose CT Grand Challenge.

10132-107, Session PS3

MDCT cardiac imaging via data consistency classification and SMART-RECON method

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In recent years, cardiac CT imaging technology has been greatly advanced with faster gantry rotation or multi-source techniques to improve temporal resolution, to boost volume scan speed by adding more detector rows or by using high pitch helical scan approach. However, further improvement in temporal resolution is still very much desired for the purpose new cardiac applications such as cardiac function studies and improvement of the performance of CT coronary angiography with improved reliability and consistency over a wider range of patients conditions. The purpose of this work is to present a new cardiac MDCT image reconstruction framework in which projection data are classified into different consistency classes, and images are jointly reconstructed by a newly developed SMART-RECON method for each data consistency class with improved image quality. Both phantom studies with ground truth and in vivo human subject studies have been conducted to validate the proposed new method.

10132-108, Session PS3

Projection-based motion estimation for cardiac functional analysis with high temporal resolution: a proof-of-concept study with digital phantom experiment

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Cardiac motion (or functional) analysis has shown promise not only for non-invasive diagnosis of cardiovascular diseases but also for prediction of cardiac future events. Current imaging modalities has limitations that could degrade the accuracy of the analysis indices. In this paper, we present a projection-based motion estimation method for x-ray CT that estimates cardiac motion with high spatio-temporal resolution using projection data and a reference 3D volume image. The experiment using a synthesized digital phantom showed promising results for motion analysis.

10132-109, Session PS3

Investigation of image quality difference between total variation and nonlinear sparsifying transform based compressed sensing

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Compressed sensing (CS) is attracting growing concerns in sparse-view CT image reconstruction. The most standard approach of CS is total variation (TV) minimization. However, images reconstructed by TV usually suffer from distortions such as patchy artifacts, improper serrate edges and loss of image textures, especially in reconstruction of practical CT images. Most existing CS approaches including TV achieve image quality improvement by using linear transforms to object image, but linear transforms usually fail to take discontinuities such as edges and image textures into account, which is considered to be the key reason of image distortions. Actually, discussions on nonlinear filter based image processing has a long history, and it has been clarified that the nonlinear filters bring good results compared to linear filters in image processing such as denoising. Median root prior was first utilized as nonlinear transform in CT image reconstruction by Alenius, and significant gains were obtained. Consequently, Zhang developed the application of nonlocal means-based CS. A fact is gradually becoming clear that nonlinear transform based CS has superiority in improving image quality compared with linear transform based CS. However, it has not been clearly concluded in any previous paper within the scope of our knowledge. In this work, we investigated the image quality differences between the conventional TV minimization and nonlinear sparsifying transform based CS, as well as image quality differences between different nonlinear sparisying transforms based CS in sparse-view CT image reconstruction. Additionally, we accelerated the nonlinear sparifying transform based CS.

10132-110, Session PS3

Image-based metal artifact reduction in x-ray computed tomography utilizing local anatomical similarity

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Purpose: X-ray computed tomography (CT) has been widely used in radiation therapy treatment planning in recent years. However, metal implants such as dental fillings and hip prostheses can cause severe bright and dark streaking in reconstructed CT images. These artifacts decrease image contrast and degrade HU accuracy, leading to inaccuracies in target delineation and dose calculation. In this work, we propose a metal artifact reduction method, which utilizes anatomical similarity between neighboring CT slices.

Methods: Neighboring CT slices from the same patient show similar anatomical features. Utilizing this anatomical similarity, a gamma map is calculated as a weighted summation of relative HU error and distance error for each pixel in an artifact-corrupted CT image relative to an adjacent artifact-free image. The minimum value in each pixel's gamma map is used to identify a pixel from the adjacent CT slice to replace the corresponding artifact-corrupted pixel.

Results: With the proposed method, the mean CT HU error was reduced from 360 HU and 460 HU to 24 HU and 34 HU on head and pelvic CT images respectively. The dose calculation accuracy was also significantly improved; with the dose difference being reduced from over 20% to less than 4%. With the 3%/3mm gamma criteria, the failing rate was reduced from 23.25% to 0.02%.

Conclusions: We proposed an image-based metal artifact correction method, which replaces corrupted image pixels with pixels from neighboring slices that are free of metal artifacts. This method proved capable of suppressing streaking artifacts, improving HU and dose calculation accuracy.

10132-111, Session PS3

Compressed sensing of sparsity-constrained total variation minimization for CT image reconstruction

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Sparse-view CT image reconstruction is becoming a potential strategy for radiation dose reduction of CT scans. Compressed sensing (CS) has been utilized to address this problem. Total Variation (TV) minimization, a method who can reduce streak artifacts and preserve object boundaries well, is treated as the most standard approach of CS. However, TV minimization cannot be solved by using classical differentiable optimization techniques such as the gradient method, because the expression of TV (TV norm) is non-differentiable. In early stages, approximated solving methods were proposed by changing TV to be differentiable in the way of adding a small constant in TV norm to enable the usage of gradient methods. But this reduces the power of TV in preserving accuracy object boundaries. Subsequently, approaches who can optimize TV norm exactly were proposed based on the convex optimization theory, such as generalizations of the iterative soft-thresholding (GIST) algorithm and Chambolle-Pock algorithm. However, these methods are simultaneous-iterative-type algorithms. It means that their convergence is rather slower compared with row-action-type algorithms. The proposed method, called sparsity-constrained total variation (SCTV), is developed using the alternating direction method of multipliers (ADMM). By which we succeeded in solving the main optimization problem by iteratively splitting to processes of row-action-type algebraic reconstruction technique (ART) procedure and TV minimization using Chambolle algorithm. Experimental results show that the convergence speed of the proposed method is much faster than the conventional simultaneous iterative methods.

10132-112, Session PS3

FBP embedded iterative method to efficiently solve the low-dose CT

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Low-dose CT is the reconstruction method for the reduction of the radiation exposure by decreasing the X-ray intensity. In exchange for the intensity reduction, the noise level increases relatively. To reduce the artifacts due to the noise, the Statistical Iterative Reconstruction (SIR) method and Compressed Sensing (CS) framework are effective. The SIR use a given prior information, e.g., noise distribution model, which leads to the penalized weighted least square (PWLS) method. Also, prior information gives the regularization term. In this study, total variation (TV) regularization is applied, which is widely used in CS framework. Because the SIR method and CS framework use the iterative method, they have a large computational cost. The well-known technique for reduction of the iteration number is Iterative FBP, which embed the FBP filter to the iteration scheme. However, Iterative FBP cannot compute the exact solution. For medical imaging, reliability of the reconstruction is required. Hence, the scheme which can compute the exact solution is favorable. In this paper, to accomplish both the low computational cost and the exact solution, we propose a new iterative method. The method based on the Alternating Projection Proximal (APP) and FBP. The accelerated APP method can also compute the exact solution. The results by FBP, Iterative FBP, APP and the proposed method are shown. Then, we show that the proposed method can computes the exact solution with less computational cost. The artifacts due to the noise can be reduced.

10132-113, Session PS4

Discrimination of clinically significant calcium salts using MARS Spectral CT

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Calcium compounds within tissues are usually a sign of pathology, and calcium crystal type is often a pointer to the diagnosis. There are clinical advantages in being able to determine the quantity and type of calcifications non-invasively in a range of medical diseases. Several calcium crystals play a role in the pathogenesis of various musculoskeletal disorders, such as MSU in gout, CPPD in pseudogout, and BCP in calcific tendinitis and osteoarthritis. Treatment differs depending on the crystal type and quantity. Calcium oxalate is almost always a sign of benign breast disease, whereas complex calcium salts such as calcium or magnesium hydroxyapatite are frequently a sign of malignant breast disease. Calcium hydroxyapatite is a marker of atherosclerotic plaque at risk for rupturing and causing stroke or heart attack.

The problem arises when trying to distinguish between different calcium compounds within the same image due to their similar attenuation properties. There are potential spectroscopic differences between calcium salts at low energies; we wished to determine whether MARS Spectral CT could distinguish between them.

Energy thresholds within 15 to 36keV and tube voltages of 50, 80 and 110kVp were chosen, and images were analysed using ImageJ® and Excel® to determine any difference in the attenuation coefficients of diluted samples calcium hydroxyapatite and calcium oxalate. Results show that there is a potential to distinguish between these compounds within a Spectral CT scan. Such protocols may, in future, aid the understanding of pathophysiology/pathogenesis and accurate diagnosis of pathology linked to calcium using less invasive procedures.

10132-116, Session PS4

Response functions of multi-pixel-type CdTe detector-Toward development of precise material identification on diagnostic X-ray images by means of photon counting-

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Currently, multi-pixel-type CdTe detectors, in which each pixel has the ability to measure the energy of X-rays, are being developed, and it is expected that information concerning material identification is analyzed using a photon counting technique. The response function of the CdTe detector is important to estimate the accuracy of the material identification. Our aim was to simulate the response function of the CdTe detector using the Monte-Carlo simulation; at this time, the transportations of incident and scattered photons and secondary produced electrons were precisely simulated without considering the charge spread in the collecting process of the produced charges. First, we set pixel sizes of 50-500 micrometers, the minimum irradiation fields which give the equilibrium conditions were determined. Then, observed peaks in the response function were analyzed with consideration of interactions between incident X-rays and detector components, Cd and Te. The secondary produced characteristic X-rays play an important role. Finally, ratios of full energy peak (FEP), scattering X-rays and penetrating X-rays in the calculated response functions were analyzed. When the pixel size of 200 micrometers was used, the scattered X-rays were saturated at the equilibrium condition with relatively small fields (side length of 1200 micrometers) and efficiency of FEP was kept at a high value (>50%). Even if the charge sharing effect is not completely corrected by using the electric circuit, it is a possibility that disturbed portions in the measured X-ray spectra will be corrected by a proper calibration, in which above considerations are taken account in.

10132-117, Session PS4

Dual energy CT kidney stone differentiation in photon counting computed tomography

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This study evaluates the capabilities of a whole-body photon counting CT system to differentiate between four common kidney stone materials, namely uric acid (UA), calcium oxalate monohydrate (COM), cystine (CYS), and apatite (APA) ex vivo. Two different X-ray spectra (120 kV and 140 kV) were applied and two acquisition modes were investigated; The macro-mode generates two energy threshold based image-volumes and two energy bin based image-volumes. In the chesspattern-mode, however, four energy thresholds are applied. A statistical decorrelation allows to derive both a virtual low and a virtual high energy image out of the initial threshold-based images. The energy bin based images of the macro-mode, as well as the virtual low and high energy image of the chesspattern-mode serve as input for our dual energy evaluation. The dual energy ratio of the individually segmented kidney stones were utilized to quantify the discriminability of the different materials. The dual energy ratios of both acquisition modes showed high correlation for both applied spectra. Wilcoxon-rank sum tests and the evaluation of the area under the receiver operating characteristics curve suggest that the UA kidney stones are best differentiable from all other materials (AUC = 1.0), followed by CYS (AUC ≈ 0.9 compared against COM and APA). COM and APA, however, are hardly distinguishable (AUC between 0.63 and 0.76). The results hold true for the measurements of both spectra and both acquisition modes.

10132-118, Session PS4

Statistical iterative material image reconstruction for spectral CT using a semi-empirical forward model

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In spectral computed tomography (spectral CT), the additional information about the energy dependence of attenuation coefficients can be exploited to generate material selective images. These images have found applications in various areas such as artifact reduction, quantitative imaging or clinical diagnosis. However, significant noise amplification on material decomposed images remains a fundamental problem of spectral CT. Most spectral CT algorithms separate the process of material decomposition and image reconstruction. Separating these steps is suboptimal because the full statistical information contained in the spectral tomographic measurements cannot be exploited. Statistical iterative reconstruction (SIR) techniques provide an alternative, mathematically elegant approach to obtaining material selective images with improved tradeoffs between noise and resolution. Furthermore, image reconstruction and material decomposition can be performed jointly. This is accomplished by a forward model which directly connects the (expected) spectral projection measurements and the material selective images. To obtain this forward model, detailed knowledge of the different photon energy spectra and the detector response was assumed in previous work. However, accurately determining the spectrum is often difficult in practice. In this work, a new algorithm for statistical iterative material decomposition is presented. It uses a semi-empirical forward model which relies on simple calibration measurements. Furthermore, an efficient optimization algorithm based on separable surrogate functions is employed. This partially negates one of the major shortcomings of SIR, namely high computational cost and long reconstruction times. Numerical simulations and real experiments show strongly improved image quality and reduced statistical bias compared to projection-based material decomposition.

10132-119, Session PS4

Development of a novel method based on a photon counting technique with the aim of precise material identification in clinical x-ray diagnosis

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Photon counting system has the ability of energy discrimination, therefore obtaining new information about material identification is expected for diagnosis using X-rays. The aim of our study is to propose a novel method for material identification. The following experiment was carried out under the assumption that the response of our single-probe-type CdTe detector is equal to the response of one pixel of a multi-pixel-type CdTe detector. First, we measured the X-ray spectra at 40 kV without phantoms using a CdTe detector. Second, four phantoms which give the same digital value in a computed radiography system were put in front of the detector, and the X-ray spectra penetrating phantoms were measured. These spectra were divided into two energy regions, and then linear attenuation factors concerning these regions were obtained. Here, beam hardening effects in X-ray spectra were properly corrected. Then, using linear attenuation factors determined for two energy regions, the normalized linear attenuation coefficient was derived. Finally, an effective atomic number was determined using a reference curve of the relationship between normalized linear attenuation coefficient and atomic number. The four different phantoms which cannot be separated in the traditional system can be identified using our method. Moreover, we evaluated the accuracy in terms of feasibility for the present medical diagnosis with help of the Monte-Carlo simulation. The accuracy of material identification is +/-0.1 in the range of effective atomic number when total X-ray intensity (counts) of 10^6 can be measured in the region of interest of the X-ray image.

10132-121, Session PS4

Material decomposition using noise compensating projection in an arbitrary number of dimensions

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Multi-energy CT (e.g., dual energy or photon counting) facilitates the identification of certain elements via data decomposition. However, the standard approach to decomposition (i.e., solving a system of linear equations) fails if – due to noise - a pixel's vector of HU values falls outside the boundary of values describing possible pure or mixed components. Typically, this is addressed by either throwing away those pixels or projecting them onto the closest point on this boundary. However, when acquiring four (or more) energy volumes, the space bounded by materials that may be found in the human body (either naturally or through injection) can be quite small. Noise may significantly limit the number of those pixels to be included. Therefore, projection onto the boundary becomes an important option. But, projection in higher than 3 dimensional space is not possible with standard vector algebra: the cross-product is not defined. In this paper, we describe a technique using Clifford Algebra for projection in higher than 3 dimensions and apply it to the problem of material decomposition. We demonstrate on a phantom containing calcium, iodine, gold nanoparticles, gadolinium, and their mixtures.

10132-122, Session PS4

Theoretical characterization of performance effectiveness of photon-counting technique for digital radiography applications

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Photon-counting (PC) technique has been interested in digital radiography applications due to its low-dose and multi energy imaging capabilities. We investigated a theoretical effectiveness of PC detectors compared than the conventional energy-integrating (EI) detectors in terms of signal-to-noise ratio (SNR), modulation-transfer function (MTF), and dose efficiency under general radiography condition RQA5. Monte Carlo technique was used to simulate energy absorption in x-ray converters and cascaded linear-systems approach was applied to reflect the differences of imaging scheme for each detector technologies. To investigate feasibility of further applications, carbon nanotube (CNT) cathode for x-ray tube was also considered which have low beam current rate compared than a conventional filament cathode. From the results, performance changes in SNR and MTF for CNT cathode were negligible and dose efficiency of 10-20% was observed with respect to various technology combinations. We expect that this result will be useful to understand an upper limit of the imaging performances of each technology.

10132-123, Session PS4

Effects of dead time on quantitative dual energy imaging using a position-sensitive spectroscopic detector

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Dual energy imaging (DE) is a potential alternative to conventional mammography for patients with dense breasts. It requires intravenous injection of contrast agent (CA) and subsequent acquisition of images at two different energies between which the attenuation of the CA should vary significantly more than the background, for example across its K-edge. In DE, each pixel is seen as a vector and is projected onto a two material basis, e.g. {water, CA}, to form separate water-equivalent and CA-equivalent images. On conventional detectors, this requires two separate exposures. Spectroscopic detectors allow acquisition of multiple images with a single exposure by integrating appropriate energy bands.

This work investigates the effects of dead time on quantitative DE imaging using a novel CdTe spectroscopic detector. A limitation of the detector is its long dead time [(10)]^(-3) s), which limits the photon rate that can be used before linearity between incident and detected counts is lost. Initially a simulation was used to model detector response of a test object containing iodine or water components only, based on different dead times and incident count rates. Using a known iodine thickness of 0.03 cm, and a dead time of [(10)]^(-3) s, the reconstructed thickness of iodine was found to be 100%, 95% and 82% of the true value for an initial count rate of 100, 1000 and 10000 photons/pixel/s respectively.

The simulation will be validated by imaging a water-equivalent test phantom containing different iodine concentrations at different currents, to determine the optimum beam conditions for DE applications.

10132-124, Session PS4

X-ray spectral calibration from transmission measurements using Gaussian blur model

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In recent years, there has been a resurgence of interest towards spectral computed tomography (CT) driven by a growing demand in photon-

counting detectors. In performing spectral CT scanning, a practical issue is to accurately calibrate the spectral response of the X-ray imaging system. Mis-calibrated detector elements can lead to strong ring artifacts in the reconstructed tomographic image. For the purpose of modeling the spectral response, we propose a Gaussian blur model combined with the prior information on the X-ray spectra that accurately predicts the transmission curve and at the same time recovers realistic estimate of the spectra. This proposed method uses a low dimensional representation of the X-ray spectra by enforcing a sparsity constraint on the parameters of the Gaussian blur model. These parameters are estimated by formulating a constrained optimization problem, and two algorithms are suggested to solve such problem in an efficient way. The effectiveness of the model is evaluated on the simulated transmission measurements of known thicknesses of known materials. The performance of the two algorithms are also compared through the error between estimated and model X-ray spectra and the error between the predicted and simulated transmission curves.

10132-125, Session PS4

Explorations of the physics-based decomposition space for a clinical spectral-detector CT

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Since 2015, the UT Southwestern Spectral CT research team has acquired significant clinical and phantom imaging experience with the Philips IQon spectral detector CT scanner installed in an outpatient facility. In addition to evaluating the final reconstructions, we have developed software and procedures for exploring the intermediate Spectral Basis Images based on the classical Alvarez-Macovski decomposition into photoelectric effect and Compton scattering. Ideally, this approach should produce perfectly beam-hardened corrected images that are invariant between systems and peak tube voltages (120 and 140 kVp with the IQon). In this work, we describe efforts to identify the precise location of certain tissues in clinical images, to compare these to known materials in databases and in phantoms, and to characterize any residual artifacts.

10132-126, Session PS4

A TV-constrained decomposition method for spectral CT

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Spectral CT has attracted more and more attention in medicine, industrial nondestructive testing and security inspection field. Material decomposition is an important issue in a spectral CT to discriminate materials. Because of the overlap of energy spectra, as well as the correlation of basis functions, it is well acknowledged that decomposition step in spectral CT imaging causes noise amplification and artifacts in component coefficients. In this work, we propose materials decomposition via an optimization method to improve the quality of decomposed coefficient images. On the basis of general optimization problem, total variance minimization is constrained on coefficient images in our overall objective function with adjustable weights. We solve this constrained optimization problem under the framework of ADMM. Validation on both a numerical dental phantom in simulation and a real phantom of pig leg on a practical CT system using dual-energy imaging is executed. Both numerical and physical experiments give visually-obvious better reconstructions than a general direct inverse method. SNR and SSIM are adopted to quantitatively evaluate the image quality of decomposed component coefficients. All results demonstrate that the TV-constrained decomposition method performs well in reducing noise without losing spatial resolution so that improving the image quality. The method can be easily incorporated into different types of spectral imaging modalities, as well as for cases with energy channels more than two.

10132-127, Session PS4

A study of modeling x-ray transmittance for material decomposition without contrast agents

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This study concerns how to model x-ray transmittance of the object using a small number of energy-dependent bases, which plays an important role for estimating basis line-integrals in photon counting detector (PCD)-based computed tomography (CT). Recently, we found that low-order polynomials can model the smooth x-ray transmittance, i.e. object without contrast agents, with sufficient accuracy, and developed a computationally efficient three-step estimator. The algorithm estimates the polynomial coefficients in the first step, estimates the basis line-integrals in the second step, and corrects for bias in the third step. We showed that the three-step estimator was ~1,000 times faster than conventional maximum likelihood (ML) estimator while it provided comparable bias and noise. The three-step estimator was derived based on the modeling of x-ray transmittance; thus, the accurate modeling of x-ray transmittance is an important issue that can improve the performance of the estimator. For this purpose, we introduce a modeling of the x-ray transmittance via dictionary learning approach. We show that the relative modeling error of dictionary learning-based approach is smaller than that of the low-order polynomials.

10132-128, Session PS4

A polychromatic adaption of the Beer-Lambert model for spectral decomposition

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Purpose: We present a semi-empirical forward-model for spectral photon-counting CT which is fully compatible with state-of-the-art maximum-likelihood estimators (MLE) for basis material line-integrals. The model relies on a minimum calibration effort to make the method applicable in routine clinical set-ups with the need for periodic re-calibration. In this work we present an experimental verification of our proposed method.

Method: The proposed method uses an adapted Beer-Lambert model, describing the energy dependent attenuation behavior of a polychromatic x-ray spectrum by additional proposed exponential terms. Thereby, we assume that the full polychromatic spectrum can be modeled by only a few dominant energies in each energy bin. The associated calibration routine relies on the measurement of different thickness combinations of materials with well-known properties. The required spectral binning is provided by a photon-counting detector with several energy thresholds.

Results: In an experimental dual-energy photon-counting CT based on a CdTe detector, the model demonstrates an accurate prediction of the registered counts for an attenuated polychromatic spectrum. Thereby deviations between model and measurement data lie within the Poisson statistic of the performed acquisitions, providing an effectively unbiased forward-model. The experimental data also shows that the model is capable of handling possible spectral distortions introduced by the photon-counting detector and CdTe sensor.

Conclusion: The simplicity and high accuracy of the proposed model provides a viable forward-model for MLE-based spectral decomposition methods without the need of costly and time-consuming characterization.

10132-129, Session PS4

Establishing a method to measure bone structure using spectral CT

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Combined bone structure and density measurement in 3D is required for bone quality assessment. MARS spectral molecular imaging is a new X-ray-based imaging technology that could achieve this as it simultaneously allows for quantification and differentiation of multiple materials. To produce optimal bone images, it is important to calibrate bone structure and density measurement. In this study, we focused on bone structure by calibrating cortical and trabecular bone measurements using the following experiments.

1- Eight different thicknesses of Aluminium (Al) sheets were scanned one in air and the other around a falcon tube and then analysed to calibrate thickness measurement.

2- To test if trabecular measurements were equal for the axial scan and the re-sliced orthogonal scan, a bone sample was scanned in both directions and analysed.

3- Bone samples were prepared in two conditions (in air and in PBS) then scanned to assess the effect of air on trabecular thickness measurement.

The results showed that the MARS scanner (with 90µm pixel size) is able to accurately measure the Al (in air) thicknesses over 200µm but it underestimates the thicknesses below 200µm because of partial volume effect in Al-air interface. The Al thickness measured from the highest energy bin is overestimated at Al-falcon tube interface. Bone scanning in two orthogonal directions gives the same trabecular thickness and air in the bone structure reduced measurement accuracy.

We have established a bone structure assessment protocol on MARS scanner. The next step is to combine this with bone densitometry to assess bone quality.

10132-130, Session PS4

Renal stone characterization using high resolution imaging mode on a photon counting detector CT system

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In addition to the standard-resolution (SR) acquisition mode, a high-resolution (HR) mode is available on a research photon-counting-detector (PCD) whole-body CT, whereby each detector element used in SR is divided into a 2x2 array of 0.45 mm x 0.45 mm elements, resulting in 0.25 mm resolution at isocenter. In this study, we quantified ex vivo the capabilities of the HR mode to characterize renal stones in terms of morphology and mineral composition. 40 pure stones - 10 uric acid (UA), 10 cystine (CYS), 10 calcium oxalate monohydrate (COM) and 10 apatite (APA) - and 14 mixed stones were placed in a 20 cm water phantom and scanned in SR and HR modes, at radiation dose matched to that of routine dual energy stone exams. Data from microCT provided a reference for the quantification of morphology and mineral composition of the mixed stones. The area under the ROC curve was 1.0 for discriminating UA from CYS, 0.89 for CYS vs COM and 0.84 for COM vs APA. The root mean square error (RMSE) of the percent UA composition of mixed stones was 11.0% with a medium-sharp kernel, and worsened with thinner slice thicknesses and sharper kernels. HR showed good characterization of stone morphology, which is performed using all detected photons and thus less susceptible to noise. Therefore, a hybrid acquisition mode for PCD-CT that provides HR for the lower energy threshold and SR for the higher one has the potential to best characterize renal stones in vivo.

10132-131, Session PS4

BVMF-B algorithm for nonconvex nonlinear regularized decomposition of spectral x-ray projection images

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Spectral computed tomography (SCT) can exploit the measurements obtained from photon counting detectors to reconstruct a 3D description of the patient in a material basis. In particular, spectral CT has shown a very good ability to image k-edge contrast agent.

SCT is an inverse problem that requires solving two subproblems, namely the basis material decomposition (BMD) problem and the tomographic reconstruction problem. In this work, we focus on the BMD problem, which is ill-posed and non-linear. This problem is classically either linearized, which enables reconstruction based on compressed sensing methods, or nonlinearly solved with no-explicit regularization schemes. In a previous communication, we proposed a Gauss-Newton (GN) [5] nonlinear regularized algorithm. However, the applicability of this algorithm is limited to differentiable regularization functionals, i.e., the exact l1 norm or the l0 quasi-norm, that are known to provider sparser solution, cannot be considered.

Our main contribution is to propose a nonlinear reconstruction framework that can handle nonconvex regularization term in order to better promote the sparsity of contrast agent images. Our approach also allows the positivity of the material images to be easily enforced. In particular, the approximation of l1 or the new smoothed approximation of l1 /l2 [9] are used to promote the sparsity. The problem is solved iteratively using the Block Variable Metric Forward-Backward (BVMF-B) algorithm [2]. The proposed method is validated on numerical data simulated in a thorax phantom made of soft tissue, bone and gadolinium scanned with a 90 kV source and a 3-bin photon counting detector.

10132-132, Session PS4

Calibration methods influence quantitative material decomposition in photon-counting spectral CT

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Photon-counting detectors and nanoparticle contrast agents can potentially enable quantitative molecular imaging and material decomposition in computed tomography (CT). Material decomposition has been investigated using both simulated and acquired data sets. However, the effect of calibration methods on resultant basis matrix values and subsequent material decomposition quality has not been systematically investigated. Therefore, the objective of this study was to investigate the influence of the number and range of contrast agent concentrations within a modular calibration phantom on material decomposition. A commercially-available spectral micro-CT (MARS Bioimaging) was used to acquire images with five energy bins selected to normalize photon counts and leverage the contrast agent k-edge. Basis matrix values were determined using either single point evaluation or multiple linear regression models. Material decomposition was performed using a maximum a priori estimator and evaluated by root mean squared error (RMSE), specificity, sensitivity and accuracy. RMSE and specificity were improved using multiple linear regression while sensitivity was highest using a selected single point calibration. The overall results show that quantitative material decomposition in spectral CT is significantly influenced by calibration methods and phantom design, which must therefore be carefully considered for the intended diagnostic imaging application.

10132-133, Session PS4

Sensitivity analysis of pulse pileup model parameter in photon counting detectors

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Photon counting detectors (PCDs) provide several benefits over energy-integrating detectors (EIDs), including spectral information for tissue characterization and the elimination of electronic noise. PCDs, however, suffer from pulse pileup, which distorts the detected spectrum and degrades the accuracy of material decomposition. Several analytical models have been proposed to address this problem. The performance of these models are dependent on the assumptions used, including the estimated pulse shape whose parameter values could differ from the actual physical ones. As the incident flux increases and the corrections become more significant the needed parameter value accuracy may be more crucial. In this work, the sensitivity of model parameter accuracies is analyzed for the pileup model of Taguchi et al. The spectra distorted by pileup at different count rates are simulated using either the model or Monte Carlo simulations, and the basis material thicknesses are estimated by minimizing the negative log-likelihood with Poisson or multivariate Gaussian distributions. From simulation results, we find that the accuracy of the deadtime and the timing to the end of the pulse peak are more important than most other parameters, and they matter more with increasing count rate. The sensitivity can also depend on the energy bins used, with parameter values for the pulse's tail being less relevant with the inclusion of counts at higher energy. This result can help facilitate further work on parameter calibrations.

10132-134, Session PS4

Enhancement of weakly tagged fecal materials in dual-energy CT colonography using spectral-driven iterative reconstruction technique

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Dual-energy computed tomography (DECT) is increasingly used in CT colonography (CTC). The combination of computer-aided diagnosis (CAD) and DE-CTC has a high clinical value because it is able to automatically detect clinically significant colonic lesions in CTC images with higher accuracy than dose single-energy CTC. While CAD has demonstrated its ability to detect small polyps, its performance is highly dependent on the quality of the input images. The presence of artifacts such as beam-hardening and noise in ultra-low-dose CTC may severely degrade detection performances of small polyps. A further limitation to the effectiveness of CAD is the weakly tagged fecal material in the colon that may result in the false positive detections. In this work, we developed a method to enhance the appearance of weak tagged fecal material in the CTC image. The proposed method consists of two stages: 1) the detection of the weakly tagged fecal material by using sinogram-based image decomposition and 2) the enhancement of the detected tagged fecal materials in the image using iterative reconstruction methods. In the first stage, ultra-low dose dual-energy projection data obtained from a CT scanner is decomposed into two materials – soft tissue and tagged material (iodine). Then, a virtual monochromatic projection data at a pre-determined energy is calculated. The iodine-decomposed sinogram and the virtual monochromatic projection data are used as an input to an iterative reconstruction scheme. In the second stage, the virtual monochromatic image is iteratively reconstructed, while at the same time the intensity of the weakly tagged iodine is enhanced. The performance of the proposed method was qualitatively and quantitatively assessed. Preliminary results showed that the method enhances the appearance of the weakly tagged fecal materials in the reconstructed CT image, while improving the overall quality of the images.

10132-135, Session PS4

Detection of increased vasa vasorum in artery walls: improving CT number accuracy using image deconvolution

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Changes in arterial wall perfusion are an indicator of early atherosclerosis. This is characterized by an increase in the spatial density of vasa vasorum (VV), the micro-vessels that supply oxygen and nutrients to the arterial wall. Detection of increased VV during contrast-enhanced CT imaging, however, is limited due to contamination from blooming effect from the contrast-enhanced lumen. We report the application of an image deconvolution technique based on hyper-Laplacian prior, in combination with a measured system point spread function (PSF), on CT data obtained from a photon-counting CT (PCCT) system to minimize the blooming and to improve the accuracy of CT number measurement of the arterial wall, which enables detection of increased VV. Phantom studies were performed to assess the accuracy of the deconvolution technique. A porcine model was created with enhanced VV in one carotid artery; the other carotid artery served as a control. CT images using an energy bin of 25-120 keV were reconstructed for all time points. CT numbers were measured for multiple locations in the carotid walls and for multiple time points, pre and post contrast injection. Mean CT number in the carotid wall was compared between the left (increased VV) and right (control) carotid arteries, before and after

image deconvolution. Prior to deconvolution, results showed similar mean CT numbers in the left and right carotid wall due to the contamination of blooming effect, limiting the detection of increased VV in the left carotid artery. After deconvolution, the mean CT number difference between the left and right carotid arteries was substantially increased at all the time points, enabling detection of the increased VV.

10132-136, Session PS4

Exploiting partial-volume artifacts in spectral CT imaging to localize surgical mesh

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Surgical mesh and textiles have routinely been used in the surgical treatment of female pelvic floor disorders. Recent evidence however indicates that a significant subpopulation of patients experience severe complications post-treatment, including scarring, mesh dislocation, migration, infection, erosion, and organ perforation. Many patients present after one or more revision surgeries and imaging is then needed to evaluate mesh status for further treatment planning. Most surgical textiles are reported to be iso-attenuating on conventional CT. Compared to the system resolution, the mesh may represent a very small volume fraction. Here we experimentally estimate the location of surgical mesh in the photoelectric-Compton spectral basis set with the goal of exploring possible image processing filters based on this a priori information.

10132-137, Session PS4

Lung nodule volume quantification and shape differentiation with an ultra-high resolution technique on a photon counting detector CT system

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A new ultra high-resolution (UHR) mode has been implemented on a whole body photon counting-detector (PCD) CT system. This mode had pixel size of 0.25 mm by 0.25 mm at the iso-center, while conventional Macro mode was limited to 0.5 mm by 0.5 mm. A set of synthetic lung nodules (two shapes, five sizes, and two radio-densities) were scanned using both UHR and Macro modes and reconstructed with 2 reconstruction kernels (4 sets of images in total). Linear regression analysis was used to compare measured nodule volumes from CT images to reference volumes. Surface curvature was calculated for each nodule and the full width half maximum (FWHM) of the curvature histogram was used as a shape index to differentiate sphere and star shape nodules. Receiver operating characteristic (ROC) analysis was performed and area under the ROC curve (AUC) was used as a figure of merit for the differentiation task. Results showed UHR mode with a sharp kernel (S80) had the highest accuracy of volume estimation for low contrast lung nodules ($R2 = 0.9999$, RMSE = 1.87). Images from UHR mode with S80f kernel consistently demonstrated the best performance (AUC = 0.875) when separating star from sphere shape nodules among all acquisition and reconstruction modes. Our results showed the advantages of UHR mode on a PCD CT scanner in lung nodule characterization. Various clinical applications, including quantitative imaging, can benefit substantially from this high resolution mode.

10132-138, Session PS4

Development of a photon counting detector response model using multiple transmission spectra

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Photon counting x-ray detectors (PCD) offer a great potential for energy-resolved imaging that would allow for promising applications such as low-dose imaging, quantitative contrast-enhanced imaging, as well as spectral tissue decomposition. However, physical processes in photon counting detectors produce undesirable effects like charge sharing and pulse-pile up that can adversely affect the imaging application. Existing detector response models for photon counting detectors have mainly used either X-ray fluorescence imaging or radionuclides to calibrate their detector and estimate the model parameters. The purpose of our work was to apply one such model to our photon counting detector and to determine the model parameters from transmission measurements. This model uses a polynomial fit to model the charge sharing response and energy resolution of the detector as well as an Aluminum filter to model the modification of the spectrum by the X-ray. Our experimental setup includes a Si-based PCD to generate transmission spectra from multiple materials at varying thicknesses, concentrations and x-ray tube potentials. Materials were selected so as to exhibit k-edges within the 15-35 keV region. Molybdenum foil of 25, 50 and 100 micron thickness resulted in double-peaked spectra with varying peak intensities that were used to tune the model parameters. We find that transmission measurements can be used to successfully model the detector response. Ultimately, this approach could be used for practical detector energy calibration. A fully validated detector response model will allow for exploration of imaging applications for a given detector.

10132-139, Session PS4

Empirical neural network forward model for maximum likelihood material decomposition in spectral CT

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CT measurements using photon counting detectors provide spectral information that can be used to estimate a material's composition. This material decomposition task is complicated by pulse pileup and charge-sharing phenomena. Physics-based methods that use maximum likelihood to estimate a material's composition rely on accurate modeling of the forward spectral measurement process, including the source spectrum and detector response. An empirical projection-domain decomposition method is proposed that uses energy-bin measurements from known basis material path lengths. The known basis material path lengths and energy-bin measurements are used to train a neural network to model the forward spectral measurement process. The neural network is used with a maximum likelihood algorithm to estimate basis material path lengths with optimal noise properties. The method does not require a model of the source spectrum or detector response. Simulations of a step-wedge phantom containing 10 path lengths of polymethyl methacrylate and 10 path lengths of aluminum resulted in 100 calibration measurements for training. Path lengths not included in calibration were used to evaluate the estimator's performance. Projections of the test path lengths contained 1000 Poisson noise realizations and the bias and variance of the estimated path lengths were used as evaluation metrics. The proposed method had less than 2% bias in the test path lengths and had a variance that achieved the Cramer-Rao lower bound. The proposed method is an efficient estimator that estimates basis material path lengths with optimal noise properties.

10132-140, Session PS4

Impact of Compton scatter on material decomposition using a photon counting spectral detector

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Photon counting spectral detectors are being investigated to allow better discrimination of multiple materials by collecting spectral data for every detector pixel. The process of material decomposition or discrimination starts with an accurate estimation of energy dependent attenuation of the composite object. Photoelectric effect and Compton scattering are two important constituents of the attenuation. Compton scattering while results in a loss of primary photon, also results in an increase in photon counts in the lower energy bins via multiple orders of scatter. This contribution to lower energy bins may change with material properties, thickness and x-ray energies. There has been little investigation into effect of this increase in counts at lower energies due to presence of these Compton scattered photons. Our preliminary investigations show that it is important to account for this effect in spectral decomposition problems. Complete work will examine careful characterization of this spectral distortion, correction methods and comparison of estimation inaccuracies relative to other known causes of spectral distortions.

10132-141, Session PS5

Novel geometries for efficient and cost-effective megavolt imaging detectors

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Megavolt (MeV) x-rays are commonly used in external beam radiotherapy to treat a wide range of cancerous tumors. MeV x-rays have the ability to penetrate much further into the body to deliver dose to the tumor compared to x-rays used for medical imaging (<150 keV). In addition to medical applications, MeV x-ray imaging/detection capabilities are used in applications such as border security, weld inspection and ...

The dominant interaction of MeV x-rays with matter is Compton scattering, which has very different properties compared to the more well-known photoelectric effect. Resolution in images is limited to blur caused by the Compton scattering. Different detectors are required to image with MeV x-rays compared to those commonly used with low energy x-ray imaging.

We have investigated a variety of geometries for use in efficient, large area imaging detectors based on segmented scintillators and storage phosphors. The former utilizes fiber-optic scintillators embedded in a high Z metal matrix and the latter uses metal plates stacked both axially with- and transverse to- gamma-ray beams. Both experimental results using Co-60 and megavolt betatrons are presented. Monte Carlo results which guide our designs are also presented along with simple, physics-based exponential fitting models and parameters. We demonstrate DQE values in excess of 10% and 50% MTF values better than 0.5 lp/mm at 1 MeV.

10132-142, Session PS5

High density scintillating glass proton imaging detector

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In recent years, proton therapy has achieved remarkable precision in dose delivery to cancerous cells while avoiding healthy tissue. However, to utilize this high precision treatment, a greater accuracy in positioning the patient is needed. A 3% range of uncertainty exists in the current practice of proton therapy due to the conversion of units for x-rays to stopping power. This study focuses on the use of protons instead, which would eliminate this conversion entirely, determine a more accurate stopping power, and lessen exposure to the patient.

There have been two separate detectors designed with unique glasses. The first detector design utilizes the scintillating high density glass bars, the other semiconducting glass fibers. The unique geometry of these detectors allows for the measurement of both the position and residual energy of pencil beams of protons, eliminating the need for trackers in the system. The simplicity, compactness, and efficiency was the major objectives in these models for the purpose of presenting a novel imaging technique that is both precise and practical for a clinical setting. The same devices can also be suitable to detect the prompt gammas (2-15 MeV) for in vivo tracking of the Bragg peaks.

This report summarizes the optical and electrical detector designs, resolution of the imager, data collection and the image reconstruction methods, as well as the properties of the materials specifically developed for these systems. Preliminary images created via Geant4 simulations, and the approaches using prompt gammas during the proton therapy will be reported.

10132-143, Session PS5

A CMOS-based high-resolution fluoroscope (HRF) detector prototype with 49.5 μm pixels for use in endovascular image guided interventions (EIGI)

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X-ray detectors to meet the high-resolution requirements for endovascular image-guided interventions (EIGIs) are being developed and evaluated. A new 49.5-micron pixel prototype detector is being investigated and compared to the current suite of high-resolution micro-angiographic fluoroscopic (MAF) detectors. This detector featuring a 300-micron thick CsI(Tl) scintillator, and low electronic noise CMOS readout is designated the MAF-CMOS50. To compare the abilities of this detector with other existing MAF detectors, a standard performance metric analysis was applied, including the determination of the modulation transfer function (MTF), noise power spectra (NPS), noise equivalent quanta (NEQ), and detective quantum efficiency (DQE) for a range of energies and exposure levels. The advantage of the smaller pixel size and reduced blurring due to the thin phosphor was exemplified when the MTF of the MAF-CMOS50 was compared to the other MAF detectors, which utilize larger pixels, other optical designs or thicker scintillators. However, the thinner scintillator has the disadvantage of a lower quantum detective efficiency (QDE) for higher diagnostic x-ray energies. The performance of the detector as part of an imaging chain was examined by employing the generalized metrics GMTF, GNEQ, and GDQE, taking standard focal spot size and clinical imaging parameters into consideration. As expected, the disparaging effects of focal spot unsharpness, exacerbated by increasing magnification, degraded the higher-frequency performance of the MAF-CMOS50, while increasing scatter fraction diminished low-frequency performance. Nevertheless, the MAF-CMOS50 brings improved resolution capabilities for EIGIs, but would require increased sensitivity and dynamic range for future clinical application.

10132-144, Session PS5

2x2 oversampling in digital radiography imaging for CsI-based scintillator detectors

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In order to efficiently conduct the anti-aliasing filtering in digital radiography imaging, the oversampling scheme using an oversampling detector, in which the sampling frequency is higher than that of the desired detector, is considered in this paper. Instead of using difficult analog anti-aliasing filters, digital anti-aliasing filters are applied to the oversampled data and then their downsampling enables acquiring the desired x-ray images. Supposing an ideal anti-aliasing filtering, the detective quantum efficiency (DQE) performance of the desired detector can be close to that of the oversampling detector since the overlap of the adjacent noise aliases can be minimized while maintaining the frequency amplitude response for the fundamental frequency range. In this paper, a 2x2 oversampling is conducted for the desired pixel pitch of 152 um/pixel and various filters are tested as the anti-aliasing filter. It is shown that securing an enough transition band is important to avoid the ringing artifacts even though the anti-aliasing performance deteriorates due to the wide transition band. From an experiment using a CsI-based detector, the aliasing artifact problem is alleviated and a DQE improvement of 0.1 is achieved at 3.0 lp/mm from the oversampling radiography imaging over the binning scheme.

10132-145, Session PS5

High spatial resolution performance of pixelated scintillators

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In indirect conversion flat panel detectors (FPDs) for digital X-ray imaging, scintillating materials such as Terbium-doped Gadolinium Oxysulfide (Gadox) convert x-ray into visible light, and an amorphous silicon (a-Si) photodiode array converts the light into electrons. However, it is desired that the detector spatial resolution is improved because the light spreading inside scintillator causes crosstalk to next a-Si photodiode pixels and the resolution is degraded compared with direct conversion FPDs which directly convert x-ray into electrons by scintillating material such as amorphous selenium. In this study, the scintillator was pixelated with same pixel pitch as a-Si photodiode array by barrier rib structure to limit the light spreading, and detector resolution was improved.

The FPD with pixelated scintillator was manufactured as follows. The barrier rib structure with 127?m pitch was fabricated on a substrate by a photosensitive organic-inorganic paste method, and a reflective layer was coated on the surface of the barrier rib, then the structure was filled up with Gadox particles. The pixelated scintillator was aligned with 127?m pixel pitch of a-Si photodiode array and set as a FPD.

The FPD with pixelated scintillator showed high modulation transfer function (MTF) and 0.94 at 1lp/mm and 0.90 at 2lp/mm were achieved. The MTF values were almost equal to the maximum value that can be theoretically achieved in FPDs with 127µm pixel pitch of a-Si photodiode array.

Thus the FPD with pixelated scintillator has great potential to apply for high spatial resolution applications such as mammography and nondestructive testing.

10132-146, Session PS5

Comparison of high resolution x-ray detectors with conventional FPDs using experimental MTFs and apodized aperture pixel design for reduced aliasing

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Apodized Aperture Pixel (AAP) design, proposed by Ismailova et.al, is an alternative to the conventional pixel design1. The advantages of AAP processing with a sinc filter in comparison with using other filters include non-degradation of MTF values and elimination of signal and noise aliasing, resulting in an increased performance at higher frequencies, approaching the Nyquist frequency. If high resolution small field-of-view (FOV) detectors with small pixels used during critical stages of Endovascular Image Guided Interventions (EIGIs) could also be extended to cover a full field-of-view typical of flat panel detectors (FPDs) and made to have larger effective pixels, then methods must be used to preserve the MTF over the frequency range up to the Nyquist frequency of the FPD while minimizing aliasing. In this work, we convolve the experimentally measured MTFs of two Microangiographic Fluoroscope (MAF) detectors, (the MAF-CCD with 35µm pixels and the MAF-CMOS50 with 49.5µm pixels) with the AAP filter and show the superiority of the results compared to MTFs resulting from simple pixel binning and to the MTF of a standard FPD. For detectors in neurovascular interventions, where high resolution is the priority during critical parts of the intervention, but full FOV with larger pixels are needed during less critical parts, AAP design provides an alternative to simple pixel binning while effectively eliminating signal and noise aliasing yet allowing the small FOV high resolution imaging to be maintained during critical parts of the EIGI.

10132-147, Session PS5

1D pixelated MV portal imager with structured privacy film: a feasibility study

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Modern amorphous silicon flat panel-based electronic portal imaging devices that utilize thin gadolinium oxysulfide scintillators suffer from low quantum efficiencies (QEs). Thick two dimensionally (2D) pixelated scintillator arrays offer an effective but expensive option for increasing QE. To reduce costs, we have investigated the possibility of combining a thick one dimensional (1D) pixelated scintillator (PS) with an orthogonally placed 1D structured optical filter to provide for overall good 2D spatial resolution. In this work, the studied the potential for using a 1D video screen privacy film (PF) to serve as a directional optical attenuator and filter. A Geant4 model of the PF was built based on reflection and transmission measurements taken with a laser-based optical reflectometer. This information was incorporated into a Geant4-based x-ray detector simulator to generate modulation transfer functions (MTFs), noise power spectra (NPS), and detective quantum efficiencies (DQEs) for various 1D and 2D configurations. It was found that the 1D array with PF can provide the MTFs and DQEs of 2D arrays. Although the PF significantly reduces the amount of optical photons detected by the flat panel, we anticipate using a scintillator with an inherently high optical yield (e.g. cesium iodide) for MV imaging, where fluence rates are inherently high, will still provide adequate signal intensities for the imaging tasks associated with radiotherapy.

10132-148, Session PS6

Dose conversion coefficients for partial-fan CBCT scans

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Many CBCT devices can operate in two different modes denoted as partial- and full-fan mode. The two modes are characterized by an asymmetric field with a complete 360°-rotation and a symmetric field with partial rotation, respectively. The geometrical difference to conventional CT devices influences the computation of patient organ doses. The feasibility to compute patient organ doses using pre-computed slices like in a previous work is examined for the partial-fan mode.

Organ doses normalized to CTDIw for partial-fan chest CBCT have been computed for the reference male phantom. These values have been compared to dose conversion coefficients (DCC) of an artificial full-fan CBCT to demonstrate that organ DCCs only mildly depend on the fan characteristic. Furthermore, it has been demonstrated that the organ DCC of a partial-fan cone-beam CT can be reproduced with an accuracy of about 25% by using precomputed slices. The relative differences in the effective DCC were less than 10%.

10132-149, Session PS6

Organ and effective dose reduction for region-of-interest (ROI) CBCT and fluoroscopy

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In some medical-imaging procedures using CBCT and fluoroscopy, it may be needed to visualize only the center of the field-of-view with optimal quality. To reduce the dose to the patient as well as enable increased contrast in the region of interest (ROI) during CBCT and fluoroscopy procedures, a 0.7 mm thick Cu ROI attenuator with a circular aperture 12% of the FOV was used. The aim of this study was to quantify the dose-reduction benefit of ROI imaging during a typical CBCT and interventional fluoroscopy procedures in the head and torso. The Toshiba Infinix C-Arm System was modeled in BEAMnrc/EGSnrc with and without the ROI attenuator. Patient organ and effective doses were calculated in DOSxynrc/EGSnrc Monte-Carlo software for CBCT and interventional procedures. We first compared the entrance dose with and without the ROI attenuator on a 20 cm thick solid-water block. Then we simulated a CBCT scan and an interventional fluoroscopy procedure on the head and torso with and without an ROI attenuator. The results showed that the entrance-surface dose reduction in the solid water is about 87% outside the ROI opening and 11% in the ROI opening. Reductions in organ and effective doses of about 35%-72% were achieved in neuro and about 40%-50% in cardiac CBCT. Reductions in organ and effective doses of about 50%-75% were achieved in our simulated interventional cardiac procedure. This work provides evidence of substantial reduction of organ and effective doses when using an ROI attenuator during CBCT and fluoroscopy.

10132-150, Session PS6

Monte Carlo investigation of backscatter point spread function for x-ray imaging examinations

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X-ray imaging examinations, especially complex interventions, may result in relatively high doses to the patient's skin inducing skin injuries. A method was developed to determine the skin-dose distribution for non-uniform x-ray beams by convolving the backscatter point-spread-function (PSF) with the primary-dose distribution to generate the backscatter distribution that, when added to the primary dose, gives the total-dose distribution. This technique was incorporated in the dose-tracking system (DTS), which provides a real-time color-coded 3D-mapping of skin dose during fluoroscopy procedures. The aim of this work is to investigate the variation of the backscatter PSF with different parameters. A backscatter PSF of a 1-mm x-ray beam was generated by EGSnrc Monte-Carlo code for different x-ray beam energies, different soft-tissue thickness above bone, different bone thickness and different entrance-beam angles, as well as for different locations on the SK-150 anthropomorphic head phantom. The results show a reduction of backscatter dose per incident photon of up to 28% when kVp increases from 60 to 120. The backscatter dose was reduced when bone was beneath the soft tissue layer and this reduction increased with thinner soft tissue and thicker bone layers. The backscatter dose increased about 60% toward the direction of the entrance beam with increased beam angle from 90° (perpendicular) to 30°. The backscatter PSF differed for different locations on the SK-150 phantom by up to 15%. The results of this study can be used to improve the accuracy of dose calculation when using PSF convolution in the DTS.

10132-151, Session PS6

Effects of sparse sampling in combination with iterative reconstruction on quantitative bone microstructure assessment

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The trabecular bone microstructure is a key to the early diagnosis and advanced therapy monitoring of osteoporosis. Regularly measuring bone microstructure with conventional multi-detector computer tomography (MDCT) would expose patients with a relatively high radiation dose. One possible solution to reduce exposure to patients is sampling fewer projection angles. This approach can be supported by fast switching X-ray source and advanced reconstruction algorithm, with its ability to achieve better image quality under reduced projection angles or high levels of noise. In this work, we collected 9 cases routine in-vivo MDCT scans of human spines and investigated the performance of iterative reconstruction from sparse sampled projection data for trabecular bone microstructure. Statistical iterative reconstruction was performed with ordered-subset separable paraboloidal surrogate (OS-SPS). The computed MDCT images were evaluated by calculating bone microstructure parameters. We demonstrated that bone microstructure parameters were still computationally distinguishable when half or less of the radiation dose was employed.

10132-152, Session PS6

Evaluation of methods to produce an image library for automatic patient model localization for dose mapping during fluoroscopically guided procedures

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The purpose of this work is to evaluate methods for producing a library of 2D-radiographic images to be correlated to clinical images obtained during a fluoroscopically-guided procedure for automated patient-model localization. The localization algorithm will be used to improve the accuracy of the skin-dose map superimposed on the 3D patient-model of the real-time Dose-Tracking-System (DTS). For the library, 2D images were generated from CT datasets of the SK-150 anthropomorphic phantom using Schmid's 3D-visualization tool and Folkert's digitally-reconstructed-radiograph (DRR) code. Those images, as well as a standard 2D-fluoroscopic image of the phantom, were correlated to a 2D reference patient radiograph, which represented the clinical-fluoroscopic image, using the Corr2 function in Matlab. The Corr2 function takes two images and outputs the relative correlation between them, which is fed into the localization algorithm. Higher correlation means better alignment of the 3D patient-model with the patient image. In this instance, it was determined that the localization algorithm will succeed when Corr2 returns a relative correlation of at least 35% compared to the reference radiograph. The 3D-visualization tool images returned 55-78% correlation relative to the radiograph, which was better than the correlation for the standard 2D-fluoroscopic image. The DRR images take longer to produce and yielded only 1% relative correlation. While the DRR method produces more accurate grey-levels, the 3D-visualization images obtained using Schmid's tool prove to be sufficient for the localization algorithm and can be produced quickly. Using the 3D-visualization tool, a library at varying angles will be produced for the localization algorithm.

10132-153, Session PS6

Estimation of breast dose reduction potential for organ-based tube current modulated CT with wide dose reduction arc

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Organ-based tube current modulation has been shown to significantly reduce breast dose, while challenged by the fact that the dose reduction zone is smaller than the extent of patients' breasts. In this study we evaluated the organ dose reduction potential for a new organ-dose-based tube current modulation scheme (ODM) (GE Healthcare) with a wide dose reduction arc across a patient population. This study included 21 female computational XCAT phantoms (age range: 27–75 y.o., weight range: 52.0-105.8 kg) representing clinical anatomical variations. A commercial CT scanner (Revolution, GE Healthcare) was simulated. The standard tube current modulation (TCM) (SmartmA, GE Healthcare) profile was modeled using a ray tracing program. The ODM profile was generated by reducing the TCM profile by 40% approximately 180° anterior of the phantom. Organ dose was calculated by a validated Monte Carlo program for a typical thoracic CT protocol. As ODM decreased ~20% of the CTDIvol, an additional set of organ dose, retaining the same CTDIvol (thus image quality) between ODM and TCM, was also reported. ODM significantly reduced organ doses for all radiosensitive organs ($p<0.01$); breast and thyroid doses were reduced by 30 ± 2% and 28 ± 3% respectively. For ODM simulations using the same CTDIvol as TCM, the breast dose was reduced by 15 ± 2%. The organs in anterior region (e.g. thyroid, stomach) exhibited substantial decreases. The medial, distributed and posterior region organ doses were increased less than 5 % from ODM to TCM. The ODM scheme was found to significantly reduce organ doses especially for superficial anterior organs.

10132-154, Session PS7

Detection of microcalcification and tumor tissue in mammography using a CdTe-series photon-counting detector

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In this study, we propose a method to detect microcalcifications and tumor tissue using a cadmium telluride (CdTe) series linear detector. We use the CdTe series detector as a photon-counting mammography detector. We designed the CdTe series linear detector and two types of phantom using a MATLAB simulation. Each phantom consisted of mammary gland and adipose tissue. One phantom contained microcalcifications and the other contained tumor tissue. We varied the size of these structures and the mammary gland composition. We divided the spectrum of an X-ray, which is transmitted to each phantom, into three energy bins and calculated the corresponding linear attenuation coefficients from the numbers of input and output photons. Then, we calculated the absorption vector length that is expressed by the amount of absorption. When the material composition was different between objects, for example mammary gland and microcalcifications, the absorption vector length was also different. We compared each absorption vector length and then tried to detect the microcalcifications and tumor tissue. However, these were become more difficult to distinguish as the size of microcalcifications and tumor tissue decreased and/or the mammary gland content rate increased. If we increase the X-ray dosage, we can distinguish the microcalcifications and tumor tissue despite the reduction in size or increase in mammary gland content rate. Hence, we should find a condition under which a low exposure dose is optimally balanced with high detection sensitivity.

10132-155, Session PS7

Contrast-enhanced spectral mammography based on a photon-counting detector: quantitative accuracy and radiation dose

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Contrast-enhanced mammography has been used to demonstrate functional information about a breast tumor by injecting contrast agents. However, a conventional technique with a single exposure degrades the efficiency of tumor detection due to structure overlapping. Dual-energy techniques with energy-integrating detectors (EIDs) also cause an increase of radiation dose and an inaccuracy of material decomposition due to the limitations of EIDs. On the other hands, spectral mammography with photon-counting detectors (PCDs) is able to resolve the issues induced by the conventional technique and EIDs using their energy-discrimination capabilities. In this study, the contrast-enhanced spectral mammography based on a PCD was implemented by using a polychromatic dual-energy model, and the proposed technique was compared with the dual-energy technique with an EID in terms of quantitative accuracy and radiation dose. The results showed that the proposed technique improved the quantitative accuracy as well as reduced radiation dose comparing to the dual-energy technique with an EID. Therefore, the contrast-enhanced spectral mammography based on a PCD is able to provide useful information for detecting breast tumors and improving diagnostic accuracy.

10132-156, Session PS7

An adaptive toolkit for image quality evaluation in system performance test of digital breast tomosynthesis

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Digital breast tomosynthesis (DBT) is a relatively new diagnostic imaging modality for women. Currently, various models of DBT systems are available on the market and the number of installations is rapidly increasing. EUREF, the European Reference Organization for Quality Assured Breast Screening and Diagnostic Services, has proposed a preliminary guideline: protocol for the quality control of the physical and technical aspects of digital breast tomosynthesis systems, with an ultimate aim of providing limiting values guaranteeing proper performance for different applications of DBT. In this work, we introduce an adaptive toolkit that is developed following this guideline to facilitate the process of image quality evaluation in system characterization and periodic constancy test. This toolkit implements robust algorithms to quantify various technical parameters of DBT images and provides a convenient user interface in practice. Test modules and configurations are set corresponding to those as described in the European guideline, but can be adapted to different settings and applications as well. This toolkit can largely improve the efficiency of image quality evaluation with DBT datasets. It is also going to evolve with the development of protocols in quality control of DBT systems.

10132-157, Session PS7

Evaluation of effective detective quantum efficiency considering breast thickness and glandularity in prototype digital breast tomosynthesis system

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Digital breast tomosynthesis (DBT) system is a novel imaging modality which is strongly depended on the performance of a detector. Recently, effective detective quantum efficiency (eDQE) has been introduced to solve the disadvantages of conventional DQE evaluations which do not consider clinical operating conditions. For eDQE evaluation, the variety of patient breast, especially the glandularity and thickness needed to be studied to consider different races of patient. For these reasons, eDQE in a prototype DBT system considering different breast thickness and glandularity was evaluated. In this study, we used the prototype DBT system with CsI(Tl) scintillator/CMOS flat panel digital detector developed by Korea Electrotechnology Research Institute (KERI). A scatter fraction, a transmission fraction, a modulation transfer function (MTF) and a normalized noise power spectrum (NNPS) were measured in different thickness and glandularity of breast equivalent phantom. As a result, scatter fraction increased from 12% to 39%, and transmission fraction decreased from 22% to 0.25% as both glandularity and thickness of the breast phantom increased. NNPS also increased with increasing glandularity and thickness. On the other hand, MTF was not affected by glandularity of breast phantom, while MTF decreased with increasing the thickness. These indicated that eDQE was strongly affected by phantom thickness, but the effect of glandularity seemed to be trivial. Consequently, the measured eDQE for our DBT system at the frequency of 1 cycles/mm decreased approximately 14% by comparing minimum and maximum eDQE values.

10132-158, Session PS7

Stationary digital breast tomosynthesis reconstruction using distance driven method

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Stationary digital breast tomosysthesis is an effective x-ray imaging technique for early breast cancer detection with fast image acquisition and low radiation dosage. This paper is continuation of our study using distance driven method for breast tomosynthesis reconstruction. Simultaneous algebraic reconstruction technique (SART) based on distance driven was developed to generate three dimensional reconstruction information of a breast phantom. Tomosynthesis data set of 15 projection images was acquired over view angle of 48 degrees. Reconstruction results were demonstrated and line profile was used to evaluate the results.

10132-159, Session PS7

Geometric calibration for a next generation digital breast tomosynthesis system

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A method for geometric calibration of a Next Generation tomosynthesis (NGT) system is proposed and tested. A phantom was created to project small Tungsten-Carbide ball bearings (bb's) onto the detector at different magnifications. Using a bandpass filter and template matching, a MatLab program was written to identify the locations of the bb's on the image. These locations were compared to the expected projection locations based on the nominal location of the source. An optimization was then used to minimize the locational differences between the two sets of locations, finding an effective location for the source for each projection. Tomographic image reconstructions with computed Super Resolution (SR) were performed for one of the geometric configurations using these source locations.

10132-160, Session PS7

Scatter reduction for grid-less mammography using the convolution-based image post-processing technique

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Mammography examinations are highly affected by scattered radiation, as it degrades the quality of the image and complicates the diagnosis process. Anti-scatter grids are currently used in planar mammography

examinations as the standard scattering reduction technique. This method has been found to be inefficient, as it increases the dose delivered to the patient, does not remove all the scattered radiation and increases the price of the equipment. Alternative scattering reduction methods, based on post-processing algorithms, are being developed to substitute anti-scatter grids. Methods such as the convolution-based scatter estimation have lately become attractive as they are faster and more flexible than pure Monte Carlo (MC) simulations. In this study we make use of this specific method, which is based on the idea that the scatter in the system is spatially diffuse, thus it can be approximated by a two-dimensional low-pass convolution filter of the primary image. This algorithm uses the narrow pencil beam method to obtain the scatter kernel used to convolve an image, acquired without anti-scatter grid. Preliminary results show an improvement in the contrast to noise ratio of the image but do not show an improvement over the images acquired with an anti-scatter grid. The chosen phantom images were heterogeneous, with test objects of unknown materials that were simplified in the simulation, leading to an underestimation of the scatter. The subsequent study will include extra kernels to account for the heterogeneity of the phantoms as well as the analysis of homogeneous images.

10132-161, Session PS7

Comparison of effects of dose on image quality in digital breast tomosynthesis across multiple vendors

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In traditional radiography and CT, contrast is an important measure of image quality that, in theory, does not vary with dose. While increasing dose may increase overall signalcontrast-to-noise ratio (CNR), the contrast in an image should be primarily dependent on variation in tissue density and linear attenuation. Investigation intoWe investigated the behavior of two all three currently FDA-approveddifferent vendors' 3D DBT systems (Siemens and, Hologic, and GE) using the CIRS Model 011A Breast Phantom revealed that both systems show a positive relationship between contrast and dose. Upon closer investigation, it appeared that for both Siemens and Hologic systems, contrast increased with dose across multiple repeated trials., while noise followed the expected trend of increasing linearly with 1/√dose. Additionally, experimental CNR appeared to increase above the expected CNR, all of which suggests that these systems appear to have introduced post-processing by manipulation of contrast, and thus DBT data cannot be used to reliably quantify tissue characteristics., as these systems appear to have introduced an artificial improvement of overall image quality post-processing by manipulation of contrast.

Additional experimentation with both 2D mammography and 3D DBT systems from GE in addition to the previously mentioned vendors, however, suggested that this relationship is not true for all systems. An initial comparison of contrast vs. dose showed no relationship between contrast and dose for 2D mammography, with the contrast remaining relatively constant in the dose range of 50% AEC to 300% AEC for all three vendors. While we did find that increasing dose seems to correlate with increasing contrast for both the Hologic and Siemens DBT systems, tThe GE DBT system also did not exhibit this behaviorincreased contrast with increased dose, suggesting that the behavior of 3D DBT systems is vendor-specific.

10132-162, Session PS7

Denoised ordered subset statistically penalized algebraic reconstruction technique (DOS-SPART) in digital breast tomosynthesis

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A novel implementation of the Denoised Ordered Subset Statistically Penalized Algebraic Reconstruction Technique (DOS-SPART) has been developed for digital breast tomosynthesis (DBT), allowing for an efficient and modular statistical iterative reconstruction by separating data consistency updates and regularization using the alternating descent of multipliers method (ADMM). In this work the DOS-SPART algorithm was adapted for use with DBT by implementing a 3D automated breast mask, and parameter optimization for the limited angular range scans. Several datasets were acquired using a Hologic Selenia Dimensions DBT system and reconstructed using the commercial reconstruction method and DOS-SPART to explore artifacts and dose performance for the two methods. Through plane blurring artifacts were assessed for high contrast calcifications in the ACR accreditation phantom, and dose performance was assessed using the measured contrast-to-noise ratio (CNR) for normal breast tissues in a cadaver specimen imaged at a range of doses. Finally, a clinical exam was reconstructed using both methods and assessed subjectively. It was found that DOS-SPART can significantly limit through-plane-blurring artifacts by about 40%, maintain image sharpness, and match the full dose CNR performance for the commercial reconstructions at doses reduced by as much as 50%. In addition, in a clinical breast exam featuring a high contrast calcified mass additional features were visualized using DOS-SPART that could not be clearly seen in the commercial reconstruction.

10132-163, Session PS7

Scattered radiation in DBT geometries with flexible breast compression paddles: a monte carlo simulation study

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Scattered radiation is an undesired signal largely present in most digital breast tomosynthesis (DBT) projection images as no physically rejection methods, i.e. anti-scatter grids, are employed, in contrast to full-field digital mammography. This scatter signal might reduce the visibility of small objects in the image, and potentially affect detection of small lesions. Thus accurate scatter models are needed to minimise the scattered radiation signal via post-processing algorithms. All prior work on scattered radiation estimation has used a rigid breast compression paddle (RP) and reported large contribution of scatter signal from RP in the detector. However, in this work, flexible paddles (FPs) tilting from 0º to 10º (depending on the model) will be studied using Monte Carlo simulations to analyse if the scatter distribution differs from RP geometries. After reproducing the Hologic Selenia Dimensions geometry (narrow angle) with a 50 mm thick compressed breast phantom (glandularity 20%), results illustrate that the scatter distribution recorded at the detector varies up to 25% between RP and FP geometries, mainly due to the decrease in thickness of the breast observed for FP. However, the relative contribution from the paddle itself (3-12% of the total scatter) remains the same for both setups and their magnitude depends on the distance to the breast edge.

10132-164, Session PS8

New high-resolution imaging technology; application of advanced radar technology for medical imaging

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Image resolution for RF/microwave relatively long waves limited by diffraction limit (Abbe diffraction limit). Each point of reflecting object will work as source of diffractive waves. But phase front of diffracted waves still will consist information about object shape. Image can be recovered from multi frequency digital hologram by combination of interferograms. Regular hologram normally recording on one color (frequency) and intensity of each next color hologram significantly dropping. Ultra-wide band Software

Defined Radio (SDR) allows real time record of multiple diffracted waves in time domain (waterfall). Resolution of recovered image will defined by accuracy for recorded phase front, means phases and amplitudes of diffracted waves, which determined by accuracy of digitizing. In this case resolution of recovered image will be determined by receiver bandwidth, digitizing frequency and accuracy of processor time. Better processor - better image resolution. Important conclusion: Image resolution in proposed technology do not depends from wavelength.Second image resolution limit related to beam width. High resolution azimuth and range measurement can be done by application of monopulse method proposed. Two overlap antenna patterns provide high accuracy phase measurement, 2-3 orders better than any, even conical scanning radar. Low frequency non-scanning wide beam covering all object and same time provides high resolution phase measurement if reference beam applied. High resolution measurement means high resolution imaging. Technology can be applied for creation of momentary images insensitive to human body movements because full image information can be recorded in a few microseconds.

10132-165, Session PS8

Multi-grid finite element method used for enhancing the reconstruction accuracy in Cerenkov luminescence tomography

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Cerenkov luminescence tomography (CLT), as a promising optical molecular imaging modality, can be applied to cancer diagnostic and therapeutic. Most current CLT reconstruction research was based on the finite element method (FEM) framework. The most attractive feature of FEM is its ability to handle complicated geometries with relative convenience. However, the quality of FEM mesh grid is still a vital factor to restrict the accuracy of the CLT reconstruction result. In this paper, we proposed a multi-grid finite element method framework, which combined the spatial optimization with a modified iterative algorithm to improve the reconstruction accuracy. Multi-grid strategy can obtain more abundant structural information, which improves the accuracy and stability of reconstruction essentially. More importantly, in each iterative process, a modified updating strategy was devised, which mainly considered the relevance between spatial coordinates and Cerenkov luminescence intensities. In numerical simulation experiments, feasibility and robustness of our proposed method were evaluated. Results showed that the multi-grid strategy can obtain 3D spatial information of tumor lesions much more accurately compared with the traditional FEM which based on a single grid. Lastly, in vivo results indicated that our method had a significant improvement to noninvasively monitor and quantify uptake of radiopharmaceutical in physiological and metabolic processes of mice. In conclusion, multi-grid FEM can obtain 3D spatial distribution information of radiopharmaceutical more accurately by combining the multi-grid strategy and the modified iterative algorithm.

10132-166, Session PS8

Accelerated x-ray scatter projection imaging using multiple continuously-moving pencil beams

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Coherent x-ray scatter varies with angle and photon energy in a manner dependent on the chemical composition of the scattering material, even for amorphous materials. Therefore, images generated from scattered photons can have much higher contrast than conventional projection radiographs. We are developing a scatter projection imaging prototype at the BioMedical Imaging & Therapy (BMIT) facility of the Canadian Light Source (CLS) synchrotron in Saskatoon, Canada. The best images are obtained using step-and-shoot scanning with a single pencil beam and area detector to capture sequentially the scatter pattern for each primary beam location on the sample. Primary x-ray transmission is recorded simultaneously using photodiodes. The technological challenge is to acquire the scatter data in a reasonable time. Using multiple pencil beams producing partially-overlapping scatter patterns reduces acquisition time but increases complexity due to the need for a disentangling algorithm to extract the data. Continuous sample motion, rather than step-and-shoot, also reduces acquisition time at the expense of introducing motion blur, which is corrected using a deconvolution algorithm. With a five-beam (33.2 keV, 2.7 mm^2 beam area) step-and-shoot configuration, a hexagonal array of 58x50 pixels with 1.68 mm pitch has been acquired in 8.8 minutes (330 px/min.), on the time scale of nuclear medicine scans. Our continuous motion acquisition protocol is expected to exceed 2000 px/min. Future improvements to the disentangling and deconvolution algorithms are needed to reduce artefacts. Our prototype development, image acquisition of plastic and biological phantoms, and data processing algorithms are described.

10132-167, Session PS8

Coded aperture coherent scatter spectral imaging for clinical use in ex vivo imaging for intraoperative margin assessment of breast cancers

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A Coded Aperture Coherent Scatter Spectral Imaging (CACSSI) system was previously developed in our group to differentiate cancer and healthy tissue (i.e. adipose and fibroglandular) in the breast. The utility of the experimental system was demonstrated using anthropomorphic breast phantoms and breast biopsy specimens1-4. Here we demonstrate the CACSSI system in scanning fresh breast lumpectomy specimens within the clinical workflow. Lumpectomy specimens were obtained from Surgical Pathology with the cancerous area designated on the specimen, scanned in the system as fresh samples, and then rescanned post-formalin-fixation the following day. The acquired data were reconstructed into form factor spectra and compared against reference literature form-factors to determine their tissue classification. The resulting images were verified with pathology reports to determine the presence and location of the tumor. The system was found to be capable of consistently differentiating cancerous and healthy specimens without disrupting clinical workflow. The spectral distributions obtained from the specimens correlated well with the pathology results. We now aim to develop CACSSI as an ex vivo clinical imaging tool for intra-operative margin assessment or other diagnostic purposes.

10132-168, Session PS8

Mono-energy coronary angiography with a compact light source

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While conventional x-ray tube sources reliably provide high-power x-ray beams for everyday clinical practice, the broad spectra that are inherent to these sources compromise the diagnostic image quality. For a monochromatic x-ray source on the other hand, the x-ray energy can be adjusted to optimal conditions with respect to contrast and dose.

However, large-scale synchrotron sources impose high spatial and financial demands, making them unsuitable for clinical practice. During the last decades, research has brought up compact synchrotron sources based on inverse Compton scattering, which deliver a highly brilliant, quasi-monochromatic, tunable x-ray beam, yet fitting into a standard laboratory.

One application that could benefit from the invention of these sources in clinical practice is coronary angiography. Being an important and frequently applied diagnostic tool, a high number of complications in angiography, such as renal failure, allergic reaction, or hyperthyroidism, are caused by the large amount of iodine based contrast agent that is required for achieving sufficient image contrast.

Here we demonstrate monochromatic angiography of a porcine heart acquired at the MuCLS, the first commercially sold compact synchrotron source. By means of a simulation, the CNR in a coronary angiography image achieved with the quasi-mono-energetic MuCLS spectrum is analyzed and compared to a conventional x-ray-tube spectrum. The results imply that the improved CNR achieved with a quasi-monochromatic spectrum can allow for a significant reduction of iodine contrast material. Furthermore, we demonstrate the feasibility of dual-energy K-edge subtraction imaging with an Iodine filter technique at a compact synchrotron source.

10132-169, Session PS8

Full three-dimensional direction-dependent x-ray scattering tomography

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Small-angle X-ray scattering (SAXS) can provide high contrast among different types of tissues or materials in medical diagnosis and other applications. Combining coherent scattering of X-ray photons with computed tomography (CT) enables the detection of spatially-resolved, material-specific scattering profile inside an extended object. However, conventional coherent-scattering computed tomography (CSCT) lacks the ability to distinguish direction-dependent coherent scattering signal from the object. By incorporating detector movement into CSCT projection measurement, here we propose a CSCT modality that can resolve three-dimensional scattering profile for each pixel in the object using a table-top quasi-monochromatic X-ray source and a two-dimensional detector array. To prove the feasibility of this concept, we demonstrate the anisotropic coherent scattering profile of different materials observed from our setup, and perform a numerical simulation to reconstruct the full three-dimensional momentum transfer space of each pixel in a two-dimensional object. This proposed method shows the potential to achieve low-cost, high-specificity X-ray tissue imaging or material characterization.

10132-170, Session PS8

3D reconstruction of synapses with deep learning based on EM Images

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Recently, due to the rapid development of electron microscope (EM) with its high resolution, stacks delivered by EM can be used to analyze a variety of components that are critical to understand brain function. Since synaptic study is essential in neurobiology and can be analyzed by EM stacks, the automated routines for reconstruction of synapses based on EM Images can become a very useful tool for analyzing large volumes of brain tissue and providing the ability to understand the mechanism of brain.

In this article, we propose a novel automated method to realize 3D reconstruction of synapses for Automated Tape-collecting Ultra Microtome Scanning Electron Microscopy (ATUM-SEM) with deep learning. Being different from other reconstruction algorithms, which employ classifier to segment synaptic clefts directly. We utilize deep learning method and segmentation algorithm to obtain synaptic clefts as well as promote the accuracy of reconstruction. The proposed method contains five parts: (1) using modified Moving Least Square (MLS) deformation algorithm and Scale Invariant Feature Transform (SIFT) features to register adjacent sections, (2) adopting Faster Region Convolutional Neural Networks (Faster R-CNN) algorithm to detect synapses, (3) utilizing screening method which takes context cues of synapses into consideration to reduce the false positive rate, (4) combining a practical morphology algorithm with a suitable fitting function to segment synaptic clefts and optimize the shape of them, (5) applying the plugin in FIJI to show the final 3D visualization of synapses. Experimental results on ATUM-SEM images demonstrate the effectiveness of our proposed method.

10132-171, Session PS8

Estimating internal tissue temperature using microwave radiometry data and bioheat models

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An ability to noninvasively measure the temperature of internal tissue regions would be valuable for applications including the detection of malignancy, inflammation, or ischemia. The output power of a microwave radiometer with an antenna at the skin surface is a weighted average of temperature in a tissue volume beneath the antenna. It is difficult, however, to translate radiometric measurements into temperature estimates for specific internal tissue regions. The chief difficulty is insufficient data: in a realistic system there are no more than a few measurements to characterize the entire volume. Efficient use must be made of available prior information together with the radiometric data in order to generate a useful temperature map. In this work we assume that we know the tissue configuration (obtained from another modality), along with arterial blood temperature, skin temperature, and nominal tissue-specific values for metabolic and blood perfusion rates, thermal conductivity, and dielectric constants. The Pennes bioheat equation can then be used to construct a nominal temperature map, and electromagnetic simulation software to construct the radiometric weighting functions for any given radiometer configuration. We show that deviations from the nominal conditions in localized regions (due, e.g., to the presence of a tumor) lead to changes in the tissue temperature that can also be approximated in terms of the nominal bioheat model. This enables the development of algorithms that use the nominal model along with radiometric data to detect areas of elevated temperature and estimate the temperature in specified tissue regions.

10132-172, Session PS8

Optically tracked, single-coil, scanning magnetic induction tomography

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Recent work has shown the feasibility of single-coil, magnetic induction tomography, for visualizing a 3D distribution of electrical conductivity in portions of the human body. Loss is measured in a single, planar coil consisting of concentric circular loops all while the coil is relocated to various non-redundant positions and orientations in the vicinity of the target. These loss values, together with measured coil position and orientation, are processed by a quantitative mapping equation that enables reconstruction of an electrical conductivity image. Up until now, the position of the coil had to be established by a template, which required assignment of locations for the coil to visit without necessarily giving any prior consideration to target geometry. We have now added optical tracking to our existing single-coil device so that position and orientation are tracked automatically, allowing collection of coil loss data at arbitrary positions or orientations as needed. Optical tracking is accomplished via a set of IR reflective spheres mounted on the same enclosure that supports the coil. Position for a select sphere within the set, together with the four quaternions specifying optical body orientation is fed to a laptop at the same time coil loss data is streamed to the same laptop via Blue Tooth. By tracking position and orientation of the optical body during a pivot step that involves sweeping the coil enclosure within a conical region while the coil center is engaged with a static pivot, the origin of coordinates may be relocated to the coil center. Thus, the coil center can be tracked with sub-millimeter accuracy while orientation angle is known to a fraction of a degree. This presentation will illustrate the use of single-coil MIT in full, position-orientation-tracked scan mode while imaging several simple laboratory phantoms. Phantoms are either based upon simple materials having biologic conductivity (< 5 S/m), or include various cuts of bone-in steak. In either case, the goal is not just to reconstruct an image that contains the features of the actual target, but also return correct conductivity values for the various features within the image - referred to by some authors as absolute conductivity imaging.

10132-173, Session PS8

Quantitative 1D diffraction signatures during dual detector scatter VOI breast CBCT

Robert J. LeClair, Laurentian Univ. (Canada)

Dual detector VOI scatter CBCT is similar to dual detector VOI CBCT except that during the high resolution scan, the low resolution flat panel detector is also used to capture the scattered photons. Previous simulations showed a potential use of scatter to diagnose suspicious VOIs. Energy integrated signals due to scatter (EISs) were computed for a specific imaging task and were labelled as a hypothetical experiment result. The signal was then compared to predictions using benign and malignant lesions. The EISs|expt - EISs|pred displayed eye catching diffraction structure that can be used to diagnose a suspicious lesion.

In this work the 2D EISs|expt - EISs|pred patterns are transformed to 1D signals. The diffraction structure has a circularly symmetric behavior because tissues are amorphous in nature. The 1D signals were obtained by calculating the mean signals in rings. The mean pixel values were a function of the momentum transfer argument q=4pi sin(theta/2)/lambda which ranged from 14 to 46 nm^-1.

The 1D signals correlated well with the 2D profiles. Of particular interest were scatter signatures between q = 20 and 30 nm^-1 where malignant tissue is predicted to scatter more than benign fibroglandular tissue.

The 1D diffraction signatures could allow a better method to diagnose a suspicious lesion during dual detector scatter VOI CBCT. A technique that uses the 1D signals along with the scatter properties of tissues will be devised so that a quantitative metric could be extracted for diagnostic purposes.

10132-174, Session PS8

Infrared microscopy imaging apply to obtain the index finger pad´s thermoregulation curves

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In this work mid wavelenght infrared microscopy imaging videos of several index finger pads are recorded to obtain the finger pad thermoregulation curves. The proposed non-invasive method capture the spatial and temporal thermal information emitted from blood vessels under-skin, and the irrigation finger pad system, making possible to see thermal features that a visual-spectrum imaging microscopy cannot detect. The mid wavelength infrared microscope is a built in system formed by a Sofradir-EC IRE-320M MWIR camera, with a spatial resolution of 320 ? 256 pixels, spectral response between 3.7–4.8 [?m], 14 bits of digital output, detector material mercury cadmium telluride, coupled with a cooling system to increase sensitivity performance. The camera is coupled to a 4X infrared microscope objective lens, acquiring scenes with micrometer spatial resolution, milli kelvin thermal resolution, and 200 frames per second temporal resolution. Using an infrared laboratory prepared method several voluntary patients exposed theirs fingers to thermal stress while the infrared data is captured. Using standard infrared imaging and signal processing techniques the thermoregulation curves of several fingerprints were measured. All volunteers were exposed to the same environmental initial conditions; the men registered an initial average temperature of 36 ºC, while the women registered an initial average temperature of 35 °C. The finger is cold/hot stressed then being immobilized while the data is acquired, the whole process take five minutes. The Cold/Hot Stress experiments have shown infrared data with exponential trend curves.

10132-175, Session PS8

Reconstruction method for x-ray imaging capsule

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Colon imaging capsule has been developed by Check-Cap Ltd (C-Scan Cap®). For the procedure, the patient swallows a small amount of standard Iodinated contrast agent. To create images, three rotating collimated X-ray beams are emitted towards the colon wall. Part of the X-ray photons are backscattered from the contrast media and the colon. These photons are collected and measured by an omnidirectional array of energy discriminating photon counting detectors (CdTe/CZT) within the capsule. X-ray fluorescence (XRF) and Compton backscattering photons pertain different energies and are counted separately by the single photon detection electronics.

The current work examines a statistical approach for the algorithm that reconstructs the lining of the colon wall from the X-ray detector readings. The algorithm performs numerical optimization for finding the solution to the inverse problem applied to the physical forward model, reflecting the behavior of the system.

The forward model that was employed, accounts for the following major factors: the two mechanisms of dependence between the distance to the colon wall and the amount of XRF and backscattered Compton photons; Scatter directional distributions; Relative orientations between beams and detectors. Calibration procedure has been put in place to adjust the coefficients of the forward model for the specific capsule geometry, radiation source strength and uniformity, and the detector response.

The performance of the algorithm was examined in phantom experiments and demonstrated high correlation between the actual phantom data and the x-ray image reconstruction.

Evaluation is underway to assess the algorithm performance in clinical setting.

10132-176, Session PS9

Design of a new DOI detector module with a single layer scintillator array using depth-dependent reflector patterns

Seung-Jae Lee, Chaeyeong Lee, Hankyeol Song, Chan Woo Park, Yong Hyun Chung, Yonsei Univ. (Korea, Republic of)

We designed a depth of interaction (DOI) PET detector using depth-dependent reflector patterns in a single layer scintillator array. Due to the different reflector pattern in depth, the light distribution on the photosensor is altered according to the depth. As a preliminary experiment, the detector module with 4-layer DOI capability was developed. The detector module consists of 9 x 9 array of 2 mm x 2 mm x 20 mm LSO crystals. The crystal array was optically coupled to a 64 channel position sensitive photomultiplier tube whose sensitive area is 18.1 mm x 18.1 mm. The flood image was acquired by anger-type calculation. It was confirmed that DOI layers were distinguished in the obtained images. Preclinical PET scanners based on this detector design will offer the prospect of high and uniform spatial resolution.

10132-177, Session PS9

Optimization of the optical parameters for the depth-dependent DOI detector module

Seung-Jae Lee, Yong Hyun Chung, Hankyeol Song, Chaeyeong Lee, Chan Woo Park, Yonsei Univ. (Korea, Republic of)

In this study, the optical parameters of depth of interaction (DOI) PET detector using depth-dependent reflector patterns in single layer scintillation crystal was optimized. The new DOI detector employs four-layer reflectors that have the dedicated patterns depending on the crystal depth. A DOI performance of the detector is determined by surface treatment of crystals, coupling materials and reflector materials. DETECT 2000 simulation was carried out and it was compared by an experiment. To assemble the detector, 2x2x20 mm3 of LYSO crystals were arranged in 6x6 array. Two crystal surface conditions were selected as polish and ground. The coupling materials were classified into air gap and optical grease. ESR(Enhanced Specular Reflector) film and BC 620 reflector paint were employed as the reflector materials. Using these parameters, eight different detector modules were modeled. A flood map of each detector was obtained and its line profiles were analyzed to evaluate DOI capability. The result indicated that the polish surface was suitable for the BC-620 reflector paint and the ground surface was well-matched with both ESR and BC 620. In case of the coupling materials, optical grease showed a better performance for DOI than air gap.

10132-178, Session PS9

A simulation study of the square-shaped preclinical PET system with DOI detector

Seung-Jae Lee, Chan Woo Park, Chaeyeong Lee, Hankyeol Song, Yong Hyun Chung, Yonsei Univ. (Korea, Republic of)

The purpose of this study is to design square-shaped preclinical PET system with 4-layer DOI detector using depth-dependent reflector patterns in a single-layer crystal array. The four modules are arranged in a square with an inner side of length 80 mm without empty space between modules. Each module consists of four sub-modules, composed of LSO crystals and MPPCs array, connected in a row. The 12 x 12 array of 2 mm x 2 mm x 20 mm polished LSO crystals is optically coupled to an 8 x 8 MPPCs array, which has 3 mm x 3 mm pixel area and pixel pitch of 3.2 mm. The spatial resolution and sensitivity of the PET system were evaluated by GATE simulation. A point source was simulated at radial offsets of 0, 10, 20 and 30 mm from the center of the field of view (FOV). To evaluate the effect of DOI measurement on the system performance, the tomographic images were reconstructed with 4-layer DOI information and without DOI. The spatial resolution with and without DOI ranged from 1.69 mm to 3.07 mm with an average of 2.39 mm and from 4.03 mm to 8.58 mm with an average of 6.3 mm, respectively. The sensitivity was 8.28 % in the center of FOV.

10132-179, Session PS9

Dynamic PET Image reconstruction for parametric imaging using the HYPR kernel method

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Dynamic PET image reconstruction is a challenging problem because of the ill-conditioned nature of PET and the low-counting statistics resulted from short time-frames in dynamic imaging. The kernel method for image reconstruction has been developed to improve image reconstruction of low-count PET data by incorporating prior information derived from high-count composite data. In contrast to most of the existing regularization-based methods, the kernel method embeds image prior information in the forward projection model and does not require an explicit regularization term in the reconstruction formula. Inspired by the existing highly constrained back-projection (HYPR) algorithm for dynamic PET image denoising, we propose in this work a new type of kernel that is simpler to implement and further improves the kernel-based dynamic PET image reconstruction. Our evaluation study using a physical phantom scan with synthetic FDG tracer kinetics has demonstrated that the new HYPR kernel-based reconstruction can achieve a better bias versus standard deviation trade-off for dynamic PET parametric imaging than the post-reconstruction HYPR denoising method and the previously used nonlocal-means kernel.

10132-180, Session PS9

Stability of gradient field corrections for quantitative diffusion MRI

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In magnetic resonance diffusion imaging, gradient nonlinearity causes significant bias in the estimation of quantitative diffusion parameters such as diffusivity, anisotropy, and diffusion direction in areas away from the magnet isocenter.

This bias can be substantially reduced if the scanner- and coil-specific gradient field nonlinearities are known. Using a set of field map calibration scans on a large (29 cm diameter) phantom combined with a solid harmonic approximation of the gradient fields, we predicted the obtained b-values and applied gradient directions throughout a typical field of view for brain imaging for a typical 32-direction diffusion imaging sequence. We measured the stability of these predictions over time. At 80 mm from scanner isocenter, predicted b-value was 1-6% different than intended due to gradient nonlinearity, and predicted gradient directions were in error by up to 1 degree. Over the course of one month the change in these quantities due to calibration-related factors such as scanner drift and variation in phantom placement was <0.5% for b-values, and <0.5 degrees for angular deviation. The proposed calibration procedure allows the estimation of gradient nonlinearity to correct b-values and gradient directions ahead of advanced diffusion image processing for high angular resolution data, and requires only a five-minute phantom scan that can be included in a weekly or monthly quality assurance protocol.

10132-181, Session PS9

Regularized ECT reconstruction on unstructured grid

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Emission Computed Tomography (ECT) reconstruction is an ill-posed inverse problem. Reconstruction on unstructured grid can alleviate the ill-posedness of the problem by reducing the dimension of the solution space, and preserve important features via characterizing structural tissue information from unstructured grid. To suppress noise and preserve important singularities, edge-preserving regularization method on unstructured grid is necessary to be developed to regularize the reconstructed images. In this study, we consider regularized ECT reconstruction method on unstructured grid based on the proposed regularization method on unstructured grid in our previous research. Motivated form the Bayesian framework and maximum a posteriori estimation, we proposed a convex optimization problem with two non-differentiable terms, with one as the regularization term and the other one as the positive constrain. However, two non-differentiable terms bring difficulty to the development of the fast solver. A fixed-point proximity algorithm with expectation maximization method (EM), characterized the object adaptively, is developed for solving the related optimization problem. The extrapolation technique is applied to accelerate the convergence, which can efficiently reduce iteration numbers. Finally, we compare the regularized ECT reconstruction method to EM algorithm with no regularization on unstructured grid, and the fixed-point proximity algorithm with total variation regularization in pixel domain, using Zubal Voxelman thorax phantom with different noise levels. Numerical experiments demonstrated that the regularized ECT reconstruction method on unstructured grid is effective to suppress noise and preserve edge features. Compared to the reconstruction in pixel domain, the regularized ECT reconstruction method is effective to reduce the computational cost.

10132-182, Session PS9

Attenuation correction in SPECT images using attenuation map estimation with its emission data

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Photon attenuation during SPECT imaging significantly degrades the diagnostic outcome and the quantitative accuracy of final reconstructed images. It is well known that attenuation correction can be done by using iterative reconstruction methods if we access to attenuation map. Two methods have been used to calculate the attenuation map: transmission-based and transmissionless techniques. Whilst the second one is appropriate for brain studies, more enough approaches must be applied in clinical application for areas of inhomogeneous attenuation like the chest. In this study, we evaluated the importance of attenuation correction by quantitative evaluation of errors associated with attenuation in SPECT in a phantom study. To obtain attenuation map an appropriate approach was used from the emission data or projections, without the use of transmission scans. The developed EM algorithm with attenuation model was developed and used for attenuation correction during image reconstruction. Finally a comparison was done between reconstructed images using our OSEM code and analytical FBP method. The results of measurements show that: Our programs are capable to reconstruct SPECT images and correct the attenuation effects. Moreover to evaluate reconstructed image quality before and after attenuation correction we applied a novel approach using Image Quality Index. Attenuation correction increases the quality and quantity factors in both methods. This increase is independent of activity in quantity factor and decreases with activity in quality factor. In EM algorithm, it is necessary to use regularization algorithms to obtain true distribution of attenuation coefficients.

10132-183, Session PS9

Accelerated MRI image gormation by stochastic RF excitation

Jun Shen, National Institute of Mental Health and Neuro Sciences (United States)

Current MRI imaging acceleration by compressed sensing requires a fully sampled k-space core, which contains most of the signal power. As a result, the k-space signals are largely coherent instead of incoherent, leading to large reconstruction errors when acceleration factors are not very small. In this work, numerical simulations were performed to evaluate the feasibility of compressed sensing MRI using a fully randomized undersampling strategy and total variation image reconstruction. The proposed scheme uses stochastic RF pulses to excite a slab followed by conventional readout in the perpendicular direction. As a proof-of-concept example, we reconstructed an image of a simulated spherical phantom with a matrix size of 128 x 128. We used eight stochastic RF pulses to generate eight k-space lines in the phase encoding direction for 16-fold acceleration. The frequency profiles of the stochastic pulses were mutually orthogonal. While the conventional SparseMRI and total variation reconstruction method resulted in gross deviations from the ground truth image for the very large acceleration factor we found that the image can be reconstruction nearly perfectly with 16 fold acceleration when the k-space signals in the phase encoding direction were completely randomized. Because the stochastic excitation encoding/decoding matrix was orthonormal, noise was not amplified. One significant drawback of the proposed method is that a single 2D image would require an additional refocusing pulse for slice selection. However, extension to 3D imaging would eliminate the extra slice-selective refocusing pulse.

10132-184, Session PS9

Evaluation of the clinical efficacy of the PeTrack motion tracking system for respiratory gating in cardiac PET imaging

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Rationale: Respiratory motion during cardiac PET imaging can lead to inaccurate estimates of myocardial perfusion that may impact patient management. Respiratory gating is commonly used to evaluate and potentially compensate for patient breathing motion and decrease the prevalence of unwanted image artifacts. The purpose of this study was to compare a new gating method with conventional optical tracking when sub-optimal respiratory gating was observed.

Methods: The PeTrack (Positron emission based Tracking) algorithm was developed to determine the 3D location of a positron-emitting fiducial marker placed on the abdomen of the patient. PeTrack calculated the position of the marker throughout the scan using raw list-mode data. Respiratory triggers were generated from the motion trace of the marker in 6 rubidium-82 cardiac PET scans. The performance of respiratory gating using PeTrack was evaluated by comparing the number of respiratory triggers, patient breathing intervals and observed respiratory motion in the reconstructed PET images, with those obtained from a conventional optical motion tracking system.

Results: The PeTrack system showed reduced variability in measured breathing intervals compared to the optical system. In cases of sub-optimal trigger response of the optical system, PeTrack was able to allow visualization of respiratory motion during the scan. Respiratory-gated image reconstruction using PeTrack triggers showed comparable image quality to those obtained in the subset of patients with adequate optical system gating.

Conclusion: PeTrack was able to accurately capture patient respiratory motion for the purpose of respiratory gating in rubidium-82 cardiac PET scans. This method appears to be more robust and potentially more accurate than conventional optical motion tracking.

10132-185, Session PS10

Comparison of detectability in step-and-shoot mode and continuous mode digital tomosynthesis systems

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Digital tomosynthesis system has been widely used in chest, dental, and breast imaging. Since the digital tomosynthesis system provides volumetric images from multiple projection data, structural noise inherent in x-ray radiograph can be reduced, and thus signal detection performance is improved. Currently, tomosynthesis system uses two data acquisition modes: step-and-shoot mode and continuous mode. Several studies have been conducted to compare the system performance of two acquisition modes with respect to spatial resolution and contrast. In this work, we focus on signal detectability in step-and-shoot mode and continuous mode. For evaluation, uniform background is considered, and eight spherical objects with diameters of 0.5, 0.8, 1, 2, 3, 5, 8, 10 mm are used as signals. Projection data with and without spherical objects are acquired in step-and-shoot mode and continuous mode, respectively, and quantum noise are added. Then, noisy projection data are reconstructed by FDK algorithm. To compare the detection performance of two acquisition modes, we calculate task signal-to-noise ratio (SNR) of channelized Hotelling observer with Laguerre-Gauss channels for each spherical object. While the task-SNR values of two acquisition modes are similar for spherical objects larger than 1 mm diameter, step-and-shoot mode yields higher detectability for small signal sizes. The main reason of this behavior is that small signal is more affected by x-ray tube motion blur than large signal. Our results indicate that it is beneficial to use step-and-shoot data acquisition mode to improve the detectability of small signals (i.e., less than 1 mm diameter) in digital tomosynthesis systems.

10132-186, Session PS10

Improvements in low contrast detectability with iterative reconstruction and the effect of slice thickness

Scott S. Hsieh, Norbert J. Pelc, Stanford Univ. (United States)

Iterative reconstruction has become a popular route for dose reduction in CT scans. One method for assessing the dose reduction of iterative reconstruction is to use a low contrast detectability phantom. The apparent improvement in detectability can be very large on these phantoms, with many studies showing dose reduction in excess of 50%. In this work, we show that much of the advantage of iterative reconstruction in this context can be explained by differences in slice thickness. After adjusting the effective reconstruction kernel by blurring filtered backprojection images to match the shape of the noise power spectrum of iterative reconstruction, we produce thick slices and compare the two reconstruction algorithms. The remaining improvement from iterative reconstruction, at least in scans with relatively uniform statistics in the raw data, is significantly reduced. Hence, the effective slice thickness in iterative reconstruction may be larger than that of filtered backprojection, explaining some of the improvement in image quality.

10132-187, Session PS10

The effect of a finite focal spot size on location dependent detectability in a fan beam CT system

Byeongjoon Kim, Jongduk Baek, Yonsei Univ. (Korea, Republic of)

A finite focal spot size is one of the sources to degrade the resolution performance in a fan beam CT system. In this work, we investigate the effect of the finite focal spot size on signal detectability. For the evaluation, five spherical objects with diameters of 2 mm, 4 mm, 6 mm, 8 mm, and 10 mm were used. The optical focal spot size viewed at the iso-center was a 1 mm (height) ? 2 mm (width) with a 7 degrees target angle, corresponding to an 8.21 mm (i.e., 1 mm / sin (7°)) focal spot length. Simulated projection data were acquired using 8 ? 8 source lets and detector lets, and reconstructed by Hanning weighted filtered backprojection. For each spherical object, the detectability was calculated at (0 mm, 0 mm) and (0 mm, 200 mm) using two image quality metrics: pixel signal to noise ratio (SNR) and detection SNR. The detection SNR was calculated in frequency domain. For all signal sizes, the pixel SNR is higher at the iso-center since the noise variance at the off-center is much higher than that at the iso-center due to the backprojection weightings used in direct fan beam reconstruction. In contrast, detection SNR shows similar values for different spherical objects except a 2 mm diameter spherical object. Overall, the results indicate the resolution loss caused by the finite focal spot size degrades the detection performance, especially for small objects less than 2 mm diameter.

10132-188, Session PS10

In vivo detectability index: development and validation of an automated methodology

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The purpose of this study was to develop and validate a method to estimate patient-specific detectability indices directly from patients' CT images (i.e., "in vivo"). The method works by automatically extracting noise (NPS) and resolution (MTF) properties from each patient's CT series based on previously validated techniques. Patient images are thresholded into skin-air interfaces to form edge-spread functions, which are further binned, differentiated, and Fourier transformed to form the MTF. The NPS is likewise estimated from uniform areas of the image. These are combined with assumed task functions (reference function: 10 mm disk lesion with contrast of 15 HU) to compute detectability indices for a non-prewhitening matched filter model observer predicting observer performance. The results were compared to those from a previous human detection study on 105 subtle, hypo-attenuating liver lesions, using a two-alternative-forced-choice (2AFC) method, over 6 dose levels using 16 readers. The in vivo detectability indices estimated for all patient images were compared to binary 2AFC outcomes with a generalized linear mixed-effects statistical model (Probit link function, linear terms only, no interactions, random term for readers). The model showed that the in vivo detectability indices were strongly predictive of 2AFC outcomes ($P = 4.64e-19$). A linear comparison between the human detection accuracy and model-predicted detection accuracy (for like conditions) resulted in Pearson and Spearman correlations coefficients of 0.86 and 0.87, respectively. These data provide evidence that the in vivo detectability index could potentially be used to automatically estimate and track image quality in a clinical operation.

10132-189, Session PS10

Using non-specialist observers in 4AFC human observer studies

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Virtual clinical trials (VCTs) are an emergent approach for rapid evaluation and comparison of various breast imaging technologies and techniques using computer-based modeling tools. Increasingly 4AFC (Four alternative forced choice) virtual clinical trials are used to compare detection performances of different breast imaging modalities. Most prior studies have used physicists and/or radiologists and physicists interchangeably. However, large scale use of statistically significant 4AFC observer studies is challenged by the individual time commitment and cost of such observers, often drawn from a limited local pool of specialists. This work aims to investigate whether non-specialist observers can be used to supplement such studies.

A team of four specialist observers (medical physicists) and four non-specialists participated in a preliminary 4AFC study containing simulated 2D-mammography and DBT (digital breast tomosynthesis) images, produced using the OPTIMAM toolbox for VCTs. The images contained 4mm irregular solid masses and 4mm spherical targets at a range of contrast levels embedded in a realistic breast phantom background. There was no statistically significant difference between the detection performance of medical physicists and non-specialists ($p>0.05$). However, non-specialists took longer to complete the study than their physicist counterparts, which was statistically significant ($p<0.05$). Overall, the results from both observer groups indicate that DBT has a lower detectable threshold contrast than 2D-mammography for both masses and spheres, and both groups found spheres easier to detect than irregular solid masses.

10132-190, Session PS10

Optimization of the simulation parameters for improving realism in anthropomorphic breast phantoms

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Virtual clinical trials (VCTs) were introduced as a preclinical alternative to clinical imaging trials, and for the evaluation of breast imaging systems. Realism in computer models of breast anatomy (software phantoms), critical for VCT performance, can be improved by optimizing simulation parameters based on the analysis of clinical images.

We optimized the simulation to improve the realism of simulated tissue compartments, defined by the breast Cooper's ligaments. We utilized the anonymized, previously acquired CT images of a mastectomy specimen to manually segment 205 adipose compartments. We generated 1,440 anthropomorphic breast phantoms based on octree recursive partitioning. These phantoms included variations of simulation parameters—voxel size, number of compartments, percentage of dense tissue, shape and orientation of the compartments. We compared distributions of the compartment volumes in segmented CT images and phantoms using Kolmogrov-Smirnov (KS) distance, Kullback-Leibler (KL) divergence and a novel distance metric (based on weighted sum of distribution descriptors differences). We identified phantoms with the size distributions closest to CT images. For example, KS resulted in the phantom with 1000 compartments, ligament thickness of 0.4mm and skin thickness of 12mm. We applied ANOVAN to these distance measures to identify parameters that most significantly influence the simulated compartment size distribution.

We have demonstrated an efficient method for the optimization of phantom parameters to achieve realistic distribution of adipose compartment size. The proposed methodology could be extended to other phantom parameters (e.g., ligament and skin thicknesses), to further improve realism of the simulation and VCTs.

10132-191, Session PS10

Validation study of the thorax phantom Lungman for optimization purposes

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This work aims to investigate the advantages and limitations of the Kyoto Kagaku thorax phantom 'Lungman' for use in chest radiography optimization studies. First, patient survey data were gathered for chest posterior anterior (PA) and lateral (LAT) examinations in a standard chest X-ray room over a period of one year, using a Caesium Iodide (CsI) based flat panel detector with automatic exposure control (AEC). Parameters surveyed included Exposure Index (EI), Dose Area Product (DAP) and AEC exposure time. PA and LAT projections of the phantom were then acquired. Additionally, the equivalence in millimetres of poly (methyl methacrylate) (PMMA) was established for the different regions of the Lungman phantom (lungs and mediastinum). Finally, a voxel model of the Lungman phantom was developed by the segmentation of a volumetric dataset of the phantom acquired using CT scanning. Subsequently, the model was used in Monte Carlo simulations with PENELOPE/penEasy code to calculate the energy deposited in the organs of the phantom. This enabled comparison of the phantom tissue-equivalent materials with materials defined by ICRP 89 in terms of absorbed dose. For the survey data, close agreement was found between phantom and the median values for the patient data (ranging from 4% to 31%, with one outlier). The phantom lung region is equivalent to 89 mm to 106 mm of PMMA, depending on tube voltage. Organ doses for the phantom material compared to those for ICRP defined material differed by at most 30%, with typical values lying within 10%.

10132-192, Session PS10

Method for decreasing CT simulation time of complex phantoms and systems through separation of material specific projection data

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Computer simulation is a powerful tool in CT; however, long simulation times of complex phantoms and systems, especially when modeling many physical aspects (e.g., spectrum, finite detector and source size), hinder the ability to realistically and efficiently evaluate and optimize CT techniques. Long simulation times primarily result from the tracing of hundreds of line integrals through each of the hundreds of geometrical shapes defined within the phantom. However, when the goal is to perform dynamic simulations or test many scan protocols using a particular phantom, traditional simulation methods inefficiently and repeatedly calculate line integrals through the same set of structures although only a few parameters change in each new case. Therefore, we have developed a new simulation framework that overcomes such inefficiencies by dividing the phantom into material specific regions with the same time attenuation profiles, acquiring and storing monoenergetic projections of the regions, and subsequently scaling and combining the projections to create equivalent polyenergetic sinograms. The simulation framework is especially efficient for the validation and optimization of CT perfusion which requires analysis of many stroke cases and testing hundreds of scan protocols on a realistic and complex numerical brain phantom. Using this updated framework to conduct a 20-time point simulation of one 5 mm slice of the brain phantom, we have reduced the simulation time from 112 minutes to under 18 minutes, an 84% improvement.

10132-193, Session PS10

Phantom system for intraluminal x-ray imaging of the human colon

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The Check-Cap capsule, C-Scan Cap®, performs intraluminal imaging of the human colon based on X-Ray scatter processes. Basic performance of such a system can be demonstrated using various tube-like phantom objects. Also, from a perspective of capsule dynamics, actuators can and have been used for capsule manipulation. Nevertheless the actual situation of a capsule in use is extremely complex, both in terms of the imaging-target object itself and the capsule dynamics within the same. In order to allow study of imaging system performance in a pseudo-clinical environment, a specialized phantom system has been developed.

A tissue-equivalent material has been developed in-house, so as to allow simple usage and flexibility for making a wide variety of phantoms, simple tubes as well as extremely complex segments of the human colon which can possibly demonstrate adenomas. The material itself is durable, flexible, and very similar to water in terms of X-Ray scattering. Based on real abdominal CT images, real colon segments have been extracted to become 3D molds, which were used for producing a set of pseudo-clinical human colon segments.

In the aspect of capsule and colon dynamics, capsule propulsion within these phantoms is based on the contents, i.e. capsule is hydro-dynamically propelled by surrounding medium rather than actuators. In addition, a system for generating peristaltic contractions along these colon segments has been developed; this system allows stimulation of the colon and the capsule within using arbitrary programmable contraction waves. This phantom system allows demonstration of pseudo-clinical imaging scenarios in the lab.

10132-194, Session PS10

Validation of Cooper’s ligament thickness in software breast phantoms

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Anthropomorphic breast phantoms are important tools for a wide range of tasks including pre-clinical validation of novel imaging techniques. In order to improve the realism in the phantoms, assessment of simulated anatomical structures is crucial. Thickness of simulated Cooper’s ligaments influences percentage of dense tissue, and qualitative and quantitative properties of simulated images.

We introduce three methods (2-dimensional watershed, 3-dimensional watershed, and facet counting) to assess the thickness of the simulated Cooper’s ligaments in the breast phantoms. For the validation of simulated phantoms, the thickness of ligaments has been measured and compared with the input thickness values. These included a total of 64 phantoms with nominal ligament thicknesses of 200, 400, 600, and 800 ?m.

The 2-dimensional and 3-dimensional watershed transformations were performed to obtain the median skeleton of the ligaments. In the 2-dimensional watershed, the median skeleton was found cross-section by cross-section, while the skeleton was found for the entire 3-dimensional space in the 3-dimensional watershed. The thickness was calculated by taking the ratio of the total volume of ligaments and the volume of median skeleton. In the facet counting method, the ligament thickness was estimated as a ratio between estimated ligaments’ volume and average ligaments’ surface area.

We demonstrated that the 2-dimensional watershed technique overestimates the ligament thickness. Good agreement was found between the facet counting technique and the 3-dimensional watershed for assessing thickness. The proposed techniques are applicable for ligaments’ thickness estimation on clinical breast images, provided segmentation of Cooper’s ligaments has been performed.

10132-195, Session PS10

Computer simulation of the breast subcutaneous and retromammary tissue for the use in virtual clinical trials

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Computer simulation of breast anatomy is an essential component of Virtual Clinical Trials (VCTs), a pre-clinical approach to validate breast imaging systems. Realism of such obtained breast phantoms affects simulation studies and their acceptance among researchers. Previously, we developed a simulation of tis-sue compartments defined by the hierarchy of Cooper’s ligaments, based upon recursive partitioning using octrees. In this work, we optimize the simulation parameters to represent realistically the breast subcuta-neous and retromammary tissue regions. As seen in clinical images, the subcutaneous and retromammary regions contain predominantly fat organized into relatively large compartments, as opposed to predominantly glandular breast interior. To mimic such organization, we divided the phantom volume into “subcu-taneous”, “retromammary”, and “interior” regions. Within each region, parameters controlling the size and orientation of tissue compartments were selected separately. In this preliminary study, we varied pa-rameter values and calculated the corresponding average compartment volume in each region. The pro-posed method was evaluated using anatomy descriptors at the radiological and pathological spatial

scales. We simulated subcutaneous region as spanning 20% of the breast diameter, comparable to the published analysis of breast CT images. In addition, we simulated tissue compartments with the average volume of 0.94cm3, 0.89cm3, and 0.31cm3 in subcutaneous, retromammary, and interior regions, respectively. Those average volumes match within 15% the values reported from histological analyses. Future evaluation may include a comparison of simulated and clinical parenchymal descriptors. The proposed method may be extended to automate the parameter optimization, and simulate detailed spatial variation, to further im-prove the realism.

10132-196, Session PS10

Improved virtual cardiac phantom with variable diastolic filling rates and coronary artery velocities

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To facilitate studies of measurement uncertainty in computed tomography angiography (CTA), we investigate the cardiac motion profile and resulting coronary artery motion utilizing innovative dynamic virtual and physical phantoms.

The four-chamber cardiac finite element (FE) model developed in the Living Heart Project (LHP) serves as the computational basis for our virtual cardiac phantom. This model provides deformation or strain information at high temporal and spatial resolution, exceeding that of speckle tracking echocardiography or tagged MRI.

We extend this model by fitting its motion profile to left ventricular (LV) volume-time curves obtained from patient echocardiography data. By combining the dynamic patient variability from echo with the local strain information from the FE model, a series of virtual 4D cardiac phantoms were developed. Using the computational phantoms, we characterize the coronary motion and its effect on plaque imaging under a range of heart rates subject to variable diastolic function. In a separate abstract by Richards et al., a similar investigation is performed using a physical cardiac phantom (Shelley Medical Imaging DHP-01).

The coronary artery motion was sampled at 248 spatial locations over 500 consecutive time frames. The coronary artery velocities were calculated as their average velocity during an acquisition window centered at each time frame, which minimized the discretization error. For the initial set of twelve patients, the diastatic coronary artery velocity ranged from 36.5 mm/s to 2.0 mm/s with a mean of 21.4 mm/s assuming an acquisition time of 75 ms.

The phantoms developed here have great potential in cardiac imaging, providing a known truth and multiple realistic cardiac motion profiles to evaluate different image acquisition or reconstruction methods.

10132-197, Session PS10

Quantification of the uncertainty in coronary CTA plaque measurements using dynamic cardiac phantom and 3D-printed plaque models

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The purpose of this study was to quantify measurement uncertainty of stenosis and plaque extent using newly developed physical coronary plaque models attached to a base dynamic cardiac phantom (Shelley Medical DHP-01). Coronary plaque models (5 mm diameter, 50% stenosis, and 32 mm long) were designed and 3D-printed with tissue equivalent materials (calcified plaque with iodine enhanced lumen). Realistic cardiac motion was achieved using left ventricle volume-time curves to create synchronized heart motion profiles executed by the base cardiac phantom. Realistic coronary CTA acquisition was accomplished by synthesizing corresponding ECG waveforms for gating and reconstruction purposes. All scans were acquired using a retrospective gating technique on a dual-source CT system (Siemens SOMATOM FLASH) with 75ms temporal resolution. Images were reconstructed at 60% of the R-R interval, vessel centerlines were determined, enhanced lumens were segmented, and measurement uncertainties were calculated. Stenosis measurement uncertainty increased with increasing heart rate. A 6.4% stenosis measurement uncertainty (width of the 95% confidence interval) at 60 bpm increased to 10.0% uncertainty at the highest heart rate of 90 bpm. Plaque extent measurement uncertainty also increased with increasing heart rate. A plaque extent uncertainty of 0.59 mm at 60 bpm increased to 1.70 mm uncertainty at 90 bpm. These results demonstrate successful implementation of the base cardiac phantom with 3D-printed coronary plaque models, adjustable motion profiles, and coordinated ECG waveforms. They further show the utility of the model to ascertain and optimize metrics of coronary CT image quality under a variety of plaque, motion, and acquisition conditions.

10132-198, Session PS10

Accuracy and variability of texture-based radiomics features of lung lesions across CT imaging conditions

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Texture analysis for lung lesions is sensitive to changing imaging conditions but these effects are not well understood, in part, due to a lack of ground-truth phantoms with realistic textures. The purpose of this study was to determine which imaging conditions provides the most accurate texture features compared to voxel-based 3D printed textured lesions for witch the true texture features are known. The seven features of interest are based on the Grey Level Co-Occurrence Matrix (GLCM). The lesion phantoms were designed with three shapes (spherical, lobulated, spiculated), two textures (homogenous, heterogeneous), and two sizes (diameter < 1.5cm, 1.5cm< diameter<3cm), resulting in 24 lesions (replica of each). The lesions were inserted into an anthropomorphic thorax phantom (Multipurpose Chest Phantom N1, Kyoto Kagaku) and imaged using a commercial CT system (SOMATOM Definition Flash, Siemens Healthcare) at three CTDI levels (0.67, 1.42, 5.80mGy), three reconstruction algorithm (FBP, IR-2, IR-4), four reconstruction kernels (standard, soft, edge), and two slice thicknesses (0.6mm, 5mm). Texture features from these images were extracted and compared to the ground truth feature values. The feature variability (coefficient of variation across lesions) was highly dependent on imaging condition, ranging from 13% to 77%. The highest accuracy imaging condition for homogeneous lesions was high dose, thin slice thickness, high-strength IR and standard kernel while there was not a consistent most-accurate condition for heterogeneous lesions.

10132-199, Session PS11

Preclinical x-ray dark-field imaging: foreign body detection

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Purpose: To evaluate the performance of X-ray dark-field imaging for detection of retained foreign bodies in ex-vivo hands and feet. X-ray dark-field imaging, acquired with a three-grating Talbot-Lau interferometer, has proven to provide access to sub-resolution structures due to small-angle scattering. Materials and Methods:

The study was institutional review board (IRB) approved. Foreign body parts included pieces of wood and metal which were placed in fresh and formaline fixated human ex-vivo hands and feet. The samples were imaged with a grating-based interferometer consisting of a standard microfocus X-ray tube (60 kVp, 100 W) and a Varian 2520-DX detector (pixel size: 127 ?m). Results: The absorption and the dark-field signals provide complementary diagnostic information for this clinical task. With regard to detecting of wooden objects, which are clinically the most relevant, only the dark-field image revealed the locations. The signal is especially strong for dry wood which in comparison is poorly to non-visible in computed tomography. The sensitivity of small-angle scattering to sub-resolution features allows to detect wood samples smaller than the resolution of the conventional absorption image. The detection of high atomic-number or dense material and wood-like or porous materials in a single X-ray scan is enabled by the simultaneous acquisition of the conventional absorption and dark-field signal.

Conclusion: Our results reveal that with this approach one can reach a significantly improved sensitivity for detection of foreign bodies, while an easy implementation into the clinical arena is becoming feasible.

10132-200, Session PS11

Advanced hyperspectral imaging system with edge enhancement

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One of the problems in physical processing of microscopic images in medical diagnostics is visualization of low-contrast objects: unstained cytological smears and histological samples, live cells. This can be done using different techniques: phase contrast microscopy, quantitative phase imaging, fluorescence imaging etc. e developed a hyperspectral imaging (HSI) system which can be switched from standard wide-field HSI operation mode to simultaneous HSI with edge enhancement. The system is based on a wide-aperture acousto-optic tunable filter (AOTF) in a confocal optical scheme. Usually, AOTFs are used in HSI instruments in a noncritical phase matching geometry of diffraction because this configuration provides maximum image quality. It is known that slight detuning of an AOTF from noncritical phase matching results in a ring-shaped transfer function. This operation mode corresponds to band-pass spatial filtering. We used this type of the transfer function for edge-enhancement processing of the images. Switching between standard HSI and edge-enhancement modes is performed by means of a telecentric amplitude mask. Without the mask, the system operates a standard HSI instrument. With the mask, lower frequencies of the beam angular spectrum are suppressed that results in the desired edge-enhancement effect. Unlike previous experiments of this kind, edge-enhancement does not require special coherent illumination of the samples. Thus, edge-enhancement is obtained simultaneously with tunable spectral filtering. We illustrate the performance of the instrument prototype with unstained histological sections of human thyroid tumors.

10132-202, Session PS11

Weighted singular value decomposition (wSVD) to improve the radiation dose efficiency of grating based x-ray phase contrast imaging with a photon counting detector

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In grating-based differential phase contrast (DPC) imaging, the noise performance depends on both the fringe visibility and the total number of photons used to extract the DPC signal. An interferometer system is usually designed to work at a specific energy, and any deviation from that energy may lead to certain visibility loss. By incorporating an energy-discriminating photon counting detector (PCD) into the system, photons with energies close to the operation energy of the interferometer can be selected, which offers the possibility of noise reduction and contrast-to-noise ratio (CNR) improvement. In our previous work, a singular value decomposition (SVD)-based rank-one approximation method is proposed to improve the CNR of DPC imaging. However, as the noise level and energy sensitivity of the interferometer may vary significantly from one energy bin to another, the signal and noise may not be well separated using the conventional SVD method, therefore the full potential of the SVD method may not be achieved. This work presents a novel weighted SVD-based method, which maintains the noise reduction capability regardless of the similarity in the noise level of raw images. The optimal weighting scheme was theoretically derived, and experimental phantom studies were performed to validate the theory and demonstrate the superior radiation dose efficiency of the proposed weighted SVD method.

10132-204, Session PS11

First in-vivo x-ray dark-field chest radiography: a feasibility study in a living pig

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X-ray chest radiography is a cheap and broadly available tool for the initial assessment of the human lung in daily clinical routine, however, it lacks diagnostic sensitivity when it comes to the detection of pulmonary diseases in their early stages. Recent x-ray dark-field (XDF) imaging studies on dead and living mice have broadened the horizon of imaging-based lung diagnostics, by showing that the XDF signal is highly sensitive towards

the pulmonary microstructure and its potential disorders. Especially in the case of early diagnosis of lung diseases like chronic obstructive pulmonary disease (COPD) and fibrosis, XDF imaging clearly demonstrated its potential to outperform conventional radiography. Until now, however, a translation of this technique from aforementioned small-animal models towards the investigation of larger mammals and finally humans has proven to be extremely challenging. Here, we present the very first in-vivo XDF full-field chest radiography (35x35cm2) of a living pig at acquisition parameters suitable for in-vivo imaging and clinical demands (scan time of 40s, estimated effective dose of 80 μSv). In order to acquire those images, we developed a novel high-energy XDF scanner, which overcomes the limitations of currently established setups. Our XDF radiography yields a sufficiently high image contrast and quality to enable radiographic evaluation of the lungs. We consider this as a milestone in the bench-to-bedside translation of XDF imaging as we successfully demonstrated the translation of XDF radiography from mouse to human-sized animals. Thus, presupposed the diagnostic value of XDF imaging can be equally transferred to humans in the future, we expect it to become a valuable diagnostic tool in clinical practice both as a general imaging and disease staging modality for a wide range of patients.

10132-205, Session PS11

High resolution laboratory grating-based x-ray phase-contrast CT

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The conventional form of computed tomography using X-ray attenuation without any contrast agents is of limited use for the characterization of soft tissue in many fields of medical and biological studies.

Grating-based phase-contrast computed tomography (gbPC-CT) is a promising alternative imaging method solving the problems of soft tissue contrast without the need of any contrast agent.

The combination of high resolution and high sensitivity already showed convincing results at the synchrotron.

While high sensitivity measurements are possible using conventional x-ray sources the spatial resolution does often not fulfil the requirements for specific imaging tasks, such as visualisation of pathologies . The focus of this study is the increase in spatial resolution without loss in sensitivity.

To overcome this limitation and further decrease the effective pixel size a super-resolution reconstruction based on sub-pixel shifts involving an iterative deconvolution of the image data is applied.

In our study we could achieve an effective pixel sizes of 28?m.

The results show the increase in resolution without any drawback in terms of sensitivity or the ability to measure quantitative data. The combination of sparse sampling and statistical iterative reconstruction allowed to maintain the total measurement time to be equal to the standard measuring procedure using filtered backprojection. In conclusion, we present high quality and high resolution tomographic images of biological samples to demonstrate the experimental feasibility of super-resolution reconstruction.

10132-206, Session PS11

In-vivo x-ray dark-field imaging of lung cancer in mice

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Purpose: The purpose of the present study was to evaluate if x-ray dark-field radiography can help to visualize lung cancer in mice.

Materials and Methods: The experiments were performed using mutant mice with high-grade adenocarcinomas. Eight animals with pulmonary carcinoma and eight control animals were imaged using a prototype small-animal x-ray dark-field scanner. After imaging, the lungs were harvested for histological analysis. To determine their diagnostic value, x-ray dark-field and conventional attenuation images were analyzed by three experienced readers in a blind assessment.

Results: The lung nodules were much clearer visualized on the dark-field radiographs compared to conventional radiographs. The loss of air-tissue interfaces in the tumor leads to a significant loss of x-ray scattering, reflected in a strong dark-field signal change. The difference between tumor and healthy tissue in terms of x-ray attenuation is significantly less pronounced. Furthermore, the signal from the overlaying structures on conventional radiographs complicates the detection of pulmonary carcinoma.

Conclusion: We found a superior diagnostic performance of dark-field imaging compared to conventional radiography, especially when it comes to the detection of small lung nodules. These results support the motivation to further develop this technique and translate it towards a clinical environment.

10132-207, Session PS11

Classification of the micromorphology of breast calcifications in x-ray dark-field mammography

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Purpose: To reduce the number of invasive procedures associated with breast micro calcification biopsies, by improving and refining conventional BIRADS micro calcification assessments with x-ray dark-field mammography.

Materials and Methods: The study was institutional review board (IRB) approved. A dedicated grating-based radiography setup (Mo-target, 40 keV, 70 mA) was used to investigate one breast mastectomy and 31 biopsies with dark-field mammography. Comparing the absorption and scattering properties of micro calcifications clusters enable accessing information on the interior morphology on the micron-scale retrieved in a non-invasive manner. Insights underlying the micro morphological nature of breast calcifications were verified by comprehensive high-resolution micro-CT measurements.

Results: Dark-field mammography allows a micro-structural rather than chemical classification of breast micro calcification as ultra-fine, fine, pleomorphic and coarse textured using conventional detectors. Dark-field mammography is thereby highly sensitive to minor structural deviations. Finally, the micro-texture of micro calcifications may be an indicator for tissue malignancy.

Conclusion: Our results demonstrate that dark-field mammography yields the potential to enhance diagnostic validity of current micro calcification analysis - which is yet limited to the exterior appearance of micro calcification clusters - and thereby reduce the number of invasive procedures.

10132-208, Session PS11

Phase unwrapping with differential phase image

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Absorption imaging is widely used by many imaging devices such as X-ray CT. However, its limitations are becoming obvious because it cannot provide adequate contrast when imaging weakly absorbing object such as biological tissue. Actually, X-phase imaging attracting growing concerns since its high ability to address the problem. It is known that the phase images are wrapped and phase unwrapping is essential to recover true phase from its modulo phase. Many phase unwrapping methods have been proposed for Magnetic Resonance Imaging (MRI) and interferometric synthetic aperture radar (In SAR), and they can be generally classified into path-following and path-independent methods. Nevertheless, different from the conventional phase image, differential image are directly measured by many X-ray phase imaging such as Talbot interferometer. So it is necessary to develop the unwrapping method which is used to unwrap the differential image, and this has not been discussed in any previous paper within the scope of our knowledge. In this paper, we investigated how to get correct image from differential image. We also found that many usual integral method give completely wrong unwrapping results for differential image, and give idea how to exclude incorrect integral methods. In simulation, combining the path-independent method successfully restricted the error in local field that is better than previous one in which error will propagate along path.

10132-209, Session PS12

Focal spot size reduction using asymmetric collimation to enable reduced anode angles with a conventional angiographic x-ray tube for use with high resolution detectors

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The high-resolution requirements for neuro-endovascular image-guided interventions (EIGIs) necessitate the use of a small focal-spot size; however, the maximum tube output limits for such small focal-spot sizes may not enable sufficient x-ray fluence after attenuation through the human head to support the desired image quality. This may necessitate the use of a larger focal spot, thus reducing resolution. A method for creating a higher-output small effective focal spot based on the line-focus principle has been demonstrated and characterized. By tilting the C-arm gantry, the anode-side of the x-ray field-of-view is accessible using a detector placed off-axis. This tilted central axis diminishes the resultant focal spot size in the anode-cathode direction by the tangent of the effective anode angle, allowing a medium focal spot to be used in place of a small focal spot with minimal losses in resolution but with increased tube output. Images were acquired of three different objects at the central axis, and with the C-arm positioned at 1° increments from 0°-8°. With standard collimation settings, only 6° was accessible, but using asymmetric extended collimation a maximum of 8° was accessed for enhanced comparisons. All objects were positioned perpendicular to the anode-cathode direction and images were compared qualitatively. The increasing advantage of the off-axis focal spots was quantitatively evidenced at each subsequent angle using the Generalized Measured-Relative Object Detectability metric (GM-ROD). This anode-tilt method is a simple and robust way of increasing tube output for a small field-of-view detector without diminishing the overall apparent resolution for neuro-EIGIs.

10132-210, Session PS12

Experimental investigation of a HOPG crystal fan for x-ray fluorescence molecular imaging

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Imaging with x-ray fluorescence generally generates a conflict between the best image quality or highest sensitivity and lowest possible dose. Consequently many experimental studies investigating the feasibility of this molecular imaging method, deal with either monochromatic x-ray sources that are not practical in clinical environment or accept high x-ray doses in order to maintain the advantage of high sensitivity and producing high quality images.

In this work we present a x-ray fluorescence imaging setup using a HOPG crystal fan construction consisting of a Bragg reflecting analyzer array together with a scatter reducing radial collimator. This method allows for the use of polychromatic x-ray tubes that are in general easily accessible in comparison to monochromatic x-ray sources such as synchrotron light sources. Moreover this energy-selecting device minimizes the amount of Compton scattered photons while simultaneously increasing the fluorescence signal yield. Thus the fan construction significantly reduces the signal to noise ratio and ensures that count-rate limitations of the detector are not violated even in large objects.

The aim is to show the feasibility of this approach by measuring the Bragg reflected K? fluorescence signal of an object containing an iodine solution using a large area detector with moderate energy resolution. Taking advantage of the anisotropic energy distribution of background scattered x-rays we compare the detection sensitivity, applying two different detector angular configurations. First results of our measurements prove that even for large area detectors with limited energy resolution, iodine concentrations of 0.6 mg/ml can be detected. However, the potentially large scan times and therefore high radiation dose need to be decreased in further investigations.

10132-211, Session PS12

Real time implementation of anti-scatter grid artifact elimination method for high resolution x-ray imaging CMOS detectors using Graphics Processing Units (GPUs)

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Scatter is one of the most important factors effecting image quality in radiography. One of the best scatter reduction methods in dynamic imaging is an anti-scatter grid. However, when used with high resolution imaging detectors these grids may leave grid-line artifacts with increasing severity as detector resolution improves. . The presence of such artifacts can mask important details in the image and degrade image quality. We have previously demonstrated that, in order to remove these artifacts, one must first subtract the residual scatter that penetrates through the grid followed by dividing out a reference grid image; however, this correction must be done fast so that corrected images can be provided in real-time to clinicians.

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 Dexela 1207 (pixel size - 75 micron) to image anthropomorphic head phantoms. For a 15 x 15cm field-of-view (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 head phantoms taken with the grid, before and after the corrections, were compared, demonstrating almost total elimination of the artifact over the full FOV. This correction is done fast using Graphics Processing Units (GPUs), with 4-5 iterations and total time taken to obtain the corrected image of only 87 ms, hence, demonstrating the virtually real-time implementation of the grid-artifact correction technique.

10132-212, Session PS12

Quantitative flow and velocity measurements of pulsatile blood flow with 4D DSA

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Time resolved 3D angiographic data from 4D DSA provides a unique environment to explore physical properties of blood flow. The 3D geometry of the vasculature coupled with the pulsatile waveforms created via contrast mixing over the cardiac cycle allows properties such as blood flow rate and velocity to be determined with high confidence. Utilizing the pulsatility of the signal waveform, the Fourier components can be used to track the waveform motion through vessels. Areas of strong local pulsatility are determined comparing the FFT power spectrum and its sideband values. With this sideband ratio (SBR) map as a guide, uncertainty in the velocity and flow can be substantially reduced. Using this method, flow conservation has been verified to be within 6% and we find an accuracy of the 4D-DSA flow measurements to be within 7.6% and 6.8% RMSE of ICA PCVIPR and phantom flow probe validation measurements, respectively. The availability of velocity and flow information with fast acquisition could provide a more quantitative approach to treatment planning and evaluation in interventional radiology.

10132-213, Session PS12

Development of a prototype chest digital tomosynthesis R/F system

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Digital tomosynthesis has an advantage of low radiation dose compared to conventional computed tomography (CT) by utilizing small number of projections (~80) acquired from limited angle range. It can produce 3D volumetric data although they may have some artifacts due to incomplete samplings. Based upon these attractive merits, we have developed a prototype digital tomosynthesis R/F system especially for the purpose of an application in chest imaging. Our prototype chest digital tomosynthesis (CDT) R/F system contains an X-ray tube with high power R/F pulse generator, flat-panel detector, R/F table, electromechanical radiographic subsystems including precise motor controller, and reconstruction server. For image reconstruction, the user could select the reconstruction option between analytic and iterative methods. The results indicated that our reconstructed images of chest phantom were clearly described the lung nodules with different sizes for both analytic and iterative reconstructions. Contrast-to-noise ratio (CNR) values of 12 mm diameter lung nodule were measured as 6.02 and 10.90 for filtered back-projection (FBP) image and simultaneous algebraic reconstruction technique (SART), respectively. The total radiation dose of our system was measured as ~5.68 mGy in a single sweep. Our prototype tomosynthesis R/F system can lead one step ahead in digital tomosynthesis technology.

10132-214, Session PS12

Localization of cardiac volume and patient features in inverse geometry x-ray fluoroscopy

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The scanning-beam digital x-ray (SBDX) system is an inverse geometry x-ray fluoroscopy technology that performs real-time tomosynthesis at planes perpendicular to the source-detector axis. The live display is a composite image which portrays sharp features (e.g. coronary arteries) extracted from a 16 cm thick reconstruction volume. We present a method for automatically determining the position of the cardiac volume prior to acquisition of a coronary angiogram. In the algorithm, a single non-contrast frame is reconstructed over a 44 cm thickness using shift-and-add digital tomosynthesis. Gradient filtering is applied to each plane to emphasize features such as the cardiomediastinal contour, diaphragm, and lung texture, and then a sharpness vs. plane position curve is generated. Three sharpness metrics were investigated: average gradient, maximum gradient, and the number of gradients exceeding a threshold. A model correlating the peak sharpness in a non-contrast frame and the midplane of the coronary arteries in a contrast-enhanced frame was established using 37 SBDX angiographic loops (64-136 kg human subjects, 0-30° cranial-caudal). The average gradient in the bright field (primarily lung) and the number of normalized gradients >50% each yielded peaks correlated to the coronary midplane. The RMS deviation between the predicted and true midplane was 1.49 cm. For a 16 cm reconstruction volume and the 5.5-11.5 cm thick cardiac volumes in this study, midplane estimation errors of 2.25-5.25 cm were tolerable. Tomosynthesis-based localization of cardiac volume is feasible. This technique could be applied prior to coronary angiography, or to assist in isocentering the patient for rotational angiography.

10132-215, Session PS12

X-ray vector radiography of a human hand

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X-ray phase-contrast reveals differential phase-contrast (DPC) and dark-field contrast (DFC) on top of the conventional absorption image. X-ray vector radiography (XVR) exploits the directional dependence of the DFC and yields the mean scattering strength, the degree of anisotropy and the orientation of scattering structures by combining several DFC-projections. Here, we perform an XVR of an ex vivo human finger as well as a human hand specimen. The conventional absorption image has a good contrast between the bones and the surrounding soft tissue. Within the bones, trabecular structures are visible. However, XVR detects subtler differences within the trabecular structure: there is strong isotropic scattering in the extremities of the phalanx in contrast to anisotropic and relatively weak scattering in its body. The orientation changes as well from relatively random in the extremities to an alignment along the longitudinal trabecular orientation in the body. In the other bones measured, a similar behavior was found. These findings indicate a deeper insight into the anatomical configuration using XVR compared to conventional radiography. Since microfractures cause a discontinuous trabecular structure, XVR could help to detect so-called radiographically occult fractures of the trabecular bones.

10132-216, Session PS12

Performance evaluation of algebraic reconstruction technique (ART) for prototype chest digital tomosynthesis (CDT) system

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Chest digital tomosynthesis (CDT) system has recently introduced to cope with overlap of anatomical structures of conventional chest radiography. In the present study, we confirmed the feasibility of algebraic reconstruction technique (ART) method with CDT system, and quantified the performance of ART method in simulation and experimental study.

Reconstructed images were acquired from the total 41 projection images over a total angular range of ±20°. We evaluated contrast-to-noise ratio (CNR) to investigate the effect of reconstruction parameters such as number of iterations, relaxation parameter and initial guess on image quality.

We found that CNR values after maximum CNR were decreased slightly with increasing iteration number regardless of relaxation parameter in both simulation and experimental results. According to the results, proper ART relaxation parameter could improve image quality from the same projection. In this study, back-projection (BP) initial guess for ART method could provide better CNRs with a faster speed than zero initial (ZI) guess. The results indicated that proper reconstruction parameters are needed to fit the best CDT exam for ART method.

10132-217, Session PS12

Dental non-linear image registration and collection method with 3d reconstruction and change detection

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The capability of a software algorithm to automatically align same-patient dental bitewing and panoramic x-rays over time is complicated by differences in collection perspectives. We successfully used image correlation with an affine transform for each pixel to discover common image borders, followed by a non-linear homography perspective adjustment to closely align the images. However, significant improvements in image registration could be realized if images were collected from the same perspective, thus facilitating change analysis. The perspective differences due to current dental image collection devices are so significant that straightforward change analysis is not possible. To address this, a new custom dental tray could be used to provide the standard reference needed for consistent positioning of a patient's mouth. Similar to sports mouth guards, the dental tray could be fabricated in standard sizes from plastic and use integrated electronics that have been miniaturized. In addition, the x-ray source needs to be consistently positioned in order to collect images with similar angles and scales. Solving this pose correction is similar to solving for collection angle in aerial imagery for change detection. A standard collection system would provide a method for consistent source positioning using real-time sensor position feedback from a digital x-ray image reference. Automated, robotic sensor positioning could replace manual adjustments. Given an image set from a standard collection, a disparity map between images can be created using parallax from overlapping viewpoints to enable change detection. This perspective data can be rectified and used to create a three-dimensional dental model reconstruction.

10132-56, Session 12

3D-printed focused collimator for intra-operative gamma-ray detection

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Recent developments in targeted radiopharmaceutical labels have increased the need for sensitive, real-time gamma detection during cancer surgery and biopsy. Additive manufacturing (3D printing) in metal has now made it possible to design and fabricate complex metal collimators for compact gamma probes. We describe the design and implementation of a 3D-printed focused collimator that allows for real-time detection of gamma radiation from within a small volume of interest, using a single-crystal large-area detector. The collimator was fabricated using laser fusion of powdered stainless steel (316L), using a commercial 3D metal printer (AM125, Renishaw plc). The prototype collimator is 20 mm thick, with hexagonal close-packed holes designed to focus to a point 35 mm below the surface of the collimator face. Tests were carried out with a low-activity (<1 μCi) 241Am source, using a conventional gamma-ray detector probe, incorporating a 2.5 cm diameter, 2.5 cm thick NaI crystal coupled to a photomultiplier. The measured full-width half maximum (FWHM) was less than 5.5 mm, and collimator detection efficiency was 48%. The ability to fabricate fine features in solid metal makes it possible to develop optimized designs for high-efficiency, focused gamma collimators for real-time intraoperative imaging applications.

10132-57, Session 12

Blood-pool contrast agent for pre-clinical computed tomography

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Recent advances in nanotechnology have led to the development of blood pool contrast agents for pre-clinical computed tomography (CT). Although long-circulating nanoparticle-based agents exist for pre-clinical imaging, they are predominantly based on iodine, which has a low atomic number. Superior radiographic contrast can be achieved using elements with higher atomic numbers (i.e. lanthanides), particularly at higher energies. The purpose of our work was to develop and evaluate a lanthanide-based blood pool contrast agent suitable for pre-clinical in vivo CT. We synthesized a contrast agent in the form of polymer-encapsulated gadolinium nanoparticles and evaluated the agent's stability in vitro. The polymer-encapsulated nanoparticles in the contrast agent were shown to have a diameter of 250 ± 6 nm, with medium size dispersity. Particle size distribution – evaluated by dynamic light scattering over the period of two days – demonstrated no change in shape and size distribution of the contrast agent in water and saline; the agent was stable in a mouse serum mimic for over 30 minutes. CT images of the initially synthesized contrast agent (containing 27 mg/mL of gadolinium) demonstrated an attenuation of over 1200 Hounsfield Units. This approach to synthesizing gadolinium-based blood pool contrast agent promises to enhance the capabilities of pre-clinical CT imaging.

10132-58, Session 12

Automated 3D coronary sinus catheter detection using a scanning-beam digital x-ray system

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Scanning-beam digital x-ray (SBDX) is an inverse geometry x-ray fluoroscopy system capable of tomosynthesis-based 3D tracking of catheter tips and electrodes concurrent with fluoroscopic display. To determine localized points belonging to a coronary sinus (CS) catheter, an automated catheter detection algorithm was created which uses the 3D localization capability of SBDX and prior knowledge of the catheter shape. Candidate groups of points representing the CS catheter are obtained from a 3D shape-constrained search. A catheter cost function is then minimized over the groups to select the most probable CS catheter candidate. The algorithm was implemented in MATLAB and tested offline using recorded image sequences of a chest phantom containing a 10-element CS catheter, 4-element ablation catheter, and 9 added fiducials. Fiducial placement was varied to create challenging detection scenarios. Table panning and elevation was used to create motion. Detection sensitivity was evaluated from frames where the catheter was completely visible. Specificity was measured by running the CS detection algorithm on the localized points corresponding to the ablation catheter and fiducials only, with CS catheter points excluded. The algorithm was found to have 98.1% sensitivity and 100% specificity in 2755 frames of imaging. Average processing time was 12.7 ms/frame on a PC with a 3.4 GHz CPU and 8 GB memory, corresponding to 78 fps performance. This work demonstrates a computationally efficient method of automated CS catheter detection in 3D tracking data from SBDX. This method is intended for use in a motion-compensated 3D display of catheters and cardiac anatomy.

10132-59, Session 12

An x-ray based capsule for colorectal cancer screening incorporating single photon counting technology

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An ingestible capsule for colorectal cancer screening, based on ionizing-radiation, has been developed and is in advanced stages of system stabilization and clinical evaluation. The imaging principle allows future patients using this technology to avoid bowel cleansing, and to continue the normal life routine during procedure.

The Check-Cap capsule, or C-Scan Cap ®, imaging principle is essentially based on reconstructing scattered radiation, while both radiation source and radiation detectors reside within the capsule. The radiation source is a custom-made radioisotope encased in a small canister, collimated into rotating beams. While traveling along the human colon, irradiation occurs from within the capsule towards the colon wall. Scattering of radiation occurs both inside and outside the colon segment; some of this radiation is scattered back and detected by sensors onboard the capsule.

During procedure, the patient receives small amounts of contrast agent as an addition to his/her normal diet. The presence of contrast agent inside the colon dictates the dominant physical processes to become Compton Scattering and X-Ray Fluorescence (XRF), which differ mainly by the energy of scattered photons. The detector readout electronics incorporates low-noise Single Photon Counting channels, which allow separation between the products of these different physical processes.

Separating between radiation energies essentially allows estimation of the distance from the capsule to the colon wall, hence structural imaging of the intraluminal surface. This allows imaging of structural protrusions into the colon volume, especially focusing on adenomas that might develop into colorectal cancer.

10132-201, Session 12

Simulation of a compact analyzer-based imaging system with a regular x-ray source

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Analyzer-based Imaging (ABI) belongs to a broader family of phase-contrast (PC) X-ray techniques. PC measures X-ray deflection phenomena when interacting with tissue, which is known to provide higher contrast images of soft tissue than other X-ray methods. This has a very important interest in the medical field, specially for mammogram applications.
This paper presents a simulation tool for table-top ABI systems using a conventional polychromatic X-ray source.

10132-61, Session 13

Airways, vasculature, and interstitial tissue: anatomically-informed computational modeling of human lungs for virtual clinical trials

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This study aimed to model virtual human lung phantoms including both non-parenchyma and parenchyma structures. Initial branches of the non-parenchyma structures (airways, arteries, and veins) were segmented from anatomical data (Visible Male) in each lobe separately. A volume-filling branching algorithm was utilized to grow the higher generations of the airways and vessels to the level of terminal branches. Arteries and airways followed proximity rules, while veins were grown based on volume rules. The diameters of the airways and vessels were estimated using established relationships between flow rates and diameters. The parenchyma was then modeled as a tree structure, which was started from the terminal bronchioles and bifurcated up to 7 generations representing the gas exchanging units of the lung. This parenchyma model included alveolar ducts and sacs as cylinders and alveoli as 3/4 spheroids, informed by previous anatomic and morphometric studies. The resulting lung phantoms were added into the existing library of whole-body extended cardiac-torso (XCAT) phantoms. The phantoms were then used as known geometries in a pilot study to investigate the impact of multiple pitch values (0.5, 1, 2, and 4) on geometrical distortions in spiral CT. Results showed the progressive degradation of 3D rendition with increased pitch. Overall, the enhanced lung models combined with the XCAT phantoms proved to provide a powerful toolset to perform virtual clinical trials in the context of thoracic imaging. Such trials, not practical using clinical datasets or simplistic phantoms, can quantitatively evaluate and optimize advanced imaging techniques towards patient-based care.

10132-62, Session 13

A virtual clinical trial using projection-based nodule insertion to determine radiologist reader performance in lung cancer screening CT

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Task-based image quality assessment using model observers is promising to provide an efficient, quantitative, and objective approach to CT dose optimization. Before this approach can be reliably used in practice, its correlation with radiologist performance for the same clinical task needs to be established. Determining human observer performance for a well-defined clinical task, however, has always been a challenge due to the tremendous amount of efforts needed to collect a large number of positive cases. To overcome this challenge, we developed an accurate projection-based insertion technique. In this study, we present a virtual clinical trial using this tool and a low-dose simulation tool to determine radiologist performance on lung-nodule detection as a function of radiation dose, nodule type, nodule size, and reconstruction methods. The lesion insertion and low-dose simulation tools together were demonstrated to provide flexibility to generate realistically-appearing clinical cases under well-defined conditions. The reader performance data obtained in this virtual clinical trial can be used as the basis to develop model observers for lung nodule detection, as well as for dose and protocol optimization in lung cancer screening CT.

10132-63, Session 13

Inter-algorithm tumor volumetry comparison of real and 3D simulated lesions in CT

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The purpose of this study was to establish volumetric exchangeability between real and computational lung lesions in CT. We compared the overall relative volume estimation performance of segmentation tools when used to measure real lesions in actual patient CT images and computational lesions virtually inserted into the same patient images (i.e., hybrid datasets). 30 thoracic patient cases from RIDER database with pathologically confirmed malignancies of a variety of sizes and morphologies were modeled and used as the basis for the comparison. While some lesions were isolated, others were attached to the pleura or lung structures. Patient images were acquired using a 16 detector row or 64 detector row (Lightspeed 16 or VCT; GE Healthcare). Scans were acquired using standard chest protocols during a breath-hold. Virtual 3D lesion models based on real lesions were developed in Duke Lesion Tool (Duke University), and inserted using a validated image-domain insertion program. Nodule volumes were estimated using multiple commercial segmentation tools (iNtuition, TeraRecon, Inc., Syngo-via, Siemens Healthcare, and IntelliSpace, Philips Healthcare). Consensus based volume comparison showed consistent trends in volume measurement between real and virtual lesions across all software. The average percent bias (± standard error) shows $-9.2\pm3.2\%$ for real lesions versus $-6.7\pm1.2\%$ for virtual lesions with tool A, $3.9\pm2.5\%$ and $5.0\pm0.9\%$ for tool B, and $5.3\pm2.3\%$ and $1.8\pm0.8\%$ for tool C, respectively. Virtual lesions were quantitatively similar to real lesions (<4% difference) with $p > .05$ in most cases. Results suggest that hybrid datasets had similar inter-algorithm variability compared to real datasets.

10132-64, Session 13

Learning-based stochastic object models for use in optimizing imaging systems

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The optimization of imaging systems based on objective, or task-based, measures of image quality via computer-simulation requires use of a stochastic object model (SOM). However, the development of computationally tractable SOMs that can accurately model the statistical variations in anatomy within a specified ensemble of patients remains a challenging task. By only use of image data corresponding a single patient, previously reported numerical anatomical models lack of the ability to accurately model inter-patient variations in anatomy. In this work, a novel and tractable methodology for learning a SOM from a set of volumetric training images is developed. The proposed method is based upon geometric attribute distribution (GAD) models, which characterize the inter- and intra-structural variations of individual anatomical structures. The GAD models are scalable and deformable, and constrained by their respective principal attribute variations learned from training data. By use of the GAD models, random organ shapes and positions can be generated and integrated to form an anatomical phantom. To demonstrate the methodology, a SOM corresponding to the adult male pelvis was computed and a corresponding ensemble of phantoms was created. Additionally, computer-simulated X-ray projection images corresponding to the phantoms were computed, from which tomographic images were reconstructed.

10132-65, Session 13

False dyssynchrony: problem with image-based cardiac functional analysis using x-ray computed tomography

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We have developed a digitally synthesized patient which we call “Zach” (Zero millisecond Adjustable Clinical Heart) phantom, which allows for an access to the ground truth and assessment of image-based cardiac functional analysis (CFA) using CT images using clinically realistic settings. The study using Zach phantom revealed a major problem with image-based CFA: “False dyssynchrony.” Even though the true motion of wall segments is in synchrony, it may appear to be dyssynchrony with the reconstructed cardiac CT images. It is attributed to how cardiac images are reconstructed and how wall locations are updated over cardiac phases. The presence and the degree of false dyssynchrony may vary from scan-to-scan, which could degrade the accuracy and the repeatability (or precision) of image-based CT-CFA exams.

10132-66, Session 13

Reanimating patients: cardio-respiratory CT and MR motion phantoms based on clinical CT patient data

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Until today several algorithms have been developed that reduce or avoid artifacts caused by cardiac and respiratory motion in computed tomography (CT).

The motion information is converted into so-called motion vector fields (MVFs) and used for motion compensation (MoCo) during the image reconstruction. To analyze these algorithms quantitatively there is the need for ground truth patient data displaying realistic motion.

We developed a method to generate a digital ground truth displaying realistic cardiac and respiratory motion that can be used as a tool to assess MoCo algorithms. By the use of available MoCo methods we measured the motion in CT scans with high spatial and temporal resolution and transferred the motion information onto patient data with different anatomy or imaging modality, thereby reanimating the patient virtually. In addition to these images the ground truth motion information in the form of MVFs is available and can be used to benchmark the MVF estimation of MoCo algorithms.

We here applied the method to generate 20 CT volumes displaying detailed cardiac motion that can be used for cone beam CT (CBCT) simulations and a set of 8 MR volumes displaying respiratory motion.

Our method is able to reanimate patient data virtually. In combination with the MVFs it serves as a digital ground truth and provides an improved framework to assess MoCo algorithms.

10132-67, Session 14

High-resolution, anthropomorphic, computational breast phantom: fusion of rule-based structures with patient-based anatomy

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While patient-based breast phantoms are realistic, they are limited by low resolution due to the image acquisition and segmentation process. The purpose of this study is to restore the high resolution components to the patient-based phantoms by adding power law noise (PLN) and features from anthropomorphic rule-based models. First, 3D radial symmetric PLN with was added at the boundary between adipose and glandular tissue to connect broken tissue and create a high frequency contour of the glandular tissue. Next, selected high-frequency features from the FDA rule-based computational phantom (Cooper’s ligaments, ductal network, and blood vessels) were also added to the phantom. The effects of restoration were demonstrated by 2D mammography projections and DBT reconstructed images. The addition of PLN and rule-based models leads to a continuous decrease in beta. The new beta is 2.76, which coincides with the normal

behavior of DBT. The new combined breast phantoms preserve the realism from segmentation and gain higher resolution after restoration.

10132-68, Session 14

Detectability of artificial lesions in anthropomorphic virtual breast phantoms of variable glandular fraction

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In previous work, we developed computational breast phantoms with normal anatomy. These include rule-based phantoms from FDA and patient-based phantoms from Duke. The goal of the current study is to develop multiple lesion models, demonstrate their insertion into the latest versions of these phantoms, and perform preliminary human and model observer studies. We insert simulated lesions into 10 of these phantoms each from Duke and FDA, representing a wide range of anatomical structures and content, with the intent of determining their detectability as affected by phantom type, lesion type, and local density. The lesions themselves are representative of three distinctly different classes: well-circumscribed, irregular (with or without diffuse margins), and spiculated masses. Both human readers as well as a Gabor channelized hotelling model observers (G-CHO) perform comparably in most instances, with overall ROC AUC of 0.896 and 0.888 respectively for cases that both the radiologist and G-CHO observer reported results on. Average G-CHO AUC is .977 for the Duke phantoms and detectability is variable between lesion models, with average G-CHO AUC of .976 for well-circumscribed, .968 for irregular, and .988 for spiculated masses. Local density also affected performance, with average G-CHO AUC of .994, .976, .956, .986, .969, .968, and .978 for the separate density classes (in order of increasing average density).

10132-69, Session 14

Third generation anthropomorphic physical phantom for mammography and DBT: Incorporating voxelized 3D printing and uniform chest wall QC region

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Physical breast phantoms provide a standard method to test, evaluate, and optimize clinical mammography systems, including new digital breast tomosynthesis (DBT) systems, in a controlled setting. In previous work, we produced an anthropomorphic phantom based on human subject breast CT data using commercial 3D printing. We now introduce a new breast phantom with voxelized 3D printing, which provides higher resolution and allows us more control over contrast. Compared to our previous phantoms that were based on 500x500x500 μm breast CT data, this latest phantom is based on a new cohort of virtual models with 155x155x155 μm voxels. We also added a uniform chest wall extension for evaluating conventional QC metrics. This uniform region contained a grayscale step wedge, chest wall coverage markers, fiducial markers, spheres, and metal ink stickers with line pairs and edges. Lastly, we experimented with doping photopolymer material to increase our current contrast. We doped samples of VeroBlue with either 3 wt% calcium, 1 wt% iodine, and 3 wt% zinc acetate to increase density. We also used 8 wt% Span 60 surfactant and sonication to retain microbubbles and reduce density. Zinc doping showed significantly different attenuation with 36% increase compared to the control, followed by 3 wt% calcium-doped VeroBlue with an 11% increase. As we move towards our long term goal of phantoms that are indistinguishable from patients, this new generation of anthropomorphic physical breast phantom validates our voxelized printing process, demonstrates the utility of a uniform QC region with features from 3D printing and metal ink stickers, and shows potential for improved contrast via doping.

10132-70, Session 14

A novel, realistic breast phantom for 2D and 3D x-ray imaging

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Purpose: Physical phantoms are central for evaluating 2D and 3D breast imaging systems. However, the presently available phantoms are uniform, not realistic enough, expensive, or may fall short of fully characterizing 3D systems. To address this need, a novel, anthropomorphic breast phantom was created for use with full field digital mammography (FFDM) and digital breast tomosynthesis (DBT) through inkjet printing.

Methods: A virtual breast phantom was first produced through analytical modeling and then realized through an inkjet printing process. Printing was performed in a slice-by-slice fashion using a glandular-mimicking ink, synthesized by combining pigmented ink with iodine, and an adipose-like material background, using parchment paper. Lesions were also inserted throughout the phantom. The phantom was imaged on clinical FFDM and DBT systems under typical mammographic beam conditions. The printing process was evaluated in terms of material realism, printing accuracy, consistency, reproducibility, and resolution.

Results: The linear attenuation of the ink and parchment closely matched those of the glandular and adipose tissues. High accuracy was found in the printing process. The ink was consistent across multiple prints and highly reproducible across different batches of ink. The resolution was of the printer was close to that of the detector pixels.

Conclusion: An anthropomorphic breast phantom was created using a novel technique. The phantom can be fabricated using inexpensive, easily available materials. It was observed to have realistic tissue properties with high accuracy, resolution, consistency, and reproducibility. This promising phantom generation methodology can be used to evaluate 2D and 3D breast imaging systems.

10132-71, Session 14

In silico imaging clinical trials for regulatory evaluation: initial considerations for a demonstration study

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Expensive and lengthy clinical trials can delay regulatory evaluation and add significant burden that stifles innovation affecting patient access to novel, high-quality imaging technologies. We define emph{in silico} imaging as a computer simulation of an entire imaging system (including source, object, detection and observer components) used for research, development, optimization, technology assessment, and regulatory evaluation of new technology. In this work we will describe an attempt to build an entire imaging pipeline emph{in silico} including device (physics), patient (anatomy, disease), and image interpretation models for regulatory evaluation using open-source tools.

10132-72, Session 15

An alternate design for the Defrise phantom to quantify resolution in digital breast tomosynthesis

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Our previous work analyzed the Defrise phantom as a test object for evaluating image quality in digital breast tomosynthesis (DBT). The phantom is assembled from multiple plastic plates at low-frequency spacing. The resultant object effectively consists of square waves arranged in a continuous vertical stack. In our previous work, there was no explicit analysis of how image quality varies with the thickness of the stack. To investigate this concept, a modified design of the phantom is now considered. For this purpose, each rectangular plate was laser-cut along an angle, creating a slope along which thickness varies continuously. The phantom was imaged using a clinical DBT system, and the relative modulation of the plastic-air separations was calculated in the reconstruction. In addition, a theoretical model was developed to determine whether modulation can be optimized by modifying the x-ray tube trajectory. It is demonstrated that modulation is dependent on the orientation of the frequency. Modulation is within detectable limits over a broad range of phantom thicknesses if frequency is parallel with the tube travel direction. Conversely, there is loss of modulation if frequency is oriented along the posteroanterior direction. In particular, as distance from the chest wall increases, there is a smaller range of thicknesses over which modulation is within detectable limits. Theoretical modeling suggests that this anisotropy is minimized by introducing tube motion along the posteroanterior direction. In conclusion, this paper demonstrates that the Defrise phantom is a tool for analyzing the limits of resolution in DBT systems.

10132-73, Session 15

Comparing the imaging performance of computed super-resolution and magnification tomography

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Computed super-resolution (SR) is a method of reconstructing higher resolution images than a detector can physically provide. Magnification mammography is a method of projection imaging that uses geometric magnification to increase spatial resolution thereby aiding diagnosis. This study explores the development and application of Magnification Digital Breast Tomography (MDBT). Four different acquisition geometries were compared in terms of various image metrics, including high-contrast spatial resolution in various axes, both in planes parallel to detector and oblique planes. A modified Defrise phantom was used to determine the low-frequency spatial resolution for the various techniques. An anthropomorphic phantom was used to simulate clinical imaging. Each experiment was conducted at three different magnifications: contact (1.06x), MAG1 (1.34x), and MAG2 (1.78x). All images were taken on the Next Generation Tomography system, an in-house solution designed to optimize SR. It has been demonstrated that SR and MDBT (MAG1 and MAG2) both provide resolution improvement over non-SR contact imaging. MDBT, however, suffers from the potential of amplified patient motion at higher magnifications. In addition, it requires more radiation dose and delays diagnosis, since MDBT would be conducted upon a recall. SR, in comparison, can be conducted with the initial acquisition data. In conclusion, this study demonstrates that MDBT is a viable method of imaging the breast, but that SR is a superior alternative. For increased resolution, SR + MDBT provides the highest sub-pixel accuracy.

10132-74, Session 15

Metal artifact reduction using a patch-based reconstruction for digital breast tomosynthesis

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Digital breast tomosynthesis (DBT) is rapidly emerging as the main clinical tool for breast cancer screening. Although several reconstruction methods for DBT are described by the literature, one common issue are the interplane artifacts caused by out-of-focus features. For breasts containing high-attenuation features, such as surgical clips, artifacts are an even more relevant issue and can harm the performance of radiologists while looking for features that indicate the development of a tumor. In this work, we propose a novel method of combining backprojected data into tomographic slices using a patch-based approach, commonly explored in the denoising field. Preliminary tests were performed on a geometry phantom and on an anthropomorphic phantom. The reconstructed images are compared to the ones reconstructed using commercial software. Qualitative assessment of the algorithm provides evidence that the proposed method reduces artifacts while maintaining a low level of noise. Objective assessment support the visual findings. The artifact spread function shows that the proposed method is capable of suppressing artifacts generated by high-attenuation features. The signal difference to noise ratio shows that the noise levels of the proposed and commercial methods are comparable, even though the commercial method applies filtering steps, while the proposed method does not have any extra filtering implemented. Thus, the proposed method can produce tomosynthesis reconstructions with reduced artifacts and low noise levels.

10132-75, Session 15

Metal and calc artifact reduction for digital breast tomosynthesis

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Tomosynthesis images of the breast suffer from artifacts caused by the presence of highly absorbing materials. This can be either induced by metal objects like needles or clips inserted during biopsy devices, or larger calcifications inside the examinated breast. Mainly two different kinds of artifacts appear after the filtered backprojection procedure. The first types are undershooting artifacts near edges of high-contrast objects caused by the filtering step. The second types are out-of-plane (ripple) artifacts that appear even in slices where the metal object or macrocalc does not exist. Due to the limited angular range of tomosynthesis systems, overlapping structures have high influence on neighboring regions. To overcome these problems, a segmentation of artefact introducing objects is done on the projection images. Both projection versions, with and without high-contrast objects are filtered independently to avoid undershootings. During backprojection a decision is made for each reconstructed voxel, if it is artifact or high-contrast object. This is based on a mask image, gained from the segmentation of high-contrast objects. This procedure avoids undershooting artifacts and additionally reduces out-of-plane ripple. Results are demonstrated for different kinds of artefact inducing objects and calcifications.

10132-76, Session 15

Contrast enhanced imaging with a stationary digital breast tomosynthesis system

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Contrast enhanced digital breast tomosynthesis (CE DBT) has been demonstrated to provide both functional, and 3D information. There are many factors that affect the quality of CE DBT imaging, including the energy spectrum, scan time, motion of the x-ray source, and the presence of scatter.

By utilizing a carbon nanotube x-ray source array, we have developed and demonstrated the stationary breast tomosynthesis system, which eliminates the x-ray source motion, improves spatial resolution, and reduces scanning time. The second generation s-DBT system (2G s-DBT) has shown a 50% improvement in spatial resolution than existing rotation gantry DBT systems. We have also demonstrated that the s-DBT system enables a unique scatter correction technique using a primary sampling device (PSD), which can lead to 30-60% improvement in contrast, and signal differential to noise ratio (SdNR) with minimal increase in radiation dose.

In this study we report the preliminary result of applying the PSD scatter correction technique for CE s-DBT imaging with quantification of the iodine contrast. The results show that the PSD scatter correction technique is effective in improving contrast for temporal subtraction (TS) and dual energy subtraction (DE) imaging, and the results of TS perform substantially better that DES.

10132-77, Session 15

Effects of detector blur and correlated noise on digital breast tomosynthesis reconstruction

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Digital breast tomosynthesis (DBT) was developed to alleviate the problem of overlapping tissue in 2-D mammography. To improve DBT image quality, we are developing model-based iterative reconstruction method based on models of the imaging system physics. Our preliminary implementation (SQS-DBCN) incorporated detector blur into the system model and correlation into the noise model under some simplifying assumptions, and used a separable quadratic surrogate (SQS) algorithm for minimizing the cost function. We have shown that SQS-DBCN improves DBT image quality, especially for microcalcification clusters (MCs) that are an early sign of breast cancer.

This work further improves the regularization method by incorporating neighbors along the diagonal directions, whereas the previous regularization used only the horizontal and vertical neighbors. To further understand the role of the different components in the system model of the SQS-DBCN method, we reconstructed DBT images without modeling either the detector blur or noise correlation for comparison.

Visual comparison of the reconstructed images showed that regularizing with diagonal directions reduced artifacts and the noise level. It effectively eliminated the square texture resulting from enhancing sharp edges along only the horizontal and vertical directions in the previous implementation. The SQS-DBCN reconstructed images had better image quality than reconstructions without models for detector blur or correlated noise, as indicated by the contrast-to-noise ratios (CNR) of MCs and textural artifacts. These results indicated that regularized DBT reconstruction with detector blur and correlated noise modeling, even with simplifying assumptions, can improve DBT image quality compared to that without system modeling.

10133-1, Session 1

Fovea detection in optical coherence tomography using convolutional neural networks

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The fovea is an important clinical landmark that is used as a reference for assessing various quantitative measures, such as central retinal thickness or drusen count. In this paper we propose a novel method for automatic detection of the foveal center in Optical Coherence Tomography (OCT) scans. Although the clinician will generally aim to center the OCT scan on the fovea, post-acquisition image processing will give a more accurate estimate of the true location of the foveal center. A Convolutional Neural Network (CNN) was trained on a set of 781 OCT scans that classifies each pixel in the OCT B-scan with a probability of belonging to the fovea. Dilated convolutions were used to obtain a large receptive field, while maintaining pixel-level accuracy. In order to train the network more effectively, negative patches were sampled selectively after each epoch. After CNN classification of the entire OCT volume, the predicted foveal center was chosen as the voxel with maximum output probability, after applying an optimized three-dimensional Gaussian blurring. We evaluate the performance of our method on a data set of 99 OCT scans presenting different stages of Age-related Macular Degeneration (AMD). The fovea was correctly detected in 96.9% of the cases, with a mean distance error of 73 ?m (±112 ?m). This result was comparable to the performance of a second human observer who obtained a mean distance error of 69 ?m (± 94 ?m). Experiments showed that the proposed method is accurate and robust even in retinas heavily affected by pathology.

10133-2, Session 1

Real time coarse orientation detection in MR scans using multi-planar deep convolutional neural networks

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Automatically detecting anatomy orientation is an important task in medical image analysis. Specifically, the ability to automatically detect coarse orientation of structures is useful to minimize the effort of fine/accurate orientation detection algorithms, to initialize non-rigid deformable registration algorithms or to align models to target structures in model-based segmentation algorithms. In this work, we present a deep convolutional neural network (DCNN)-based method for fast and robust detection of the coarse structure orientation, i.e., the hemi-sphere where the principal axis of a structure lies. That is, our algorithm predicts whether the principal orientation of a structure is in the northern hemisphere or southern hemisphere, which we will refer to as UP and DOWN, respectively, in the remainder of this manuscript. The only assumption of our method is that the entire structure is located within the scan's field-of-view (FOV). To efficiently solve the problem in 3D space, we formulated it as a multi-planar 2D deep learning problem. In the training stage, a large number coronal-sagittal slice pairs are constructed as 2-channel images to train a DCNN to classify whether a scan is UP or DOWN. During testing, we randomly sample a small number of coronal-sagittal 2-channel images and pass them through our trained network. Finally, coarse structure orientation is determined using majority voting. We tested our method on 114 Elbow MR Scans. Experimental results suggest that only five 2-channel images are sufficient to achieve a high success rate of 97.39%. Our method is also extremely fast and takes approximately 50 milliseconds per 3D MR scan. Our method is insensitive to the location of the structure in the FOV.

10133-3, Session 1

Marginal shape deep learning: applications to pediatric lung field segmentation

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Representation learning through deep learning (DL) architecture has shown tremendous potential for identification, localization, and texture classification in various medical imaging modalities. However, DL applications to segmentation of objects especially to deformable objects are rather limited and mostly restricted to pixel classification. In this work, we propose marginal shape deep learning (MaShDL), a framework that extends the application of DL to deformable shape segmentation by using deep classifiers to estimate the shape parameters. MaShDL combines the strength of statistical shape models with the automated feature learning architecture of DL. Unlike the iterative shape parameters estimation approach of classical shape models that often leads to a local minima, the proposed framework is robust to local minima optimization and illumination changes. Furthermore, since the direct application of DL framework to a multi-parameter estimation problem results in a very high complexity, our framework provides an excellent run-time performance solution by independently learning shape parameter classifiers in marginal eigenspaces. We evaluated MaShDL for segmenting the lung field from 314 normal and abnormal pediatric chest radiographs and obtained a mean Dice similarity coefficient of 0.927 using only the four highest modes of variation (compared to 0.888 with classical ASM (p-value=0.01) using same configuration). To the best of our knowledge this is the first demonstration of using DL framework for parametrized shape learning for the delineation of deformable objects.

10133-4, Session 1

Accurate segmentation of lung fields on chest radiographs using deep convolutional networks

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Accurate segmentation of lung fields on chest radiographs is the primary step for computer-aided detection of various conditions such as lung cancer and tuberculosis. The size, shape and texture of lung fields are key parameters for chest X-ray (CXR) based lung disease diagnosis in which the lung field segmentation is a significant primary step. Although many methods have been proposed for this problem, lung field segmentation remains a challenge. In recent years, deep learning has shown state of the art performance in many visual tasks such as object detection, image classification and semantic image segmentation. In this study, we propose a deep convolutional neural network (CNN) framework for segmentation of lung fields on 167 clinical posterior-anterior (PA) CXR image collected retrospectively from picture archiving and communication system (PACS) of Geisinger Health System. The proposed network composed of five convolutional layer and one fully connected layer. The framework achieved IOU (intersection over union) of 0.96 in the test dataset as compared to manual segmentation. The suggested framework outperforms state of the art registration-based segmentation by a significant margin. To our knowledge, this the first study of lung segmentation on CXR images based

on deep neural network on a heterogeneous clinical dataset. The results suggest that convolutional neural networks can be employed reliably for lung field segmentation on CXR images.

10133-5, Session 1

Intervertebral disc segmentation in MR images with 3D convolutional networks

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The vertebral column is a complex anatomical construct, composed of vertebrae and intervertebral discs (IVDs) supported by ligaments and muscles. During life, all components undergo degenerative changes, which may in some cases cause severe, chronic and debilitating low back pain. The main diagnostic challenge is to locate the pain generator, and degenerated IVDs have been identified to act as such. Accurate and robust segmentation of IVDs is therefore a prerequisite for computer-aided diagnosis and quantification of IVD degeneration, and can be also used for computer-assisted planning and simulation in spinal surgery. In this paper, we present a novel fully automated framework for supervised segmentation of IVDs from three-dimensional (3D) magnetic resonance (MR) spine images. By considering global intensity appearance and local shape information, a landmark-based approach is first used for the detection of IVDs in the observed image, which then initializes the segmentation of IVDs by combining deformable models with convolutional networks. For this purpose, a 3D convolutional network architecture called the IVD-Net was designed that learns rich high-level appearance representations from a training repository of IVDs, and then generates spatial IVD probability maps that guide deformable models towards IVD boundaries. By applying the proposed framework to 15 3D MR spine images containing 105 IVDs, quantitative comparison of the obtained against reference IVD segmentations yielded an overall mean Dice coefficient of 92.8%, mean symmetric surface distance of 0.4 mm and Hausdorff surface distance of 3.7 mm.

10133-6, Session 2

An atlas of the (near) future: cognitive computing applications for medical imaging *(Keynote Presentation)*

Anne LeGrand, IBM Watson Health (United States)

Keynote Speaker - TBD

10133-7, Session 2

An iterative method for airway segmentation using multiscale leakage detection

Syed Ahmed Nadeem, Dakai Jin, The Univ. of Iowa (United States); Eric A. Hoffman, The Univ. of Iowa Hospitals and Clinics (United States); Punam K. Saha, The Univ. of Iowa (United States)

There is a growing use of quantitative computed tomography to assess the lung both in terms of parenchymal characteristics as well as characteristics of the bronchial tree. Numerous large multi-center studies incorporating lung imaging as a study component are interested in airway phenotypes, wall-thickness, and other morphological measures. To our knowledge, there are no fully automated airway tree segmentation methods, free of the need for user review. When there is a failure of even a fraction of the segmentations, the airway tree masks must be manually reviewed for all subjects which is extremely cumbersome when many thousands of image data sets are being evaluated. In this paper, we present a novel iterative algorithm using multi-scale leakage detection for CT-based airway tree segmentation. The method is fully automated requiring no manual inputs or post-editing. It uses simple intensity based connectivity and a new leakage detection algorithm to iteratively grow an airway tree starting from an initial seed inside the trachea. It begins with a conservative threshold and then, iteratively shifting toward more generous values. The method was applied on chest CT scans of ten normal non-smoking subjects at total lung capacity. Airway segmentation results were compared to an expert user's manually edited segmentations. Branch level accuracy of the new segmentation method was examined along five standardized airway paths (RB1, RB4, RB10, LB1, LB10) and continuing two generations beyond these segmental bronchi. The method successfully detected all branches up to two generations beyond these segmental bronchi with no visual leakages.

10133-8, Session 2

Multi-atlas spleen segmentation on CT using adaptive context learning

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Automatic spleen segmentation on CT is challenging due to the complexity of abdominal structures. Multi-atlas segmentation (MAS) has shown to be a promising approach to conduct spleen segmentation. To deal with the substantial registration errors between the heterogeneous abdominal CT images, the context learning method for performance level estimation (CLSIMPLE) method was previously proposed. The context learning method generates a probability map for a target image using a Gaussian mixture model (GMM) as the prior in a Bayesian framework. However, the CLSSIMPLE typically trains a single GMM from the entire heterogeneous training atlas set. Therefore, the estimated spatial prior maps might not represent specific target images accurately. Rather than using all training atlases, we propose an adaptive GMM based context learning technique (AGMMCL) to train the GMM adaptively using subsets of the training data with the subsets tailored for different target images. Training sets are selected adaptively based on the similarity between atlases and the target images using cranio-caudal length, which is derived manually from the target image. To validate the proposed method, a heterogeneous dataset with a large variation of spleen sizes (100 cc to 9000 cc) is used. We designate a metric of size to differentiate each group of spleens, with 0 to 100 cc as small, 200 to 500cc as medium, 500 to 1000 cc as large, 1000 to 2000 cc as XL, and 2000 cc and above as XXL. From the results, AGMMCL leads to more accurate spleen segmentations by training GMMs adaptively for different target images.

10133-9, Session 2

Multi-atlas segmentation enables robust multi-contrast MRI spleen segmentation for splenomegaly

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Non-invasive spleen volume estimation is essential in detecting splenomegaly. Magnetic resonance imaging (MRI) has been used to facilitate splenomegaly diagnosis in vivo. However, achieving accurate spleen volume estimation from MR images is challenging given the great inter-subject

variance of human abdomens and wide variety of clinical images/modalities. Multi-atlas segmentation has been shown to be a promising approach to handle heterogeneous data and difficult anatomical scenarios. In this paper, we propose to use multi-atlas segmentation frameworks for MRI spleen segmentation for splenomegaly. To the best of our knowledge, this is the first work that integrates multi-atlas segmentation for splenomegaly as seen on MRI. To address the particular concerns of spleen MRI, automated and novel semi-automated atlas selection approaches are introduced. The automated approach interactively selects a subset of atlases using selective and iterative method for performance level estimation (SIMPLE) approach. To further control the outliers, semi-automated craniocaudal length based SIMPLE atlas selection (L-SIMPLE) is proposed to introduce a spatial prior in a fashion to guide the iterative atlas selection. A dataset from a clinical trial containing 55 MRI volumes (28 T1 weighted and 27 T2 weighted) was used to evaluate different methods. Both automated and semi-automated methods achieved median DSC > 0.9. The outliers were alleviated by the L-SIMPLE (≈1 min manual efforts per scan), which achieved 0.9713 Pearson correlation compared with the manual segmentation. The results demonstrated that the multi-atlas segmentation is able to achieve accurate spleen segmentation from the multi-contrast splenomegaly MRI scans.

10133-10, Session 3

Improving 3D surface reconstruction from endoscopic video via fusion and refined reflectance modeling

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Shape from shading (SFS) has been studied for decades; nevertheless, its overly simple assumptions and its ill-conditioning have resulted in infrequent use in real applications. Price et al. recently developed an iterative scheme named shape from motion and shading (SFMS) that models both shape and reflectance of an unknown surface simultaneously. SFMS produces a fairly accurate, dense 3D reconstruction from each frame of a pharyngeal endoscopic video, albeit with inconsistency between the 3D reconstructions of different frames. We present a comprehensive study of the SFMS scheme and several improvements to it: (1) We integrate a deformable registration method into the iterative scheme and use the fusion of multiple surfaces as a reference surface to guide the next iteration's reconstruction. This can be interpreted as incorporating temporal regularity into each single surface reconstruction. (2) We show that the reflectance model estimation is crucial and very sensitive to noise in the data. Moreover, even when the surface reflection is not assumed to be Lambertian, the reflectance model estimation function in SFMS is still overly simple for endoscopy of human tissue. By removing outlier pixels, by preventing unrealistic BRDF estimation, and by reducing the falloff speed of illumination in SFS to account for the effect of multiple bouncing of the light, we improve the reconstruction accuracy.

10133-11, Session 3

Automatic estimation of retinal nerve fiber bundle orientation in SD-OCT images using a structure-oriented smoothing filter

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Optical coherence tomography is used for detecting the glaucomatous damage. A better understanding of retinal nerve fiber bundle (RNFB) trajectories in combination with visual field data is important for diagnosis and monitoring glaucoma. Manual tracing of these bundles is a tedious task. In this work, we present an automatic technique to estimate the orientation of RNFBs from OCT images. Our method consists of several steps, starting from automatic segmentation of the RNFL. Afterwards, a stack of enface images around the posterior nerve fiber layer interface was extracted. The image with the most visible trajectories of the RNFBs was selected for further processing. After denoising the selected enface image, we applied semblance structure-oriented filter to this image. A Gaussian-based model was fitted to the filter response at different orientations and the least fit residue variance was used to select the dominant orientation. A confidence map was created and applied iteratively for smoothing the filter response. Finally, an orientation field corresponding to the strongest local orientation was obtained. The RNFB orientations of 6 macular scans from 3 subjects were estimated. For all scans, the estimated orientation fields show a good agreement with the RNFB trajectories in the enface images by visual inspection. Additionally, a good correlation between the orientation fields of two scans of the same subject was observed. A manual tracing of the RNFB trajectories can help us to validate our results quantitatively. Additionally, we will apply this method to a larger field of view around macula and optic nerve head.

10133-12, Session 3

Detection of coronary arteries using Gabor filters with automatic parameter selection

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Automatic detection of coronary arteries in X-ray angiograms is an important and challenging task for computer-aided diagnosis (CAD) systems in cardiology. Since the main disadvantages of the coronary angiograms are the uneven illumination and low contrast between blood vessels and image background, vessel detection methods play an essential role. In this paper, a novel unsupervised objective function to select the optimal Gabor filter parameters for the detection of coronary arteries in X-ray angiograms is proposed. Because the Gabor filters are defined by the parameters of average thickness, elongation, and number of oriented filters, an optimization process to select the optimal parameter values is highly desirable in order to increase the vessel detection rate while reducing the computational cost of a training stage. On the other hand, the proposed objective function is based on the measures of contrast and correlation from the gray-level co-occurrence matrix, which is computed from the Gabor filter response avoiding a training stage involving ground-truth images. The vessel detection performance of the proposed method is compared with those obtained by different methods of the state-of-the-art in terms of the area (Az) under the receiver operating characteristic (ROC) curve. In the experimental results, the proposed method obtained the highest detection rate with Az=0.9592, achieving a similarity rate of 0.9905 between the highest Az value and the Az value acquired by the proposed objective function using a test set of 60 angiograms.

10133-14, Session 3

Boundary segmentation for fluorescence microscopy using steerable filters

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Fluorescence microscopy is used to image multiple subcellular structures in living cells which are not readily observed using conventional optical microscopy. Moreover, two-photon microscopy is widely used to image structures deeper in tissue. Recent advancement in fluorescence microscopy has enabled the generation of large data sets of images at different depths, times, and spectral channels. Thus, automatic object segmentation is necessary since manual segmentation would be inefficient and biased. However, automatic segmentation is still a challenging problem as regions of interest may not have well defined boundaries as well as non-uniform pixel intensities. This paper describes a method for segmenting tubular structures in fluorescence microscopy images of rat kidney and liver samples using adaptive histogram equalization, foreground/background segmentation, steerable filters to capture directional tendencies, and connected-component analysis. The results from several data sets demonstrate that our method can segment tubular boundaries successfully. Moreover, our method has better performance when compared to other popular image segmentation methods when using ground truth data obtained via manual segmentation.

10133-15, Session 4

Large deep neural networks for MS lesion segmentation

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Multiple sclerosis (MS) is a multi-factorial autoimmune disorder, characterized by spatial and temporal dissem- ination of brain lesions that are visible in T2-weighted and Proton Density (PD) MRI. Assessment of lesion burden and is useful for monitoring the course of the disease, and assessing correlates of clinical outcomes.

Although there are established semi-automated methods to measure lesion volume, most of them require human interaction and editing, which are time consuming and limits the ability to analyze large sets of data with high accuracy. The primary objective of this work is to improve existing segmentation algorithms and accelerate the time consuming operation of identifying and validating MS lesions.

In this paper, a Large Scale Deep Neural Network for MS Lesion Segmentation is implemented. The MS lesion samples are extracted from the Partners Comprehensive Longitudinal Investigation of Multiple Sclerosis (CLIMB) study. A set of 6000 cases with T2 and PD images and a corresponding label map were used to train a Deep Neural Network to identify the white matter (WM) and MS lesion classes. Initial tests using this network achieved a 93% accuracy rate. A secondary goal was to enable this data repository for big data analysis by using this algorithm to segment the remaining cases available in the CLIMB repository.

10133-16, Session 4

Generative adversarial networks for brain lesion detection

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Supervised learning techniques, especially deep CNNs require large numbers of labelled data. In the medical imaging domain, the amount of labelled data is scarce and pixel labeling is laborious. In this work, Generative Adversarial Networks (GAN) are used to generate MR image patches of the brain and distinguish between healthy and lesion tissues. GAN consists of a generator and a discriminator network. The generator synthesizes images corresponding to an input array of Gaussian distributed random numbers. The discriminator in turn is trained to differentiate between the generated images i.e. fake images and real images of the brain. GAN's generator was trained to generate images of healthy brain tissue, the discriminator trained simultaneously, then classified input patches as real or generated fakes. It was expected that patches of brain lesions and healthy tissue would be classified as fake and real respectively. An open source GAN network model was trained by extracting healthy tissue patches of size 64x64 from FLAIR, T2 and T1 weighted images of brain tumor patients. The network was trained and validated on 13000 and 233 patches respectively. The GAN classified correctly (242483/324415) healthy tissues and brain tumor components such as Necrotic region (4776/6068), Edema (94044/123636), Non Enhancing tumor (13600/17906) and Enhancing tumor (17894/23842). Entire patient data volumes from the BRATS challenge data set will be tested and the feasibility of using GAN to delineate brain tumor lesions will be evaluated.

10133-17, Session 4

Machine learning in a graph framework for subcortical segmentation

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Automated and reliable segmentation of subcortical structures from human brain magnetic resonance images is of great importance for volumetric and shape analyses in quantitative neuroimaging studies. However, the poor boundary contrast and variable shape of these structures make the automated segmentation a tough task. We propose a 3D graph-based machine learning method to segment the caudate and the putamen from brain MRI scans in a robust and accurate way. An atlas-based tissue classification and bias-field correction method is applied to the images to generate an initial segmentation for each structure. Then a 3D graph framework is utilized to construct a geometric graph for each initial model mesh. A locally trained random forest classifier is used to determine the cost of each graph node. A max-flow algorithm is applied to solve the segmentation problem. For evaluation, a dataset with T1-weighted MRI of 62 subjects was used with 42 images for training and 20 images for testing. For comparison, FreeSurfer, FSL and BRAINSCut approaches were also evaluated using the same dataset. Dice overlap coefficients and surface-to-surfaces distances between the automated segmentation and the manual segmentation indicate the results of our method are statistically more accurate than all other three methods, for both caudate (Dice: 0.89+/-0.03) and putamen (0.89+/-0.03).

10133-18, Session 4

Sulci segmentation using geometric active contours

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Sulci are groove-like regions lying in the depth of the cerebral cortex between gyri, which together, form a folded appearance in human and mammalian brains. Sulci play an important role in the structural analysis of the brain, morphometry (i.e., the measurement of brain structures), anatomical labeling and landmark-based registration. Moreover, Sulcal morphology changes is related to cortical thickness which its measurement could provide useful information for studying variety of psychiatric disorders. Manually extracting sulci requires complying with complex protocols, which make the procedure both tedious and erroneous. To be able to compute different characteristics of the cortex, a number of 3D analyses have been developed using dynamic programming, watershed technique and Parametric representation. We have developed a method, employing geometric active contours. The initial curve evolved according to the external force, derived from geometry of the surface as well as the internal curvature flow, which is the conformal curve shortening flow on the surface. The curvature flow is responsible for the inward motion of the curve towards sulci regions and the evolving curve tend to lie along a high mean curvature groove. The Level set technique which can handle merging and splitting of curves naturally was used for the curve evolution implementation. Geometric variables needed in the implementation of curve evolution equation were computed based on the level-set function utilizing numerical methods.

10133-19, Session 4

Multi-modal and targeted imaging improves automated mid-brain segmentation

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The basal ganglia and limbic system, particularly the thalamus, putamen, internal and external globus pallidus, substantia nigra, and sub-thalamic nucleus, comprise a clinically relevant signal network for Parkinson's Disease. In order to manually trace these structures, a combination of high-resolution and specialized sequences at 7T are used, but these sequences are not feasible for clinical patients. Targeted imaging sequences at 3T (such as F-GATIR and other optimized inversion recovery sequences) have been presented to enhance contrast in a select group of these structures. In this work, we show that a series of atlases generated at 7T can be used to accurately segment basal ganglia and limbic structures at 3T using a combination of standard and optimized imaging sequences, though no single approach provided the best result across all structures. In the thalamus and putamen, a median Dice coefficient over 0.88 and a mean surface distance less than 1.0mm was achieved using a combination of T1 and an optimized inversion recovery imaging sequences. In the internal and external globus pallidus a Dice over 0.75 and a mean surface distance less than 1.2mm was achieved using a combination of T1 and F-GATIR imaging sequences. In the substantia nigra and sub-thalamic nucleus a Dice coefficient of over 0.6 and a mean surface distance of less than 1.0mm was achieved using the optimized inversion recovery imaging sequence. On average, using T1 and optimized inversion recovery together produced significantly improved segmentation results than any individual modality ($p<0.05$ Wilcoxon sign-rank test).

10133-20, Session 4

An algorithm for automatic parameter adjustment for skull extraction in BrainSuite

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Skull Extraction (classification of brain and non-brain tissue) of MRI brain image is a crucial preprocessing step necessary for imaging based anatomical studies of the human brain. This paper presents an automated and accurate parameter tuning algorithm for the Brain Surface Extraction (BSE) step of the BrainSuite Software. The algorithm can automatically and intelligently choose the parameters of BSE which gives the best skull extraction results for each subject. The algorithm starts the search with default parameters of edge constant and diffusion constant and optimizes over the 2-Dimensional parameter space for the fixed diffusion iteration and erosion size parameters. The volume and the surface area of the brain mask are computed. The cost function is computed as a ratio of surface area to the volume. This cost function is minimized over the parameters of BSE to obtain the accurate mask. The optimization is performed using a simplex search. This iterative process is repeated for different values of discrete parameters of BSE (erosion size and diffusion iteration). The parameter results and the mask for the optimal parameters are displayed as the output. The algorithm converges within 30-45 minutes for each subject. We observed that we were able to find optimal parameters for BSE as well as good skull extraction results in most cases using this algorithm.

10133-21, Session 5

Comparison of multi-fiber reproducibility of PAS-MRI and Q-ball with empirical multiple b-value HARDI

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Crossing fibers are prevalent in human brains and a subject of intense interest for neuroscience. Diffusion tensor imaging (DTI) can resolve tissue orientation but is blind to these crossing fibers. Many advanced diffusion-weighted magnetic resolution imaging (MRI) approaches have been presented to extract crossing-fibers from high angular resolution diffusion imaging (HARDI), but the relative sensitivity and specificity of approaches remains unclear. Here, we examine two leading approaches (PAS and Q-ball) in the context of a large-scale, single subject reproducibility study. A single healthy individual was scanned 11 times with 96 diffusion weighted directions and 10 reference volumes for each of five b-values (1000, 1500, 2000, 2500, 3000 s/mm2) for a total of 5830 volumes (over the course of 3 sessions). We examined the reproducibility of the number of fibers per voxel, volume fraction, and cross-fiber angles. For each method, we determined the minimum resolvable angle for each acquisition. Reproducibility of fiber counts per voxel was generally high (~80% consensus for PAS and ~70% for Q-ball), but there was substantial bias between individual repetitions and model estimated with all data (~10% lower consensus for PAS and ~15% lower for q-ball). Both PAS and Q-ball predominantly discovered fibers crossing at near 90 degrees, but reproducibility was higher for PAS across most measures. Within voxels with low anisotropy, q-ball finds more intra-voxel structure; meanwhile, PAS resolves multiple fibers at greater than 75 degrees for more voxels. These results can inform researchers when deciding between HARDI approaches or interpreting findings across studies.

10133-22, Session 5

Identifying HIV associated neurocognitive disorder using large-scale Granger causality analysis on resting-state functional MRI

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We investigate the applicability of large-scale Granger Causality (lsGC) for extracting a measure of multivariate information flow between pairs of regional brain activities from resting-state functional MRI (fMRI) and test the effectiveness of these measures for predicting a disease state. Such pairwise multivariate measures of interaction provide high-dimensional representations of connectivity profiles for each subject and are used in a machine learning task to distinguish between healthy controls and

individuals presenting with symptoms of HIV Associated Neurocognitive Disorder (HAND). Cognitive impairment in several domains can occur as a result of HIV infection of the central nervous system. The current paradigm for assessing such impairment is through neuropsychological testing. With fMRI data analysis, we aim at non-invasively capturing differences in brain connectivity patterns between healthy subjects and subjects presenting with symptoms of HAND. To classify the extracted interaction patterns among brain regions, we use a prototype-based learning algorithm called Generalized Matrix Learning Vector Quantization (GMLVQ). Our approach to characterize connectivity using lsGC followed by GMLVQ for subsequent classification yields good prediction results with an accuracy of 87% and an area under the ROC curve (AUC) of up to 0.90. We obtain a statistically significant improvement (p<0.01) over a conventional Granger causality approach (accuracy = 0.76, AUC = 0.74). High accuracy and AUC values using our multivariate method to connectivity analysis suggests that our approach is able to better capture changes in interaction patterns between different brain regions when compared to conventional Granger causality analysis known from the literature.

10133-23, Session 5

Effects of b-value and number of gradient directions on diffusion MRI measures obtained with Q-ball imaging

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High-angular-resolution diffusion-weighted imaging (HARDI) MRI acquisitions have become common for use with higher order models of diffusion. Despite successes in resolving complex fiber configurations and probing microstructural properties of brain tissue, there is no common consensus on the optimal b-value and number of diffusion directions to use for these HARDI methods. While this question has been addressed by analysis of the diffusion- weighted signal directly, it is unclear how this translates to the information and metrics derived from the HARDI models themselves. Using a high angular resolution data set acquired at a range of b-values, and repeated 11 times on a single subject, we study how the b-value and number of diffusion directions impacts the reproducibility and precision of metrics derived from Q-ball imaging, a popular HARDI technique. We find that Q-ball metrics associated with tissue microstructure and white matter fiber orientation are sensitive to both the number of diffusion directions and the spherical harmonic representation of the Q-ball, and often are biased when under sampled. These results can advise researchers on appropriate acquisition and processing schemes, particularly when it comes to optimizing the number of diffusion directions needed for metrics derived from Q-ball imaging.

1. INTRODUCTION

Diffusion tensor imaging (DTI) is arguably the most commonly used diffusion-weighted magnetic resonance imaging (dMRI) technique due to its simplicity and its ability to provide unique insights into tissue microstructure [1]. These insights include metrics that have been associated with white matter integrity as well as estimates of dominant white matter directions, which enable fiber tractography [2]. However, DTI only models a single diffusion direction per voxel, and is inadequate in areas that contain multiple fiber populations, often resulting in incorrect estimates of fiber orientation or misleading microstructural indices. The “crossing fiber” problem has been shown to be prevalent in dMRI datasets, affecting as much as 90% of all voxels in the brain [3]. To address this issue, a variety of higher order diffusion models have been introduced. These methods are generally referred to as high-angular-resolution diffusion-weighted imaging (HARDI), a term which encompasses nearly all acquisition and analysis pipelines that provide more information than the diffusion tensor – but most commonly indicating the acquisition of a large number of diffusion weighted images (DWIs) sensitized to diffusion along varying directions all acquired at the same b-value, or diffusion weighting (DW).

Despite the rapidly growing popularity of HARDI techniques, there is currently no fixed consensus on the optimal b- value for these methods, or on the appropriate number of diffusion directions for these methods. Early DTI studies addressed the optimal b-value and diffusion direction schemes by acquiring multiple repeats of unique acquisition schemes, and assessed the impact on the precision and accuracy of orientation estimates and microstructural indices [4]. However, similar studies have not been performed on HARDI models, in part due to the tremendous acquisition requirements needed for this type of analysis. Thus, most knowledge of appropriate acquisition requirements comes from simulations and phantom data [5].

Rather than analyze a specific HARDI model, Tournier et al. have addressed this question of sampling directions by analyzing the frequency content of the DW signal itself, fit to spherical harmonics (SH) [6]. They concluded that the angular profile of the DW signal at a b-value of 1000 s/mm2 could be captured with order 4 SH, requiring only 15 unique sampling directions. Similarly, b-values up to 3000 s/mm2 require only 28 unique directions (6 SH) to capture the necessary information. However, these numbers represent lower bounds, much like the diffusion tensor only requires 6 measurements, but in practice up to 30 are typically acquired. Thus, it remains to be seen how many sampling directions, and what b-value, are needed for HARDI models in practice.

In this study, we focus on one common HARDI model called Q-Ball imaging, or just Q-ball [7]. By acquiring 11 repeats of a high-angular-resolution dataset, we probe the precision and accuracy of estimating various Q-ball metrics as a function the number of sampling directions. Specifically, we use Q-ball to derive the diffusion orientation distribution function (dODF), from which we derived reproducibility measures of fractional anisotropy (FA), generalized fractional anisotropy (GFA). We then extract peaks of the dODF in order to assess the reproducibility of the orientations and strengths of the peaks, the Hessian of each peak (which describes its curvature), as well as the number of detected fiber populations (or peaks) in each voxel. Finally, we assess the angular correlation coefficient (ACC) of the dODFs between each individual dataset and the dataset acquired with the full complement of diffusion directions. This work has not been previously published in any format.

2. METHODS

2.1 MRI acquisition

All imaging was performed on the same healthy volunteer scanned on a 3T Phillips Achieva Scanner (Philips Medical Systems, Best, The Netherlands), in three different two-hour long sessions, on three consecutive days. The scanning protocol consisted of five diffusion shells (b-values of 1000, 1500, 2000, 2500, and 3000 s/mm2) with 96 diffusion- weighted directions each, plus five repeats of the non-DW (b0) volume, which were formed by 10 scanner averages. The data was acquired at 2.5mm isotropic resolution using DW PGSE-EPI sequence (TR=2.65s, TE=101ms). Each shell was preceded by a reverse phase-encoded b0 image. This protocol was repeated four times on days 1 and 2, and three times on day 3, resulting in a total of 11 repeats of each diffusion shell.

2.2 Q-ball processing

All volumes were corrected for movement, susceptibility induced distortions, and eddy currents using FSL’s topup and eddy [8, 9]. All data was registered to a common space using a 6 degrees-of-freedom rigid registration to facilitate a voxel-wise comparison, followed by appropriate re-orientation of diffusion gradient vectors. The full 96 gradient directions were re-ordered to minimize the electrostatic potential of any partial set of the first “N” directions, ensuring that the first “N” directions are as maximally uniformly distributed. From this, for each diffusion shell, subsets of DWIs from 20 to 96 directions (in increments of 4) were created and analyzed with the Q-ball model using UCL’s Camino Diffusion MRI Toolkit [10]. This results in an approximation of the dODF (represented using SH coefficients), from which various microstructural and fiber orientation metrics are derived. It is important to note that the Q-ball is derived using the highest order SH coefficients possible (up to order 8) given the number of sampling points (i.e. < 28 directions = SH order 4; 28-44 directions = SH order 6; > 44 directions = SH order 8).

2.3 Metrics and analysis

For every diffusion shell (11 repeats of each of 5 b-values), and all subsets of directions within each shell, various metrics were derived, and compared directly to the corresponding full 96-direction dataset as a gold standard. First, FA was calculated using the DTI model, while GFA was calculated directly from the Q-ball SH coefficients. Next, local maxima, or peaks, in the dODF were detected following Jansons and Alexander [5]. From each peak, one can first determine its curvature (or sharpness) using the trace of the hessian. Because each peak is traditionally assumed to represent a distinct population of fiber bundles, the fiber fraction of each peak can be calculated (in this study DFF represents the dominant fiber fraction) and the number of fiber bundles (peaks) per voxel. The ability of each subset to detect crossing fiber voxels can be described by the consistency fraction (CF). A voxel is consistent with the gold standard if it has the same number of peaks and each peak is within a small angular tolerance of those in the gold standard. The CF is then the fraction of voxels that are consistent with the 96-direction dataset. Finally, the ACC, a measure that describes agreement between spherical functions, is calculated for all voxels in each subsampled dataset.

3. RESULTS

Figure 1 shows Q-ball glyphs in an area containing both single and crossing fiber voxels. Qualitatively, they glyphs seem to share the same basic shape and orientations across all b-values and for all diffusion-weighting schemes. Many glyphs appear more sharp or “spiky” at higher b-values, while very little change is noticeable with changing number of gradient directions.

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The average percent deviation from the gold-standard datasets for FA and GFA are shown in Figure 2 (A, B). The percent deviation of FA (Fig 2. A) is monotonically decreasing, and is less than 10% for all b-values after 30 directions. The higher b-values show a consistently higher positive bias than low b-value acquisitions. Unlike FA, the GFA (Fig 2. B) shows very high positive biases at transitions zones that occur when the data first allows the next higher order SH coefficients to be estimated. However, bias decreases as the number of DWIs increases.

Next, the effect of gradient directions on the bias and accuracy of DFF and TH were assessed (Fig 2. C, D). At low DW directions, the DFF is overestimated at all b-values. This is likely due to the inability to resolve multiple fibers, resulting in a DFF of 1 for most voxels. However, at SH of order 6 and 8, the DFF is consistently underestimated, and shows high deviations at the transition zones. Similarly, the deviation of the TH peaks is high at the 28 and 48 (first dataset > 45) direction sets. As the number of DWI’s increases, the peaks sharpness gradually decreases towards the gold-standard TH.

An analysis of the ACC shows that nearly all directions (besides N=28 and N=48) have similar Q-ball SH representations as that of the N=96 dataset, with the average ACC typically 0.8 or higher across the entire brain. Qualitatively, the WM dODF profiles agree very well with the gold standard, even at very low gradient directions (Fig2. H).

4. DISCUSSION AND CONCLUSION

In this study, the aim was to determine the appropriate number of DW-directions for robust estimates of measures derived from Q-ball imaging. What is clear from the data is that the variance and precision of many parameters is dependent on not only the number of directions sampled, but also on the reconstruction scheme, specifically the SH order that the data was fit to. Tournier et al. determine that 8th order SH are high enough to capture the angular profile of the DW signal, which implies that as low as 45 sampling directions is sufficient for all HARDI analysis, although the authors recommend acquisition of more to increase the effective SNR [6]. Here, we find that fitting to just 45 coefficients (or to 28 for SH order 6) leads to noisy and inaccurate estimates of a variety of measures.

Due to fitting the data exactly, the dODFs are noisy at these measurements, overestimate the number of fiber populations in each voxel, and have erroneous peaks. Even more concerning, the fraction of fibers containing crossing fibers did not plateau, suggesting that either (A) even 96 directions is not enough to correctly identify all fiber crossings, or (B) the Q- ball model may break down with a large number of measurements, effectively “blurring” any identifiable peaks or crossings. It is also interesting to note that we did not find significant differences in any measures across b-values.

Based on this work, we suggest collecting significantly more than the minimum 45 measurements to fit to 8th order SH. It remains to be seen how a 6th order fit to the larger datasets (N>45) compares to the 8th order, and if the accuracy is of a comparable scale. Finally, similar analysis should be performed on a range of HARDI models, to not only optimize acquisitions based on clinical or research needs, but also to determine the limitations of varying HARDI models and suggest future refinements.

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10133-24, Session 5

Subparcellation of cortical ROIs based on resting state fMRI

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Resting state fMRI (rsfMRI) provides complementary information to the sulcal brain anatomy about the cytoarchitecture and function of the human brain and therefore parcellation based on rsfMRI is becoming increasingly popular. In this paper, we present a method for subparcellation of a given anatomical ROI of the cortex based on rsfMRI time series. First, a distance metric between a given pair of time series based on correlation is defined and then used to define a distance matrix between every pair of points in the ROI. Using the distance matrix, a spectral clustering of the ROI is performed. The number of clusters is determined based on Silhouette score. Additionally, to check the consistency of this parcellation across subjects, the parcellation was repeated for 40 subjects from tNLM filtered HCP dataset and intensity modulated map of the clustering results was plotted. The results for precuneus and cingulate show a remarkable consistency across subjects and an interesting differentiation between the connectivity patterns for the different subdivisions found. The Silhouette plots for different number of ROIs is also shown. An extension of this study to generate a finer subparcellation of the cortex based on anatomy and function is planned.

10133-25, Session 5

White matter fiber-based analysis of T1w/T2w ratio map

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Purpose: To develop, test, evaluate and apply a novel tool for the diffusion fiber-based analysis of T1w/T2w ratio maps quantifying myelin content. Background: The cerebral white matter in the human brain develops from a mostly non-myelinated state to a nearly fully mature white matter myelination within the first few years of life. The study of myelination is of interests in a number of brain development studies. High resolution T1w/T2w ratio maps are believed to be effective in quantitatively estimating myelin content on a voxel-wise basis. We propose the use of a fiber-tract-based analysis of such T1w/T2w ratio data, as it allows us to separate fiber bundles that regional analysis imprecisely groups together, and to associate effects to specific tracts rather than large, broad regions. Methods: We developed an intuitive tool to facilitate such fiber-based studies of T1w/T2w ratio maps. Via its Graphical User Interface (GUI) the tool is accessible to non-technical users. The framework uses calibrated T1w/T2w ratio maps and a prior fiber atlas as an input to generate profiles of T1w/T2w values using a version of the UNC atlas-based fiber analysis toolkit that we adapted to handle non-diffusion data. The resulting fiber profiles are used in a statistical analysis that performs along-tract functional statistical analysis. We applied this approach to a study of early brain development in neonates. Results: We implemented a publicly available tool for the fiber based analysis of T1w/T2w ratio maps and tested it in a study of brain development.

10133-26, Session 6

Rapid perfusion quantification using Welch-Satterthwaite approximation and analytical Spectral Filtering

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CT/MR perfusion enable quantification of perfusion parameters in stroke studies. These parameters are calculated from the residual impulse response function (IRF) based on physiological model for tissue perfusion. The standard approach for estimating the IRF is deconvolution using oscillatory-limited singular value decomposition (oSVD) and frequency domain deconvolution (FDD). FDD is widely recognized as the fastest approach currently available for deconvolution of perfusion data and was introduced as a Real Time Analysis method in the DEFUSE2 and EXTEND trials. In this work, three faster methods are proposed. The first is a direct (model based) approximation to the final perfusion quantities (Blood flow, Blood volume, Mean Transit Time and Delay) using the Welch-Satterthwaite approximation for gamma fitted concentration time curves (CTC). The second is a fast deconvolution method, we call Analytical Fourier Filtering. The third is another fast deconvolution technique using Showalter's method, we call Analytical Showalter Spectral Filtering. Through systematic evaluation on phantom and clinical data, we show that the proposed methods are computationally faster (2.3 to 8 times) and quantitatively accurate compared to FDD and oSVD. For a CTC of length L, FDD requires one forward Discrete Fourier Transform (DFT), one linear filtering and one inverse DFT, and therefore has a computational complexity O(L log(L)). The bcoSVD is slower and has an approximate complexity of O(L^3). By contrast, AFF and Showalter require just one circular convolution of length L. GvWS requires a few multiplications/exponentiations, regardless of the length of the signal, but assumes the CTC's have been gamma fitted.

10133-27, Session 6

Classification of coronary artery calcifications according to motion artifacts in chest CT using a convolutional neural network

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Coronary artery calcification (CAC) is a strong and independent predictor of cardiovascular events (CVEs). CAC can be quantified in chest CT scans acquired in lung screening. However, in these images the reproducibility of CAC quantification is compromised by cardiac motion artifacts that occur during scanning, which limits the reproducibility of CVE risk assessment.

We present a system for detection of severe cardiac motion artifacts affecting CACs by using a convolutional neural network (CNN).

This study included 125 chest CT scans from the National Lung Screening Trial (NLST). The images were acquired with CT scanners from four major CT scanner vendors (GE, Siemens, Philips, Toshiba) with varying tube voltage and slice thickness settings, and without ECG synchronization. An observer manually identified CAC lesions and labelled each CAC according to presence of cardiac motion (strongly affected, not affected).

A CNN was designed to automatically label the identified CAC lesions according to the presence of cardiac motion by analyzing a patch from the axial CT slice around each CAC lesion.

From 125 CT scans, 9201 CAC lesions were analyzed. 8001 lesions were used for training (19% positive) and the remaining 1200 (50% positive) were used for testing. The CNN achieved a classification accuracy of 85% (86% sensitivity, 84% specificity).

The proposed algorithm can identify CAC lesions that are strongly affected by motion. This enables further investigation into the relation of CAC scoring reproducibility and presence of cardiac motion artifacts.

10133-28, Session 6

Automatic quality assessment of apical four-chamber echocardiograms using deep convolutional neural networks

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Echocardiography (echo) is a skilled technical procedure and the quality of the acquired cine depends on the experience of the operator. In many cases, the operator is not experienced enough to examine the acquired echo to adjust the transducer accordingly; therefore, she ends up with suboptimal images which may further affect the clinical diagnosis. In this work, we aim to aid the operator during image acquisition by automatically assessing

the quality of the echo and generating the Echo Quality Score (EQS). This system is based on a deep convolutional neural network, trained in an end-to-end fashion on a large dataset of apical four-chamber (A4C) echo images. For this project, an expert cardiologist went through 3,000 A4C images obtained from independent studies and assessed their condition based on a 6-scale grading system. The scores assigned by the expert ranged between 0 (not acceptable) and 5 (excellent). The distribution of data among the 6 levels was almost uniform. The network was then trained on 80% of the data (2,500 samples). The average absolute error of the trained model in calculating the EQS was 0.87 The computation time of the network was 5 milliseconds per image, sufficient for real-time deployment. The proposed approach makes no assumptions about the A4C echo and can be generalized to other standard echo views.

10133-29, Session 6

Automatic localization of cochlear implant electrodes in CTs with a limited intensity range

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Cochlear implants (CIs) are neural prosthetics for treating severe-to-profound hearing loss. Our group has developed an image-guided cochlear implant programming (IGCIP) system that uses image analysis techniques to recommend patient-specific CI processor settings to improve hearing outcomes. One crucial step in IGCIP is the localization of CI electrodes in post-implantation CTs. Manual localization of electrodes requires time and expertise. To automate this process, our group has proposed automatic techniques that have been validated on CTs acquired with scanners that produce images with a full range of intensity values. However, there are clinical CTs acquired with many scanners that have a limited intensity range, in which the intensity values above a threshold are mapped to the same maximum value. This limitation complicates the electrode localization process. In this work, we present a pre-processing step for CTs with a limited intensity range and show that the methods we proposed for full intensity range CTs can be successfully extended to limited intensity range CTs. We evaluate our method on CTs of 20 subjects implanted with CI arrays produced by different manufacturers. Our method achieves a mean localization error as 0.21 mm. This indicates our method is robust for automatic localization of CI electrodes in different types of CTs, which represents a crucial step for translating IGCIP from research laboratory to clinical use.

10133-30, Session 6

Fully automated lobe-based airway taper index calculation in a low dose MDCT CF study over 4 time-points

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Cystic Fibrosis (CF) results in severe bronchiectasis in nearly all cases.

Bronchiectasis is a disease where parts of the airways are permanently dilated.

The development and the progression of bronchiectasis is not evenly distributed over the entire lungs -- rather, individual functional units are affected differently.

Accurate lobe-based detection and monitoring of the course of bronchiectasis is needed for individualized treatment, particularly in the initial stage of the disease.

We developed a fully automated method for the precise calculation of lobe-based airway taper indices (ATI).

To calculate ATI, some preparatory algorithms are needed.

The airway tree is segmented, skeletonized and transformed to a rooted acyclic graph.

This graph is used to label the airways.

Then a modified version of the previously validated integral based method (IBM) for airway geometry determination is utilized.

The rooted graph and the airway lumen information is then used to calculate ATI.

The new method was applied to 144 volumetric inspiratory low-dose MDCT scans.

The scans were acquired from 36 children with mild CF at 4 time-points (baseline, 3 month, 1 year, 2 years).

ATI was able to identify enlarged airway parts in the segmented airway trees.

The index has the potential to be a precise imaging biomarker for the early detection of CF or non-CF bronchiectasis.

In combination with other imaging biomarkers, ATI can be an important tool for monitoring the progression and the individual treatment of patients with bronchiectasis.

10133-31, Session 6

Segmentation and feature extraction of retinal vascular morphology

Henry Leopold, John S. Zelek, Vasudevan Lakshminarayanan, Jeffery J. Orchard, Univ. of Waterloo (Canada)

Analysis of retinal fundus images is essential for physicians, optometrists and ophthalmologists in the diagnosis, care and treatment of patients. The first step of almost all forms of automated fundus analysis begins with the segmentation and subtraction of the retinal vasculature, while analysis of that same structure can aid in the diagnosis of certain retinal and cardiovascular conditions, such as diabetes or stroke. This paper investigates the use of a Convolutional Neural Network as a multi-channel classifier of retinal vessels using DRIVE, a database of fundus images. The result of the network without post-processing was slightly below the 2nd observer and gold standard, with an accuracy of 0.9419, sensitivity of 0.6823 and specificity of 0.9801.

10133-32, Session 7

An octree based approach to multi-grid B-spline registration

Pingge Jiang, James A. Shackleford, Drexel Univ. (United States)

In this paper, we propose a new strategy for the recovery of complex anatomical deformations that exhibit local discontinuities, such as the shearing found at the lung rib cage interface, using multi-grid octree B-splines. This technique efficiently captures deformations within and at organ boundaries without the need for prior segmentation. Experimental results show that the proposed method achieves more plausible deformations than traditional global B-spline methods.

10133-33, Session 7

Nonrigid registration of 3D longitudinal optical coherence tomography volumes with choroidal neovascularization

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In this paper, we propose a 3D registration method for retinal 3D optical coherence tomography volumes. The proposed method consists of five main steps: First, a projection image of the 3D OCT scan is created. Second, the vessel enhancement filter is applied on the projection image to detect vessel shadow. Third, landmark points are extracted based on both vessel positions and layer information. Fourth, the Coherent Point Drift method is used to align retinal OCT volumes. Finally, a nonrigid B-spline-based registration method is applied to find the optimal transform to match the data. We have applied this registration method on 15 3D OCT scans of patients with Choroidal Neovascularization (CNV). The Dice coefficients (DSC) between layers are greatly improved after applying the nonrigid registration.

10133-34, Session 7

Active registration models

Kasper Marstal, Stefan Klein, Erasmus MC (Netherlands)

We present the Active Registration Model (ARM), a generalization of Active Shape Models (ASMs) and Active Appearance Models (AAMs) that couples image registration with matching of statistical appearance models. The models are embedded in the image registration procedure as similarity metrics that penalizes differences between a target image and a synthesized model reconstruction of that image. This approach addresses three key limitations of ASMs and AAMs, namely generalization to arbitrary transformation models, generalization to higher-dimensional images (3D, 4D), and the ability to take advantage of optimization methods typically employed in the field medical image registration. We demonstrate the appearance-based metric on Magnetic Resonance (MR) images of human brains.

10133-35, Session 7

Evaluation of non-rigid registration parameters for atlas-based segmentation of CT images of human cochlea

Mai Elfarnawany, S. Riyahi Alam, Sumit K. Agrawal, Hanif M. Ladak, Western Univ. (Canada)

Cochlear implant surgery is a hearing restoration procedure for patients with profound hearing loss. In this surgery, an electrode is inserted into the cochlea to stimulate the auditory nerve and restore the patient's hearing. Clinical computed tomography (CT) images are used for planning and evaluation of electrode placement, but their low resolution limits the visualization of internal cochlear structures. Therefore, high resolution micro-CT images are used to develop atlas-based segmentation methods to extract these nonvisible anatomical features in clinical CT images. Accurate registration of the high and low resolution CT images is a prerequisite for reliable atlas-based segmentation. In this study, we evaluate and compare different non-rigid B-spline registration parameters using micro-CT and clinical CT images of five cadaveric human cochleae. The varying registration parameters are cost function [normalized correlation (NC), mutual information (MI) and mean square error (MSE)], interpolation method (linear, windowed-sinc and B-spline) and initialization transform mode (none, moments and geometry). We compare the registration results visually and quantitatively using the Dice similarity coefficient (DSC), Hausdorff distance (HD) and absolute percentage error in cochlear volume. Using MI or MSE cost functions and linear or windowed-sinc interpolation resulted in visually undesirable deformation of internal cochlear structures. Quantitatively, the transform initialization using moments yielded the highest DSC and smallest HD and volume error. Therefore, B-spline registration with cost function: NC, interpolation: B-spline and initialization: moments can be the foundation of developing an optimized atlas-based segmentation algorithm of intracochlear structures in clinical CT images.

10133-36, Session 7

ACIR: automatic cochlea image registration

Ibraheem Al-Dhamari, Sabine Bauer, Dietrich W. Paulus, Univ. Koblenz-Landau (Germany); Fredirich Lesseck M.D., Roland Jacob M.D., Central Military Hospital, Koblenz (Germany)

Efficient Cochlear Implant (CI) surgery requires prior knowledge of the cochlea's size and its characteristics. This information helps to select suitable implants for different patients. To get these measurements, a segmentation method of cochlea medical images is needed. An important pre-processing step for good cochlea segmentation involves efficient image registration. The cochlea's small size and complex structure, in addition to the different resolutions and head positions during imaging, reveals a big challenge for the automated registration of the different image modalities. In this paper, an Automatic Cochlea Image Registration (ACIR) method for multi-modal human cochlea images is proposed. This method is based on using small areas that have clear structures from both input images instead of registering the complete image. It uses the Adaptive Stochastic Gradient Descent Optimizer (ASGD) and Mattes's Mutual Information metric (MMI) to estimate 3D rigid transform parameters. The use of state of the art medical image registration optimizers published over the last two years are studied and compared, visually using 3 experts and quantitatively using the standard Dice Similarity Coefficient (DSC). ACIR requires only 4.86 seconds on average to align cochlea images automatically and put all the modalities in the same spatial locations without human interference. The source code is based on the tool elastix and is provided for free as a 3D Slicer plugin. Another contribution of this work is a proposed public cochlea standard dataset which can be downloaded for free from a public XNAT server.

10133-37, Session 7

Whole-body diffusion-weighted MR image stitching and alignment to anatomical MRI

Jakub Ceranka, Mathias Polfliet, Vrije Univ. Brussel (Belgium); Frederic Lecouvet, Nicolas Michoux, Cliniques Univ. Saint-Luc (Belgium); Jef Vandemeulebroucke, Vrije Univ. Brussel (Belgium)

Whole-body diffusion-weighted (WB-DW) MRI in combination with anatomical MRI has shown a great potential in bone and soft tissue tumour detection, evaluation of lymph nodes and treatment response assessment. Because of the vast body coverage, whole-body MRI is acquired in separate stations, which are subsequently combined into a whole-body image. However, inter-station and inter-modality image misalignments can occur due to image distortions and patient motion during acquisition, which may lead to inaccurate representations of patient anatomy and hinder visual assessment. Automated and accurate whole-body image formation and alignment of the multi-modal MRI images is therefore crucial. We investigated several registration approaches for the formation or stitching of the whole-body image stations, followed by a deformable alignment of the multi-modality whole-body images. We compared a pairwise approach, where diffusion-weighted (DW) image stations were sequentially aligned to a reference station (pelvis), to a groupwise approach, where all

stations were simultaneously mapped to a common reference space while minimizing the overall transformation. For each, a choice of input images and corresponding metrics was investigated. Performance was evaluated by assessing the quality of the obtained whole-body images, and by verifying the accuracy of the alignment with whole-body anatomical sequences. We found that the groupwise registration approach resulted in higher image quality for the formation of WB-DW images, and led to a higher registration accuracy with anatomical MRI. The fully automated method was found to be robust, making its use in the clinic feasible.

10133-38, Session 7

A novel model-based evolutionary algorithm for multi-objective deformable image registration with content mismatch and large deformations: benchmarking efficiency and quality

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Taking a multi-objective optimization approach to deformable image registration has recently gained attention, because such an approach removes the requirement of manually tuning the weights of all the involved objectives. Especially for problems that require large complex deformations, this is a non-trivial task. From the resulting Pareto set of solutions one can then much more insightfully select a registration outcome that is most suitable for the problem at hand. To serve as an internal optimization engine, currently used multi-objective algorithms are competent, but rather inefficient. In this paper we largely improve upon this by introducing a multi-objective real-valued adaptation of the recently introduced Gene-pool Optimal Mixing Evolutionary Algorithm (GOMEA) for discrete optimization. In this work, GOMEA is tailored specifically to the problem of deformable image registration to obtain substantially improved efficiency. This improvement is achieved by exploiting a key strength of GOMEA: iteratively improving small parts of solutions, exploiting faster, partial evaluations of the impact of such updates on the objectives at hand. We performed experiments on three registration problems. In particular, an artificial problem containing a disappearing structure, a pair of pre- and post-operative breast CT scans and a pair of breast MRI scans acquired in prone and supine position were considered. Results show that compared to the previously used evolutionary algorithm, GOMEA obtains a speed-up of up to a factor of ~1600 on the tested registration problems while achieving registration outcomes of similar quality.

10133-13, Session PS1

AWM: Adaptive Weight Matting for medical image segmentation

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Image matting is a method that separates foreground and background objects in an image, and has been widely used in medical image segmentation. Previous work has proven that matting can be formulated as a graph Laplacian matrix. In this paper, we derive matting from a local regression and global alignment view which has a clearer physical meaning compared to conventional matting method. In addition, we improve the matting by weight extension and call the proposed approach Adaptive Weight Matting (AWM), where an adaptive weight is added to each local regression term to reduce the bias of outliers. We compared the proposed method and several state-of-the-art segmentation methods, including conventional matting, graph-cuts and random walker, on medical images from different organs and different modalities. Experimental results demonstrated the advantages of AWM on medical image segmentation.

10133-59, Session PS1

Laplacian eigenmaps for multimodal groupwise image registration

Mathias Polfliet, Vrije Univ. Brussel (Belgium) and iMinds (Belgium) and Erasmus MC (Netherlands); Stefan Klein, Erasmus MC (Netherlands); Wiro J. Niessen, Erasmus MC (Netherlands) and Technische Univ. Delft (Netherlands); Jef Vandemeulebroucke, Vrije Univ. Brussel (Belgium) and iMinds (Belgium)

Groupwise registration has been of growing interest to the image processing community due to developments in scanner technologies (e.g. multiparametric MRI, DCE-CT or PET-MR) that increased both the number of modalities and number of images under consideration. In this work a novel groupwise registration methodology is presented that is based on Laplacian eigenmaps, a nonlinear dimensionality reduction technique. Compared to recently proposed dissimilarity metrics based on principal component analysis, the proposed metric should enable a better capture of the intensity relationships between different images in the group. The metric is constructed to be the second smallest eigenvalue from the eigenvector problem defined in Laplacian eigenmaps. The method was validated in three distinct experiments: a non-linear synthetic registration experiment, the registration of quantitative MRI data of the carotid artery and the registration of multimodal data of the brain (RIRE). The results show increased accuracy and robustness compared to other state-of-the-art groupwise registration methodologies.

10133-60, Session PS1

Using flow feature to extract pulsatile blood flow from 4D flow MRI images

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Problem: 4D flow MRI images make it possible to retrieve pulsatile blood flow inside deforming vessel walls, which is critical in accurate blood flow visualization, simulation, and evaluation. Such data has great potential to overcome problems in existing work, which usually does not reflect the dynamic nature of elastic vessels and blood flows in cardiac cycles. However, the 4D flow MRI imaging suffers long scanning time and its data is often low-resolution with strong noise. Due to these challenges, few efforts have been successfully conducted to extract dynamic blood flow fields and deforming vessels over cardiac cycles, especially for smaller arteries like carotid.

Method: we use a reliable and robust fluid mechanical attribute, the mean flow intensity, to segment blood flow regions inside vessels from 4D flow MRI images. The approach has solid foundation based on turbulent fluid mechanics to handle noisy image data. The extracted boundaries at different time steps then reconstruct high quality deforming vessel walls and extract pulsatile blood flows in a cardiac cycle.

Result: the computational method is applied to the clinical 4D flow MRI data of a patient's neck area. Dynamic vessel walls and blood flows are effectively

generated in a cardiac cycle in the relatively small carotid arteries. Good image segmentation results on 2D slices are presented, together with the visualization of 3D vessels and blood flows. Evaluation of the method was performed by clinical doctors.

10133-61, Session PS1

Super-resolution convolutional neural network for the improvement of the image quality of magnified images in chest radiographs

Kensuke Umehara, Junko Ota, Naoki Ishimaru, Shunsuke Ohno, Kentaro Okamoto, Takanori Suzuki, Naoki Shirai, Takayuki Ishida, Osaka Univ. (Japan)

Super-resolution (SR) method can generate a high-resolution (HR) image from a low-resolution (LR) image by enhancing spatial resolution and is useful for medical imaging to make an accurate diagnosis. However, it has a limitation of processing speed in clinical application. The super-resolution convolutional neural network (SRCNN) which achieves superior performance and fast speed has been proposed in recent years. In this study, we applied the SRCNN scheme to improve the image quality of magnified images in chest radiographs. For evaluation, 154 chest X-rays were sampled from the JSRT database. We compared the image quality of the SRCNN and the traditional interpolation methods, Nearest neighbor, Bilinear and Bicubic interpolations. For quantitative evaluation, we measured two objective image quality metrics, Peak Signal-to-Noise Ratio (PSNR) for evaluating the image restoration quality and Structural Similarity (SSIM) for assessing the perceptual image quality. In the SRCNN method, PSNR and SSIM were higher than those of three interpolation methods. The differences of PSNR and SSIM between the SRCNN and three interpolation methods were statistically significant ($p<0.001$). Visual evaluation confirmed that the SRCNN yielded much sharper edge than traditional interpolation methods without any obvious artifacts. Our experimental results indicate that the SRCNN method significantly outperformed conventional interpolation methods, and could be a robust approach for clinical application of SR scheme. The use of the SRCNN can yield substantial improvement of the image quality in chest radiographs.

10133-62, Session PS1

Graph search: active appearance model based automated segmentation of retinal layers for optic nerve head centered OCT images

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In this paper, a novel approach that combiningAAM and graph searchwas proposedto segment retinal layers forOptic Nerve Head(ONH) centered Optical coherence tomography(OCT) images.The method includes two parts: preprocessing and layer segmentation. During the preprocessing phase, images was firstly filtered, then theB-scans were flattened. During layer segmentation, the AAM was first used to obtain the coarse segmentation results. Then a multi-resolution GS–AAM algorithm is applied to further refine theresults, in which AAM model was efficiently integrated into the graph search segmentation process. The proposed method was tested on a dataset which contains 11 SD-OCT images.The preliminary results demonstrated the feasibility and efficiency of the proposed method.

10133-63, Session PS1

Fast recovery of compressed multi-contrast magnetic resonance images

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In many cases, multiple Magnetic Resonance Imaging (MRI) scans are performed with different contrast characteristics at a single patient visit. Unfortunately, MRI data-acquisition process is inherently slow and there is a persistent need to accelerate the imaging process.

Multi-contrast MRI deals with the reconstruction of different contrasts simultaneously. Previous approaches suggest solving a regularized optimization problem using group sparsity and/or color total variation, using composite-splitting denoising and FISTA. Yet, there is significant room for improvement in existing methods regarding computation time, ease of parameter selection, and robustness in reconstructed image quality.

Selection of sparsifying transformations is critical in applications of compressed sensing. Here we propose using non-convex p-norm group sparsity (with $p < 1$), and apply color total variation (CTV). Our method is readily applicable to magnitude images rather than each of the real and imaginary parts separately. We use the constrained form of the problem, which allows an easier choice of data-fidelity error-bound (based on noise power determined from a noise-only scan without any RF excitation). We solve the problem using an adaptation of Alternating Direction Method of Multipliers (ADMM), which provides faster convergence in terms of CPU-time. We demonstrated the effectiveness of the method on two MR image sets (numerical brain phantom images and SRI24 atlas data) in terms of CPU-time and image quality. We show that a non-convex group sparsity function that uses the p-norm instead of the convex counterpart accelerates convergence and improves the peak-Signal-to-Noise-Ratio (pSNR), especially for highly undersampled data.

10133-64, Session PS1

Evaluation of the sparse coding super-resolution method for improving image quality of up-sampled images in computed tomography

Junko Ota, Kensuke Umehara, Naoki Ishimaru, Shunsuke Ohno, Kentaro Okamoto, Takanori Suzuki, Naoki Shirai, Takayuki Ishida, Osaka Univ. (Japan)

As the capability of high-resolution displays grows, high-resolution images are required in Computed Tomography (CT), however, acquiring high-resolution images requires a much higher radiation dose and a longer scanning time. In this study, we applied the Sparse Coding Super-Resolution (ScSR) method to generate high-resolution images without increasing the radiation dose. We prepared the over-complete dictionary learned the mapping between low- and high-resolution patches and seek a sparse representation of each patch of the low-resolution input. These coefficients were used to generate the high-resolution output. For evaluation, 44 CT cases were used for the generation of high-resolution output. We up-sampled images up to 2 times and compared the image quality of the ScSR scheme and bilinear and bicubic interpolations, which are the traditional interpolation schemes. We also compared three kinds of learning datasets. A total of 45 CT images, 91 general images, and 93 chest radiographs were used for dictionary preparation respectively. Image noise was evaluated quantitatively by measuring peak signal-to-noise ratio (PSNR). The difference of PSNRs between the ScSR method and bilinear or bicubic method was statistically significant ($p<0.001$, respectively). Conventional interpolation methods generated over-smoothed images, whereas the ScSR method generated a high-resolution image. In terms of optimal training images in CT, CT images were better than general images or chest radiographs as training images for application of the ScSR. These results suggest that the ScSR provides a robust approach for application of up-sampling CT images and yields substantial high image quality of extended images in CT.

10133-65, Session PS1

Motion correction of dynamic contrast enhanced MRI of the liver

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Motion correction of dynamic contrast enhanced MR images is a challenging task. Conventional sequential registration methods lack the ability to achieve temporal smoothness. In this study groupwise registration using a PCA-based dissimilarity metric, which can realize spatial and temporal smoothness, is applied to clinical DCE MRI of the liver. The groupwise registration registers the images in a common space, rather than registering to a reference volume.

The results of the groupwise registration are compared with a sequential approach using a mutual information metric. Clinical DCE MRI of the abdomen of eight patients were used for this study. Per patient one lesion is manually segmented in all the 16 volumes. The comparison is by groupwise Dice similarity coefficient (DSC) of the segmented lesions. Both registrations improve the DSC, but the groupwise approach performs better. The DSC increases from 0.25 for the original images to 0.37 and 0.41 for sequential and groupwise registration respectively.

In a recently started clinical study groupwise registered clinical DCE MRI of the abdomen of nine patients are scored by three radiologists. The results suggested that in case of motion the alignment of the images increases after groupwise registration. A gain in reading time for the radiologist of almost a minute is estimated. A slight increase in reader confidence was observed. Registration has no added value for images with little motion.

The groupwise registration of DCE MR images results in better alignment than achieved by sequential registration, which is beneficial for clinical assessment and further image processing.

10133-66, Session PS1

Supervised local error estimation for nonlinear image registration using convolutional neural networks

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Error estimation in medical image registration is valuable when validating, comparing, or combining registration methods. To validate a nonlinear image registration method, ideally the registration error should be known for the entire image domain. Here we propose a supervised method for the estimation of a registration error map for nonlinear image registration. The method is based on a convolutional neural network that estimates the norm of the residual deformation from patches around each pixel in two registered images. This norm is interpreted as the registration error, which is defined for every pixel in the image domain. The network is trained using a set of artificially deformed images. Each training example is a pair of images: the original image, and a random deformation of that image. Because the true deformation is known, we require no manually labeled ground truth error maps. During test time, only the two registered images are required as input. We train and validate the network on registrations in a set of 2D digital subtraction angiography sequences, such that errors up to eight pixels can be estimated. We show that for this range of errors the convolutional network is able to learn the registration error in pairs of 2D registered images at subpixel precision. Finally, we present a proof-of-principle for the extension to 3D registration problems in chest CTs, showing that the method has the potential to estimate errors in 3D registration problems.

10133-67, Session PS1

Computer aided analysis of prostate histopathology images to support a refined Gleason grading system

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The Gleason grading system used to render prostate cancer diagnosis has recently been updated to allow more accurate grade stratification and higher prognostic discrimination when compared to the traditional grading system. In spite of progress made in trying to standardize the grading process, there still remains approximately a 30% grading discrepancy between the score rendered by general pathologists and those provided by experts while reviewing needle biopsies for Gleason pattern 3 and 4, which accounts for more than 70% of daily prostate tissue slides at most institutions. We propose a new computational imaging method for Gleason pattern 3 and 4 classification, which better matches the newly established prostate cancer grading system. The computer-aided analysis method includes two phases. First, the boundary of each glandular region is automatically segmented using a deep convolutional neural network. Second, color, shape and texture features are extracted from superpixels corresponding to the outer and inner glandular regions and are subsequently forwarded to a random forest classifier to give a gradient score between 3 and 4 for each delineated glandular region. The F1 score for glandular segmentation is 0.85 and the classification accuracy is 0.83.

10133-68, Session PS1

Pseudo CT estimation from MRI using patch-based random forest

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We propose a pseudo CT estimation method from MR images based on patch-based random forest. Patient-specific anatomical features are extracted from the aligned training images and adopted as signatures for each voxel. The most robust and informative features are identified using the feature selection process to train the random forest. The well-trained random forest is used to predict the pseudo CT of a new patient. This prediction technique was tested with human brain images and the prediction accuracy was assessed using the original CT images. Peak signal-to-noise ratio (PSNR) and feature similarity (FSIM) indexes were used to quantify the differences between the pseudo and original CT images. The experimental results showed the proposed method could accurately generate pseudo CT images from MR images. In summary, we have developed a new pseudo CT prediction method based on patch-based random forest, demonstrated its clinical feasibility, and validated its prediction accuracy. This pseudo CT prediction technique could be a useful tool for MRI-based radiation treatment planning and attenuation correction in PET/MRI scanner.

10133-69, Session PS1

Automatic segmentation of left ventricle in cardiac cine MRI images based on deep learning

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To develop novel treatments for cardiovascular diseases, cine MRI has been used widely as a valuable tool for determining properties of global cardiac structure and function, e.g. ventricle dimensions, stroke volume, and ejection fraction. However, accurate assessment of these cardiac characteristics often requires image segmentation of cine MRI data with high precision, which is a laborious task when performed manually. Herein, based on deep learning, a fully automatic framework is proposed for the segmentation of the left ventricle from the imaging slices of short axis cine MRI data. During the training phase of model development, a large set of data was applied by leveraging a public database of human cine MRI scans. To validate the model, experimental cardiac MRI dataset comprising of 900 images from two pig subjects were used. Our data have shown that when comparing the automatic and manual segmentations, the mean slice-wise Dice coefficient is about 0.93 and the mean slice-wise Hausdorff distance is around 4.4 mm, highlighting the accuracy and robustness of the proposed inter-species translational approach.

10133-70, Session PS1

Random walk and graph cut based active contour model for three-dimension interactive pituitary adenoma segmentation from MR images

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Accurate volume measurements are important to the diagnosis and treatment for pituitary adenoma. In this paper we describe an interactive method to segment the pituitary adenoma from brain MR data by combining graph cut based active contour model (GCACM) and random walk (RW) algorithm. In GCACM framework, the segmentation task is formulated as an energy minimization problem by a hybrid active contour model (ACM), and then the energy formulation is discretized and solved numerically by the max-flow/min-cut method. The region-based term in the hybrid ACM considers the local image intensities which are described by Gaussian distributions with different means and variances, expressed as maximum a posteriori probability (MAP). RW is utilized as an initialization tool to provide initialized closed surface for GCACM with two user defined seeds (a foreground seed and a background seed). The proposed method is tested on 23 three-dimension (3-D) T1-weighted (T1W) MR data from 23 patients diagnosed with pituitary adenoma. Compared with the GrowCut method planted in 3D Slicer and a GCACM method which considers global mean intensity in region forces, experimental results show that the proposed method achieves more accurate segmentation of pituitary adenoma than those methods. The average dice similarity coefficients (DSCs) are 81.61%, 70.88% and 88.36%, respectively. The proposed method can provide clinicians with accurate information of the pituitary adenoma to assist diagnose and treatment.

10133-71, Session PS1

Auto-focused panoramic dental tomosynthesis imaging with exponential polynomial based sharpness indicators

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In this paper, we are using the exponential polynomial based sharpness indicator for auto-focused dental panoramic image.

10133-72, Session PS1

Blind deconvolution combined with level set method for correcting cupping artifacts in cone beam CT

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To reduce cupping artifacts and enhance contrast resolution in cone-beam CT (CBCT), in this paper, we introduce a new approach which combines blind deconvolution with a level set method. The proposed method focuses on the reconstructed image without requiring any additional physical equipment, is easily implemented on a single-scan acquisition. The results demonstrate that the algorithm is practical and effective for reducing the cupping artifacts and enhance contrast resolution on the images, preserves the quality of the reconstructed image, and is very robust.

10133-73, Session PS1

3D ultrasound volume reconstruction using global filling mode

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This work proposes a novel method for accurate 3D reconstruction of ultrasound volume from a series of 2D ultrasound acquisitions. First, all pixels in the B-model ultrasound slices are traversed, and the vacant voxels are assigned by their neighboring voxels according to the presupposed distance threshold. The intensity value of the vacant voxel is interpolated by the distance weight of every neighboring voxels. Second, all the vacant regions are counted and separated in the ultrasound volume, for which the assignment weights of all edge voxel of vacant regions are calculated. Then, the best matching patch is optimized by searching the largest weight assignment. The vacant voxels are iteratively assigned by the best matching patches, and the assignment weights of the vacant regions are updated simultaneously. The process continues until there is no vacant voxel. Experimental results demonstrate the effectiveness and robustness of the proposed method for the reconstruction of ultrasound volume.

10133-74, Session PS1

Optimized 3D stitching algorithm for whole body SPECT based on transition error minimization (TEM)

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Standard Single Photon Emission Computed Tomography (SPECT) has a limited field of view (FOV) and cannot provide a 3D image of an entire long whole body SPECT. To produce 3D SPECT with whole body parts, two to five overlapped SPECT FOVs from head to foot are acquired and assembled using image stitching. Most commercial software from medical imaging manufacturers applies a direct mid-slice stitching method to avoid blurring or ghosting from 3D image blending, using either the slices average or weighted cross-fade technique. Direct mid-slice stitching often produces visible seams in coronal and sagittal views and maximal intensity projection (MIP) due to intensity changes across the middle slice of overlapping images. In this study, we proposed an optimized algorithm to reduce visibility of stitching edges. The new algorithm computed a 3D stitching interface between two overlapped 3D SPECT images based on transition error minimization (TEM). Four sets of 2-FOV whole body SPECT studies were used to test the suggested algorithm. They included two different reconstruction methods of filtered back projection (FBP) and ordered subset expectation maximization (OSEM), and two different radiopharmaceuticals of Tc-99m MDP for bone metastases and I-131 MIBG for tumors. Relative transition errors of stitched whole body SPECT using mid-slice stitching and the TEM-based algorithm were measured for objective evaluation. Preliminary experiments show that the new algorithm reduces the visibility of the stitching interface obviously in coronal, sagittal, and MIP views. Average relative transition errors were reduced from 56.7% of mid-slice stitching to 11.7% of TEM-based stitching. The proposed algorithm also avoids blurring artifacts without image blending.

10133-75, Session PS1

Hyperspectral image processing for detection and grading of skin erythema

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No Abstract Available.

10133-76, Session PS1

Multi-contrast MRI registration of carotid arteries based on cross-sectional images and lumen boundaries

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Ischemic stroke has great correlation with carotid atherosclerosis and is mostly caused by vulnerable plaques. It's particularly important to analysis the components of plaques for the detection of vulnerable plaques. Recently plaque analysis based on multi-contrast magnetic resonance imaging technique has attracted great attention. Though multi-contrast MR imaging has potentials in enhanced demonstration of carotid wall, its performance is hampered by the misalignment of different imaging sequences. In this study, a coarse-to-fine registration strategy based on cross-sectional images and wall boundaries is proposed to solve the problem. It includes two steps: a rigid step using the iterative closest points to register the centerlines of carotid artery extracted from multi-contrast MR images, and a non-rigid step using the thin plate spline base on the boundaries of carotid artery. In the rigid step, the centerline was extracted by tracking the cross-sectional images along the vessel direction calculated based on Hessian matrix. In the non-rigid step, a shape context descriptor is introduced to find corresponding points of two similar boundaries. In addition, the deterministic annealing technique is used to find a globally optimized solution. The proposed strategy was evaluated by newly developed three-dimensional, fast and high resolution multi-contrast black blood MR imaging. Quantitative validation indicated that after registration, the overlap of two boundaries from different sequences is 95.24%, and their mean surface distance is 0.12 mm. In conclusion, the proposed algorithm has improved the accuracy of registration effectively for further component analysis of carotid plaques.

10133-77, Session PS1

Automated segmentation of 3D anatomical structures on CT images by using a deep convolutional network based on end-to-end learning approach

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In this paper, we propose an end-to-end learning approach that trains a deep convolutional neural network (CNN) for automatic CT image segmentation that accomplishes a voxel-wised multiple classification to directly map each voxel on 3D CT images to an anatomical label automatically. The novelties of this proposed method are (1) transforming the anatomical structure segmentation on 3D CT images into a majority voting the results of 2D semantic image segmentation on a number of 2D-slices from different image orientations, and (2) using "convolution" and "de-convolution" networks to achieve the traditional "organ localization" and "contour decision" functions which are integrated into a compact all-in-one deep CNN for image segmentation. The advantage comparing to previous works is its capability to accomplish real-time image segmentations on 2D slices of arbitrary CT-scan-range (e.g. body, chest, abdomen) and produce correspondingly-sized output". We applied this approach to train a deep CNN to segment a wide range of anatomical structures that consisted of 19 types of target regions in human torso. A database consisting of 240 3D CT scans and a humanly annotated ground truth was used for training (228 cases) and testing (the remaining 12 cases). The preliminary results showed that the target regions for the entire set of CT test scans were segmented with acceptable accuracies (79% voxels were labeled correctly) against the human annotations. This performance was comparable to other recently reported state-of-the-art results. The experimental results demonstrated the potentials of using a single deep CNN to segment complicated anatomical structures on 3D CT images.

10133-78, Session PS1

Microscopic neural image registration based on the structure of mitochondria

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Microscopic image registration is a key component of the neural structure reconstruction with serial sections of neural tissue. The goal of microscopic neural image registration is to recover the 3D continuity and geometrical properties of specimen. During image registration, various distortions need to be corrected, including image rotation, translation, tissue deformation et.al, which come from the procedure of sample cutting, staining and imaging. Furthermore, there is only certain similarity between adjacent sections, and the degree of similarity depends on local structure of the tissue and the thickness of the sections. These factors make the microscopic neural image registration a challenging problem. To tackle the difficulty of corresponding landmarks extraction, we introduce a novel image registration method for Scanning Electron Microscopy (SEM) images of serial neural tissue sections based on the structure of mitochondria. The ellipsoidal shape of mitochondria ensures that the same mitochondria has similar shape between adjacent sections, and its characteristic of broad distribution in the neural tissue guarantees that landmarks based on the mitochondria distributed widely in the image. The proposed image registration method contains three parts: (1) landmarks extraction through mitochondria segmentation, (2) determining corresponding landmarks, (3) image deformation. We demonstrate the performance of our method with SEM images of drosophila brain.

10133-79, Session PS1

High precision automated face localization in thermal images: oral cancer dataset as test case

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Automated face detection is the pivotal step in computer vision aided facial medical diagnosis and biometrics. This paper presents an automatic, subject adaptive framework for accurate face detection in the long infrared spectrum on our database for oral cancer detection consisting of malignant, precancerous and normal subjects of varied age group. Previous works on oral cancer detection using Digital Infrared Thermal Imaging(DITI) reveals that patients and normal subjects differ significantly in their thermal emissivity signatures. Therefore, it is a challenging task to formulate a completely adaptive framework to veraciously localize face from such a subject specific modality. Our model consists of first extracting the most probable facial regions by minimum error thresholding followed by ingenious adaptive methods to leverage the horizontal and vertical projections of the segmented thermal image. Additionally, the model incorporates our domain knowledge of exploiting temperature difference between strategic locations of the face. To our best knowledge, this is the pioneering work on detecting faces in thermal facial images comprising both patients and normal subjects. Previous works on face detection have not specifically targeted automated medical diagnosis; face bounding box returned by those algorithms are thus loose and not apt for further medical automation. Our algorithm significantly outperforms contemporary face detection algorithms in terms of commonly used metrics for evaluating face detection accuracy. Since our method has been tested on challenging dataset consisting of both patients and normal subjects of diverse age groups, it can be seamlessly adapted in any DITI guided facial healthcare or biometric applications.

10133-80, Session PS1

Segmentation of cortical bone using fast level sets

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Cortical bone plays a big role in the mechanical competence of bone. The analysis of cortical bone requires accurate segmentation methods. Level set methods are state-of-the-art for segmenting medical images. However, traditional implementations of this method are computationally expensive. This drawback was recently tackled through the so-called coherent propagation extension of the classical algorithm which has decreased computation times dramatically. In this study we assess the potential of this technique for segmenting cortical bone in interactive time in images acquired through high resolution peripheral quantitative computed tomography (HR-pQCT). The segmentations are used to estimate cortical thickness and cortical porosity of the investigated specimen. Qualitative comparison between the segmentations of our proposed algorithm and a previously published approach reveals superior smoothness properties of the level set approach. Further, our estimations of cortical thickness and porosity are reasonable as compared to literature. We conclude that it is worthwhile to investigate the influence of the smoothing parameter inherent to the level set approach on these parameters in more detail in the future.

10133-81, Session PS1

View-interpolation of sparsely sampled sinogram using convolutional neural network

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In computed tomography (CT) imaging, various approaches to reducing radiation dose to the patient without image quality degradation are actively investigated. One of such approaches is to sparsely sample the patient projection data. This will reduce the exposure to the patient with possible reduction of scanning time or of motion contamination. Due to insufficient amount of data for analytic image reconstruction, iterative reconstruction methods have been devised such as compressed sensing inspired algorithms. However, the iterative reconstruction algorithms are computationally burdensome and the reconstruction results are often subject to characteristic artifacts such as cartooning and over-smoothing. An alternative way to reconstruct image from the sparsely sampled projection data is to fill in, or interpolate, missing projection data and reconstruct the image by use of the analytic reconstruction algorithms. There are several approaches to interpolating the missing data with their success to varying degrees. In this study, inspired by the recent progresses in deep learning, we developed a convolution neural network method to interpolate the missing projections and compared the reconstruction results with those reconstructed by a conventional linear interpolation based method.

10133-82, Session PS1

Deep learning and shapes similarity for joint segmentation and tracing single neurons in SEM images

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Extracting the structure of single neurons is critical for understanding how they function within the neural circuits. Recent developments in machine learning and the microscopy and the widely recognized need for openness and standardization provide a community resource for automated reconstruction of dendritic and axonal morphology of single neurons. In order to look into the fine structure of neurons, we use the Automated Tape-collecting Ultra Microtome Scanning Electron Microscopy (ATUM-SEM) to get images sequence of serial sections of animal brain tissue that densely packed with neurons. Different from other neuron reconstruction method, we propose a method that enhances the SEM images by detecting the neuronal membranes with deep convolutional neural network (DCNN) and segments single neurons by active contour with group shape similarity. We joint the segmentation and tracing together and they interact with each other by alternate iteration that tracing aids the selection of candidate region patch for active contour segmentation while the segmentation provides the neuron geometrical features which improve the robustness of tracing. The tracing model mainly relies on the neuron geometrical features and is updated after neuron being segmented on the every next section. Our method enables the reconstruction of neurons of the drosophila mushroom body which is sectioned to serial sections and imaged under SEM. Our method provides a primitive step for the whole reconstruction of neuronal networks in the brain tissue.

10133-83, Session PS1

Learning deep similarity in fundus photography

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Similarity learning is one of the most fundamental tasks in image analysis. The ability to extract similar images in the medical domain as part of content-based image retrieval (CBIR) systems has been researched for many years. The vast majority of methods used in CBIR systems are based on hand-crafted feature descriptors; hence, their quality is limited by the human ingenuity. The approximation of a similarity mapping for medical images is difficult due to big variety of pixel-level structures of interest. In fundus photography (FP) analysis, a subtle difference in e.g. lesions and vessels shape and size can result in a different diagnosis. In this work, we demonstrated how to learn a similarity function for image patches derived from FP directly from image data without the need of manually designed feature descriptors. We used a convolutional neural network (CNN) with a novel architecture adapted for similarity learning to accomplish this task. Furthermore, we explored and studied multiple CNN architectures and training scenarios combinations. We show that our method can approximate the similarity between FP patches more efficiently and accurately than state-of-the-art feature descriptors, including SURF and SIFT using publicly available datasets. Finally, we observe that our approach, which is purely data-driven, learns that features such as vessel's calibre and orientation are important discriminative factors, which resembles the way how humans reason about similarity. To the best of authors' knowledge, this is the first attempt to approximate a visual similarity mapping in FP.

10133-84, Session PS1

Cascaded deep decision networks for classification of endoscopic images

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Both traditional and wireless capsule endoscopes can generate tens of thousands of images for each patient. It is desirable to have the majority of irrelevant images filtered out by automatic algorithms during an offline review process or to have automatic indication for highly suspicious areas during an online guidance. This also applies to the newly invented endomicroscopy, where online indication of tumor classification plays a significant role. Image classification is a standard pattern recognition problem and is well studied in the literature. However, performance on the challenging endoscopic images still has room for improvement. In this paper, we present a novel Cascaded Deep Decision Network (CDDN) to improve image classification performance over standard Deep neural network based methods. During the learning phase, CDDN automatically builds a network which discards samples that are classified with high confidence scores by a previously trained network and concentrates only on the challenging samples which would be handled by the subsequent expert {shallow} networks. We validate CDDN using two different types of endoscopic imaging, which includes a polyp classification dataset and a tumor classification dataset. From both datasets we show that CDDN can outperform other methods by about 10%. In addition, CDDN can also be applied to other image classification problems.

10133-85, Session PS1

Personalized design and virtual evaluation of physician-modified stent grafts for juxta-renal abdominal aortic aneurysms

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Background:

Endovascular aneurysm repair (EVAR) of juxtarenal aortic aneurysms (JAA) is particularly challenging owing to the requirement of suprarenal EVAR graft fixation, in contrast with preferred strategy of infrarenal EVAR fixation with a sufficient proximal landing zone below the renals. Both open surgical repair as well as suprarenal fixation EVAR grafts have been reported to be associated with significant declines in long term renal function. Further, even temporary interruption of flow through the suprarenal visceral arteries may cause hepatic or mesenteric ischemia as well as renal dysfunction leading to haemodialysis. Therefore, the ability to design fenestrated EVAR grafts on a personalized basis in order to ensure visceral and renal perfusion, is highly desirable.

Objectives: a) To demonstrate novel 3D geometric methods to virtually design and deploy EVAR grafts into patient-specific models of juxta-renal aortic aneurysms, reconstructed from 3D segmentation of medical images; and b) To virtually evaluate patient-specific renal flow and wall stresses in these patient-specific virtually EVAR geometries.

Methods:

We present a framework to design patient-specific EVAR grafts with personalized fenestration, for JAAs, in virtual and interactive fashion. In this study, we demonstrate this framework in a simulated JAA. An in-house computational geometry environment named Surgery Explorer (QuantMD LLC, Pittsburgh, PA) is employed to parametrically define a diseased aorta with a JAA, starting with a patient-specific computed tomography (CT) image based abdominal aorta reconstruction, by employing an interactive

mesh morphing tool in an infrarenal location < 1.5-cm proximal to the renal branches of the aorta. Next, a patient-specific EVAR stent graft is designed interactively and fit into the parametrically modeled JAA, based on a user-specified suprarenal fixation distance. EVAR graft personalization is conducted in two distinct steps: a) A parametric stent template loop is designed interactively and swept along the patient-specific aortic vascular centerline, starting suprarenal and ending above the illiac bifurcation; and b) The aortic graft diameter is then virtually adjusted in a radially outward direction until it makes contact with the endovascular walls at a supra-renal location and before the illiac bifurcation, and the renal stents are adjusted in diameter using a similar approach based on the expected normal renal arterial diameters, while intersecting the main aortic graft at locations of renal fenestrations to be created on the graft surface, to ensure proper renal perfusion. Finally, computational fluid dynamics (CFD) simulation is conducted in the EVAR-deployed geometry, factoring in precise fenestrations for the renal ostia, under assumptions of Newtonian blood flow (?=0.00319 Pa.s, ?=1050 kg/m3), considering rigid, impermeable walls. Parabolic inlet velocity profiles with peak velocities of 0.12, 0.29 and 0.38 m/s were modeled, for each geometry, and geometry-specific hemodynamics were studied in terms of aortic flow patterns, renal outflow rates, wall shear stress and energy dissipation.

Results & Conclusions:

Preoperative planning, virtual EVAR graft deployment, fenestration design and virtual postoperative hemodynamic simulations can help predict avoidable failures owing to graft malpositioning and guarantee optimal visceral and renal perfusion. The presented framework may provide the modern cardiovascular surgeon the ability to leverage non-invasive, pre-operative imaging equipment to personalize and guide EVAR therapeutic strategy. CFD studies revealed that virtual EVAR grafting with optimal fenestration sites and renal stenting led to a 179.67±15.95% and 1051.43±18.34% improvement in right and left renal flow rates, respectively, when compared with the baseline patient-specific aortic geometry with renal stenoses, whereas a right and left renal flow improved by 36.44±2.24% and 885.93±12.41%, respectively, relative to the equivalently modeled JAA with renal stenoses, considering averages across the three simulated inflow rate cases. The proposed framework may in future be utilized to iteratively optimize suprarenal EVAR fixation length, to achieve normal renal wall shear stress and streamlined juxtarenal hemodynamics.

10133-86, Session PS1

Multi-scale hippocampal parcellation improves atlas-based segmentation accuracy

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Known for its distinct role in memory, the hippocampus is one of the most studied regions of the brain. Recent advances in magnetic resonance imaging have allowed for high-contrast, reproducible imaging of the hippocampus. Typically, a trained rater takes 45 minutes to manually trace the hippocampus and delineate the anterior from the posterior segment at millimeter resolution. As a result, there has been a significant desire for automated and robust segmentation of the hippocampus. In this work, we use a population of 195 atlases based on T1-weighted MR images with the left and right hippocampus delineated into the head and body. We initialize the multi-atlas segmentation to a region directly around each lateralized hippocampus to both speed up and improve the accuracy of registration. This initialization allows for incorporation of nearly 200 atlases, an accomplishment which would typically involve hundreds of hours of computation per target image for whole-brain processing. The proposed segmentation results in a Dice similarity coefficient over 0.9 for the full hippocampus. This result outperforms a multi-atlas segmentation using the BrainCOLOR atlases (Dice 0.85) and FreeSurfer (Dice 0.75). Furthermore, the head and body delineation resulted in a Dice coefficient over 0.87 for both structures. The head and body volume measurements also show high reproducibility on the Kirby 21 reproducibility population (R2 greater than 0.95, p < 0.05 for all structures). This work signifies the first result in an ongoing work to develop a robust tool for measurement of the hippocampus and other temporal lobe structures.

10133-87, Session PS1

Comparison of parametric methods for modeling corneal surfaces

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Corneal topography is a medical imaging technique to get the 3D shape of the cornea as a set of 3D points of its anterior and posterior surfaces. From these data, topographic maps can be derived to assist the ophthalmologist in the diagnosis of disorders. In this paper, we compare three different mathematical parametric representations of the corneal surfaces least-squares fitted to the data provided by corneal topography. The parameters obtained from these models reduce the dimensionality of the data from several thousand 3D points to only a few parameters and could eventually be useful for diagnosis, biometry etc. The first representation is based on Zernike polynomials that are used in optics, and in our case, for modeling the corneal surfaces. A variant of these polynomials, named Bhatia-Wolf smoothing will also be investigated. These two sets of polynomials are defined over a circular domain which is convenient to model the elevation (height) of the corneal surface. The third representation uses Spherical Harmonics that are particularly well suited for nearly-spherical object modelling, which is the case for cornea. We compared the three methods using the following three criteria: the root-mean-square error (RMSE), the number of parameters and the visual accuracy of the reconstructed topographic maps. A large dataset of 210 corneal topographies was used. Our results showed that Spherical Harmonics were superior with a RMSE mean lower than 2 microns with 36 coefficients (order 5) for normal corneas and lower than 5 microns for keratoconus (a corneal disorder).

10133-89, Session PS1

Accurate bolus arrival time estimation using piecewise linear model fitting

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Dynamic contrast-enhanced computed tomography (DCE-CT) provides functional measurements of the vascular support of tissues through the analysis of tissue kinetics. The acquisition involves an injection of contrast agent and rapid sequences of CT images to monitor the temporal changes in the tissues and blood vessels due to the passage of the contrast agent. The temporal changes in the tissues results in a tissue attenuation curve (TAC). The relation between the feeding artery and the tissue of interest is modelled by an integral convolution equation. The bolus arrival time (BAT) has a strong influence on the estimated perfusion parameters. Direct estimation of this parameter is problematic and a tedious task. We present a robust method to estimate the bolus arrival time by fitting a piecewise model to the TAC by using a nonlinear optimisation technique. The method was tested on 2500 different simulated TACs with different level of noises and on two clinic subjects. The proposed method provides a precise estimation for the BAT even for extremely noisy TACs and converges fast to the best fitted model.

10133-90, Session PS1

A multi-object statistical atlas adaptive for deformable registration errors in anomalous medical image segmentation

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Statistical Atlases have played an important role towards automated medical image segmentation. However, a challenge has been to make the atlas more adaptable to possible errors in deformable registration of anomalous images, given that the body structures of interest for segmentation might present significant differences in shape and texture. Recently, deformable registration errors have been accounted by a method that locally translates the statistical atlas over the test image, after registration, and evaluates candidate objects from a delineation algorithm in order to choose the best one as final segmentation. In this paper, we improve its delineation algorithm and extend the model to be a multi-object statistical atlas, built from control images and adaptable to anomalous images, by incorporating a texture classifier. In order to provide a first proof of concept, we instantiate the new method for segmenting, object-by-object and all objects simultaneously, the left and right brain hemispheres, and the cerebellum, without the brainstem, and evaluate it on MRT1-images of epilepsy patients before and after brain surgery, which removed portions of the temporal lobe. The results show efficiency gains with statistically significant higher accuracy, using the mean Average Symmetric Surface Distance, with respect to the original approach.

10133-91, Session PS1

Automatic MR prostate segmentation by deep learning with holistically-nested networks

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Accurate automatic prostate magnetic resonance (MR) images segmentation is a challenging task due to the high variability of prostate anatomy structure. Artifacts such as noise and homogeneous tissues around the prostate boundary inhibit traditional methods from achieving high segmentation accuracy. The proposed method performs end-to-end prediction by integrating holistically nested edge detection (HED) on prostate MR images by means of deep learning that leverages fully convolutional neural networks. Holistically-Nested Networks (HNN) automatically learn the hierarchical representation that can improve prostate boundary detection. Quantitative evaluation is performed on 247 (patients) prostate MR axial images in 5-fold cross-validation. We achieve a mean Dice Similarity Coefficient of 88.79% and a mean Jaccard of 80.29% without trimming any erroneous contours at apex and base.

10133-92, Session PS1

Fully automated lumen segmentation of intracoronary optical coherence tomography images

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Optical coherence tomography (OCT) provides high-resolution cross-sectional images of arterial luminal morphology. Traditionally lumen segmentation of OCT images is performed manually by expert observers; a laborious, time consuming effort, sensitive to inter-observer variability process. Although several automated methods have been developed, the majority cannot be applied in real time because of processing demands.

To address these limitations we propose a new method for fast image segmentation of arterial lumen borders using OCT images that involves the following steps: 1) OCT image acquisition using the raw OCT data, 2) reconstruction of longitudinal cross-section (LOCS) images from four different acquisition angles, 3) segmentation of the LOCS images and 4) lumen contour construction in each 2D cross-sectional image.

The efficiency of the developed method was evaluated using 613 annotated images from 10 OCT pullbacks acquired from 10 patients at the time of coronary arterial interventions. High Pearson’s correlation coefficient was obtained when lumen areas detected by the method were compared to areas annotated by experts (r=0.98, R2=0.96); Bland-Altman analysis showed no significant bias with good limits of agreement.

The proposed methodology permits reliable border detection especially in lumen areas having artifacts and is faster than traditional techniques making it capable of being used in real time applications. The method is likely to assist in a number of research and clinical applications - further testing in an expanded clinical arena will more fully define the limits and potential of this approach.

10133-93, Session PS1

Accurate registration of temporal CT images for pulmonary nodules detection

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Interpretation of temporal CT images could help the radiologists significantly improve the detection of some subtle interval changes in the sequential examinations. The purpose of this study was to develop a fully automated scheme for accurate registration of temporal CT images for pulmonary nodule detection. Our method consisted of three major registration steps. Firstly, affine transformation was applied in the segmented lung region to obtain global coarse registration images. Secondly, B-splines based free-form deformation (FFD) was used to refine the coarse registration images. Thirdly, Demons method was performed to align the feature points extracted from the registered images in the second step and the reference images. Our database consisted of 91 temporal CT cases, including 63 and 28 images acquired, respectively, with two CT scanners produced by Shanghai United Imaging Healthcare and GE Healthcare. The preliminary results showed that approximately 96.7% cases could obtain accurate registration based on subjective observation. The subtraction images of the rigid and non-rigid registered images and the reference images could effectively remove the normal structures (i.e. blood vessels) and retain the abnormalities (i.e. pulmonary nodules). This would be useful for the screening of lung cancer in our future study.

10133-94, Session PS1

Automatic polyp detection in colonoscopy videos

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Colon cancer is the second cancer killer in the US. Colonoscopy is the primary method for screening and prevention of colon cancer, but during colonoscopy, a significant number (25%) of polyps (precancerous abnormal growths inside of the colon) are missed; therefore, the goal of our research is to reduce the polyp miss-rate of colonoscopy. This paper presents a method to detect polyp automatically in a colonoscopy video. Our system has two stages: Candidate generation and candidate classification. In candidate generation, we chose 3,463 frames (including 1,718 "with-polyp" frames) from real-time colonoscopy video database. We firstly applied processing procedures, namely intensity adjustment, edge detection and morphology operations, as pre-preparation. Then we extracted each connected component (edge contour) as one candidate patch. With the help of ground truth (GT) images, 2 constraints were implemented on each candidate patch, dividing and saving them into polyp group and non-polyp group. In candidate classification, we trained and tested convolutional neural networks (CNNs) with AlexNet architecture to classify each candidate into class "with-polyp" or "non-polyp". Each "with-polyp" patch was processed by rotation, translation and scaling for invariant to get a much robust CNNs' system. We applied leave-2-patients-out cross-validation on this model (4 of 6 cases were chosen as training set and the rest 2 were as testing set). The accuracy of polyp detection shows is 91.47%.

10133-95, Session PS1

High frequency ultrasound in-plane registration of deformable finger vessels

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Ultrasound imaging is widely used in clinical imaging because it is non-invasive, real-time, and inexpensive. Due to the freehand nature of clinical ultrasound, analysis of an image sequence often requires registration between the images. Of the previously developed mono-modality ultrasound registration frameworks, only few were designed to register small anatomical structures. Monitoring of small finger vessels, in particular, is essential for the treatment of vascular diseases such as Raynaud's Disease. High frequency ultrasound (HFUS) can now image smaller anatomic details down to 30 microns within the vessels, but no work has been done to date on such small-scale ultrasound registration. Due to the complex internal finger structure and increased noise of HFUS, it is difficult to register 2D images of finger vascular tissue, especially under deformation. We studied a variety of similarity measurements with different pre-processing techniques to find which registration similarity metrics were best suited for HFUS vessel tracking. The overall best performance was obtained with a normalized correlation metric coupled with HFUS downsampling and a one-plus-one evolutionary optimizer, yielding a mean registration error of 0.05 mm. We also used HFUS to study how finger tissue deforms under an ultrasound transducer, comparing internal motion vs. transducer motion. Improving HFUS registration and tissue modeling may lead to new research and improved treatments for peripheral vascular disorders.

10133-96, Session PS1

Automatic selection of landmarks in T1-weighted head MRI with regression forests for image registration initialization

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Image registration is at the core of many applications in medical imaging but registration methods often depend on a good initialization to lead to accurate results. Prior work has shown that landmark-based point set registration is a good approach to initialize the registration process but the selection of landmarks is important. Landmarks should cover the entire structure and make the correspondences between individuals as robust as possible. In this work, we present a learning-based method to automatically find a set of robust landmarks in 3D MR image volumes of the head to initialize non-rigid transformations. Our dataset contains images of 101 individuals, the images are partitioned into a training dataset of 60 images that is used to train regression forests to localize a set of landmarks, a second training set of 20 images that is used to identify among the set of landmarks which ones are the most robust, a testing set of 20 images, and one atlas image. Our technique includes 4 training steps: (1) the generation of the candidate landmark set using the atlas image, (2) the creation of a series of RF models that are each trained to localize one landmark, (3) the localization of the candidate landmarks in the second training set and (4) the selection of the most reliable landmarks using a random sample consensus (RANSAC) algorithm and the second training set. In the testing phase, the most reliable landmarks are localized in unknown volumes and they are used to compute a thin-plate splines transformation that registers the atlas to the volume. We show that our method leads to good registration initialization results.

10133-97, Session PS1

A task-related and resting state realistic fMRI simulator for fMRI data validation

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Despite more than 25 years of published functional magnetic resonance imaging (fMRI) studies, reporting localized activation clusters in human brain corresponding to specific tasks, the extent and location of these activation clusters lack validation under careful scrutiny. Such lack of validated results reported by most task related fMRI studies makes it difficult to interpret decisively and necessitates development of realistic fMRI simulators with synthetic ground truth to serve as surrogates for experimentally acquired data. We present a MATLAB toolbox based realistic fMRI simulator called STANCE (Spontaneous & Task-related Activation of Neuronally Correlated Events) simulator. What will ultimately set STANCE apart from others is an attempt to handle correlated time-series of activations. This is necessary to realistically model spontaneous activations (the unconstrained spontaneous "tasks" that occur during a so called "resting state"), which is in turn a necessary psychological "noise" component present when modelling task-related activations with time-series which are constrained by the experimental design. This will allow for the simulation of resting state functional connectivity studies with a modeled ground truth. However, true-to-reality simulation cannot be fully achieved because of our incomplete knowledge of how real-world data is generated. We take a hybrid approach, allowing for progressive building of new modules that can grow with the interests of the research community, while also allowing for comparisons with existing simulators and validation measures.

10133-99, Session PS1

Automatic segmentation of the prostate on CT images using deep learning and multi-atlas fusion

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Automatic prostate segmentation on CT images is an important but a challenging task because of the low contrast of soft tissue on CT images. In this paper, we propose an automatic prostate segmentation method on CT images by combining the deep learning method and multi-atlas refinement. First, instead of segmenting the whole image, we extract the region of interesting (ROI) to delete irrelevant regions. Then, we use the convolutional neural networks (CNN) to learn the deep features for distinguishing the prostate pixels from the non-prostate pixels to obtain the preliminary segmentation results. CNN can automatically learn the deep feature adapting to data, which is different from some handcrafted features. The CNN method achieved a good classification performance. Finally, we select some similar atlases to refine the preliminary segmented prostate for final segmentation results. The proposed method has been evaluated on the dataset containing 92 prostate CT images. Experimental results show that our method achieved a DSC of 86.80% as compared to the manual segmentation. The CT segmentation method can have variety applications in prostate cancer diagnosis and therapy.

10133-100, Session PS1

Semi-automatic 3D lung nodule segmentation in CT using dynamic programming

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We present a method for semi-automatic segmentation of lung nodules in chest CT that can be extended to general lesion segmentation in multiple modalities. Most semi-automatic algorithms for lesion segmentation or similar tasks use region-growing or edge-based contour finding methods such as level-set. However, lung nodules and other lesions are often connected to surrounding tissues, which makes these algorithms prone to growing the nodule boundary into the surrounding tissue. To solve this problem, we apply a 3D extension of the 2D edge linking method with dynamic programming to find a closed surface in a spherical representation of the nodule ROI. The algorithm requires a user to draw a maximal diameter across the nodule in the slice in which the nodule cross section is the largest. Using the LIDC public lung nodule dataset, we report DICE values for our segmentation as compared to an expert radiologist, and compare the results against a level-set implementation using ITK.

10133-101, Session PS1

Learning-based interactive segmentation using the maximum mean cycle weight formalism

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The maximum mean cycle weight (MMCW) segmentation framework is an alternative to approaches such as GraphCut or Markov Random Fields. Like them, it offers time- and space-efficient computation and guaranteed optimality in a graph-based formulation. Its focus on segmenting a single optimal object makes MMCW attractive to interactive segmentation settings. However, a provably correct way of performing interactive segmentation by MMCW has never been demonstrated. Further, the question of how to develop a good objective function based on user-provided information has never been addressed. We propose a three-component objective function designed for use with interactive MMCW segmentation. Two components, representing object boundary and interior information, can be learned from a modest amount of user-labelled data. The third component extends the MMCW framework to allow interactive segmentation. We prove that a weighted combination of the three components guarantees the object produced by MMCW segmentation encloses pixels selected interactively by the user. The component weights can be computed a priori, based on image characteristics, or at segmentation time via an adaptive reweighting scheme. We evaluated our approach by comparing MMCW-segmented objects to manual segmentations, and to GraphCut segmentation, where GraphCut is provided similar training data. We tested on three domains: segmenting muscle fibers from images of H&E-stained muscle sections, and from fluorescently labeled muscle sections, and segmenting blood cells from light microscope images. In all cases, MMCW segmentation with our three-component weighting was better than the with individual components, better than any blend of boundary and interior weights, and better than GraphCut.

10133-102, Session PS1

Unsupervised quantification of abdominal fat from CT images using greedy snakes

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Adipose tissue has been associated with adverse consequences of obesity. Total adipose tissue (TAT) is divided into subcutaneous adipose tissue (SAT) and visceral adipose tissue (VAT). Intra-abdominal fat (VAT), located inside the abdominal cavity, is a major factor for the classic obesity related pathologies. Since direct measurement of visceral and subcutaneous fat is not trivial, substitute metrics like waist circumference (WC) and body mass index (BMI) are used in clinical settings to quantify obesity. Abdominal fat can be assessed effectively using CT or MRI, but manual fat segmentation is rather subjective and time-consuming. Hence, an automatic and accurate quantification tool for abdominal fat is needed. The goal of this study is to extract TAT, VAT and SAT fat from abdominal CT's in a fully automated unsupervised fashion using energy minimization techniques. We applied a four step framework consisting of 1) initial body contour estimation, 2) approximation of the body contour, 3) estimation of inner abdominal contour using Greedy Snakes algorithm, and 4) voting, to segment the subcutaneous and visceral fat. We validated our algorithm on 952 clinical abdominal CT images (from 476 patients with a very wide BMI range) collected from various radiology departments of Geisinger Health System. To our knowledge, this is the first study of its kind on such a large and diverse clinical dataset. Our algorithm obtained a 3.4% error for VAT segmentation compared to manual segmentation. These personalized and accurate measurements of fat can complement traditional population health driven obesity metrics such as BMI and WC.

10133-39, Session 8

Multi-atlas propagation based left atrium segmentation coupled with super-voxel based pulmonary veins delineation in late gadolinium-enhanced cardiac MRI

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Late Gadolinium-Enhanced Cardiac MRI (LGE CMRI) is a non-invasive technique, which has shown promise in detecting native and post-ablation atrial scarring. To visualize the scarring, a precise segmentation of the left atrium (LA) and pulmonary veins (PVs) anatomy is performed as a first step—usually from an ECG gated CMRI roadmap acquisition—and the enhanced scar regions from the LGE CMRI images are superimposed. The anatomy of the LA and PVs in particular is highly variable and manual segmentation is labor intensive and highly subjective. In this paper, we developed a multi-atlas propagation based whole heart segmentation (WHS) to delineate the LA and PVs from ECG gated CMRI roadmap scans. While this captures the anatomy of the atrium well, the PVs anatomy is less easily visualized. The process is therefore augmented by semi-automated manual strokes for PVs identification in the registered LGE CMRI data. This allows us to extract more accurate anatomy than the fully automated WHS. Both qualitative visualization and quantitative assessment with respect to manual segmented ground truth showed that our method is efficient and effective with an overall mean Dice score of 0.91.

10133-40, Session 8

Three-dimensional whole breast segmentation in sagittal MR images with dense depth field modeling and localized self-adaptation

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Whole breast segmentation is the first step in quantitative analysis of breast MR images. This task is challenging due mainly to the chest-wall line's (CWL) spatially varying appearance and nearby distracting structures, both being complex. In this paper, we propose an automatic three-dimensional (3-D) segmentation method of whole breast in sagittal MR images. This method distinguishes itself from others in two main aspects. First, it reformulates the challenging problem of CWL localization into an equivalence that searches for an optimal smooth depth field and so fully utilizes the 3-D continuity of the CWLs. Second, it employs a localized self-adapting algorithm to adjust to the CWL's spatial variation. Experimental results on real patient data with expert-outlined ground truth show that the proposed method can segment breasts accurately and reliably, and that its segmentation is superior to that of previously established methods.

10133-41, Session 8

An automated segmentation for direct assessment of adipose tissue distribution from thoracic and abdominal multi-echo Dixon MR images

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Magnetic Resonance Imaging (MRI) and Magnetic Resonance Spectroscopy (MRS) together have become the gold standard in the precise quantification of body fat. The study of the quantification of fat in the human body has matured in recent years from a simplistic interest in the whole-body fat content to detailing regional fat distributions. The realization is that body-fat, or adipose tissue (AT), far from being a mere aggregate mass or deposit, is a biologically active organ in and of itself, which may play a role in the association between obesity and the various pathologies that are the biggest health issues of our time. Furthermore, a major bottleneck in most medical image assessments of adipose tissue content and distribution is the lack of automated image analysis. This motivated us to develop an automated and direct methodology to accurately and reproducibly determine both body fat content and distribution in the human body for cross-sectional and longitudinal studies of obesity and associated diseases such as cardiovascular disease and diabetes. The AT considered here is located beneath the skin (subcutaneous) as well as around the internal organs and between muscles (visceral and inter-muscular). There are also special fat depots on and around the heart (pericardial = epicardial + paracardial) as well as around the aorta (peri-aortic). Our methods focus on measuring and classifying these various AT deposits in the human body in an intervention study that involves the acquisition of thoracic and abdominal MR images via multi-echo Dixon MRI.

10133-42, Session 8

Seed robustness of oriented relative fuzzy connectedness: core computation and its applications

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In this work, we present a formal definition and an efficient algorithm to compute the cores of Oriented Relative Fuzzy Connectedness (ORFC), a recent seed-based segmentation technique. The core is a region where the seed can be moved without altering the segmentation, an important aspect for robust techniques and reduction of user effort.

We show how ORFC cores can be used to build a powerful hybrid image segmentation approach. We also provide some new theoretical relations between ORFC and Oriented Image Foresting Transform (OIFT), as well as their cores. Experimental results among several methods show that the hybrid approach conserves high accuracy, avoids the shrinking problem and provides robustness to seed placement inside the desired object due to the cores properties.

10133-43, Session 8

Comparison of thyroid segmentation techniques for 3D ultrasound

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The segmentation of the thyroid in ultrasound images is a field of active research. The thyroid is a gland of the endocrine system and regulates several body functions. Measuring the volume of the thyroid is regular practice of diagnosing pathological changes. In this work, we compare three approaches for semi-automatic thyroid segmentation in freehand-tracked three-dimensional ultrasound images. The approaches are based on level set, graph cut and feature classification. For validation, eight 3D ultrasound records were created with ground truth images, which we make publicly available. The properties analyzed are the dice coefficient when compared against the ground truth reference and the effort of required interaction.

Our results show that in terms of dice coefficient, all algorithms perform similarly. For interaction, however, each algorithm has advantages over the other. The graph cut-based approach gives the practitioner direct influence on the final segmentation. Level set and feature-based approaches require less interaction, but offer less control over the result. All three compared methods show promising results for future work and provide several possible extensions.

10133-44, Session 9

Robust nuclei segmentation in cyto-histopathological images using statistical level set approach with topology preserving constraint

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Computerized assessments for diagnosis or malignancy grading of cyto-histopathological specimens have drawn increased attention in the field of digital pathology. Automatic segmentation of cell nuclei is a fundamental step in such automated systems. Despite considerable research, nuclei segmentation is still a challenging task due noise, nonuniform illumination, and most importantly, in 2D projection images, overlapping and touching nuclei. In most published approaches, nuclei refinement is a post-processing step after segmentation, which usually refers to the task of detaching the aggregated nuclei or merging the over-segmented nuclei. In this work, we present a novel segmentation technique which effectively addresses the problem of individually segmenting touching or overlapping cell nuclei during the segmentation process. The proposed framework is a region-based segmentation method, which consists of three major modules: i) the image is passed through a color deconvolution step to extract the desired stains; ii) then the generalized fast radial symmetry transform is applied to the image followed by non-maxima suppression to specify the initial seed points for nuclei, and their corresponding GFRS ellipses which are interpreted as the initial nuclei borders for segmentation; iii) finally, these nuclei border initial curves are evolved through the use of a statistical level-set approach along with topology preserving criteria for segmentation and separation of nuclei at the same time. The proposed method is evaluated using Hematoxylin and Eosin, and fluorescent stained images, performing qualitative and quantitative analysis, showing that the method outperforms thresholding and watershed segmentation approaches.

10133-45, Session 9

Direct spondylolysis identification and spondylolisthesis measurement in MR/CT using detectors trained by articulated parameterized spine model

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The identification of spondylolysis and spondylolisthesis is important in spinal diagnosis, rehabilitation, and surgery planning. Accurate and automatic detection of the spinal portion with spondylolysis problem will significantly reduce the manual work of the physician and provide a more robust evaluation of the spine condition. Most existing automatic identification methods adopted the indirect approach which used vertebrae location to measure the spondylolysis. However, these methods relied heavily on automatic vertebra detection which often suffered from the pool spatial accuracy and the lack of validated pathological training samples. In this study, we present a novel spondylolysis/spondylolisthesis detection method which can directly locate the irregular spine portion and output the corresponding grading. The detection is done by a set of learning-based detectors which are discriminatively trained by spondylolysis/spondylolisthesis image samples. To provide sufficient pathological training samples, we used a parameterized spine model to synthesize different types of spondylolysis images from real MR/CT scans. The parameterized model can automatically locate the vertebrae in spine images and estimate their pose orientations, and can inversely alter the vertebrae locations and poses by changing the corresponding parameters. Various training samples can then be generated from only a few spine MR/CT images. The preliminary results suggest great potential for the fast and efficient spondylolysis identification and spondylolisthesis measurement in both MR and CT spine images.

10133-46, Session 9

Subject-specific longitudinal shape analysis by coupling spatiotemporal shape modeling with medial analysis

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Modeling subject-specific shape change is one of the most important issues in longitudinal shape analysis of disease progression. Anatomical change over time is not only a function of normal aging; anatomy can also be impacted by disease related degeneration. Shape changes to anatomy may also be affected by external structural changes from neighboring shapes, which may cause non-linear pose variation. In this paper, we propose a framework to analyze disease related shape changes by coupling extrinsic modeling of the ambient anatomical space via spatiotemporal deformations with intrinsic shape properties from medial surface analysis. We compare intrinsic shape properties of a subject-specific shape trajectory to a 4D shape atlas representing normal aging to quantify shape changes related to disease. The spatiotemporal shape modeling establishes inter/intra subject anatomical correspondence which enables comparisons between subjects and the 4D shape atlas, and quantitative analysis of disease related shape change. The medial surface analysis provides intrinsic shape properties which capture local patterns of deformation. The proposed framework therefore models extrinsic longitudinal shape changes in the ambient anatomical space, as well as intrinsic shape properties which give localized measurements of degeneration. Six high risk subjects and six controls are randomly sampled from a Huntington's disease database for quantitative and qualitative comparison.

10133-47, Session 9

Simultaneous segmentation and correspondence improvement using statistical modes

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Statistical shape models used in medical applications require high accuracy to minimize errors during medical procedures. Many shape models are built using homologous shapes obtained by propagating a template shape to each patient space using deformation fields obtained from deformable registration between template and patient images. However, registration algorithms are not perfect, and patient segmentations often contain some errors. Several methods have been presented that improve these segmentations. However, since the vertices of each shape are moved independently of other shapes, segmentation improvement can often lead to deterioration of the correspondences. We present a method that iteratively improves both segmentation as well as correspondences using statistical modes. We build an initial statistical model using the shapes obtained from deformable registration, and use this model to constrain the movement of vertices during segmentation improvement. Once the segmentation for each patient in the data-set has been improved, the model is used to improve the correspondence between shapes. Finally, once correspondence for each patient has been improved, a new shape model is built, and this process is repeated until convergence. We evaluate our segmentation against hand-segmented maxillary sinuses, and our correspondences via the leave-one-out analysis, and show that our methods improves both segmentation and correspondence.

10133-48, Session 9

Improved automatic optic nerve radius estimation from high resolution MRI

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The optic nerve (ON) is a vital structure in the human visual system and transports all visual information from the retina to the cortex for higher order processing. Due to the lack of redundancy in the visual pathway, measures of ON damage have been shown to correlate well with visual deficits. These measures are typically taken at an arbitrary anatomically defined point along the nerve and do not characterize changes along the length of the ON. We propose a fully automated, three-dimensionally consistent technique building upon a previous independent slice-wise technique to estimate the radius of the ON and surrounding cerebrospinal fluid (CSF) on high-resolution heavily T2-weighted isotropic MRI. We show that by constraining results to be three-dimensionally consistent this technique produces more anatomically viable results. We compare this technique with the previously published slice-wise technique using a short-term reproducibility data set, 10 subjects, follow-up <1 month, and show that the new method is more reproducible in the center of the ON. The center of the ON contains the most accurate imaging because it lacks confounders such as motion and frontal lobe interference. Long-term reproducibility, 5 subjects, follow-up of approximately 11 months, is also investigated with this new technique and shown to be similar to short-term reproducibility, indicating that the ON does not change substantially within 11 months. The increased accuracy of this new technique provides increased power when searching for anatomical changes in ON size amongst patient populations.

10133-49, Session 9

Model-based correction of ultrasound image deformations due to probe pressure

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Freehand 3D ultrasound (US) consists in acquiring a US volume by moving a tracked conventional 2D probe over an area of interest. To maintain good acoustic coupling between the probe and the skin, the operator applies pressure on the skin with the probe. This pressure deforms the underlying tissues in a variable way across the excursion of the probe, which, in turn, leads to inconsistencies in the volume. To address this problem, this paper proposes a method to estimate the deformation field sustained by each image with respect to a reference deformation free image. The method is based on a 2D biomechanical model that takes into account the mechanical parameters of the tissues depicted in the image to predict a realistic deformation field. These parameters are estimated along with the deformation field such as to minimize the mean squared difference between the reference and the corrected images. The image is then corrected by applying the inverse deformation field. Preliminary validation was conducted with synthetic US images generated using a 3D biomechanical model. Results show that the proposed method improves image correction compared to a purely image-based method.

10133-50, Session 10

A segmentation editing framework based on shape change statistics

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Segmentation is a key task in medical image analysis because its accuracy significantly affects successive steps. Automatic segmentation methods often produce inadequate segmentations, which require the user to manually edit the produced segmentation slice by slice. Because editing is time-consuming, an editing tool that enables the user to produce accurate segmentations by only drawing a sparse set of contours would be needed. This paper describes such a framework as applied to a single object. Constrained by the additional information enabled by the manually segmented contours, the proposed framework utilizes object shape statistics to transform the failed automatic segmentation to a more accurate version. Instead of modeling the object shape, the proposed framework utilizes shape change statistics that were generated to capture the object deformation from the failed automatic segmentation to its corresponding correct segmentation. An optimization procedure was used to minimize an energy function that consists of two terms, an external contour match term and an internal shape change regularity term. The high accuracy of the proposed segmentation editing approach was confirmed by testing it on a simulated data set based on 10 in-vivo infant magnetic resonance brain data sets using four similarity metrics. Segmentation results indicated that our method can provide efficient and adequately accurate segmentations (Dice segmentation accuracy increase of 10%), with few added contours (only 10%), which is promising in greatly decreasing the work expected from the user.

10133-51, Session 10

Structural-functional relationships between eye orbital imaging biomarkers and clinical visual assessments

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Eye diseases and visual impairment affect millions of Americans and induce billions of dollars in annual economic burdens. Expounding upon existing knowledge of eye diseases could lead to improved treatment and disease prevention. This research investigated the relationship between structural metrics of the eye orbit and visual function measurements in a cohort of 557 patients from a retrospective study of ophthalmology records for patients (with thyroid eye disease, orbital inflammation, optic nerve edema,

glaucoma, intrinsic optic nerve disease), clinical imaging, and visual function assessments. Orbital magnetic resonance imaging (MRI) and computed tomography (CT) images were retrieved and labeled in 3D using multi-atlas label fusion. Based on the 3D structures, both traditional radiology measures (e.g., Barrett index, volumetric crowding index, optic nerve length) and novel volumetric metrics were computed. Using stepwise regression, the associations between structural metrics and visual field scores (visual acuity, functional acuity, visual field, functional field, and functional vision) were assessed. Across all models, the explained variance was reasonable (R2 ~ 0.1-0.2) but highly significant ($p < 0.001$). Instead of analyzing a specific pathology, this study aimed to analyze data across a variety of pathologies. This approach yielded a general model for the connection between orbital imaging biomarkers and visual function.

10133-52, Session 10

Tumor propagation model using generalized hidden Markov model

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Tumor tracking and progression analysis using medical images is a crucial task for physicians to provide accurate and efficient treatment plans. We present a new generalized tumor propagation model considering time-series prior images and local anatomical features using a hierarchical Hidden Markov Model for tumor tracking. The propagation model describes the lesion propagation between prior and current images, and between adjacent images within the same series. We extract the anatomical tissue structure of the targeted body part and incorporate the local tissue properties in the proposed model. The model identifies a diagnostic relationship between different tissue types, their locations and neighboring regions. We validate our method using diverse tumor exams including brain tumors, lung nodules and liver cancer exams with priors. Our model has the potential to be applied to general tumor propagation problems for practical use in a tumor tracking application.

10133-53, Session 10

A four-dimensional motion field atlas of the tongue from tagged and cine magnetic resonance imaging

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Representation of human tongue motion using three-dimensional vector fields over time can be used to better understand tongue function during speech, swallowing, and other lingual behaviors. To characterize the inter-subject variability of the tongue's shape and motion of a population carrying out one of these functions it is desirable to build a statistical model of the four-dimensional (4D) tongue. In this paper, we propose a method to construct a spatio-temporal atlas of tongue motion using magnetic resonance (MR) images acquired from fourteen healthy human subjects. First, cine MR images revealing the anatomical features of the tongue are used to construct a 4D intensity image atlas. Second, tagged MR images acquired to capture internal motion are used to compute a dense motion field at each time frame using a phase-based motion tracking method. Third, motion fields from each subject are pulled back to the cine atlas space using the deformation fields computed during the cine atlas construction. Finally, a spatio-temporal motion field atlas is created to show a sequence of mean motion fields and their inter-subject variation. The quality of the atlas was evaluated by deforming cine images in the atlas space. Comparison between deformed and original cine images showed high correspondence. The proposed method provides a quantitative representation to observe the commonality and variability of the tongue motion field for the first time, and shows potential in evaluation of common properties such as strains and other tensors based on motion fields.

10133-54, Session 10

Multi-atlas-based CT synthesis from conventional MRI with patch-based refinement for MRI-based radiotherapy planning

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Accurate CT synthesis, sometimes called electron density estimation, from MRI is crucial for successful MRI-based radiotherapy planning and dose computation. Existing CT synthesis methods are able to synthesize normal tissues but are unable to accurately synthesize abnormal tissues (i.e., tumor), thus providing a suboptimal solution. We propose a multi-atlas-based hybrid synthesis approach that combines multi-atlas registration and patch-based synthesis to accurately synthesize both normal and abnormal tissues. Multi-parametric atlas MR images are registered to the target MR images by multi-channel deformable registration, from which the atlas CT images are deformed and fused by locally-weighted averaging using a structural similarity measure (SSIM). Synthetic MR images are also computed from the registered atlas MRIs by using the same weights used for the CT synthesis; these are compared to the target patient MRIs allowing for the assessment of the CT synthesis fidelity. Poor synthesis regions are automatically detected based on the fidelity measure and refined by a patch-based synthesis. The proposed approach was tested on brain cancer patient data, and showed a noticeable improvement especially for the tumor region.

10133-55, Session 11

Image enhancement in positron emission mammography

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Purpose: To evaluate an efficient iterative method for improving the quantitative accuracy of previously reconstructed breast images by commercial positron emission mammography (PEM) camera. A novel rapidly converging, iterative deconvolution algorithm (RSEMD) to reduce noise and enhance image resolution has been demonstrated.

Materials and Methods: The RSEMD method was tested on phantoms and clinical PEM imaging data. Data acquisition was performed on a commercial Naviscan Flex Solo II PEM camera. This method was applied to patient breast images previously reconstructed with Naviscan software to determine improvements in resolution, signal to noise ratio (SNR) and contrast to noise ratio (CNR.)

Results: In all of the patients' breast studies the post-processed images proved to have higher resolution and lower noise as compared with images reconstructed by conventional methods. In general, the values of SNR reached a plateau at around 6 iterations with an improvement factor of about 2 for processed Flex Solo II PEM images. Improvements in image resolution after the application of RSEMD have also been demonstrated.

Conclusions: A rapidly converging, iterative deconvolution algorithm with a novel resolution subsets-based approach RSEMD that operates on patient DICOM images has been used for quantitative improvement in breast imaging. The RSEMD method can be applied to clinical PEM images to improve image quality to diagnostically acceptable levels and will be crucial in order to facilitate diagnosis of tumor progression at the earliest stages. The RSEMD method can be considered as an extended Richardson-Lucy algorithm with multiple resolution levels.

10133-56, Session 11

Scatter correction by non-local techniques

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In X-ray imaging, scatter can produce noise, artifacts, and decreased contrast. In practice, hardware such as anti-scatter grids are often used to reduce scatter. However, the remaining scatter can still be significant and additional software-based correction are desirable. Furthermore, good software solutions can potentially reduce the amount of needed anti-scatter hardware, thereby reducing cost. In this work, we developed a software correction algorithm by adapting a class of non-local image restoration techniques to scatter reduction. In this algorithm, scatter correction is formulated as a Bayesian MAP (maximum a posteriori) problem with a non-local prior, which leads to better textural detail preservation in scatter reduction. The efficacy of our algorithm is demonstrated through experimental and simulation results.

10133-57, Session 11

Resolution enhancement for x-ray images

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X-ray machines are widely used for medical imaging and their cost is highly dependent on their image resolution. Due to economic reasons, lower-res machines still have a lot of customers, especially in developing economies. Software based resolution enhancement can enhance the capabilities of the lower-res machines without significant cost increase hence is highly desirable. In this work, we developed an algorithm for X-ray image resolution enhancement. In this algorithm, the fractal idea and cross-resolution patch matching are used to identify low-res patches that can be used as samples for high-res patch/pixel estimation. These samples are then used to generate a prior distribution and used in a Bayesian MAP optimization to produce the high-res image estimate. The efficacy of our algorithm is demonstrated by experimental results.

10133-58, Session 11

Chromaticity based smoke removal in endoscopic images

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In minimally invasive surgery, image quality is a critical pre-requisite to ensure a surgeon's ability to perform a procedure. In endoscopic procedures, image quality can deteriorate for a number of reasons such as fogging due to the temperature gradient after intra-corporeal insertion, lack of focus and due to smoke generated when using cautery to dissect tissues without bleeding. In this paper we investigate the use of vision techniques to remove surgical smoke and improve the clarity of the image. For simplicity and computational efficiency we use an adapted dark-channel prior method combined with histogram equalization to remove smoke artifacts to recover the radiance image and enhance the contrast and brightness of the final result. Our initial results on images from robotic assisted procedures are promising and show that the proposed approach may be used to enhance image quality during surgery without additional suction devices. In addition, the processing pipeline may be used as an important part of a robust surgical vision pipeline that can continue working in the presence of smoke.

10134-1, Session 1

Segmentation of inner and outer bladder wall using deep-learning convolutional neural network in CT urography

Marshall Gordon, Lubomir M. Hadjiiski, Kenny H. Cha, Heang-Ping Chan, Ravi K. Samala, Richard H. Cohan, Elaine M. Caoili, Univ. of Michigan Health System (United States)

We are developing a computerized system for detection of bladder cancer in CT urography. In this study, we used a deep-learning convolutional neural network (DL-CNN) to segment the bladder wall. This task is challenging due to differences in the wall between the contrast and non-contrast-filled regions, significant variations in appearance, size, and shape of the wall among cases, overlap of the prostate with the bladder wall, and the wall being extremely thin and occasionally invisible compared to the overall size of the bladder. We trained a DL-CNN to estimate the likelihood that a given pixel would be inside the wall of the bladder using neighborhood information. A segmented bladder wall was then obtained using level sets with this likelihood map as a term in the level set energy equation to obtain a contour of the inner and outer bladder wall. The accuracy of the segmentation was evaluated by comparing the segmented wall outlines to hand outlines for a set of 79 training cases and 37 test cases using average volume intersection %, average % volume error, absolute % volume error, and average distance as metrics. For the test set, the inner wall achieved values of 86.9±9.6%, -8.3±37.7%, 18.4±33.8%, and 3.4±1.8mm respectively, while the outer wall achieved values of 87.5±9.9%, 1.2±20.8%, 11.9±17.0%, and 3.5±2.3mm. The results show that the DL-CNN with level sets was effective in segmenting the inner and outer bladder wall.

10134-2, Session 1

Computer-aided detection of bladder masses in CT urography

Kenny H. Cha, Lubomir M. Hadjiiski, Heang-Ping Chan, Elaine M. Caoili, Richard H. Cohan, Alon Z. Weizer, Ravi K. Samala, Univ. of Michigan (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 and the non-contrast-enhanced regions of the bladder individually. In this study, we investigated methods for detection of bladder masses within the entire bladder. The bladder was segmented using our method that combined deep-learning convolutional neural network 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 gray level threshold was applied to the contrast and non-contrast regions separately to extract 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. A data set of 68 patients with 91 biopsy-proven bladder lesions was used, which was split into independent training and test sets: 43 training cases with 52 lesions, and 26 test cases with 39 lesions. Using the training set, feature selection was performed and a linear discriminant (LDA) classifier was designed to merge the selected features for classification of bladder lesions and false positives. The trained classifier was evaluated with the test set. FROC analysis showed that the system achieved a sensitivity of 86.5% at 3.3 FPs/case for the training set, and 84.6% at 3.8 FPs/case for the test set.

10134-3, Session 1

Bladder cancer treatment response assessment using deep learning in CT with transfer learning

Kenny H. Cha, Univ. of Michigan (United States); Lubomir M. Hadjiiski, Heang-Ping Chan, Ravi K. Samala, Richard H. Cohan, Elaine M. Caoili, Chintana Paramagul, Ajjai Alva, Univ. of Michigan Health System (United States); Alon Z. Weizer, Univ. of Michigan (United States)

We are developing a CAD system for bladder cancer treatment response assessment in CT. We compared the performance of the deep-learning convolution neural network (DL-CNN) using different network sizes, and with and without transfer learning using natural scene images or regions of interest (ROIs) inside and outside the bladder. The DL-CNN was trained to identify responders (T0 disease) and non-responders to chemotherapy. ROIs were extracted from segmented lesions in pre- and post-treatment scans of a patient and paired to generate pre-post-treatment paired ROIs. The 87 lesions from 82 patients generated 104 temporal lesion pairs and 6,700 pre-post-treatment paired ROIs. Two-fold cross-validation and receiver operating characteristic analysis were performed and the area under the curve (AUC) was calculated for the DL-CNN estimates. The AUCs for prediction of T0 disease after treatment were 0.77±0.08 and 0.75±0.08, respectively, for the two partitions using DL-CNN without transfer learning and small network, and were 0.74±0.07 and 0.74±0.08 with the large network. The AUCs were 0.73±0.08, and 0.62±0.08 with transfer learning using bladder inside and outside ROIs and small network. The values were 0.77±0.08 and 0.73±0.07 with the large network. With transfer learning using natural scene images, the AUCs were 0.72±0.06 and 0.64±0.09, respectively, for the two partitions. None of the differences in the methods reached statistical significance. Our study demonstrated the feasibility of using DL-CNN for the estimation of treatment response in CT. Transfer learning did not improve the treatment response estimation. The DL-CNN performed better when transfer learning with bladder images was used instead of natural scene images.

10134-4, Session 1

Convolutional neural network based deep-learning architecture for prostate cancer detection on multiparametric magnetic resonance images

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Due to the recent success in bottom-up computer learning algorithms that can learn descriptive features from the given data, we investigated a deep-learning based convolutional neural network (CNN) architecture to find an improved solution for PCa detection on multiparametric MRI (mpMRI). The training and testing cases consisted of 52 patients with T2WI, ADC, and B2000 image sequences and at least one tumor to be used as ground truth. The mpMRI images and the ground truth pair were used to train a Holistically-nested Edge Detection (HED) network architecture, a state-of-the-art edge detection tool that takes an image as an input and produces an image probability map. Its loss function was modified to make it optimal for tumor detection, but no changes were made to the neural network architecture. Two-fold cross validation along with a receiver operating characteristic (ROC) analysis was used to determine the CAD's performance.

The efficacy was compared to an existing prostate CAD system that is based on a top-down learning method, which was evaluated on the same set of test cases. HED based CAD (HED-CAD) had an 85% detection rate at 20% false positive rate while the top-down learning CAD (TDL-CAD) had 55% detection rate at the same false positive rate. Area under the curves for HED-CAD and TDL-CAD were 0.90 and 0.80. In conclusion, Holistically-nested Edge Detection network architecture based CAD is able to detect cancerous lesions on mpMRI of the prostate with a performance greater than an existing top-down learning algorithm based CAD system.

10134-5, Session 1

Quantification of oxygen changes in the placenta from BOLD MR image sequences

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Functional analysis of the placenta is important to analyze and understand its role in fetal growth and development. BOLD MR is a non-invasive technique that has been extensively used for functional analysis of the brain. During the last years, several studies have shown that this dynamic image modality is also useful to extract functional information of the placenta. We propose in this paper a method to track the placenta from a sequence of BOLD MR images acquired under normoxia and hyperoxia conditions with the goal of quantifying how the placenta adapts to oxygenation changes. The method is based on a spatiotemporal transformation model that ensures temporal coherence of the tracked structures. The method was initially applied to four patients with healthy pregnancies. An average MR signal increase of 16.96±8.39% during hyperoxia was observed. These automated results are in line with state-of-the-art reports using time-consuming manual segmentations subject to inter-observer errors.

10134-6, Session 2

Cascade of convolutional neural networks for lung texture classification: overcoming ontological overlapping

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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. Traditionally, such classification relies on a two-dimensional analysis of axial CT images. This paper proposes a cascade of the existing CNN based CAD system, specifically tuned-up. The advantage of using a deep learning approach is a better regularization of the classification output. In a preliminary evaluation, the combined approach was tested on a 10 patient database of various lung pathologies, showing an increase of 10% in the accuracy with respect to the best suited state of the art CNN for this task.

10134-7, Session 2

Identification of early-stage Usual Interstitial Pneumonia from low-dose chest CT scans using fractional high-density lung distribution

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A fully-automated computer algorithm has been developed to identify early-stage Usual Interstitial Pneumonia (UIP) using features computed from low-dose CT scans. In each scan, the pre-segmented lung region is divided into N subsections (N=8, 27, 64) by separating the lung from anterior/posterior, left/right and superior/inferior in 3D space. Each subsection has approximately the same volume. In each subsection, a classic density measurement (fractional high-density volume h) is evaluated to characterize the disease severity in that subsection, resulting in a feature vector of length 2*N (for both lungs).

The algorithm was evaluated on a dataset consisting of 51 UIP and 56 normal cases, a feature vector H ={hi } was computed for all subsections of each case and an SVM classifier (RBF kernel) was used to classify each case into UIP or normal using ten-fold cross validation. A receiver operating characteristic (ROC) area under the curve (AUC) of 0.95 was achieved. Therefore this equal-volume partition fractional high-density volume method is useful in distinguishing early-stage UIP from normal cases.

10134-8, Session 2

3D convolutional neural network for automatic detection of lung nodules in chest CT

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Deep convolutional neural networks (CNNs) form the backbone of many state-of-the-art computer vision systems for classification and segmentation of 2D images. The same principles and architectures can be extended to three dimensions to obtain 3D CNNs that are suitable for volumetric data such as CT scans. In this work, we train a 3D CNN for automatic detection of pulmonary nodules in chest CT images using volumes of interest extracted from the LIDC dataset. We then convert the 3D CNN which has a fixed field of view to a 3D fully convolutional network (FCN) which can generate the score map for the entire volume efficiently in a single pass. Compared to the sliding window approach for applying a CNN across the entire input volume, the FCN leads to a nearly 800-fold speed-up, and thereby fast generation of output scores for a single case. This screening FCN is used to generate hard negative examples that are used to train a new discriminant CNN. The overall system consists of the screening FCN for fast generation of candidate regions of interest, followed by the discrimination CNN.

10134-9, Session 2

Automatic detection of lung nodules: false positive reduction using convolution neural networks and handcrafted features

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Univ. (China); Youn Seon Han, Johns Hopkins Univ. (United States); Jun Zhao, Shanghai Jiao Tong Univ. (China)

Lung cancer is the leading cause of cancer deaths worldwide. Early diagnosis is critical in increasing the 5-year survival rate, and the efficient and accurate detection of lung nodules, potential precursors to lung cancer, is evermore important. In this paper, a computer-aided detection (CAD) system for lung nodule detection using convolution neural networks (CNN) and handcrafted features for false positive (FP) reduction was developed. The CNNs were trained with three types of images: original lung CT images, their nodule-enhanced images, and their blood vessel-enhanced images. For each nodule candidate, nine 2D patches from differently oriented planes were extracted from each type of image. Patches of the same orientation from the same type of image across different candidates were used to train the CNNs independently, which were used to extract 864 features. 88 handcrafted features including intensity, shape, and texture features were also obtained from the lung CT images. The CNN features and handcrafted features were then combined to train a classifier, and a support vector machine (SVM) was adopted to achieve the final classification results. The proposed method was evaluated on 1004 CT scans from the LIDC-IDRI database using 10-fold cross-validation. Compared with the traditional CNN method using only lung CT images, the proposed method boosts the sensitivity from 89.3% to 91.2% at 4 FPs/scan and from 71.8% to

10134-10, Session 2

The effects of slice thickness and radiation dose level variations on computer-aided diagnosis (CAD) nodule detection performance in pediatric chest CT scans

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For pediatric oncology patients, CT scans are performed to assess treatment response and disease progression. CAD may be used to detect lung nodules which would reflect metastatic disease. The purpose of this study was to investigate the effects of reducing radiation dose and varying slice thickness on CAD performance in the detection of solid lung nodules in pediatric patients. The dataset consisted of CT scans of 58 pediatric chest cases, from which 7 cases had lung nodules detected by radiologist, and a total of 28 nodules were marked. For each case, the original raw data (sinogram data) was collected and a noise addition model was used to simulate reduced-dose scans of 50%, 25% and 10% of the original dose. In addition, the original and reduced-dose raw data were reconstructed at slice thicknesses of 1.5 and 3 mm using a medium sharp (B45) kernel. CAD tool was applied on all reconstructed scans, and results were compared with the radiologist's markings. Patient level mean sensitivities at 3mm thickness were 24%, 26%, 25%, 27%, and at 1.5 mm thickness were 23%, 29%, 35%, 36% for 10%, 25%, 50%, and 100% dose level, respectively. Mean FP numbers were 1.5, 0.9, 0.8, 0.7 at 3 mm and 11.4, 3.5, 2.8, 2.8 at 1.5 mm thickness for 10%, 25%, 50%, and 100% dose level respectively. CAD sensitivity did not change with dose level for 3mm thickness, but did change with dose for 1.5 mm. False Positives increased at low dose levels where noise values were high.

10134-11, Session 2

Lung lesion detection in FDG-PET/CT with Gaussian process regression

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Purpose: We propose a novel computer-assisted detection (CAD) method for lung lesions on FDG-PET/CT. We aim to detect more remarkable lesions in FDG-PET than in CT. Our method is based on anomaly detection, which does not require lesion labels manually made during the training phase. We also examine which features are useful to describe the relationship between FDG-PET and CT.

Methods: We formulated the lesion detection problem as anomaly detection based on the conditional probability distribution over normal standard uptake values (SUVs) given the feature vector extracted from the surrounding volume of interest in CT. The feature vectors include gradient-based and texture-based features. To estimate the distribution, we use Gaussian process regression with an automatic relevance determination (ARD) kernel, which provides the relevance of the features to the estimation. If the anomaly score calculated from the distribution for each voxel is higher than some predefined threshold, the voxel is judged as a part of a lesion.

Results: Our model was trained using FDG-PET/CT volumes of 121 normal cases. According to the validation using 28 FDG-PET/CT volumes with 34 lung lesions, the sensitivity of the proposed method at 5.0 false positives per case was 81.9%, while the sensitivity of naive thresholding in SUVs was 65.1%.

Conclusion: Our proposed method exhibited higher performance than using only FDG-PET. Also, we provided the information which features are useful to describe the relationship between FDG-PET and CT by using ARD kernel.

10134-12, Session 3

Evaluation of image features and classification methods for Barrett's cancer detection using VLE imaging

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Volumetric Laser Endomicroscopy (VLE) is a promising technique for the detection of early dysplasia in Barrett's Esophagus (BE). VLE generates hundreds of high-resolution, grayscale, cross-sectional images of the esophagus. However, at present, classifying these images is a time consuming and cumbersome effort performed by an expert using a clinical prediction model. This paper explores the feasibility of using computer vision techniques to accurately predict the presence of dysplastic tissue in VLE BE images with known histology. Our contribution is twofold. First, a benchmarking is performed for widely applied machine learning techniques and feature extraction methods. Second, three new features based on the clinical detection model are proposed, with superior classification accuracy and execution speed, compared to earlier work. The results are evaluated on a clinically validated dataset of 30 dysplastic and 30 non-dysplastic VLE images with known histology. Optimal classification accuracy is obtained by applying Adaptive Boosting with decision trees and using our modified Haralick features, yielding an area under the receiver operating characteristic of 0.91 compared to the clinical prediction model at 0.81. Optimal execution time is achieved using a proposed mean and median feature, which is extracted at least factor 2.5 faster than features with comparable performance.

10134-13, Session 3

Deep multi-spectral ensemble learning for electronic cleansing in dual-energy CT colonography

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We developed a novel electronic cleansing (EC) method for dual-energy CT colonography (DE-CTC) based on ensemble deep convolution neural networks (DCNNs) and multi-slice multi-spectral image patches. In the method, an ensemble DCNN 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 voxel classifier, where an input image patch centered at the voxel is generated as input to the DCNNs. An image patch has three channels that are mapped from a region-of-interest (ROI) containing the image plane of the voxel and the two adjacent image planes. Six different types of image patches are derived using the two dual-energy CT images, two virtual monochromatic images, and two material images. An ensemble DCNN is constructed by combining multiple DCNNs, each of which is trained with multi-slice multi-spectral image patches, by a meta-classifier. The electronically cleansed CTC images are calculated by removal of the regions that were classified as other than soft tissue, followed by colon surface reconstruction. For pilot evaluation, 359 volumes of interest (VOIs) representing sources of subtraction artifacts observed in current EC schemes were sampled from 30 clinical CTC cases. The preliminary results showed that the ensemble DCNN had high accuracy in labeling the VOIs, indicating that deep learning of multi-spectral EC could accurately remove residual fecal materials from CTC images without generating major EC artifacts.

10134-14, Session 3

Fully convolutional neural networks for polyp segmentation in colonoscopy

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Colorectal cancer (CRC) is one of the most common and deadliest forms of cancer, accounting for nearly 10% of all forms of cancer in the world. Even though colonoscopy is considered the most effective method for screening and diagnosis, the success of the procedure is highly dependent on the operator skills and level of hand-eye coordination. In this work, we propose to adapt fully convolution neural networks (FCN), to identify and segment polyps in colonoscopy images. We converted three established networks into a fully convolution architecture and fine-tuned their learned representations to the polyp segmentation task. We validate our framework on the 2015 MICCAI polyp detection challenge dataset, surpassing the state-of-the-art in automated polyp detection.

Our method obtained high segmentation accuracy, with a mean pixel precision and recall of 78.5% and 93.3%, respectively.

10134-15, Session 3

Deep ensemble learning of virtual endoluminal views for polyp detection in CT colonography

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We developed an ensemble deep convolutional neural network (DCNN) scheme (EDN) for learning of virtual endoluminal (VE) images to improve the performance of computer-aided detection (CADe) of polyps in CT colonography (CTC). Nine different types of renderings were generated for the VE images of polyp candidates detected by a conventional CADe system. We re-trained eleven DCNNs representing three types of publically available DCNN models to identify polyps from VE images. An EDN was developed by combining the DCNNs using a random forest classifier as the meta-classifier. The resulting EDN can be used to review the nine types of VE images of the polyp candidates to determine the final output. For evaluation, we sampled 154 CTC cases from a large CTC screening trial and divided them randomly into a training dataset and a test dataset. At 3.9 false-positive (FP) detections, the detection sensitivities of the conventional CADe system, single DCNN, and EDN were 81.3%, 90.7%, 93.5%, respectively, for polyps ≥6 mm in size. With the application of EDN, the number of FPs was 2.9 per patient at 86.8% sensitivity for 6-9 mm polyps and 3.9 per patient at 97% sensitivity for ≥10 mm polyps. These preliminary results indicate that the EDN scheme provides an effective approach for improving the detection performance of CADe in CTC, especially for small polyps.

10134-16, Session 3

Deep learning of contrast-coated serrated polyps for computer-aided detection in CT colonography

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Recent studies have revealed a novel molecular pathway where a subtype of hyperplastic polyps, called serrated polyps, can develop into colorectal cancer. CT colonography (CTC) is able to detect serrated polyps using the radiomic biomarker of contrast coating, but this requires expertise from the reader and current computer-aided detection (CADe) systems have not been designed to detect serrated polyps. The purpose of this study was to develop a novel CADe method that makes use of the contrast coating phenomenon to detect serrated polyps in CTC. After extraction of the colorectal region from CTC images, shape-based features are used to detect potential polyp sites. The sites are imaged using multi-angular 2D image patches that are reviewed for the presence of polyps by use of a deep convolutional neural network (DCNN). The DCNN-based polyp-likelihood estimates are merged into an aggregate polyp-likelihood index. For pilot evaluation, the proposed CADe scheme was evaluated with 10-fold cross-validation using 101 cases from a CTC screening program, where the patients were prepared for CTC with saline laxative and fecal tagging by barium and iodine-based diatrizoate. There were 144 biopsy-confirmed serrated polyps.

The average per-polyp sensitivity for serrated polyps ≥6 mm in size was 93±7% at 0.8±1.8 false positives per patient on average. Our results indicate that CADe is able to detect serrated polyps automatically at high accuracy in CTC, and that deep learning can be used to differentiate images of contrast-coated polyps from those of normal colon anatomy.

10134-17, Session 3

A study of oral contrast coating on the surface of polyps: an implication for computer-aided detection and classification of polyps

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Accurate identification of polyps is the ultimate goal of Computed Tomography Colonography (CTC). While oral contrast agents were originally used to tag stool and fluid for the ultimate goal of CTC, recently their effect on coating the surface of polyps has been observed. This study aims to evaluate (1) the frequency at which the oral contrast adhered to polyp surfaces and (2) if there was a difference in contrast adherence with respect to diverse polyp types. To eliminate gravity as a factor in this study, the polyps in contact with tagged fluid pools, particularly on the bottom of the colon wall were excluded. A total of 150 polyps were selected under the above condition from a CTC database and screened for any adherent contrast on the luminal edge. Among the total, 53% of the screened polyps had adherent contrast. Serrated adenomas and hyperplastic polyps had a higher tagging percentage, 77.80% and 62.50% respectively, than tubular adenomas and tubulovillous adenomas, 44.40% and 43% respectively. Other factors that were analyzed for the effect on coating include size and location of the polyps. The higher tagging percentage of serrated adenomas and hyperplastic polyps may be due to their similar cellular features. The average size of the polyps was 8.9 mm. When the polyps were separated by size into small (5-9mm) and large (10-26mm) groups, the large group had a higher tagging percentage. The polyp types were also classified by location with the major findings being: 1) Tubular adenomas were present in all segments of the colon and 2) that serrated adenomas were present at a higher percentage in the proximal colon. These findings shall facilitate characterizing tagging agents and improve computer aided detection and classification of polyps via CTC.

10134-18, Session 3

Computer assisted optical biopsy for colorectal polyps

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We propose a method for computer-assisted optical biopsy for colorectal polyps, with the final goal of assisting the medical expert during the colonoscopy. Our approach is based on recent advancements in convolutional neural networks (CNN) for image representation. In particular, we use features obtained from a pre-trained CNN and a random forest classifier. We show the feasibility of transferring a feature extraction mechanism trained on millions of natural images, to the task of classifying adenomatous polyps. For our study 776 polyp images were acquired and histologically analysed after polyp resection. We report a performance increase w.r.t. conventional engineered features and comparable results to a state-of-the art method using videos and 3D shape features.

10134-19, Session 4

Automatic estimation of heart boundaries and cardiothoracic ratio from chest X-ray images

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Cardiothoracic ratio (CTR) is a widely used radiographic index to assess heart size on Chest X-rays (CXRs). Recent studies have suggested that also two-dimensional CTR might contain clinical information about the heart function. However, manual measurement of such indices is both subjective and time consuming. This study proposes a fast algorithm to automatically estimate CTR indices in CXRs. The algorithm has three main steps: 1) model based lung segmentation, 2) estimation of heart boundaries from lung contours, and 3) computation of cardiothoracic indices from the estimated boundaries. We extended a previously employed lung detection algorithm to automatically estimate heart boundaries without using ground truth heart markings. We used two datasets: a publicly available dataset with 247 images as well as clinical dataset with 167 studies from Geisinger Health System. The models of lung fields are learned from both datasets. The lung regions in a given test image are estimated by registering the learned models to patient CXR. Then, heart region is estimated by applying Harris operator on segmented lung fields to detect the corner points corresponding to the heart boundaries. The algorithm calculates three indices, 1D-CTR, 2D-CTR, and cardiothoracic area ratio (CTAR). The method was tested on 103 clinical CXRs and average error rates of 7.9%, 25.5%, and 26.4% (for 1D-CTR, 2D-CTR, and CTAR respectively) were achieved. The proposed method outperforms previous CTR estimation methods. Moreover, it does not require heart templates. This method can have important clinical implications as it can provide fast and accurate estimate of cardiothoracic indices.

10134-20, Session 4

Coronary artery calcification identification and labeling in low-dose chest CT images

Yiting Xie, Shuang Liu, Cornell Univ. (United States); Albert Miller, Queens College, City Univ. of New York (United States); Jeffrey A. Miller, Rutgers New Jersey Medical School, Rutgers Univ. (United States); Steven Markowitz, Queens College, City University of New York (United States); Ali Akhund, Queens College, City Univ. of New York (United States); Anthony P. Reeves, Cornell Univ. (United States)

A fully automated computer algorithm has been developed to evaluate coronary artery calcification (CAC) from low-dose CT scans. CAC is identified and evaluated in three main coronary artery groups: Left Main and Left Anterior Descending Artery (LM + LAD) CAC, Left Circumflex Artery (LCX) CAC, and Right Coronary Artery (RCA) CAC. The artery labeling is achieved by applying geometric constraints on locally pre-identified anatomy regions. This algorithm was evaluated on 1,200 low-dose ungated CT scans, in which each artery CAC content was categorically visually scored by a radiologist into none, mild, moderate and extensive. The Spearman correlation coefficient R was used to assess the agreement between two automated CAC scores (Agatston-weighted and volume) and categorical visual scores. For Agatston-weighted automated scores, R was 0.84 for total CAC, 0.79 for LM + LAD CAC, 0.65 for LCX CAC and 0.73 for RCA CAC; results using volume scores were similar. These results indicate that location specific heart risk assessment is possible from low-dose chest CT images.

10134-21, Session 4

Coronary artery calcification (CAC) classification with deep convolutional neural networks

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Coronary artery calcification (CAC) is a typical marker of the coronary artery disease, which is one of the biggest causes of mortality in the U.S. This study evaluates the feasibility of using a deep convolutional neural network (DCNN) to automatically detect CAC in X-ray images.

1768 posteroanterior (PA) view chest X-Ray images from Sichuan Province People's Hospital, China were collected retrospectively. Each image is associated with a corresponding diagnostic report written by a trained radiologist (907 normal, 861 diagnosed with CAC). One-quarter of the images were randomly selected as test samples; the rest were used as training samples. DCNN models consisting of 2,4,6 and 8 convolutional layers were designed using blocks of pre-designed CNN layers. Each block was implemented in Theano with Graphics Processing Units (GPU). Human-in-the-loop learning was also performed on a subset of 165 images with framed arteries by trained physicians. The results from the DCNN models were compared to the diagnostic reports.

The average diagnostic accuracies for models with 2,4,6,8 layers were 0.85, 0.87, 0.88, and 0.89 respectively. The areas under the curve (AUC) were 0.92, 0.95, 0.95, and 0.96. As the model grows deeper, the AUC or diagnostic accuracies did not have statistically significant changes. Human-in-the-loop learning resulted in an average AUC of 0.95 and an average accuracy of 0.90, which were comparable to automatic detection. Our DCNN models achieved high accuracies in CAC classification, and were shown to be robust under image resizing, rotation, and in the presence of thermal noise.

10134-22, Session 4

Automatic extraction of disease-specific features from Doppler images

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Flow Doppler imaging is widely used by clinicians to detect diseases of the valves. In particular, continuous wave (CW) Doppler mode scan is routinely done during echocardiography and shows Doppler signal traces over multiple heart cycles. Traditionally, echocardiographers have manually traced such velocity envelopes to extract measurements such as decay time and pressure gradient which are then matched to normal and abnormal values based on clinical guidelines. In this paper, we present a fully automatic approach to deriving these measurements for aortic stenosis retrospectively from echocardiography videos. Comparison of our method with measurements made by echocardiographers shows large agreement as well as identification of new cases missed by echocardiographers.

10134-23, Session 4

Differentiation of pre-ablation and post-ablation late gadolinium-enhanced cardiac MRI scans of longstanding persistent atrial fibrillation patients

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Late Gadolinium-Enhanced Cardiac MRI (LGE CMRI) is an emerging non-invasive technique to image and quantify pre-ablation native and post-ablation atrial scarring. Previous studies have reported that enhanced image intensities of the atrial scarring in the LGE CMRI inversely correlate with the left atrial endocardial voltage invasively obtained by electro-anatomical mapping. However, the reported reproducibility of using LGE CMRI to identify and quantify atrial scarring is variable. This may be due to two reasons: first, delineation of the left atrium (LA) and pulmonary veins (PVs) anatomy generally relies on manual operation that is highly subjective, and this could substantially affect the subsequent atrial scarring segmentation; second, simple intensity based image features may not be good enough to detect subtle changes in atrial scarring. In this study, we hypothesized that texture analysis can provide reliable image features for the LGE CMRI images subject to accurate and objective delineation of the heart anatomy based on a fully-automated whole heart segmentation (WHS) method. We tested the extracted texture features to differentiate between pre-ablation and post-ablation LGE CMRI studies in longstanding persistent atrial fibrillation patients. These patients often have extensive native scarring and differentiation from post-ablation scarring can be difficult. Quantification results showed that our method is capable of solving this classification task, and we can envisage further deployment of this texture analysis based method for other clinical problems using LGE CMRI.

10134-24, Session 5

Radiomic modeling of BI-RADS density categories

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We developed a radiomic model for BI-RADS density assessment on digital mammography (FFDM) using supervised machine learning. With IRB approval, we retrospectively collected 478 FFDMs. Including intensity distribution and texture features, a total of 73 features were extracted from regions in each breast automatically determined by keypoint distribution. Our BI-RADS density estimator was constructed by using a random forest. The computerized density categories for 412 of the 478 cases agree with radiologist's assessment (kappa = 0.93). The machine learning method with radiomic feature as predictors demonstrated a high accuracy in classifying FFDMs into BI-RADS density categories.

10134-26, Session 5

Fully automated breast density assessment from low-dose chest CT

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Breast cancer is the most common cancer diagnosed among US women and the second leading cause of cancer death. Breast density has been shown

to be an independent risk factor of breast cancer and has been mandated to be reported during the mammographic screening by legislation in over 20 states. Recent publications have demonstrated that breast density measured from low-dose chest CT (LDCT) correlates well with that measured from mammograms and MRIs, thereby providing valuable information for many women who have undergone LDCT but not recent mammograms. A fully automated framework for breast density assessment from LDCT is presented in this paper. The whole breast region is first segmented using an anatomy-orientated novel approach based on the propagation of muscle fronts to resolve the challenge of separating the fibroglandular tissue from the underlying muscles. The fibroglandular tissue regions are then identified from the segmented whole breast and the percentage density is calculated based on the volume ratio of the fibroglandular tissue to the local whole breast region. The breast region segmentation framework was validated with 1270 LDCT scans, with 96.1% satisfactory outcomes. 100 scans with satisfactory segmentation were randomly selected for the validation of breast density measurements, and 91% scans obtained automated density assessment consistent with subjective reading of an experienced radiologist.

10134-27, Session 5

Convolutional neural network approach for enhanced capture of breast parenchymal complexity patterns associated with breast cancer risk

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We assess the feasibility of a parenchymal texture feature fusion approach, utilizing a convolutional neural network (ConvNet) architecture, to benefit breast cancer risk assessment. Hypothesizing that by capturing sparse, subtle interactions between localized motifs present in two-dimensional texture feature maps derived from mammographic images, a multitude of texture feature descriptors can be optimally reduced to five meta-features capable of serving as a basis on which a linear classifier, such as logistic regression, can efficiently assess breast cancer risk. We combine this methodology with our previously validated lattice-based strategy for parenchymal texture analysis and we evaluate the feasibility of this approach in a case-control study with 424 digital mammograms. In a randomized split-sample setting, we optimize our framework in training/validation sets (N=300) and evaluate its descriminatory performance in an independent test set (N=124). The discriminatory capacity is assessed in terms of the the area under the curve (AUC) of the receiver operator characteristic (ROC). The resulting meta-features exhibited strong classification capability in the test dataset (AUC = 0.90), outperforming conventional, non-fused, texture analysis which previously resulted in an AUC=0.85 on the same case-control dataset. Our results suggest that informative interactions between localized motifs exist and can be extracted and summarized via a fairly simple ConvNet architecture.

10134-28, Session 5

Identifying key radiogenomic associations between DCE-MRI and micro-RNA expressions for breast cancer

Ravi K. Samala, Heang-Ping Chan, Lubomir M. Hadjiiski, Mark A. Helvie, Renaid Kim, Univ. of Michigan Health System (United States)

Understanding the key radiogenomic associations for breast cancer between DCE-MRI and micro-RNA expressions is the foundation for the discovery of radiomic features as biomarkers for assessing tumor progression and prognosis. We conducted a study to analyze the radiogenomic associations for breast cancer using the TCGA-TCIA data set. The core idea that tumor etiology is a function of the behavior of miRNAs is used to build the regression models. The associations based on regression are analyzed for three study outcomes: diagnosis, prognosis, and treatment. The diagnosis group consists of miRNAs associated with clinicopathologic features of breast cancer and significant aberration of expression in breast cancer patients. The prognosis group consists of miRNAs which are closely associated with tumor suppression and regulation of cell proliferation and differentiation. The treatment group consists of miRNAs that contribute significantly to regulation of metastasis thereby having the potential to be part of therapeutic mechanisms. As a first step, important miRNA expressions were identified and their ability to classify the clinical phenotypes based on the study outcomes was evaluated using the area under the ROC curve (AUC) as a figure-of-merit. The key mapping between the selected miRNAs and radiomic features were determined using least absolute shrinkage and selection operator (LASSO) regression analysis within a two-loop leave-one-out cross-validation strategy. These key associations indicated a number of radiomic features from DCE-MRI to be potential biomarkers for the three study outcomes.

10134-29, Session 5

Computer-aided theragnosis using quantitative ultrasound methods and convolutional neural networks

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A non-invasive computer-aided-theragnosis (CAT) system was developed for the early assessment of responses to neoadjuvant chemotherapy in patients with locally advanced breast cancer (LABC). The CAT system was based on quantitative ultrasound spectroscopy methods in conjunction with deep learning techniques. This study, for the first time, applied convolutional neural networks (CNNs) in the application of therapeutic cancer response assessment in order to monitor the effectiveness of neoadjuvant chemotherapy early during the course of treatment administration. "Mid-treatment" scans at three intervals during the course of treatment were compared with the baseline scans acquired before treatment onset ("pre-treatment"). Patches of 64 ? 64 pixels were extracted from differentiated scans and submitted to a CNN for training and testing. The CNN comprised three main layers including convolutional, pooling, and fully-connected layers. The implementation of the network was accomplished using the Caffe library and the results of classification were compared with handcrafted texture parameters extracted from the parametric maps using local binary patterns (LBP). The results of the classification using the developed CAT system based on deep learning indicated an improvement of performance up to 10% compared to a CAT system with handcrafted features using the LBPs. The proposed CAT system, thus, establishes a non-invasive framework for monitoring cancer treatment response in tumours using clinical ultrasound imaging in conjunction with state-of-the-art machine learning techniques. Such a framework can potentially facilitate the detection of refractory responses in patients to treatment early on during a course of therapy to enable possibly switching to more efficacious treatments.

10134-91, Session 5

Neutrosophic segmentation of breast lesions for dedicated breast CT

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We proposed the neutrosophic approach for segmenting breast lesions in

breast Computer Tomography (bCT) images. The neutrosophic set (NS) considers the nature and properties of neutrality (or indeterminacy), which is neither true nor false. We considered the image noise as indeterminate component, while treating the breast lesion and other breast areas as true and false components. We first transformed the image into the NS domain. Each voxel in the image can be described as its membership in True, Indeterminate, and False sets. Operations ?-mean, ?-enhancement, and ?-plateau iteratively smooth and contrast-enhance the image to reduce the noise level of the true set. Once the true image no longer changes, we applied one existing algorithm for bCT images, the RGI segmentation, on the resulting image to segment the breast lesions. We compared the segmentation performance of the proposed method (named as NS-RGI) to that of the regular RGI segmentation. We used a total of 138 breast lesions (48 benign, 90 malignant) of 123 non-contrasted bCT cases. We measured the segmentation performances of the NS-RGI and the RGI using the DICE coefficient. The average DICE value of the NS-RGI was 0.82 (STD: 0.09), while that of the RGI was 0.8 (STD: 0.1). The difference between the two DICE values were statistically significant (paired t test, p-value = 0.0007). We conducted a subsequent feature analysis on the resulting segmentations. The classifier performance for the NS-RGI (AUC = 0.81) improved over that of the RGI (AUC = 0.71, p-value = 0.043).

10134-30, Session 6

Superpixel-based classification of gastric chromoendoscopy images

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Gastric chromoendoscopy (CH) for cancer detection is a highly mature medical field with solid clinical taxonomies, with CH images classified into their respective classes based on color, shape and regularity of pit patterns. The specific goal of this work is to classify the manually segmented region of each image as either 'Normal' or 'Abnormal'. To do this, the dataset is split in half (88 images for training purposes, and 88 for testing), and a classification model is built. Segmentation via superpixel is performed by grouping pixels into perceptually meaningful atomic regions, used to replace the rigid structure of the pixel grid. This technique, based on k-means clustering, is fast to compute and memory efficient. For each cluster of uniform pixels, 111 features are extracted (37 for each color plane): mean intensity and standard deviation with a simple analysis; contrast, energy and homogeneity by performing GLCM statistical analysis; local texture information are expressed through an histogram of local binary pattern, one of the most descriptive features in the field of texture classification. The feature matrix is then fed to a random forest based classifier, which computes a model used to predict the class of each image through a majority vote on each superpixel's predicted class. The average general accuracy of our model is 92.05% in the pixel domain (86.62% in the superpixel domain), while detection accuracies on the normal and abnormal class are respectively 85.71% and 95%.

10134-31, Session 6

Quantification of CT images for the classification of high- and low-risk pancreatic cysts

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Pancreatic cancer is the most lethal cancer with an overall 5-year survival rate of 7% due to the late stage at diagnosis and the ineffectiveness of current therapeutic strategies. Given the poor prognosis, early detection at a pre-cancerous stage is the best tool for preventing this disease. Intraductal papillary mucinous neoplasms (IPMN), cystic tumors of the pancreas, represent the only radiographically identifiable precursor lesion of pancreatic cancer and are known to evolve stepwise from low-to-high-grade dysplasia before progressing into an invasive carcinoma. Observation is usually recommended for low-risk patients, while high-risk patients undergo resection; hence, patient selection is critically important in the management of pancreatic cysts. Radiologists use standard criteria such as main pancreatic duct size, cyst size, or presence of a solid enhancing component in the cyst to optimally select patients for surgery. However, these findings are subject to a radiologist's interpretation and have been shown to be inconsistent with regards to the presence of a mural nodule or solid component. We propose objective classification of risk groups based on quantitative imaging features extracted from CT scans. We apply new features that represent the solid component (i.e. areas of high intensity) within the cyst and extract standard texture features. An adaptive boost classifier achieves the best performance with area under receiver operating characteristic curve (AUC) of 0.73 and accuracy of 77.3% for texture features. The random forest classifier achieves the best performance with AUC of 0.71 and accuracy of 70.8% with the solid component features.

10134-32, Session 6

Automated Liver Elasticity Calculation for 3D MRE

Bogdan Dzyubak, Kevin J. Glaser, Armando Manduca, Richard L. Ehman, Mayo Clinic (United States)

Magnetic Resonance Elastography (MRE) is a phase-contrast MRI technique which calculates quantitative stiffness images, called elastograms, by imaging propagation of acoustic waves in tissues. It is used clinically to diagnose liver fibrosis. Automated analysis of MRE is difficult as the corresponding MRI magnitude images (which contain anatomical information) are affected by intensity inhomogeneity, motion artifact, and poor tissue- and edge-contrast, and areas with poor wave propagation or low amplitude must be excluded. An automated algorithm was successfully developed and validated for standard 2D MRE. 3D MRE acquires substantially more data and, due to accelerated acquisition, has exacerbated image artifacts. Also, the current 3D MRE processing does not yield a confidence map to indicate MRE wave quality and guide ROI selection. In this study, the extension of the automated method, with a simple wave-amplitude metric used to exclude areas of low wave-SNR, was validated against an expert reader in a set of 57 patient exams with both 2D and 3D MRE. The stiffness discrepancy with the expert in 3D MRE was -0.8% ± 9.45% and was better than discrepancy with the same reader in 2D MRE (-3.2% ± 10.43%), and better than the inter-reader discrepancy observed in previous studies. There were no automated processing failures in this dataset. Thus, the automated liver elasticity calculation (ALEC) algorithm is able to calculate stiffness from 3D MRE data with minimal bias and good precision, while enabling stiffness measurements to be fully reproducible and to be easily performed on the large 3D MRE datasets.

10134-33, Session 6

The effects of iterative reconstruction in CT on low-contrast liver lesion volumetry: a phantom study

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This work aimed to assess the impact of iterative reconstruction (IR) on the performance of a lesion sizing tool in volume estimation of synthetic liver lesions in a non-uniform background. An anthropomorphic abdomen phantom was built with a removable liver insert filled with gelatin-based background. Gelatins of two densities were used to mimic normal liver tissue (~60 HU) and focal fat (~30 HU). Ten solid spherical lesions (20, 14, 10, 7, 5 mm @ 95, 110 HU) were embedded. The phantom was scanned at three CTDIvol levels(19.0, 7.6 and 3.87 mGy) and reconstructed using FBP, statistical-based IRs (ASiR30%, ASiR50%, ASiR70%), and a model-based IR (VEO). We repeated each scan five times with the phantom relocated between exposures. All lesion volumes were estimated using a matched-filter algorithm. Relative contrast of lesions and signal-to-noise ratios (SNR) were evaluated for each reconstruction algorithms. Linearity, bias, and repeatability analyses were performed.

Results show that IRs improved SNRs substantially. The relative contrast was fairly consistent across different algorithms. The absolute bias of each lesion ≥10 mm was less than 5% regardless of reconstruction or dose and with standard deviation up to 12%. For lesions <10 mm, bias (standard deviation) ranged from -27 to 20% (10 to 70%) in ASiR and FBP, but from 13 to 51% (6 to 40%) in VEO. VEO improved the repeatability especially when dose was low. In conclusion, IRs reduce noise substantially but their effect on volume estimation depend on the difficulty of the task and the type of IR.

10134-34, Session 6

Preoperative assessment of microvascular invasion in hepatocellular carcinoma

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Hepatocellular carcinoma (HCC) is the most common liver cancer and the third leading cause of cancer-related death worldwide. Resection or liver transplantation may be curative in patients with early-stage HCC but early recurrence is common. Microvascular invasion (MVI) is one of the most important predictors of early recurrence. The identification of MVI prior to surgery would optimally select patients for potentially curative resection or liver transplant. Patients with large tumors are not eligible for transplant under current selection criteria. If MVI status was established preoperatively, patients without MVI and large tumors would be considered for transplant and patients with smaller tumors and MVI would be selected for surgery. MVI is not reliably evaluated by biopsy due to sampling error in these large heterogeneous tumors. MVI can only be diagnosed by microscopic assessment of the resected tumor. The aim of the present study is to apply CT-based texture analysis to identify pre-operative imaging predictors of MVI in patients with HCC. Texture features are derived from CT and analyzed individually as well as in combination, to evaluate their value in predicting MVI. Two-stage classification is employed: HCC tumors are automatically categorized into uniform or heterogeneous groups followed by classification into the presence or absence of MVI. We achieve an area under the receiver operating characteristic curve (AUC) of 0.76 and accuracy of 76.7% for uniform lesions and AUC of 0.79 and accuracy of 74.06% for heterogeneous tumors. These results suggest that MVI can be accurately and objectively assessed from preoperative CT scans.

10134-35, Session 7

Combination of lateral and PA view radiographs to study development of knee OA and associated pain

Luca Minciullo, Jessie Thomson, Timothy F. Cootes, The Univ. of Manchester (United Kingdom)

Knee Osteoarthritis (OA) is the most common form of arthritis, affecting millions of people around the world. The effects of the disease have been studied using the shape and texture features of bones in Posterior-Anterior (PA) and Lateral radiographs separately. In this work we compare the utility of features from each view, and evaluate whether combining features from both is advantageous. We built a fully automated system to independently locate landmark points in both radiographic images using Random Forest Constrained Local Models. We extracted discriminative features from the two bony outlines using Appearance Models. The features were used to train Random Forest classifiers to solve three specific tasks: (i) OA classification, distinguishing patients with structural signs of OA from the others; (ii) predicting future onset of the disease and (iii) predicting which patients with no current pain will have a positive pain score later in a follow-up visit. Using a subset of the MOST dataset we show the PA view has more discriminative features to classify and predict OA, while the lateral view contain features that achieve better performance in predicting pain, and that combining the features from both views gives a small improvement in accuracy of classification compared to the individual views.

10134-36, Session 7

Characterizing cartilage microarchitecture on phase-contrast x-ray computed tomography using deep learning with convolutional neural networks

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The effectiveness of phase contrast X-ray computed tomography (PCI-CT) in visualizing human patellar cartilage matrix has been demonstrated due to its ability to capture soft tissue contrast on a micrometer resolution scale. Recent studies have shown that off-the-shelf Convolutional Neural Network (CNN) features learned from a non-medical data set can be used for medical image classification. In this paper, we investigate the ability of features extracted from two different CNNs for characterizing chondrocyte patterns in the cartilage matrix. We obtained features from 842 regions of interest annotated on PCI-CT images of human patellar cartilage using CaffeNet and Inception-v3 Network, which were then used in a machine learning task involving support vector machines with radial basis function kernel to classify the ROIs as healthy or osteoarthritic. Classification performance was evaluated using the area (AUC) under the Receiver Operating Characteristic (ROC) curve. The best classification performance was observed with features from Inception-v3 network (AUC = 0.95), which performs comparably to all gray-level co-occurrence matrix derived features (best AUC = 0.93). These results suggest that such characterization of chondrocyte patterns using features from internal layers of CNNs can be used to distinguish between healthy and osteoarthritic tissue with high accuracy.

10134-37, Session 7

Classification of micro-CT images using 3D characterization of bone canal patterns in human osteogenesis imperfecta

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Few studies have analyzed the microstructural properties of bone in cases of Osteogenenis Imperfecta (OI), or 'brittle bone disease'. Current approaches mainly focus on bone mineral density measurements as an indirect indicator of bone strength and quality. It has been shown that bone strength would depend not only on composition but also structural organization. This study aims to characterize 3D structure of the cortical bone in high resolution micro CT images. A total of 40 bone fragments from 28 subjects (13 with OI and 15 healthy controls) were imaged using micro tomography using a synchrotron light source (SRμCT). Minkowski functionals - volume, surface, curvature, and Euler characteristics - describing the topological organization of the bone were computed from the images. The features were used in a machine learning task to classify between healthy and OI bone. The best classification performance (mean AUC – 0.96) was achieved with a combined 4-dimensional feature of all Minkowski functionals. Individually, the best feature performance was seen using curvature (mean AUC - 0.85), which characterizes the edges within a binary object. These results show that quantitative analysis of cortical bone microstructure, in a computer aided diagnostics framework, can be used to distinguish between healthy and OI bone with high accuracy.

10134-38, Session 7

Automated melanoma recognition in dermoscopic images based on extreme learning machine (ELM)

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Skin cancer in the form of malignant melanoma is one of the most dangerous types which is responsible for over 9,000 deaths each year in the US. The detection of the malignant melanoma in its early stages with dermoscopic images reduces the mortality considerably, hence this a crucial issue for the dermatologists. Dermoscopy or skin surface microscopy provides in vivo inspection of color and morphologic structures of pigmented skin lesions (PSLs), rendering higher accuracy for detecting suspicious cases than it is possible via inspecting with naked eye. However, interpretation of dermoscopic images is time consuming and subjective, even for trained dermatologists. Therefore, there is currently a great interest in the development of computer-aided diagnosis (CAD) systems for automated melanoma recognition. However, the majority of the CAD systems are still in the early development stage with lack of descriptive feature generation and benchmark evaluation in ground-truth datasets. This work is focusing on by addressing the various issues related to the development of such a CAD system with effective feature extraction from Non-Subsampled Contourlet Transform (NSCT) and Eig(Hess) histogram of oriented gradients (HOG) and lesion classification with efficient Extreme Learning Machine (ELM). Finally, the effectiveness of the system is evaluated in a benchmark data set of dermoscopic images towards the goal of realistic comparison and real clinical integration. The proposed research on melanoma recognition has huge potential for offering powerful services that would significantly benefit the present Biomedical Information Systems.

10134-39, Session 8

FDA's role in the innovation and evaluation of evolving CAD solutions *(Keynote Presentation)*

Kyle J. Myers, U.S. Food and Drug Administration (United States)

No Abstract Available

10134-40, Session 8

Organ detection in thorax abdomen CT using multi-label convolutional neural networks

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A convolutional network architecture is presented to determine bounding boxes around six organs in thorax-abdomen CT scans. A single network for each orthogonal direction determines the presence of lungs, kidneys, spleen and liver. We show that an architecture that takes additional slices before and after the slice of interest as an additional input outperforms an architecture that processes single slices. From the slice-based analysis, a bounding box around the structures of interest can be computed. The system uses 6 convolutional, 4 pooling and one fully connected layer and uses 333 scans for training and 110 for validation. The test set contains 110 scans. The average Dice score of the proposed method was 0.95 and 0.95 for the lungs, 0.59 and 0.58 for the kidneys, 0.83 for the liver and 0.63 for the spleen. This paper shows that automatic localization of organs using multi-label convolution neural networks is possible. This architecture can likely be used to identify other organs of interest as well.

10134-41, Session 8

Mammographic phenotypes of breast cancer risk driven by breast anatomy

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Image-derived features of breast parenchymal texture patterns have emerged as promising risk factors for breast cancer, paving the way towards personalized recommendations regarding women's cancer risk evaluation and screening. The main steps to extract texture features of the breast parenchyma are the selection of regions of interest (ROIs) where texture analysis is performed, the texture feature calculation and the texture feature summarization in case of multiple ROIs. In this study, we incorporate breast anatomy in these three key steps by (a) introducing breast anatomical sampling for the definition of ROIs, (b) texture feature calculation aligned with the structure of the breast and (c) weighted texture feature summarization considering the spatial position and the underlying tissue composition of each ROI. We systematically optimize this novel framework for parenchymal tissue characterization in a case-control study with digital mammograms from 424 women. We also compare the proposed approach with a conventional, non-driven-by-breast-anatomy methodology, recently shown to enhance the potential of parenchymal texture analysis in breast cancer risk assessment. The case-control discriminatory performance is assessed using support vector machines (SVMs) with 10-fold cross validation, where the evaluation measure is the area under the curve (AUC) of the receiver operating characteristic. Upon optimization, the proposed breast-anatomy-driven approach demonstrated a promising case-control classification performance (AUC=0.90). In the same dataset, the performance of conventional parenchymal texture characterization was found to be significantly lower (AUC=0.79, DeLong's test p-value<0.05). Our results suggest that breast anatomy may further leverage parenchymal texture features in breast cancer prediction, and may therefore be a valuable addition in pipelines aiming to elucidate quantitative mammographic phenotypes of breast cancer risk.

10134-42, Session 9

Validation of an image registration and segmentation method on ECG-gated CT data of a physical dynamic stent graft model

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The application of endovascular aortic aneurysm repair has expanded tremendously over the last decade. However, stent graft durability, in particular durable fixation and sealing to the aortic wall, remains the main concern of this treatment. The sealing and fixation are challenged at every heartbeat due to downward and radial pulsatile forces. Yet knowledge on cardiac-induced dynamics of implanted stent grafts is sparse, as it is not measured in routine follow-up with static imaging techniques. Such knowledge is particularly relevant to perform fatigue tests, to predict failure in the individual patient and to improve stent grafts. Using a physical dynamic stent graft model in an anthropomorphic phantom, we have evaluated the accuracy of our previously proposed segmentation and registration algorithm to detect periodic motion of endovascular stent grafts on ECG-gated 4D-CT data. Abdominal aortic motion profiles were simulated in two series of Gaussian based motion patterns with different amplitudes and frequencies. Experiments were performed on a 64-slice CT scanner with a helical scan protocol and retrospective gating. Motion patterns calculated by our algorithm were compared to motion patterns obtained from camera recordings of the physical stent graft model in motion. Absolute errors of stent graft motion were smaller than 0.28 mm. The smallest motion pattern with an amplitude of 0.23 mm was detected, although the amplitude of motion was overestimated by the algorithm. We conclude that the algorithm performs well for the detection of aortic stent graft motion in the mm and sub-mm range. This ultimately is expected to aid in patient-specific risk assessment and prevention of stent graft failure.

10134-43, Session 9

Automatic detection and quantification of pulmonary arterio-venous malformations in hereditary hemorrhagic telangiectasia

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Hereditary hemorrhagic telangiectasia (HHT) is an autosomic dominant disorder, which is characterized by the development of multiple arterio-venous malformations in the skin, mucous membranes, and/or visceral organs. Pulmonary Arterio-Venous Malformation (PAVM) is an abnormal connection where feeding arteries shunt directly into draining veins with no intervening capillary bed. This condition may lead to paradoxical embolism and hemorrhagic complications. PAVMs patients should systematically be screened as the spontaneous complication rate is high, reaching almost 50%. Chest enhanced contrast CT scanner is the reference screening and follow-up examination. When performed by experienced operators as the prime treatment, percutaneous embolization of PAVMs, is a safe, efficient and sustained therapy. The accuracy of PAVM detection and quantification of its progression over time is the key of embolotherapy success. In this paper, we propose an automatic method for PAVM detection and quantification relying on a modeling of vessel deformation, i.e. local caliber increase, based on mathematical morphology. The pulmonary field and vessels are first segmented using geodesic operators. The vessel caliber is estimated by means of a granulometric measure and the local caliber increase is detected by using the h-domes operator applied in a hysteresis scheme. The detection sensitivity can be tuned up according to the choice of the h value which models the irregularity of the vessel caliber along its axis and the PAVM selection is performed according to a clinical criterion of >3 mm diameter of the feeding artery of the PAVM. The developed method was tested on a 20 patient dataset. A sensitivity study allowed choosing the irregularity parameter to maximize the true positive ratio reaching 81% in average. A specific false positive reduction procedure targeting the vessel trunks of the arterio-venous tree near mediastinum allows 25% precision increase with an average false positives per scan of 2.85.

10134-44, Session 9

Pelvic artery calcification detection on CT scans using convolutional neural networks

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Artery calcification is observed commonly in elderly patients, especially in patients with chronic kidney disease, and may affect coronary, carotid and peripheral arteries. Vascular calcification has been associated with many clinical outcomes. Manual identification of calcification in CT scans requires substantial expert interaction, which makes it time-consuming and infeasible for large-scale studies. Many works have been proposed for coronary artery calcification detection in cardiac CT scans. In these works, coronary artery extraction is commonly required for calcification detection. However, there are few works about abdominal or pelvic artery calcification detection. In this work, we present a method for automatic pelvic artery calcification detection on CT scan. This method uses the recent advanced faster region-based convolutional neural network (R-CNN) to directly identify artery calcification without a need for artery extraction since pelvic artery extraction itself is challenging. Our method first generates category-independent region proposals for each slice of the input CT scan using region proposal networks (RPN). Then, each region proposal is jointly classified and refined by softmax classifier and bounding box regressor. We applied the detection method to 500 images from 20 CT scans of elderly patients for evaluation. The detection system achieved a 77.4% average precision and a 85% sensitivity at 1 false positive per image.

10134-45, Session 9

Vessel segmentation in 4D arterial spin labeling magnetic resonance angiography images of the brain

Renzo Phellan, Univ. of Calgary (Canada); Thomas Lindner, Univ. of Kiel (Germany); Alexandre X. Falcão, Univ. Estadual de Campinas (Brazil); Nils Daniel Forkert, Univ. of Calgary (Canada)

4D arterial spin labeling magnetic resonance angiography (4D ASL MRA) is a non-invasive and safe modality for cerebrovascular imaging procedures. It uses the patient's magnetically labeled blood as intrinsic contrast agent, so that no external contrast media is required. It provides important 3D structure and blood flow information but a sufficient cerebrovascular segmentation is important since it can help clinicians to analyze and diagnose vascular diseases faster, and with higher confidence as compared to simple visual rating of raw ASL MRA images. This work presents a new method for automatic cerebrovascular segmentation in 4D ASL MRA images of the brain. Therefore, images are denoised, corresponding image label/control image pairs of the 4D ASL MRA sequences are subtracted, and temporal intensity averaging is used to generate a static representation of the vascular system. After that, a set of vessel and background seeds

is extracted and provided as input for the image foresting transform algorithm to segment the vascular system. Four 4D ASL MRA datasets of the brain of healthy subjects and corresponding time-of-flight (TOF) MRA images were available for this preliminary study. For evaluation of the segmentation results of the proposed method, the cerebrovascular system was automatically segmented in the high-resolution TOF MRA images using a validated algorithm and the segmentation results were registered to the 4D ASL datasets. On average, a Dice similarity coefficient of 0.9025 was achieved, indicating that vessels are identified in most cases.

10134-46, Session 9

Computer-assisted measurement increases the precision and accuracy of intracranial aneurysm morphology analysis

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Clinicians currently base most intracranial aneurysm (IA) treatment decisions on crude morphological measurements made manually from 2D angiographic images. However, due to the complexity of the IA's geometry, measurements on 2D images may give imprecise results, and manual calculations can vary based on clinician experience. Furthermore, studies have shown that several more sophisticated morphological and hemodynamic indices are highly correlated with rupture risk, and yet they are not easily calculated by current approaches. The purpose of this study is to introduce and validate computer-aided adjuncts for aneurysmal assessment and to show the clinical utility of this tool. To this end, we have developed a prototype software, AView, to calculate morphometric and hemodynamic analysis of IAs. Herein, we experimentally validated the morphological measurement tools and tested the software on a retrospective clinical dataset to compare computer-aided measurement and manually measurement. Our results showed that the measurements in AView recapitulates the sizes of known spheres and compare well to established 3D morphological measurement tools. Additionally, we found that clinicians using manual measurement tend to over-estimate size for small aneurysm and under-estimate size in large aneurysms. Additionally, clinicians utilizing computer-aided size measurements are more consistent. This study validates and shows the necessity of a computer-aided approach for morphological analysis of IAs.

10134-47, Session 9

Hessian-assisted supervoxel: structure-oriented voxel clustering and application to mediastinal lymph node detection from CT volumes

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In this paper, we propose a novel supervoxel segmentation method and demonstrate its application to feature extraction for mediastinal lymph node detection. Starting from a popular supervoxel segmentation method, SLIC, which computes supervoxels by minimising differences of intensity and distance, we overcome this method's limitation of merging neighboring regions with similar intensity by introducing Hessian-based feature analysis into the supervoxel formation, resulting in a more accurate division into distinct regions. This way, different tissue types in chest CT volumes can be segmented individually, even if neighboring tissues have similar intensity or have non-spherical extent. We show that this method can be used for multi-scale feature value extraction from the supervoxels, and apply it to the detection of false positives of mediastinal lymph nodes in 47 chest CT volumes. We obtained the better false positive reduction result compared to the previous method.

10134-48, Session 11

Conditional random field modeling of interactions between findings in mammography

Thijs Kooi, Jan-Jurre Mordang, Nico Karssemeijer, Radboud Univ. Medical Ctr. (Netherlands)

Recent breakthroughs in deep learning, in particular deep Convolutional Neural Networks (CNNs), made a big impact on vision research and are increasingly responsible for advances in Computer Aided Diagnosis (CAD). Since many natural scenes and medical images vary in size and are too large to feed to the networks as a whole, two stage systems are typically employed, where in the first stage, small regions of interest in the image are located and presented to the network as training and test data. A shortcoming of this approach is that the information is local and context is not taken into account. In this paper, we present preliminary work on employing a Conditional Random Field (CRF) that is trained on top of the CNN to model contextual interactions such as the presence of other suspicious regions and microcalcifications for mammography CAD. The model is general and can easily be extended to incorporate other sources of information, such as symmetry, temporal change and various patient covariates.

10134-49, Session 11

Deep learning and three-compartment breast imaging in breast cancer diagnosis

Karen Drukker, Benjamin Q. Huynh, Maryellen L. Giger, The Univ. of Chicago (United States); Serghei Malkov, Jesus I. Avila, Bo Fan, Bonnie Joe, Karla Kerlikowske, Univ. of California, San Francisco (United States); Jennifer S. Drukteinis, H. Lee Moffitt Cancer Ctr. & Research Institute (United States); Leila Kazemi, Univ. of California, San Francisco (United States); Malesa M. Pereira, H. Lee Moffitt Cancer Ctr. & Research Institute (United States); John A. Shepherd, Univ. of California, San Francisco (United States)

We investigated whether deep learning has potential to aid in the diagnosis of breast cancer when applied to mammograms and biologic tissue composition images derived from three-compartment (3CB) imaging.

The dataset contained diagnostic mammograms and 3CB images (water, lipid, and protein content) of biopsy-sampled BIRADS 4 and 5 lesions in 195 patients. In 58 patients, the lesion manifested as a mass (13 malignant vs. 45 benign), in 87 as microcalcifications (19 vs. 68), and in 56 as (focal) asymmetry or architectural distortion (11 vs. 45). Six patients had both a mass and calcifications. For each mammogram and corresponding 3CB images, a 128x128 region of interest containing the lesion was selected by an expert radiologist and used directly as input to a deep learning method pre-trained on a very large independent set of non-medical images. We used a nested leave-one-out-by-case (patient) model selection and classification protocol. The area under the ROC curve (AUC) for the task of distinguishing between benign and malignant lesions was used as performance metric.

For the cases with mammographic masses, the AUC increased from 0.83 (mammograms alone) to 0.89 (mammograms+3CB, p=.162). For the microcalcification and asymmetry/architectural distortion cases the AUC increased from 0.84 to 0.91 (p=.116) and from 0.61 to 0.87 (p=.006), respectively.

Our results indicate great potential for the application of deep learning methods in the diagnosis of breast cancer and additional knowledge of the biologic tissue composition appeared to improve performance, especially for lesions mammographically manifesting as asymmetries or architectural distortions.

10134-50, Session 11

Performance comparison of deep learning and segmentation-based radiomic methods in the task of distinguishing benign and malignant breast lesions on DCE-MRIs

Natasha Antropova, Benjamin Q. Huynh, Maryellen L. Giger, The Univ. of Chicago (United States)

Intuitive segmentation-based CADx/radiomic features, calculated from the lesion segmentations of dynamic contrast-enhanced magnetic resonance images (DCE-MRIs) have been utilized in the task of distinguishing between malignant and benign lesions. Additionally, deep learning allows for the use of an alternative method of radiomics extraction, convolutional neural networks (CNN), where the features are derived directly from the image data. However, the comparison of computer-extracted segmentation-based and CNN features in breast lesion characterization has not yet been conducted. In our study, we used a DCE-MRI database of 640 breast cases--191 benign and 449 malignant. Thirty eight segmentation-based features were extracted automatically using our quantitative radiomics workstation. Also, 2D ROIs were selected around each lesion on the DCE-MRIs and directly input into a pre-trained CNN AlexNet, which involved transfer learning, yielding 4,096 CNN features. Each method was investigated separately and in combination in terms of performance in the task of distinguishing between benign and malignant lesions. Area under the ROC curve (AUC) served as a figure of merit. Both methods yielded promising classification performance with round-robin cross-validated AUC values of 0.88 (se =0.01) and 0.76 (se=0.02) for segmentation-based and deep learning methods, respectively. Combination of the two methods enhanced the performance in malignancy assessment resulting in an AUC value of 0.91 (se=0.01), a statistically significant improvement over the performance of the CNN method alone.

10134-51, Session 11

Classification of breast MRI lesions using small-size training sets: comparison of deep learning approaches

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Diagnostic interpretation of breast MRI studies requires meticulous work and high expertise. Computerized algorithms may assist radiologists by automatically characterizing the detected lesions. Deep learning approaches have shown promising results in natural image classification, but their applicability to medical imaging is limited by the deficiency of large annotated training sets. In this work, we address automatic classification of breast MRI lesions using two different deep learning approaches. We propose a novel image representation for dynamic contrast enhanced (DCE) breast MRI lesions, which combines the morphological and kinetics information in a single multi-channel image. We compare two classification approaches for discriminating between benign and malignant lesions: training a designated convolutional neural network and using a pre-trained deep network to extract features for a shallow classifier. The domain-specific trained network provided higher classification accuracy, compared to the pre-trained model, with area under the ROC curve of 0.91 vs. 0.81 and accuracy of 0.83 vs. 0.71. Similar accuracy was achieved in classifying benign lesions, malignant lesions and normal tissue images. The trained network was able to improve by using the multi-channel image representation, and was more robust to reductions in the size of the training set. A small-size convolutional neural network can learn to accurately classify findings in medical images using as little as few hundreds of images from few dozens of patients. With sufficient data augmentation, such network can be trained to outperform a pre-trained out-of-domain classifier. Development of domain-specific deep-learning models for medical imaging may facilitate technological advancements in computer-aided diagnosis.

10134-52, Session 11

Prediction of occult invasive disease in ductal carcinoma in situ using computer-extracted mammographic features

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Purpose: Predicting the risk of occult invasive disease in ductal carcinoma in situ (DCIS) is an important task to help address the overdiagnosis and overtreatment problems associated with breast cancer. In this work, we investigated the feasibility of using computer-extracted mammographic features to predict invasive disease in patients with biopsy proven DCIS.

Method: We proposed a computer-vision algorithm based approach to extract mammographic features from magnification views of full field digital mammography (FFDM) for patients with DCIS. After an expert breast radiologist provided a region of interest (ROI) mask for the DCIS lesion, the proposed approach is able to segment individual microcalcifications (MCs), detect the boundary of the MC cluster (MCC), and extract 113 mammographic features from MCs and MCC within the ROI. In this study, we extracted mammographic features from 99 patients with DCIS (74 pure DCIS; 25 DCIS plus invasive disease). The predictive power of the mammographic features was demonstrated through binary classifications between pure DCIS and DCIS with invasive disease using linear discriminant analysis (LDA). Before classification, the minimum redundancy maximum relevance (mRMR) feature selection method was first applied to choose subsets of useful features. The generalization performance was accessed using Leave-One-Out Cross-Validation and Receiver Operating Characteristic (ROC) curve analysis.

Result: Using the computer-extracted mammographic features, the proposed model was able to distinguish DCIS with invasive disease from pure DCIS, with an average classification performance of AUC = 0.61 ± 0.05.

Conclusion: Overall, the proposed computer-extracted mammographic features are promising for predicting occult invasive disease in DCIS.

10134-53, Session 11

Deep learning of symmetrical discrepancies for computer-aided detection of mammographic masses

Nico Karssemeijer, Thijs Kooi, Radboud Univ. Medical Ctr. (Netherlands)

When humans identify objects in images, context is an important cue; a cheetah is more likely to be a domestic cat when a television set is recognised in the background. Similar principles apply to the analysis of medical images. The detection of diseases that manifest unilaterally in symmetrical organs or organ pairs can in part be facilitated by a search for symmetrical discrepancies in or between the organs in question. In this paper, we explore 3 different fusion schemes for convolutional deep learning architectures with the goal to optimally capture such asymmetries. The methods are applied to the domain mammography CAD, but can be relevant to other medical image analysis tasks where symmetry is important such as lung, prostate or brain images.

10134-76, Session PS1

Analysis of 18F-DMFP-PET data using Hidden Markov Random Field and the Gaussian distribution to assist the diagnosis of Parkinsonism

Fermin Segovia Roman, Diego Salas González, Juan Manuel Górriz Sáez, Javier Ramírez Pérez de Inestrosa, Francisco Jesús Martínez Murcia, Univ. de Granada (Spain)

18F-DMFP-PET is a neuroimaging modality that allows us to analyze the striatal dopamine. Thus, it is recently emerging as an effective tool to assist the diagnosis of Parkinsonism and differentiate among Parkinsonian syndromes. However the analysis of these data, which require specific preprocessing methods, is still poorly covered. In this work we demonstrate a novel methodology based on Hidden Markov Random Fields (HMRF) and Gaussian Mixtures Model to preprocess 18F-DMFP-PET data. First, we performed a selection of voxels based on the analysis of the histogram in order to remove low-signal regions and regions outside the brain. Specifically, we modeled the histogram of intensities of a neuroimage with a mixture of two Gaussians and then, using a HMRF algorithm the voxels corresponding to the low-intensity Gaussian were discarded. This procedure is similar to the tissue segmentation usually applied to Magnetic Resonance Imaging data. Secondly, the intensity of the selected voxels was scaled so that the Gaussian that models the histogram for each neuroimage has same mean and standard deviation. This step made the data from different patients comparable, without removing the characteristic patterns of each patient's disorder. The proposed approach was evaluated using a computer system based on statistical classification that separated the neuroimages according to the Parkinsonian variant they represented. The proposed approach achieved higher accuracy rates than standard approaches for voxel selection (based on atlases) and for intensity normalization (based on the global mean).

10134-77, Session PS1

Automated method to compute Evans index for diagnosis of idiopathic normal pressure hydrocephalus on brain CT images

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The early diagnosis of idiopathic normal pressure hydrocephalus (iNPH) considered as a treatable dementia is important. The iNPH causes enlargement of lateral ventricles (LVs). The degree of the enlargement of the LVs on CT or MR images is evaluated by using a diagnostic imaging criterion, Evans index (EI). EI is defined as the ratio of the maximal width of frontal horns (FH) of the LVs to the maximal width of the inner skull (IS). EI-value greater than 0.3 is suggested as a hallmark for iNPH. Manual measurement of EI is a time-consuming process. In this study, we present an automated method to compute EI on brain CT images. The algorithm of the method consisted of five major steps: standardization of CT data to an atlas, extraction of FH and IS regions, the search for the outmost points of bilateral FH regions, determination of the maximal widths of both the FH and the IS, and calculation of EI. The standardization to the atlas was performed by using linear affine transformation and non-linear wrapping techniques. The FH regions were segmented by using a three dimensional region growing technique. This scheme was applied to CT scans from 44 subjects, including 13 iNPH patients. The average difference in EI between the proposed method and manual measurement was 0.01 (1.6%), and the correlation coefficient of these data for the EI was 0.98. Therefore, this computerized method may have the potential to accurately calculate EI for the diagnosis of iNPH on CT images.

10134-78, Session PS1

Case-based statistical learning applied to SPECT image classification

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Statistical learning and decision theory play a key role in many areas of science and engineering. Some examples include time series regression and prediction, optical character recognition, signal detection in communications or biomedical applications for diagnosis and prognosis. This paper deals with the topic of learning from biomedical image data in the classification problem. In a typical scenario we have a training set that is employed to fit a prediction model or emph{learner} and a testing set on which the emph{learner} is applied to in order to predict the outcome for new unseen patterns. Both processes are usually completely separated to avoid over-fitting and due to the fact that, in practice, the unseen new objects (testing set) have unknown outcomes. However, the outcome yields one of a discrete set of values, i.e. the binary diagnosis problem. Thus, assumptions on these outcome values could be established to obtain the most likely prediction model at the training stage, that could improve the overall classification accuracy on the testing set, or keep its performance at least at the level of the selected statistical classifier. In this sense, a novel case-based learning (c-learning) procedure is proposed which combines hypothesis testing from a discrete set of expected outcomes and a cross-validated classification stage.

10134-79, Session PS1

Fine-tuning convolutional deep features for MRI-based brain tumor classification

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Manual prediction of survival time from brain tumor magnetic resonance images (MRI) is not commonly performed and would ordinarily be a time consuming process. However, current cross-sectional imaging techniques, particularly MRI, generate many features that may provide information on the patient's prognosis including survival. This information can potentially be used to identify individuals who would benefit from more aggressive therapy. Rather than using pre-defined and hand-engineered features as with current radiomics methods, we investigated the use of deep features extracted from pre-trained convolutional neural networks (CNNs) in predicting survival time. We also provide evidence for the power of domain specific fine-tuning in improving the performance of a pre-trained CNN,

even though the data set is small. We fine-tuned a CNN initially trained on a large natural image recognition dataset (Imagenet ILSVRC) and transferred the learned feature representations to the survival time prediction task, obtaining over 81% accuracy in leave one out cross validation.

10134-80, Session PS1

Application of Probabilistically-Weighted Graphs to Image-Based Diagnosis of Alzheimer's Disease using Diffusion MRI

Oleg V. Michailovich, Syeda Maryam, Laura McCrackin, Mark Crowley, Univ. of Waterloo (Canada); Yogesh Rathi, Harvard Medical School, Harvard Univ. (United States)

This study addresses the problem of image-based diagnosis of Alzheimer's Disease (AD) based on information provided by Diffusion Magnetic Resonance Imaging (dMRI). We propose an extension of region-based statistical methods to simultaneous characterization of multiple brain regions, which we describe by means of an undirected, fully-connected graph with probabilistic weights. The characteristics of such graphs provide a sensitive mechanism for perfect separation of AD subjects and normal controls (NC), thereby laying ground for further developments towards finer stratification between AD and its prodromal stages (e.g. MCI). Our model is verified using samples from the ADNI database.

10134-81, Session PS1

Machine learning algorithm for automatic detection of CT-identifiable hyperdense lesions associated with traumatic brain injury

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Traumatic brain injury (TBI) is a major cause of death and disability in the United States. Time to treatment is often related to patient outcome. The performance of fast and accurate cerebral imaging is an important component of patient care. Current methods of detecting and quantifying intracranial pathology are time-consuming, in that they require careful review of the 2D/3D images by a radiologist. Additional time is allotted for image protocoling, acquisition, and processing. These steps occur in series, adding time to the process of identifying and treating brain injury - a condition where time to treatment is critical.

Using machine learning and computer vision, we demonstrate a technique to rapidly and automatically detect CT-identifiable lesions. To identify important image features that can distinguish TBI lesions, we use the scale invariant feature transform (SIFT) and deep convolutional neural networks (CNN). Our learning algorithm is a linear support vector machine (SVM). The technique was validated using 409 CT scans of the brain, acquired via the Progesterone Treatment, Experimental Clinical Trial (PROTECTIII) study considering patients with moderate to severe TBI. CT data are annotated by a central radiologist and include patients with positive and negative scans. Additionally, the largest lesion on each positive scan was manually segmented. We reserved 80% of the data for training the SVM and 20% for testing. Preliminary results are promising with prediction accuracies as high as 92.55% (sensitivity = 91.15%, specificity = 93.45%), indicating the potential usefulness of this technique in clinical scenarios.

10134-82, Session PS1

Automatic classification of patients with idiopathic Parkinson's disease and progressive supranuclear palsy using diffusion MRI datasets

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Parkinson's disease denotes a spectrum of neurodegenerative illnesses, which can be classified into various subtypes. The differentiation of these variants is typically conducted based on clinical criteria assessed by clinicians. Due to the overlap of intra-syndrome symptoms, the accurate differential diagnosis based on classical clinical guidelines remains a challenge with failure rates up to 25%. The aim of this study is to present an image-based classification of patients with idiopathic Parkinson's disease (IPD) and patients with progressive nuclear palsy (PSP), an atypical variant of Parkinson's disease, using mean apparent diffusion coefficient (ADC) values in different brain regions extracted from diffusion magnetic resonance imaging (MRI) datasets. Therefore, mean ADC values were determined in 82 different brain regions using an atlas-based approach. The extracted mean ADC values for each patient were then used as features for classification using a linear kernel support vector machine classifier. To increase the classification accuracy, a feature selection was performed, which resulted in the top 17 attributes to be selected as the final input features. A leave-one-out cross evaluation based on 56 IPD and 21 PSP subjects revealed that the proposed method is capable of differentiating IPD and PSP patients with an accuracy of 94.8%. More precisely, three IPD patients were falsely classified as PSP and one PSP patient was falsely classified as IPD. In conclusion, the classification of IPD and PSP patients based on ADC features obtained from diffusion MRI datasets is a promising alternative in the context of image-based decision support systems.

10134-83, Session PS1

Automated detection and quantification of residual brain tumor using an interactive computer-aided detection scheme

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Detection of residual brain tumor is important to evaluate efficacy of brain cancer surgery, determine optimal strategy of further radiation therapy if needed, and assess ultimate prognosis of the patients. Brain MR is a commonly used imaging modality for this task. In order to distinguish between residual tumor and surgery induced scar tissues, two sets of MRI scans are conducted pre- and post-gadolinium contrast injection. The residual tumors are only enhanced in the post-contrast injection images. However, subjective reading and quantifying this type of brain MR images faces difficulty in detecting real residual tumor regions and measuring total volume of the residual tumor. In order to help solve this clinical difficulty, we developed and tested a new interactive computer-aided detection scheme, which consists of three consecutive image processing steps namely, 1) segmentation of the intracranial region, 2) image registration and subtraction, 3) tumor segmentation and refinement. The scheme also includes a specially designed and implemented graphical user interface (GUI) platform. When using this scheme, two sets of pre- and post-contrast injection images are first automatically processed to detect and quantify residual tumor volume. Then, a user can visually examine segmentation results and conveniently guide the scheme to correct any detection or segmentation errors if needed. The scheme has been repeatedly tested using five cases. Due to the observed high performance and robustness of the testing results, the scheme is currently ready for conducting clinical

studies and help clinicians investigate the association between this quantitative image marker and outcome of patients.

10134-85, Session PS1

Improving utility of brain tumor confocal laser endomicroscopy: objective value assessment and diagnostic frame detection with convolutional neural networks

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Confocal laser endomicroscopy (CLE), although capable of obtaining images at cellular resolution in real time with significant potential to improve precision in brain tumor surgery, creates as many non-diagnostic as diagnostic images. Non-useful images are often distorted due to relative motion between probe and brain or blood artifacts. Many images, however, simply lack diagnostic features immediately informative to the physician. Examining all the hundreds or thousands of images from a single case to discriminate diagnostic images from non-diagnostic ones can be tedious. Providing a real time "diagnostic value" assessment of images (fast enough to be used during the surgical acquisition process and accurate enough for the pathologist to rely on) to automatically detect diagnostic frames would streamline the analysis of images and filter useful images for the pathologist/surgeon. We sought to automatically classify images as diagnostic or non-diagnostic. AlexNet, a deep-learning architecture, was used in a 4-fold cross validation manner. Our dataset included 16,795 images (8572 non-diagnostic and 8223 diagnostic) from 74 CLE-aided brain tumor surgery patients. The ground truth for all the images is provided by the pathologist. Average model accuracy on test data was about 91% overall (90.79 % accuracy, 90.94 % sensitivity and 90.87 % specificity). To evaluate the model reliability we also performed receiver operating characteristic (ROC) analysis yielding 0.958 average for area under ROC curve (AUC). These results demonstrate that a deeply trained AlexNet network can create a model that reliably and quickly recognizes diagnostic CLE images.

10134-86, Session PS1

Automatic classification of cardioembolic and arteriosclerotic ischemic strokes from apparent diffusion coefficient datasets using texture analysis and deep learning

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Stroke is a leading cause of death and disability in the western hemisphere. Acute ischemic strokes can be broadly classified based on the underlying cause into atherosclerotic strokes, cardioembolic strokes, small vessels disease, and stroke with other causes. The ability to determine the exact phenotype of an acute ischemic stroke is highly relevant for optimal treatment decision and preventing recurrent events. However, the differentiation of atherosclerotic and cardioembolic phenotypes can be especially challenging due to similar appearance and symptoms. The aim of this study was to develop and evaluate the feasibility of an image-based machine learning approach for discriminating between arteriosclerotic and cardioembolic acute ischemic strokes using 56 apparent diffusion coefficient (ADC) datasets from acute stroke patients. For this purpose, acute infarct lesions were semi- atomically segmented and 30,981 geometric and texture image features were extracted for the lesion segmentation. To improve the performance and accuracy, categorical Pearson's chi-squared test was used to select the most informative features while removing redundant attributes. As a result, only 289 features were finally included for training of a deep multilayer feed-forward neural network without bootstrapping. The proposed method was evaluated using a leave-one-out cross validation scheme. The proposed classification method achieved an average area under receiver operator characteristic curve value of 0.93 and a classification accuracy of 94.64%. These first results suggest that the proposed image-based classification framework can support neurologists in clinical routine differentiating between atherosclerotic and cardioembolic phenotypes.

10134-88, Session PS1

Deep learning for segmentation of brain tumors: Can we train with images from different institutions?

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Deep learning and convolutional neural networks (CNNs) in particular are increasingly popular tools for segmentation and classification of medical images. CNNs were shown to be particularly successful for segmentation of brain tumors. However, in the environment where sharing data is increasingly encouraged and multi-institutional datasets are available, a question arises: does training with data from another institution with potentially different imaging equipment, contrast protocol, and patient population impact the segmentation performance of the CNN? In this study, we present preliminary data toward answering this question. Specifically, we used magnetic resonance imaging data of glioblastoma (GBM) patients for 2 institutions present in The Cancer Imaging Archive dataset. We performed a process of training and testing CNN multiple times such that half of the time the CNN was tested on data from the same institution that was used for training and half of the time it was tested on another institution. In our experiments, the training and testing set size remained constant. We observed a decrease in performance as measured by Dice coefficient when the CNN was trained with data from a different institution as compared to training with data from the same institution. The difference in performance was from 0.72 to 0.65 for the entire tumor ($p<0.06$), 0.61 to 0.58 for the enhancing component ($p<0.49$), 0.54 to 0.51 for necrotic region ($p<0.82$), 0.31 to 0.23 for T1 abnormality ($p<0.03$), and 0.43 to 0.31 for FLAIR abnormality ($p<0.003$). In summary, we found that while data across institutions can be used for development of CNNs, this might be associated with a moderate decrease in performance.

10134-89, Session PS1

Improved brain tumor segmentation by utilizing tumor growth model in longitudinal brain MRI

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In this work, we propose a novel method to improve texture based tumor segmentation by fusing cell density patterns that are generated from tumor growth modeling. In order to model tumor growth, we solve the reaction-diffusion equation by using Lattice-Boltzmann method (LBM). Computational tumor growth modeling obtains the cell density distribution

that potentially indicates the predicted tissue locations in the brain over time. The density patterns is then considered as novel features along with other texture (such as fractal, and multifractal Brownian motion (mBm)), and intensity features in MRI for improved brain tumor segmentation. We evaluate the proposed method with about one hundred longitudinal MRI scans from five patients obtained from public BRATS 2015 data set, validated by the ground truth. The result shows significant improvement of complete tumor segmentation using ANOVA analysis for five patients in longitudinal MR images.

10134-25, Session PS2

Feature extraction using convolutional neural network for classifying breast density in mammographic images

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Breast cancer is the leading cause of death for women in most countries. The high levels of mortality relates to late diagnosis and the direct proportionally relationship between breast density and breast cancer development. Therefore, the correct assessment of breast density is important to provide better screening for higher risk patients. However, in modern digital mammography the assessment of dense breasts is highly complex. Thus, a computational system for classifying breast density might be a useful tool for aiding medical staff. Several machine-learning algorithms are capable of classifying with good accuracy tasks with a small number of classes. However, machine-learning algorithms main constraint relates to the set of features extracted and used for classification. Although well-known feature extraction techniques provide a good set of features, it is a complex task to select an initial set during design of a classifier. Thus, we propose feature extraction using a Convolutional Neural Network (CNN) for classifying breast density by a usual machine-learning classifier. We used 307 mammographic images downsampled to 260x200 pixels to train a CNN and extract features from a deep layer. After training, the activation of 8 neurons of a deep fully connected layer are extracted and used as features. Then, these features are feedforward to a single hidden layer neural network that is cross-validated using 10-folds to classify among four classes of breast density. The global accuracy of this method is 98.4%, presenting only 1.6% of misclassification. Thus, we presented a promising method for extracting features and classifying breast density.

10134-90, Session PS2

An ensemble-based approach for breast mass classification in mammography images

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Mammography analysis is an important tool that helps detecting breast cancer at the very early stages of the disease, thus increasing the quality of life of hundreds of thousands of patients worldwide. In Computer-Aided Detection systems, the identification of mammograms with and without masses (without clinical findings) is highly needed to reduce the false positive rates regarding the automatic selection of regions of interest that may contain some suspicious content. In this work, the introduce a variant of the Optimum-Path Forest (OPF) classifier for breast mass identification, as well as we employed an ensemble-based approach that can enhance the effectiveness of individual classifiers aiming at dealing with the aforementioned purpose. The experimental results also comprise the na ?ıve OPF and a traditional neural network, being the most accurate results obtained through the ensemble of classifiers, with an accuracy nearly to 86%.

10134-92, Session PS2

A novel deep learning-based approach to high-accuracy breast density estimation in digital mammography

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Mammographic breast density is a well-established marker for breast cancer risk. However, accurate measurement of dense tissue is a difficult task due to faint contrast and significant variations in background fatty tissue. This study presents a novel method for automated mammographic density estimation based on Convolutional Neural Network (CNN). A total of 397 full-field digital mammograms were selected from Seoul National University Hospital. Among them, 297 mammograms were randomly selected as a training set and the rest 100 mammograms were used for a test set. We designed a CNN architecture suitable to learn the imaging characteristic from a multitudes of sub-images and classify them into dense and fatty tissues. To train the CNN, not only local statistics but also global statistics extracted from an image set were used. The image set was composed of original mammogram and eigen-image which was able to capture the X-ray characteristics in despite of the fact that CNN is well known to effectively extract features on original image. The 100 test images which was not used in training the CNN was used to validate the performance. The correlation coefficient between the breast estimates by the CNN and those by the expert's manual measurement was 0.95. Our study demonstrated the feasibility of incorporating the deep learning technology into radiology practice, especially for breast density estimation. The proposed method has a potential to be used as an automated and quantitative assessment tool for mammographic breast density in routine practice.

10134-93, Session PS2

Does the prediction of breast cancer improve using a combination of mammographic density measures compared to individual measures alone?

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High mammographic density is associated with increased risk of breast

cancer, however whether the association is stronger when there is agreement across several density measures is unknown. This study investigates whether a combination of density measures is a better predictor of breast cancer risk than individual methods alone.

Women recruited as a part of the Predicting Risk of Cancer At Screening (PROCAS) study and with mammographic density assessed using three different methods were included (n=33,304). Density was assessed visually using Visual Analogue Scales (VAS) and by two fully automated methods, Quantra and Volpara. Percentage breast density for each method was divided into tertiles (high, medium and low) and combinations of measures were used to further categorise individuals (e.g. 'all high'). A total of 667 breast cancers were identified and logistic regression was used to determine the relationship between breast density and breast cancer risk.

In total, 44% of individuals were in the same tertile for all three measures, with 8.6% of individuals in non-adjacent (high and low) or mixed categories (high, medium and low). Of the individual methods the strongest association with breast cancer risk was for medium and high tertiles of VAS (odds ratio (OR) of 1.45 (95% CI 1.18 to 178) and 1.86 (1.53 to 2,27) respectively). The combination of density methods increased the strength of association for the 'all medium' group (OR 1.64) but not for the 'all high' group (OR 1.90).

Combining density measures provides modest improvement in risk estimates compared to VAS alone.

10134-94, Session PS2

Automated assessment of breast tissue density in non-contrast 3D CT images without image segmentation based on a deep CNN

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This paper describes a novel approach for automatic assessment of breast tissue densities in non-contrast 3D CT images. The proposed approach trains a deep convolutional neural network from scratch to accomplish the breast tissue density assessment directly from CT images without any anatomical structure segmentations required in conventional works. Our scheme determines breast tissue density in a 3D breast region by decomposing a 3D breast region into a number of radial 2D-sections from nipple and measuring the distribution of breast tissue densities on each 2D section from different orientations. The whole scheme is designed as a compact all-in-one network without any post processing to gain a superior robustness and computational efficiency for real clinical setting. We applied this scheme to a dataset that includes 400 non-contrast CT scans from 30 to 45 year-old-women in Japan. The breast tissue density on each CT scan was assigned into one of the four ranks (glandular tissue within breast composition <25%, 25%-50%, 50%-75%, and >75%) by a radiologist as ground truth. We used 300 CT scans for training the deep CNN and remained 100 CT scans for testing the performance. The experimental results demonstrated that the proposed approach successfully achieved the same judgement to the radiologist in 73% CT scans in training samples and 76% CT scans in testing samples respectively. Those results demonstrated the potentials of using a deep CNN for assessment of breast tissue density in non-contrast 3D CT images.

10134-95, Session PS2

Automated detection of microcalcification clusters in mammograms

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Mammography is the most efficient modality for detection of breast cancer at early stage. Microcalcifications are tiny bright spots in mammograms and can often get missed by the radiologist during diagnosis. The presence of microcalcification clusters in mammograms can act as an early sign of breast cancer. This paper presents a completely automated Computer Aided Detection (CAD) system for detection of microcalcifications in mammograms. High Boost filtering is used as a preprocessing step which enhances the contrast between microcalcifications and the background. The preprocessed image is thresholded and various shape and intensity-based features are extracted. Support Vector Machine (SVM) classifier is used to reduce the false positives while preserving the true microcalcification clusters. The proposed technique is applied on two different databases i.e DDSM and private database. The proposed technique shows good sensitivity with moderate false positives (FPs) per image on both databases.

10134-96, Session PS2

Automated detection of masses on whole breast volume ultrasound scanner: false positive reduction using deep convolutional neural network

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Breast cancer screening with mammography and ultrasonography is expected to improve sensitivity compared with mammography alone, especially for women with dense breast. An automated breast volume scanner (ABVS) provides the operator-independent whole breast data which facilitate double reading and comparison with past exams, contralateral breast, and multimodality images. However, large volumetric data in screening practice increase radiologists' workload. Therefore, our goal is to develop a computer-aided detection scheme of breast masses in ABVS data for assisting radiologists' diagnosis and comparison with mammographic findings. In this study, we investigated the false positive reduction scheme using deep convolutional neural network (DCNN). For training DCNN, regions of interest (ROIs) including masses were obtained from multiplanar reconstruction slices. The false positive ROIs were prepared for suspicious regions randomly selected from the result of automated detection using the vector convergence filter. In the preliminary experiment, the number of false positives were reduced by half without missing the true positive regions. The result indicates the potential usefulness of the proposed method for false positive reduction in the computer-aided mass detection framework.

10134-97, Session PS2

Agreement between a computer-assisted tool and radiologists to classify lesions in breast elastography images

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Breast elastography is a new sonographic technique that provides additional information to evaluate tissue stiffness. However, interpreting breast elastography images can vary depending on the radiologist. In order to provide quantitative and less subjective data regarding the stiffness of a lesion, we developed a tool to measure the amount of hard area in a lesion from the 2D image. The database consisted of 78 patients with 83 breast lesions (31 malignant and 52 benign). Two radiologists and one resident manually drew the contour of the lesions in B-mode ultrasound images and the contour was mapped in the elastography image. By using the system proposed, the radiologists obtained a very good diagnostic agreement among themselves (kappa = 0.86), achieving the same sensitivity and specificity (80.7 and 88.5, respectively), and an AUC of 0.883 for Radiologist 1 and 0.892 for Radiologist 2. The Resident had less interobserver agreement, as well as lower specificity and AUC, which may be related to less experience. Furthermore, the radiologists had an agreement with the tool used in the automatic method higher than 90%. Thus, the method developed was useful in aiding the diagnosis of breast lesions in strain elastography, minimizing its subjectivity.

10134-99, Session PS2

Comparison of breast DCE-MRI contrast time points for predicting response to neoadjuvant chemotherapy using deep convolutional neural network features with transfer learning

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DCE-MRI datasets have a temporal aspect to them, resulting in multiple regions of interest (ROIs) per subject, based on contrast time points. It is unclear how the different contrast time points vary in terms of usefulness for computer-aided diagnosis tasks in conjunction with deep learning methods. We thus sought to compare the different DCE-MRI contrast time points with regard to how well their extracted features predict response to neoadjuvant chemotherapy within a deep convolutional neural network. Our dataset consisted of 561 ROIs from 64 subjects. Each subject was categorized as a non-responder or responder, determined by recurrence-free survival. First, features were extracted from each ROI using a convolutional neural network (CNN) pre-trained on non-medical images. Linear discriminant analysis classifiers were then trained on varying subsets of these features, based on their contrast time points of origin. Leave-one-out cross validation (by subject) was used to assess performance in the task of estimating probability of response to therapy, with area under the ROC curve (AUC) as the metric. The classifier trained on features from strictly the pre-contrast time point performed the best, with an AUC of 0.85 (SE = 0.033). The remaining classifiers resulted in AUCs ranging from 0.71 (SE = 0.028) to 0.82 (SE = 0.027). Overall, we found the pre-contrast time point to be the most effective at predicting response to therapy and that including additional contrast time points moderately reduces variance.

10134-100, Session PS2

A new texture descriptor based on local micro-pattern for detection of architectural distortion in mammographic images

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This paper presents a new local micro-pattern texture descriptor for the detection of architectural distortion in mammographic images. Architectural Distortion (AD) is a subtle contraction of breast parenchyma that may represent an early sign of breast cancer. Due to its subtlety and variability, AD is more difficult to detect compared to microcalcifications and masses, and is commonly found in retrospective evaluations of false-negative mammograms. Several computer-based systems have been proposed for automatic detection of AD, but their performance are still unsatisfactory. The proposed descriptor, Local Mapped Pattern (LMP), is a generalization of Local Binary Pattern (LBP), which is considered one of the most powerful feature descriptor for texture classification in digital images. As compared to LBP, the LMP descriptor captures more effectively the minor differences between the local image pixels. Moreover, LMP is a parametric model which can be optimized for the desired application. In our work, the LMP performance was compared to original LBP and four Haralick's texture features for the classification of 400 regions of interest extracted from digitized mammograms. The feature vectors were used as input to a multilayer perceptron artificial neural network, with a single hidden layer. The best results achieved, in terms of area under the receiver operating characteristics curve (AUC), were 0.87 for the LBP, 0.96 for all four Haralick's descriptors combined and 0.97 for the LMP descriptor. Future works will evaluate the performance of the proposed descriptor on full-field digital mammography and 3D reconstructed digital breast tomosynthesis images.

10134-101, Session PS2

The impact of using weight estimated from mammographic images vs self-reported weight on breast cancer risk calculation

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Introduction: Fully personalised breast screening requires assessment of individual risk of breast cancer, of which one contributory factor is weight. Self-reported weight has previously been used for this purpose, but may be unreliable. We explore the potential of using the volume of fat in the breast, measured from digital mammograms, as an alternative to self-reported weight for cancer risk assessment.

Methods: Volumetric breast density measurements from VolparaTM were used to determine the volume of fat in the breasts of 40431 women who took part in the Predicting Risk Of Cancer At Screening (PROCAS) study. Tyrer-Cuzick risk using self-reported weight was calculated for each woman. Each woman's weight was also estimated from the relationship between self-reported weight and breast fat volume in the cohort, and these estimated weights were used to re-calculate Tyrer-Cuzick risk. Women were assigned to risk categories according to 10 year risk (low <2%, population 2-3.49%, moderate 3.5-4.9%, high >5%) and allocations based on the original and re-calculated Tyrer-Cuzick risks compared.

Results: 593 women (1.5%) moved into a lower risk category, and 1259 (3.1%) moved into a higher category when using weight estimated from breast

fat volume. The majority of these changes (72.8%) were between low and population risk. No individual moved more than one risk group, e.g. from low to moderate, or from high to population.

Conclusion: Automated breast fat measures may provide a suitable alternative to self-reported weight for risk assessment in personalized screening. Further validation against actual weights is necessary.

10134-102, Session PS2

Computer-aided diagnosis of mammographic masses using geometric verification-based image retrieval

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Computer-Aided Diagnosis of masses in mammograms is an important indicator of breast cancer. The use of retrieval systems in breast examination is increasing gradually. In this respect, the method of exploiting the vocabulary tree framework and the inverted file in the mammographic masse retrieval have been proved high accuracy and excellent scalability. However it just considered the features in each image as a visual word and had ignored the spatial configurations of features. It greatly affect the retrieval performance. To overcome this drawback, we introduce the geometric verification method to retrieval of mammographic masses. First of all, we obtain corresponding match features based on the vocabulary tree framework and the inverted file. After that, we grasps the main point of local similarity characteristic of deformations in the local regions by constructing the circle regions of corresponding pairs. Meanwhile we quarter the circle to express the geometric relationship of local matches in the area and generate the spatial encoding strictly. Additionally, we rotate the quartered circle to control the strictness of geometric constraints. Finally we judge whether the matched features are correct or not, based on verifying the all spatial encoding are whether satisfied the geometric consistency. The experimental results demonstrates that our method could improve the retrieval accuracy significantly with low computational cost.

10134-103, Session PS2

Can upstaging of ductal carcinoma in situ be predicted at biopsy by histologic and mammographic features?

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Purpose: Reducing the overdiagnosis and overtreatment associated with ductal carcinoma in situ (DCIS) requires accurate prediction of the invasive potential at cancer screening. In this work, we investigated the utility of pre-operative histologic and mammographic features to predict upstaging of DCIS. The goal was to provide intentionally conservative baseline performance using readily available data from radiologists and pathologists and only linear models.

Method: We conducted a retrospective analysis on 99 patients with DCIS. Of those 25 were upstaged to invasive cancer at the time of definitive surgery. Pre-operative factors including both the histologic features extracted from stereotactic core needle biopsy (SCNB) reports and the mammographic features annotated by an expert breast radiologist were investigated with statistical analysis. Furthermore, we built classification models based on those features in an attempt to predict the presence of an occult invasive component in DCIS, with generalization performance assessed by receiver operating characteristic (ROC) curve analysis.

Result: Histologic features including nuclear grade and DCIS subtype did not show statistically significant differences between cases with pure DCIS and with DCIS plus invasive disease. However, three mammographic features, i.e., the major axis length of DCIS lesion, the BI-RADS level of suspicion, and radiologist's assessment did achieve the statistical significance. Using those three statistically significant features as input, a linear discriminant model was able to distinguish patients with DCIS plus invasive disease from those with pure DCIS, with an ROC AUC equal to 0.62.

Conclusion: Overall, mammograms used for breast screening contain useful information that can be perceived by radiologists and help predict invasion in DCIS.

10134-104, Session PS3

MRI myocardium T2* measurement by a new PCA- based object recognition algorithm

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MRI myocardium T2* measurement is a very important task in MRI for the detection, for example, of myocardial iron overload. Generally, T2* values are obtained by a T2* multiecho MRI. In particular, signal intensities of selected ROIs on different TE images are valuated and the signal -TE relation is used in order to estimate the T2*. In order to correctly estimate the T2*, it is important that the different selected ROIs correspond to the same anatomical pixels. In this paper, a new PCA-based recognition algorithm is presented in order to recognize and quantify the same anatomical pixels on different TE images of a multiecho sequence. The algorithm was implemented in Matlab. A group of 10 patients, referred to MRI with presumptive, clinical diagnosis of myocardial iron overload, was examined in order to test the algorithm. All patients showed no myocardial iron overload with a T2* > 20 ms. To assess intra- and interobserver variability, two observers blindly analyzed the data by delimiting myocardial region. A good intra- and interobserver reproducibility was obtained, in fact the mean difference between the two observer measurements was 0.8 ms and the 95% limits of agreement on the Bland-Altman plot were -4.9 to 6.5 ms.

10134-105, Session PS3

Left ventricle segmentation in cardiac MRI images using fully convolutional neural networks

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According to the World Health Organization, cardiovascular diseases are the leading cause of death worldwide, accounting for 17.3 million deaths per year, a number that is expected to grow to more than 23.6 million by 2030. Most cardiac pathologies involve the left ventricle; therefore, estimation of several functional parameters from a previous segmentation of this structure can be helpful in diagnosis. Manual delineation is a time consuming and tedious task that is also prone to high intra and inter-observer variability.

Thus, there exists a need for automated cardiac segmentation method to help facilitate the diagnosis of cardiovascular diseases. In this work we propose a deep fully convolutional neural network architecture to address this issue and assess its performance. The model was trained end to end in a supervised learning stage from whole cardiac MRI images input and ground truth to make a per pixel classification. For its design, development and experimentation was used Caffe deep learning framework over an NVidia Quadro K4200 Graphics Processing Unit (GPU). The net architecture is: Conv64-ReLU (2x) – MaxPooling – Conv128-ReLU (2x) – MaxPooling – Conv256-ReLU (2x) – MaxPooling – Conv512-ReLu-Dropout (2x) – Conv2-ReLU – Deconv – Crop – Softmax. Training and testing processes were carried out using 5-fold cross validation with short axis cardiac MR images from Sunnybrook Database. We obtained a sensitivity of 0.90, specificity of 0.99, Dice score of 0.90, Jaccard index of 0.97 and Hausdorff distance of 4.48, overall mean values.

10134-106, Session PS3

A novel 3D shape descriptor for automatic retrieval of anatomical structures from medical images

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Content-based image retrieval (CBIR) aims at retrieving from a database objects that are similar to an object provided by a query, by taking into consideration a set of extracted features. While CBIR has been widely applied in the two-dimensional image domain, the retrieval of 3D objects from medical image datasets using CBIR remains to be explored. In this context, the development of descriptors that can capture information specific to organs or structures is desirable. In this work, we focus on the retrieval of two anatomical structures commonly imaged by Magnetic Resonance Imaging (MRI) and Computer Tomography (CT) techniques, the left ventricle of the heart and blood vessels. Towards this aim, we developed the Area-Distance Local Descriptor (ADLD), a novel 3D local shape descriptor that employs mesh geometry information, namely facet area and distance from centroid to surface, to identify shape changes. Because ADLD only considers surface meshes extracted from volumetric medical images, it substantially diminishes the amount of data to be analyzed. ADLD exhibited good performance, achieving 90% precision rate for retrieving both convex (left ventricle) and non-convex structures (blood vessels), allowing for detection of abnormalities associated with changes in shape. Thus, this technique has the potential to aid in the diagnosis of a wide range of vascular and cardiac diseases.

10134-107, Session PS3

Application of convolutional artificial neural networks to echocardiograms for differentiating congenital heart diseases in a pediatric population

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In this paper we describe a pilot study, where machine learning methods are used to differentiate between congenital heart diseases. Our approach was to apply convolutional neural networks (CNNs) to echocardiographic images from five different pediatric populations: normal, coarctation of the aorta (CoA), hypoplastic left heart syndrome (HLHS), transposition of the great arteries (TGA), and single ventricle (SV). Our approach was to apply a single network topology (Alex-net) that was trained in a pairwise fashion in order to evaluate the potential to differentiate between patient populations. In total we used 59,378 echo frames drawn from 1,670 clinical sequences. Approximately 80% of the data was used for training, and the remainder for validation. Data was split at sequence boundaries to avoid having related images in the training and validation sets. While training was done with echo images/frames, evaluation was performed for both single frame discrimination as well as sequence discrimination (by majority voting). In total 10 networks were generated and evaluated. The best performance was the HLHS-TGA network with 98% accuracy and sequence accuracy of 100% and 96% per class. The worst was the HLHS-Normal network with only 64% accuracy. Unlike other domains where this network topology has been traditionally used, in ultrasound there is low visual variation between classes. This work shows the potential for CNNs to be applied to this low-variation domain of medical imaging for disease discrimination.

10134-108, Session PS3

Fully automated calculation of cardiothoracic ratio in digital chest radiographs

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The calculation of Cardiothoracic Ratio (CTR) in digital chest radiographs would be useful for cardiac anomaly assessment and heart enlargement related disease indication. The purpose of this study was to develop and evaluate a fully automated scheme for calculation of CTR in digital chest radiographs. Our automated method consisted of three steps, i.e., lung region localization, lung segmentation, and CTR calculation. We manually annotated the lung boundary with 84 points in 100 digital chest radiographs, and calculated an average lung model for the subsequent work. Firstly, in order to localize the lung region, generalized Hough transform was employed to identify the upper, lower, and outer boundaries of lung by use of Sobel gradient information. The average lung model was aligned to the localized lung region to obtain the initial lung outline. Secondly, we separately applied dynamic programming method to detect the upper, lower, outer and inner boundaries of lungs, and then linked the four boundaries to segment the lungs. Based on the identified outer boundaries of left lung and right lung, we corrected the center and the declination of the original radiography. Finally, CTR was calculated as a ratio of the transverse diameter of the heart to the internal diameter of the chest, based on the segmented lungs. The preliminary results on 106 digital chest radiographs showed that the proposed method could obtain accurate segmentation of lung based on subjective observation, and achieved sensitivity of 88.9% (40 of 45 abnormalities), and specificity of 100% (i.e. 61 of 61 normal) for the identification of heart enlargements.

10134-109, Session PS4

Automatic grade classification of Barrett's esophagus through feature enhancement

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Barrett's Esophagus (BE) is a precancerous condition that affects the esophagus tube and has the risk of developing esophageal adenocarcinoma. BE is the process of developing metaplastic intestinal epithelium and

replacing the normal cells in the esophageal area. The detection of BE is considered difficult due to its appearance and properties. The diagnosis is usually done through both endoscopy and biopsy. Recently, Computer Aided Diagnosis systems have been developed to support physician's opinion when facing difficulty in detection/classification in different types of diseases. In this paper, an automatic classification of Barrett's Esophagus condition is introduced. The presented method enhances the internal features of a Confocal Laser Endomicroscopy (CLE) image by utilizing a proposed enhancement filter. This filter depends on fractional differentiation and integration that improve the features in the discrete wavelet transform of an image. Later on, various features are extracted from each enhanced image on different levels for the multi-classification process. Our approach is validated on a dataset that consists of a group of 32 patients with 262 images with different histology grades. The experimental results demonstrated the efficiency of the proposed technique. Our method helps clinicians for more accurate classification. This potentially helps to reduce the need for biopsies needed for diagnosis, facilitate the regular monitoring of treatment/development of the patient's case and can help train doctors with the new endoscopy technology. The accurate automatic classification is particularly important for the Intestinal Metaplasia (IM) type, which could turn into deadly cancerous. Hence, this work contributes to automatic classification that facilitates early intervention/treatment and decreasing biopsy samples needed.

10134-110, Session PS4

False positive reduction for wall thickness-based detection of colonic flat polyps via CT colonography

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Computer-aided detection (CAD) of flat polyps, in contrast to other polyp types, is challenging due to their lack of projections from the colonic surface and limited geometrical features that can be extracted from such polyps. In this paper, we present a new approach for CAD of flat polyps via colon wall thickness mapping, texture feature extraction and analysis. First, we integrated our previous work of detecting flat polyp candidates via colon wall thickness mapping into this study for automated detection of initial polyp candidates (IPCs). The colon wall segmentation is established on a coupled level-set method after the lumen is electronically cleansed by a sophisticated statistical algorithm, which considers the partial volume effect to preserve the mucosa layer details. The IPC detection was performed based on the wall thickness local pattern. From each IPC volume, we extracted the 14 Haralick texture features and 16 additional features that were previously demonstrated to improve polyp classification performance. Then, we adopted the R-package "randomForest" to classify the features for false positive (FP) reduction. We evaluated our method via 16 patient datasets. The proposed scheme achieved a high capacity in terms of the well-known area under the curve value of 0.930. The FPs was reduced to less than 3 FPs/per polyp. The experiment results demonstrate the feasibility of our method in achieving computer aided detection of flat polyps, therefore, improving the screening capability of computed tomography cololongraphy.

10134-111, Session PS4

A new framework for detection of initial flat polyp candidates based on a dual level set competition model

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Computer-aided detection (CAD) of colonic polyps plays an important role in advancing computed tomographic colonography (CTC) toward a screening modality. Detection of flat polyps is very challenging because of their plaquelike morphology with limited geometric features for detection purpose. In this paper, we present a novel scheme to automatically detect initial polyp candidates (IPCs) of flat polyp in CTC images. First, tagged materials in CTC images were automatically removed via the partial volume (PV) based electronic colon cleansing (ECC) strategy. We then propose a dual level set competition model to segment the volumetric colon wall from CTC images after ECC. In this model, we developed a comprehensive cost function which takes consideration of the essential characteristics of colon wall such as colon mucosa and weak boundaries, to simulate the mutual interference relationships among those compositions of the colon wall. Furthermore, we introduced a CAD scheme based on the thickness mapping of the colon wall. By tracing the gradient direction of the potential field between inner and outer borders of the colon wall, we focus on the local thickness measures for the detection of IPCs. The proposed CAD approach was validated on patient CTC scans with flat polyps. Experimental results indicate that the present scheme is very promising towards detection of colonic flat polyp candidates via CTC.

10134-112, Session PS4

Electronic cleansing for CT colonography using spectral-driven iterative reconstruction

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Dual-energy computed tomography is used increasingly in CT colonography (CTC). The combination of computer-aided detection (CADe) and dual-energy CTC (DE-CTC) has high clinical value, because it can detect clinically significant colonic lesions automatically at higher accuracy than single-energy CTC. While CADe has demonstrated its ability to detect small polyps, its performance is highly dependent on several factors, including the quality of CTC images and the quality of electronic cleansing (EC) of the images. The presence of artifacts such as beam-hardening and image noise in ultra-low-dose CTC can produce incorrectly cleansed colon images that severely degrade the detection performance of CTC for small polyps. Also CADe methods are very dependent on the quality of input images and the information about different tissues in the colon. In this work, we developed a novel method to calculate EC images using spectral information from DE-CTC data. First, the ultra-low dose dual-energy projection data obtained from a CT scanner are decomposed into two materials, soft tissue and contrast agent (CA), to detect the location and intensity of the CA. Next, the images are iteratively reconstructed while gradually removing the presence of tagged materials from the images. The performance of the proposed method was assessed qualitatively and quantitatively. Preliminary results show that the method is able to cleanse the CA correctly from DE- CTC images without affecting the appearance of surrounding tissues.

10134-113, Session PS5

Detection of retinal changes from illumination-normalized fundus images using convolutional neural networks

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Automated detection and quantification of spatio-temporal retinal changes is an important step to objectively assess disease progression and treatment effects for dynamic retinal diseases such as diabetic retinopathy (DR). However, detecting retinal changes caused by early DR lesions such as microaneurysms and dot hemorrhages from longitudinal pairs of fundus images is challenging due to intra and inter-image illumination variation between fundus images. This paper explores a method for automated detection of retinal changes using a deep convolutional neural network (CNN) using illumination normalized fundus images, and compares its performance with two other CNNs trained separately on color and green channel fundus images. Illumination variation was addressed by correcting for the variability in the luminosity and contrast estimated from a large scale retinal regions. The CNN models were trained and evaluated on image patches extracted from a registered fundus image set collected from one eye of 51 diabetic patients gathered from a regular DR screening program. The results suggest that illumination normalization greatly facilitates CNNs to quickly learn distinctive local image features of DR related retinal changes.

10134-114, Session PS5

Automated detection of nerve fiber layer defects on retinal fundus images

using fully convolutional network for early diagnosis of glaucoma

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Early detection of glaucoma is important to slow down progression of the disease and to prevent total vision loss. We have been studying an automated scheme for detection of retinal nerve fiber layer defect (NFLD), which is one of the earliest signs of glaucoma on retinal fundus images. In our previous study, we proposed a multi-step detection scheme which consists of Gabor filtering, clustering and adaptive thresholding. The problems of the previous method were that the number of false positives was still large and that the method included too many rules. In attempt to solve these problems, we investigated the end-to-end learning system without pre-specified features. A deep convolutional neural network (DCNN) with deconvolutional layers was trained to detect NFLD regions. In this preliminary investigation, we investigated the effective way of preparing the input images and compared the detection results. The network was trained with original color images of abnormal cases, original color images of both abnormal and normal cases, modified polar transformed images, transformed filtered images, or transformed region-of-interest images. The results from preliminary experiments indicate that the sensitivity increases when only abnormal cases were used for training, although with larger number of false positives. While NFLDs are most detectable in green component, inclusion of 3 color components improved the sensitivity. Compared with the conventional method, the sensitivity was slightly lower; however, the number of false positives can be reduced. Use of DCNN has a potential to improve the automated detection of NFLDs on retinal fundus images.

10134-115, Session PS5

Inferring diagnosis and trajectory of wet age-related macular degeneration from OCT imagery of retina

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Purpose

Quantitative biomarkers for assessing the presence, severity, and progression of age-related macular degeneration (AMD) would benefit research, diagnosis, and treatment. This paper explores development of quantitative biomarkers derived from OCT imagery of the retina.

Methods

OCT images for approximately 75 patients with Wet AMD, Dry AMD, and no AMD (healthy eyes) were analyzed to identify image features indicative of the patients' conditions. OCT image features provide a statistical characterization of the retina. Healthy eyes exhibit a layered structure, whereas chaotic patterns indicate the deterioration associated with AMD. Our approach uses wavelet and frangi filtering, combined with statistical features that do not rely on image segmentation, to assess patient conditions.

Results

Classification analysis indicates clear separability of Wet AMD from other conditions, including Dry AMD and healthy retinas. The probability of correct classification of was 95.7%, as determined from cross validation. Similar classification analysis predicts the response of Wet AMD patients to treatment, as measured by the Best Corrected Visual Acuity (BCVA). A statistical model predicts BCVA from the imagery features with R2 = 0.846.

Conclusions

Initial analysis of OCT imagery indicates that imagery-derived features can provide useful biomarkers for characterization and quantification of AMD:

- Accurate assessment of Wet AMD compared to other conditions
- Image-based prediction of outcome for Wet AMD treatment
- Features derived from the OCT imagery accurately predict BCVA
- Unlike many methods in the literature, our techniques do not rely on segmentation of the OCT image
- Our next steps include larger scale testing and validation

10134-116, Session PS5

Comparison of two different preprocessing steps in detection of optic nerve head in fundus images

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Identification of optic nerve head (ONH) is necessary in retinal image analysis to locate anatomical components such as fovea and retinal vessels in fundus images. In this study, we first worked on two different methods for preprocessing of images after that our main method was proposed for ONH detection in color fundus images. At first part of preprocessing we did color space conversion, illumination equalization, and contrast enhancement. On the other hand, we separately applied top-hat transformation to the image. In the next step Radon transform was applied to each of these two

preprocessed fundus image to find candidates for the location of the ONH. Then, the accurate location was found using the minimum mean square error estimation. The accuracy of this method was approved by the results. Our method detected ONH correctly in 114 out of 120 images in our local database and all color images in the DRIVE database by using Illumination equalization and contrast enhancement preprocessing. Moreover, by use of top-hat transformation our approach correctly detected the ONHs in 115 out of 120 images in the local database and 39 out of 40 images in the DRIVE set. In addition, Sensitivity and specificity of pixel base analysis of this algorithm seems to be acceptable in comparison with other methods.

10134-117, Session PS5

Retinal SD-OCT image-based pituitary tumor screening

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In most cases, the pituitary tumor compresses optic chiasma and causes optic nerves atrophy, which will reflect in retina. In this paper, we proposed an Adaboost classification based method to screen pituitary tumor from retinal spectral-domain optical coherence tomography (SD-OCT) image. The method includes four parts: pre-processing, feature extraction and selection, training and testing. First, in the pre-processing step, the retinal OCT image is segmented into 10 layers and the first 5 layers are extracted as our volume of interest (VOI). Second, 19 textural and spatial features are extracted from the VOI. Principal component analysis (PCA) is utilized to seclect the primary features. Third, in the training step, an Adaboost based classifier is trained using the above features. Finally, in the testing phase, the trained model derived is utilized to screen pituitary tumor. The proposed method was evaluated on 40 retinal OCT images from 30 patients and 30 OCT images from 15 normal subjects.The preliminary results demonstrated the feasibility and efficiency of the proposed method.

10134-118, Session PS6

Evaluation of age-related changes with cross-sectional CT imaging of teeth

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PURPOSE

Tooth pulp atrophy occurs accompanying aging. Imaging evaluation of tooth pulp cavity may be useful in forensic dentistry to estimate age. However it is not easy to evaluate the size of tooth pulp cavities quantitatively because tooth cavity is small and complicated in morphology. Therefore we paid attention to the cross sectional area of tooth pulp cavity in anterior teeth. The aim of this study was to develop an age estimation procedure using dental corn beam CT (CBCT) image of jaws.

METHOD AND MATERIALS

Firstly, micro focus CBCT (Figure 1) images of anterior tooth sample collections were obtained to define an adequate three dimensional imaging parameters including the types of the rendering technique, direction and position of cross sectional plane, and the thickness of a sectional image. Tooth pulp cavity was observed in labio-lingual, mesio-distal and axial cross sectional planes. These were set perpendicular and/or parallel to the tooth axis. Then, clinical dental CBCT images of 60 patients were evaluated to study the correlation between the cross sectional area of tooth pulp cavity and patient's age (Figure 2). The age of patients were ranged from 20 to 80 years old (average 48.3 years old). The ratio of the cross sectional area of pulp cavity to the cross sectional area of the tooth (pulp cavity ratio) was evaluated (Figure 3).

RESULTS

As a 3DCT imaging technique to depict tooth pulp cavity, it was revealed that the average (ray-sum) and minimum intensity projection (minIP) images with a thickness of approximately 2mm were appropriate to measure the area of tooth pulp cavity. Regarding the pulp cavity ratio in clinical CBCT images, labio-lingual plane of the mandibular anterior tooth and the mesio-distal plane of the maxillary anterior tooth revealed high correlational relationship with patient's age (Figure 4).

CONCLUSION

The pulp cavity ratio of anterior tooth may be a useful parameter to estimate age. However it needs to be considered that the suitable cross sectional plane to estimate age differ among types of teeth. Our next task will be to develop computer algorithm to measure pulp cavity ratio automatically.

CLINICAL RELEVANCE/APPLICATION

Dental CBCT image is useful to estimate patient's age by means of evaluation the size of tooth pulp cavity.

10134-119, Session PS6

An introductory analysis of digital infrared thermal imaging guided oral cancer detection using multiresolution rotation-invariant texture features

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This manuscript presents an analytical treatment on the feasibility of multi scale Gabor filter bank response for non-invasive oral cancer pre-screening and detection in the long infrared spectrum. Incapability of present healthcare technology to detect oral cancer in budding stage manifests in high mortality rate. The paper contributes a step towards automation in non-invasive computer-aided oral cancer detection using amalgamation of image processing and machine intelligence paradigms. Previous works have shown discriminative difference of facial temperature distribution between a normal subject and a patient. The proposed work, for the first time, exploits this difference further by representing the facial Reigon of Interest(ROI) using multiscale rotation invariant Gabor filter bank responses followed by classification using Radial Basis Function(RBF) kernelized Support Vector Machine(SVM). Proposed study reveals initial increase in classification accuracy with incrementing image scales followed by degradation of performance; an indication that addition of more and more finer scales tend to embed noisy information instead of discriminative texture patterns. Moreover, the performance is consistently better for filter responses from profile faces compared to frontal faces. This is primarily attributed to inaptness of Gabor kernels to analyse low spatial frequency components over a small facial surface area. On our dataset comprising of 81 malignant, 59 pre-cancerous, and 63 normal subjects, we achieve state-of-the-art accuracy of 85.16% for normal v/s precancerous and 84.72% for normal v/s malignant classification. This sets a benchmark for further investigation of multiscale feature extraction paradigms in IR spectrum for oral cancer detection.

10134-120, Session PS6

Tooth labeling in cone-beam CT using deep convolutional neural network for forensic identification

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Dental record plays an important role in forensic identification. However, filing of dental charts for cadavers is not an easy task for general dentists. Moreover, it is laborious and time-consuming work in cases of large scale disasters. We have been investigating a tooth labeling method on dental cone-beam CT images for the purpose of automatic filing of dental charts. In our proposed method, individual teeth in CT volumes are identified and classified into seven tooth types using deep convolutional neural network (DCNN). As a preliminary investigation, we employed the AlexNet network architecture, which consists of 5 convolution layers, 3 max pooling layers and 2 full connection layers for classifying the teeth into seven types, including the central incisors, the lateral incisors, the canines, the first and second premolars, and the first and second molars. From 52 CT volumes obtained by two imaging systems, five cases each were randomly selected as test data, and the remaining 42 cases were used as training data. In the training of the DCNN, the training data were augmented by rotation and intensity transformation for reducing the overtraining effect. The preliminary result showed the seven-class classification accuracy of 91.0%. Teeth were often misclassified as the neighbor tooth types, which may be improved by combining additional information. The result indicates the potential utility of the proposed method for automatic recording of dental information.

10134-121, Session PS6

Computer-assisted quantification of the skull deformity for craniosynostosis from 3D head CT images using morphological descriptor and hierarchical classification

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Quantitative analysis of the severity of skull deformity in infants is necessary because skull protects and affects the growth of the brain. Craniosynostosis is one of the most common causes of skull deformities in infants and indicates a variety of skull shape depending on the type of craniosynostosis. 3D CT is the most standard imaging for diagnosis of craniosynostosis. However, determination of skull deformity is still prone to inter-observer variability depending on clinical experience. Therefore, we propose 2D and 3D morphological descriptors representing the degree of skull deformity in head CT images and a hierarchical classification model distinguishing among normal and different types of deformity skulls. First, cranial reference and two representative planes are generated for extracting 2D features. Second, five 2D features are extracted for considering the degree and position of prominent area of skull. Third, to compare deformity skull with similar normal skull, 3D mean normal skull models are generated and the model is deformed to deformity skull. Fourth, four 3D features are extracted in each five cranial bone. The local distance and area ratio indices are determined by considering the degree of expansion and reduction of each cranial bone against mean normal skull model. Finally, hierarchical SVM classifier is proposed to distinguish between the normal and deformity skulls. Experimental results showed that 2D morphological descriptor can easily distinguish normal subjects and deformity subjects with bicoronal and sagittal synostosis and normal subjects and 3D morphological descriptor can efficiently distinguish asymmetric deformity skulls with unicoronal and unilambdoid synostosis.

10134-122, Session PS7

Applying a deep learning-based CAD scheme to segment and quantify visceral and subcutaneous fat areas from CT images

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In order to overcome the limitation of using only one subjectively selected CT slice to estimate volumes of fat areas, we developed and tested a new CAD scheme for adipose tissue segmentation based on a sequential of two-step process including firstly recognizing abdominal CT slices and secondly segmenting SFA and VFA from each single selected CT slices. The results illustrated that using this CNN based CAD scheme enabled to recognize abdomen part from CT scans and segment SFA and VFA from CT slices with high agreement with manual segmentation results (accuracy > 95%).

10134-123, Session PS7

An improved method for pancreas segmentation using SLIC superpixels and interactive region merging

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This paper proposes an improved pancreas segmentation method using Simple Linear Iterative Clustering (SLIC) and Interactive Region Merging (IRM) for computer-aided diagnosis systems. For convenience, we refer the improved SLIC_IRM as ISLIC_IRM for solving the problem of pancreas weak edges. In the proposed ISLIC_IRM method, different spatial distance functions are applied for distance measure to generate regular and compact superpixel image in SLIC processing, and then five texture features and one brightness feature are extracted in similarity measure to merge all superpixels belonging to object tissues in IRM processing. Thus the problem of pancreas weak edges can be nicely solved. A comparison experiment is implemented with our proposed ISLIC_IRM and initial SLIC_IRM method on four groups of abdominal CT images. Experimental results demonstrate that the reliability and accuracy of the proposed method have been effectively improved. The segmentation accuracy of ISLIC_IRM can be improved more than 92%.

10134-124, Session PS7

Advancements in automated tissue segmentation pipeline for contrast-enhanced CT scans of adult and pediatric patients

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The development of a random forests machine learning technique is presented for fully-automated neck, chest, abdomen, and pelvis tissue segmentation of CT images using Trainable WEKA Segmentation (TWS)

plugin of FIJI (ImageJ, NIH). A single classifier model was developed for six tissue classes (lung, fat, muscle, solid organ, blood/contrast agent, bone) and 1 background class. An automated unbiased scheme to sample pixels from the training images to yield a balanced training dataset over the seven classes was developed. Classifier training was developed from 12 manually segmented cross-sectional CT images from two adult and two pediatric patients. Classifier training investigated 28 image filters comprising a total of 272 features. Highly correlated and insignificant features were eliminated using Correlated Feature Subset selection with Best First search algorithms in WEKA. Training performance investigated homogenizing background pixels and varying the number of trees (25, 50, 100, and 200) in the random forest algorithm. Training cross validation was performed on nine manually segmented cross-sectional CT images (two adult one pediatric patient). Dice similarity coefficients (DSC) and true positive rate (TPR) statistics were used to determine segmentation accuracy. Best classifier training model consisted of 67 features. Performance improvement was optimized using 100 trees (correct classification 94.5%). Cross validation results using median DSC: 0.98, 0.87, 0.87, 0.80, 0.63, and 0.83, and TPR: 0.97, 0.87, 0.85, 0.97, 0.73, and 0.75 values for lung/gas, fat, muscle, solid organ, blood/contrast agent, and bone, respectively, demonstrate robust segmentation accuracy for fully-automated whole-body segmentation of pediatric and adult CT.

10134-125, Session PS7

Texture analysis of renal masses in multiple MR sequences for prediction of pathology

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We present a method that performs texture analysis on multiple MRs of common renal masses for differentiation of renal cell carcinoma (RCC). Bounding boxes were drawn around each mass on one axial slice in T1 delay sequence to use for feature extraction and classification. All sequences (T1 delay, venous, arterial, pre-contrast phases, T2, and T2 fat saturated sequences) are co-registered and texture features are extracted from each sequence simultaneously. Random Forest is used to construct models to classify lesions on 102 normal regions, 88 clear cell RCCs, 7 papillary RCCs, and 27 renal oncocytomas; ground truths are verified through pathology reports.

The highest performance is seen in random forest model when using data from all sequences are used in conjunction, achieving an overall classification accuracy of 86.6%. When using data from one single sequence, the overall accuracies achieved for T1 delay, venous, arterial, and pre-contrast phase, T2, and T2 fat saturated were 85.2%, 76.1%, 69.6%, 61.6%, 51.8%, and 62.5%, respectively. This demonstrates promising results of utilizing intensity information from multiple MR sequences for accurate classification of renal masses.

10134-126, Session PS7

The effects of TIS and MI on the texture features in ultrasonic fatty liver images

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Nonalcoholic fatty liver disease (NAFLD) is prevalent and has a worldwide distribution now. Although ultrasound imaging technology has been deemed as the common method to diagnose fatty liver, it is not able to detect NAFLD in its early stage and limited by the diagnostic instruments and some other factors. B-scan image feature extraction of fatty liver can assist doctor to analyze the patient's situation and enhance the efficiency and accuracy of clinical diagnoses. However, some uncertain factors in ultrasonic diagnoses are often been ignored during feature extraction. In this study, the nonalcoholic fatty liver rabbit model was made and its liver ultrasound images were collected by setting different Thermal index of soft tissue (TIS) and mechanical index (MI). Then, texture features were calculated based on gray level co-occurrence matrix (GLCM) and the impacts of TIS and MI on these features were analyzed and discussed. Furthermore, the receiver operating characteristic (ROC) curve was used to evaluate whether each feature was effective or not when TIS and MI were given. The results showed that TIS and MI do affect the features extracted from the healthy liver, while the texture features of fatty liver are relatively stable. In addition, TIS set to 0.3 and MI equal to 0.9 is a better choice when using a computer aided diagnosis (CAD) method for fatty liver recognition.

10134-127, Session PS8

Balance the nodule shape and surroundings: a new multichannel image-based convolutional neural network scheme on lung nodule diagnosis

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Deep learning is a trending promising method in medical image analysis area, but how to efficiently prepare the input image for the deep learning algorithms remains a challenge. In this paper, we introduced a novel artificial multichannel region of interest (ROI) generation procedure for convolutional neural networks (CNN). From LIDC database, we collected 54880 benign nodule samples and 59848 malignant nodule samples based on the radiologists' annotations. The proposed CNN consists of three pairs of convolutional layers and two fully connected layers. For each original ROI, two new ROIs were generated: one contains the segmented nodule which highlighted the nodule shape, and the other one contains the gradient of the original ROI which highlighted the textures. By combining the three channel images into a pseudo color ROI, the CNN was trained and tested on the new multichannel ROIs (multichannel ROI II). For the comparison, we generated another type of multichannel image by replacing the gradient image channel with a ROI contains whitened background region (multichannel ROI I). With the 5-fold cross validation evaluation method, the CNN using multichannel ROI II achieved the ROI based area under the curve (AUC) of 0.8823, compared to the AUC of 0.8484 generated by the original ROI. By calculating the average of ROI scores from one nodule, the lesion based AUC using multichannel ROI was 0.87930.0210. By comparing the convolved features maps from CNN using different types of ROIs, it can be noted that multichannel ROI II contains more accurate nodule shapes and surrounding textures.

10134-128, Session PS8

Automatic lung nodule graph cuts segmentation with deep learning false positive reduction

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To automatic detect lung nodules from CT images, we designed a two stage computer aided detection (CAD) system. The first stage is graph cuts segmentation to identify and segment the nodule candidates, and the second stage is convolutional neural network for false positive reduction. The dataset contains 595 CT cases randomly selected from Lung Image Database Consortium and Image Database Resource Initiative (LIDC/IDRI) and the 305 pulmonary nodules achieved diagnosis consensus by all four experienced radiologists were our detection targets. Consider each slice as an individual sample, 1208 nodules were included in our database. The graph cuts segmentation was conducted in a two-dimension manner, 1164

lung nodule ROIs are successfully identified and segmented. With a false positive reduction by a seven-layer convolutional neural network, 1062 nodules still remain detected while the false positive dropped 82.5%. The average F-measure of segmented lung nodule tissue is 0.8501.

10134-129, Session PS8

Detection of juxta-pleural lung nodules in computed tomography images

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This paper describes an approach for the detection of juxta-pleural lung nodules in computed tomography images. It is known that among the different nodule types, computer-aided diagnosis systems perform worse for nodules with radius ≤ 5mm and juxta-pleural nodules. A method for the detection of small juxta-pleural nodules is proposed. The method is developed and tested using the public Lung Image Database Consortium and Image Database Resource Initiative (LIDC-IDRI) dataset, by creating a sub-dataset of juxta-pleural nodules. The lung volume is segmented using region-growing and refined with morphological operations and active contours to include juxta-pleural nodules. Nodule candidates are searched slice-wise inside the lung volume segmentation. Solid nodules are detected by selecting an appropriate threshold inside a representative sliding window. Sub-solid and non-solid nodules are enhanced with a multiscale Laplacian-of-Gaussian filtering prior to their detection. Obvious non-nodule candidates, namely corresponding to small blood vessels, are discarded using fixed rules. Then, a support vector machine with radial basis function is trained with the remaining candidates to further reduce the number of false positives (FPs). The majority of the studied juxta-pleural nodules have solid texture. The initial candidate detection step achieves a sensitivity of 92% with 3450±2720 FPs/scan. Fixed rules reduction drops the sensitivity to 72.5% with 95.5±52.1 FPs/scan. The final system sensitivity is 57.4% with 4 FPs/scan, with an average sensitivity score of 0.39. The performance is similar or better than state-of-the-art methods, especially when considering the high number and small radius of the studied juxta-pleural nodules.

10134-130, Session PS8

Kernel descriptors for chest X-ray analysis

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In this study, we address the problem of lesion classification in radiographic scans. We adapt image kernel functions to be applicable for high-resolution, grayscale images to improve the classification accuracy of a support vector machine.

We take kernel functions inspired by the histogram of oriented gradients, and derive an approximation that can be evaluated in linear time of the image size instead of the original quadratic complexity, enabling high-resolution input. Moreover, we propose a variant of the existing instances, inspired by the matched filter, to better utilize intensity space. The new kernels are improved to be scale-invariant and combined with a Gaussian kernel built from handcrafted image features. We introduce a simple multiple kernel learning framework that is robust when one of the kernels, in the current case the image feature kernel, dominates the others. The combined kernel is input to a support vector classifier.

We tested our method on lesion classification both in chest radiographs and digital tomosynthesis scans. The radiographs originated from a database including 364 patients with lung nodules and 150 healthy cases. The digital tomosynthesis scans were obtained by simulation using 91 CT scans from the LIDC-IDRI database as input. The new kernels showed good separation capability: ROC AuC was in [0.827, 0.853] for the radiograph database and 0.763 for the tomosynthesis scans. Adding the new kernels to the image feature based classifier significantly improved accuracy: AuC increased from 0.958 to 0.967 and from 0.788 to 0.801 for the two applications.

10134-131, Session PS8

A feasibility study of automatic lung nodule detection in chest digital tomosynthesis with machine learning based on support vector machine

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Chest digital tomosynthesis (CDT) is a recently developed medical device that has several advantages for diagnosing lung disease [1]. For example, CDT provides depth information with relatively low radiation dose compared to computed tomography (CT). However, a major problem with CDT is the image artifact associated with data incompleteness resulting from limited angle data acquisition in CDT geometry [2]. For this reason, the sensitivity of lung disease was not clear compared to CT. In this study, to improve sensitivity of lung disease detection in CDT, we developed computer aided diagnosis (CAD) systems based on machine learning. For design CAD systems, we used 50 cases of lung nodules cropped images and 100 cases of normal lesion cropped images acquired by lung man phantoms and proto type CDT. We used machine learning techniques based on supporter vector machine and Gabor filter. The Gabor filter was used for extracting characteristics of lung nodules and the Gabor filter has 5 different frequency and 8 orientations [3, 4]. After extracting features, supporter vector machine (SVM) method was used for classifying lesions. The results of CAD system with machine learning showed the capability of automatically lung lesion detection. Although there are several false positive cases, all five lung nodules were exactly predicted. In conclusion, our suggested CAD system showed feasibility for improving sensitivity of lung lesion detection in CDT.

10134-132, Session PS8

Risk prediction of small pulmonary nodules based on novel CT image texture markers

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Purpose:

Computed tomography (CT) has become an important imaging technique for screening pulmonary nodules, the precursor of lung cancer. Among the detected nodules sized from 3 to 30mm, a significant portion is undetermined in terms of malignance which needs biopsy or other follow-up means, resulting in excessive risk and cost. Therefore, this study aims to find those texture features or imaging markers, which are efficient in discriminating the nodule malignance.

Methods:

In the LIDC-IDRI database, the world's largest public lung nodule database, there are five levels of malignance for the nodules (sized from 3 to 30 mm). The five levels determined by radiologists could be used to indicate the risk degree of lung cancer from benign to malignance with the values from "1" to "5". Based on these levels, we propose two novel CT image texture markers (median and variance, MV) from two- and three-dimensional gray-level co-

occurrence matrices (GLCMs) instead of average and arrange (AR) features usually used in most applications. The aim is to distinguish small nodules from most likely benign, likely benign to likely malignant and most likely malignant, and undefined. To evaluate the efficiency of the usually used and the above presented novel texture markers for the risk prediction of small nodules, experiments were designed to focus on benign and malignant classes firstly, then continue to classify the two levels of benign and the two levels of malignant nodules more specifically. Totally 1,353 nodules (483 benign, 449 undefined, 422 malignant) were included in the experiments. Firstly, the most likely benign, likely benign and undefined nodules were grouped as one class, and the most likely malignant and likely malignant nodules were grouped as the other class. Then, the texture markers vectors (namely features) and the labels of the two classes were sent to SVM classifiers for training and testing for 100 times. And the classifications of the most likely benign (or malignant) and likely benign (or malignant) were implemented in the same method.

Results:

All the classification results are shown in ROC curves and tabulated by the AUC values. For the classification of malignant and benign nodules, the biggest AUC values are 0.9117±0.0095 obtained based on AR markers, 0.9125±0.0096 obtained based on MV markers, and 0.9122±0.0083 obtained based on all the above four markers. For the most likely benign and likely benign, the three biggest AUC values are 0.9220±0.0162, 0.9239±0.0147 and 0.9224±0.0149 obtained based on AR, MV and all the four markers respectively. And for the most likely malignant and likely malignant, the biggest AUC values are 0.7567±0.0304, 0.8888±0.0197, and 0.7465±0.0366 obtained based on AR, MV and all the four markers respectively.

From the results, we can see that the proposed two novel texture markers (MV) are more efficient for the risk classifications of small nodules.

New or breakthrough work to be presented:

From the results of the above experiments, we observed that the texture markers from CT images are efficient for the risk predictions of small nodules. And the proposed two new markers for the improved texture models are more suitable for the risk prediction of lung cancer than the corresponding two old ones (average and arrange).

Conclusions

CT image texture features can be used for distinguishing the small nodules into different levels of benign or malignant, thus the risk prediction could be implemented through image analysis. In addition, the proposed two new texture markers are expressed as the texture characters instead of average and arrange. Furthermore, they were demonstrated to be more efficient for the risk prediction of small nodules in the experiments.

10134-133, Session PS8

Development and validation of a radiomics nomogram for progression free survival prediction in stage four epidermal growth factor receptor mutant non small cell lung cancer

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Accurately predict the risk of disease progression and benefit of tyrosine kinase inhibitors (TKIs) therapy for stage IV non-small cell lung cancer (NSCLC) patients with activing epidermal growth factor receptor (EGFR) mutations by current staging methods are challenge. We postulated that integrating a classifier consisted of multiple computed tomography (CT) phenotypic features, and other clinicopathological risk factors into a single model could improve risk stratification and prediction of progression-free survival (PFS) of EGFR TKIs for these patients.

Patients confirmed as stage IV EGFR-mutant NSCLC received EGFR TKIs with no resection; pretreatment contrast enhanced CT performed at approximately 2 weeks before the treatment was enrolled. A six-CT-phenotypic-feature-based classifier constructed by the LASSO Cox regression model, and three clinicopathological factors: pathologic N category, performance status (PS) score, and intrapulmonary metastasis status were used to construct a nomogram in a training set of 115 patients. The prognostic and predictive accuracy of this nomogram was then subjected to an external independent validation of 107 patients.

PFS between the training and independent validation set is no statistical difference by Mann-Whitney U test (P = 0.2670). PFS of the patients could be predicted with good consistency compared with the actual survival. C-index of the proposed individualized nomogram in the training set (0·707, 95%CI: 0·643, 0·790) and the independent validation set (0·715, 95%CI: 0·650, 0·782) showed the potential of clinical prognosis to predict PFS of stage IV EGFR-mutant NSCLC from EGFR TKIs. The individualize nomogram might facilitate patient counselling and individualise management of patients with this disease.

10134-134, Session PS8

Airway extraction from 3D chest CT volumes based on iterative extension of VOI enhanced by cavity enhancement filter

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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 an integrated 3-D airway tree structure from a CT volume is a quite challenging task.

This paper presents a novel airway segmentation method based on intensity structure analysis and bronchi shape structure analysis in volume of interest (VOI). This method segments the bronchial regions by applying the cavity enhancement filter (CEF) to trace the bronchial tree structure from the trachea. It uses the CEF in each VOI to segment each branch and to predict the positions of VOIs which envelope the bronchial regions in next level. At the same time, a leakage detection is performed to avoid the leakage by analysing the pixel information and the shape information of airway candidate regions extracted in the VOI.

The final bronchial region is obtained by unifying the extracted airway regions.

The experiments results showed that the proposed method can extract most of the bronchial region in each VOI and led good results of the airway segmentation.

10134-135, Session PS8

A study of retrieval accuracy of pulmonary nodules based on external attachment

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In this paper, retrieval accuracy of different types of pulmonary nodules (well-circumscribed, juxta-pleural, and juxta-vascular) is studied. The trainee radiologists could enrich their knowledge using the visual information of the retrieved nodules. In the proposed retrieval system, the pulmonary nodules are segmented using a semi-automated technique. Several 3D features are explored to improve the performance of the proposed retrieval system. A set of relevant shape and texture features is determined for efficient representation of the nodules in the feature space. The proposed CBIR system is validated on a data set of 542 nodules of Lung Image Database Consortium and Image Database Resource Initiative (LIDC/IDRI). The nodules with composite rank of malignancy “1”, “2” are considered as benign and “4”, “5” are considered as malignant. Considering top five retrieved images, the precision of the proposed retrieval system are 84.76%, 80.75%, and 80.34% for well-circumscribed, juxta-pleural, and juxta-vascular nodules, respectively.

10134-136, Session PS8

An experimental study of interstitial lung tissue classification in HRCT images using ANN and role of cost functions

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In this paper, we investigate the effect of the error criteria used during a training phase of the artificial neural network (ANN) on the accuracy of the classifier. Mean square error (MSE) and the cross-entropy (CE) criteria are chosen being a most popular choice in state-of-the-art implementations. The classification experiment performed on the six interstitial lung disease (ILD) patterns viz. Consolidation, Emphysema, Ground Glass Opacity, Micronodules, Fibrosis and Healthy from MedGIFT database. The texture feature from an arbitrary region of interest (AROI) extracted using Gabor filter. A neural network trained with the scaled conjugate gradient back propagation algorithm with MSE and CE error criteria function for weight up gradation. Performance is evaluated in terms of average accuracy of the classifier using 4 fold cross-validation. Each network is trained for five times for each fold with randomly initialized weight vectors and accuracies are computed. Significant improvement in classification accuracy observed when ANN is trained by using CE (67.27%) as error function compared to MSE (63.60%). Moreover, standard deviation of the classification accuracy for the network trained with CE (6.69) error criteria is found less as compared to network trained with MSE (10.32) criteria.

10134-137, Session PS8

Volume calculation of CT lung lesions based on Halton low-discrepancy sequences

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Volume calculation from the Computed Tomography (CT) lung lesions data is a significant parameter for clinical diagnosis. The volume is widely used to assess the severity of the lung nodules and track its progression, however, the accuracy and efficiency of previous studies are not well achieved for clinical uses. It remains to be a challenging task due to its tight attachment to the lung wall, inhomogeneous background noises and large variations in sizes and shape.

In this paper, we employ Halton low-discrepancy sequences to calculate the volume of the lung lesions. The proposed method directly compute the volume without the procedure of three-dimension (3D) model reconstruction and surface triangulation, which significantly improves the efficiency and reduces the complexity. The main steps of the proposed method are: (1) generate a certain number of random points in each slice using Halton low-discrepancy sequences and calculate the lesion area of each slice through the proportion; (2) obtain the volume by integrating the areas in the sagittal direction. In order to evaluate our proposed method, the experiments were conducted on the sufficient data sets with different size of lung lesions. With the uniform distribution of random points, our proposed method achieves more accurate results compared with other methods, which demonstrates the robustness and accuracy for the volume calculation of CT lung lesions. In addition, our proposed method is easy to follow and can be extensively applied to other applications, e.g., volume calculation of liver tumor, atrial wall aneurysm, etc.

10134-138, Session PS8

Distant failure prediction for early-stage NSCLC by analyzing PET with sparse representation

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Positron emission tomography (PET) imaging has been widely explored for treatment outcome prediction. Radiomics-driven method provides a new insight to quantitatively explore underlying information from PET images. However, it is still a challenging problem to automatically extract clinically meaningful features for prognosis. In this work, we propose a PET image-guided distant failure predictive model for early stage NSCLC after stereotactic body radiation therapy (SBRT) by using sparse representation. The method does not need pre-calculated features and can learn intrinsically distinctive features contributing to classification of distant failure. In particular, the framework includes two main parts: intra-tumor heterogeneity description and dictionary pair learning based sparse representation. Heterogeneity is initially captured in tumor images through anisotropic kernel and represented as a set of concatenated vectors, which forms the training sample gallery. Then, given a test tumor image, its identity (i.e., distant failure or not) is classified by applying dictionary pair learning based sparse representation. We evaluate the proposed approach on 50 patients. Experimental results show that the proposed approach can achieve an overall accuracy of 65.67% with a sensitivity of 55.97% and specificity of 77.86% over 10 fold cross validation.

10134-139, Session PS8

Automatic body region localization

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Radiological imaging and image interpretation for clinical decision making are mostly specific to each body region such as head & neck, thorax, abdomen, pelvis, and extremities. For automating image analysis and consistency of results, standardizing definitions of body regions and the various anatomic objects, tissue regions, and zones in them becomes essential [1]. Assuming that a standardized definition of body regions is available, a fundamental early step needed in automated image and object analytics is to automatically trim the given image stack into image volumes exactly satisfying the body region definition. This paper presents a solution to this problem based on the concept of virtual landmarks introduced in this conference via a separate paper and evaluates it on whole-body PET/CT scans. The method first selects a (set of) reference object(s), segments it (them) roughly, and identifies virtual landmarks for the object(s). The geometric relationship between these landmarks and the boundary locations of body regions is then learned through a regressor neural network, and the locations are predicted. Based on the low-dose CT images of 180 whole-body PET/CT scans and the skeleton and lung space used as reference objects, the mean prediction accuracy for the boundaries of three body regions – thorax, abdomen, and pelvis – is found to be 12, 16, 20 mm in this initial effort. Improvements of this performance via optimal selection of objects and virtual landmarks and other object analytics applications are currently being pursued.

10134-140, Session PS8

A new method for predicting CT lung nodule volume measurement performance

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Purpose: To evaluate a new approach for predicting nodule volume measurement bias and variance when scanning with a specific CT scanner and acquisition protocol.

Methods: A GE LightSpeed VCT scanner was used to CT scan 3 new rolls of 3M 3/4 x 1000 Inch Scotch Magic tape with a routine chest protocol (120 kVp, 100 mA, .98 pitch, STANDARD kernel) at three different slice thicknesses and spacings. Each tape scan was independently analyzed by fully automated image quality assessment software, resulting in fundamental image quality characteristics and simulated lung nodule volume measurements for a range of sphere diameters. The same VCT scanner and protocol was then used to obtain 10 repeat CT scans of an anthropomorphic chest phantom containing Teflon spheres embedded in foam. The observed volume of the spheres in the 30 repeat scans was provided by independently developed nodule measurement software.

Results: The predicted vs observed mean volume (mm^3) and CV for 3 slice thicknesses and sphere sizes was obtained for three different slice thicknesses. For 0.625mm slice thickness scans the predicted vs observed values were (44.3,0.91)-vs-(48.2,1.17) for 4.76mm diameter spheres, (110.4,0.51)-vs-(124.1,0.47) for 6.25mm spheres, and (219.9,0.29)-vs-(250.1,0.34) for 7.94mm spheres. For 1.25mm slice thickness the corresponding values were (42.1,0.98)-vs-(47.6,1.35), (106.9,0.56)-vs-(123.1,0.61), and (214.8,0.32)-vs-(248.8,0.41). For 2.5mm slice thickness the corresponding values were (23.9,9.53)-vs-(36.8,12.50), (77.6,3.84)-vs-(110.5,3.20), and (173.0,1.57)-vs-(233.9,1.32).

Conclusion: Volume measurement bias and variability for lung nodules based on nodule size and acquisition protocol can potentially be predicted using a new method that utilizes fundamental image characteristics and first order simulation.

10134-141, Session PS8

Building confidence and credibility into CAD with belief decision trees

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To improve on existing CAD systems, we first examined Belief Decision Trees with an iterative classification approach to provide a vector of predicted probabilistic labels for each case in a balanced version of the Lung Image Database Consortium (LIDC) dataset. We then applied conformal prediction to these results in order to analyze the reliability of the predictions (which was then used in the implementation of iterative classification), and typicality of each case. Probabilistic predictions given with levels of confidence and credibility can build a smarter CAD system that provides more contextual information to the radiologist.

Keywords: Computer-aided diagnosis, belief decision tree, iterative classification, conformal prediction, reliability, confidence, credibility

INTRODUCTION

Computer-aided diagnosis (CAD) systems provide radiologists with extra information for use when analyzing medical images. These systems reduce the work required for a radiologist to assess an image by quantitatively analyzing images and predicting qualitative characteristics of the case. To improve on current CAD systems, we investigate strategies to produce better prediction performance and analysis of the quality of a CAD prediction when handling uncertain data. We first examine Belief Decision Trees with an iterative classification approach to provide a vector of predicted probabilistic labels for each case in a balanced version of the Lung Image Database Consortium (LIDC) dataset. Second, we propose to apply conformal prediction to these results in order to analyze the reliability of the predictions, and typicality of each case. Probabilistic predictions given with levels of confidence and credibility can build a smarter CAD system that provides more contextual information to the radiologist. The Belief Decision Tree itself as well as conformal prediction have been implemented with 43.5% testing accuracy, and we are in the process of refining conformal prediction.

PURPOSE

CAD systems currently have a relatively low adoption rate in clinical settings. This is partially because radiologists are unable to trust them due to the small amount of information (typically, a single diagnosis) they are given. Without a window into the CAD system's reasoning, or how well it may predict a particular case, they may come to distrust its results as they observe more misclassified cases [1]. As such, more comprehensive statistical and contextual output for each case may help build their trust in these types of systems, and give clinicians a better idea of how well a prediction fits each case. By providing probabilistic labels for potential diagnoses, along with self-evaluation features like case reliability and typicality, we hope to dispel some of the doubt in the potential of these systems.

METHODS

The LIDC dataset [2] contains between one and four radiologist ratings of malignancy for each case, on a scale of 1 (benign) to 5 (malignant). We are working with a mean-balanced subset of this data, which includes only those cases rated by four radiologists. The data were balanced between mode ratings by severely under sampling the label 3 (uncertain) cases, as there were far more of these than the rest, and slightly over sampling cases of other labels. Unfortunately, a radiologist rating is not akin to a ground truth in machine learning, and the four radiologists agree on a consensus label in only 25% of these cases [3]. This can introduce unwanted bias when classifying new nodules. In order to deal with this uncertainty, we have implemented an algorithm based on a probabilistic classifier called Belief Decision Tree (BDT). It is an adaption of a decision tree (DT) classifier that uses belief function theory to better handle cases of uncertainty.

In a similar vein to a decision tree, a BDT classifies an LIDC case by comparing calculated image feature values to the chosen threshold values to determine which path in the tree the case should follow. When a case reaches a leaf node, it can be assigned a Basic Belief Assignment (BBA) associated with this node as a method of classifying that case. This BBA is a set of probabilities for each of the five classification labels, and represents the average BBA of all cases in the training set that reached this node [4]. The training case BBA's were created using the radiologist ratings from the dataset; for example, ratings of 2, 3, 4, and 4 would yield the BBA [0 .25 .25 .5 0]. Typically the process of calculating these probabilities is much more involved for a belief decision tree, but the LIDC dataset has a few special qualities that allow us to use this method. For one, every radiologist can only pick one label for each case, and for another, we have no way to gage the uncertainty of said choice. This allows us to eliminate union labels (label1 U label2) and pure uncertainty labels in our BBA, resulting in a simple probability distribution [5].

The biggest difference between a decision tree and a BDT occurs during tree construction. When deciding whether and how a node should split, a BDT calculates the pignistic probabilities of each class for every case in the dataset (which becomes our BBA), and averages the probabilities of all the cases that reach each node in the tree. The average pignistic probabilities of the parent and child nodes can then be used to calculate the information gain of splitting, using each possible feature and threshold value in the dataset. It then computes the gain ratio, which controls for the size of the child subsets and rewards equally distributed splits, and chooses the feature and threshold that achieved the maximum gain ratio for the split. One can determine whether a node in a BDT is a leaf node if it meets one of four stopping criterion: the maximum information gain of splitting was 0, there is no split that can be made which will result in acceptable numbers of cases at the parent and child nodes (given by np and nc parameters), all of the BBA's at the node are equivalent, or all features have already been used to split [4].

We would like to incorporate an iterative classification approach with these BDTs in order to reinforce their ability to handle the uncertain radiologist labels and achieve a reasonable consensus [6, 7]. In this project, we propose the use of iterative classification with four belief decision trees, each incorporating an increasing number of radiologist ratings. After a new case is classified by each tree, the BBA output would be compared to the best previous BBA. If it was better, this would become the best overall BBA. This process provides four different possible BBA's for each case. We can then determine the optimal BBA for the case based on their respective confidence and credibility scores.

Finally, we are implementing Conformal Prediction (CP) in our BDT to produce measures of confidence and credibility for each CAD probability distribution. CP begins as a typical classification problem: the dataset is divided into a training and testing set, and from the training set is derived a calibration set, which is used to facilitate conformal prediction. The calibration set is classified using the BDT produced by the training set. Using the conformity function given in equation 1 to determine conformity scores for each case (which correlate with case typicality), we then build a set of calibration conformity values. Positive conformity scores represent more typical cases, whereas negative scores represent more atypical cases. Johansson et.al. [8] defines calibration conformity as:

?_i=p_i^Y-?max?_(j=1…C:j≠Y) p_i^j Eq. 1

In equation 1, ?_i is the conformity score for the ith case, p_i^Yis the probability of the actual classification of the case, and ?max?_(j=1…C:j≠Y) p_i^j is the maximum probability of all of the remaining labels in the case. After these calibration conformity values have been calculated, the testing set is run through the classifier to find the predicted labels for the testing cases. With these predicted labels, we can compute the testing conformity of each case using equation 2 below. Testing cases are not associated with a true label, and therefore we must calculate a conformity score for each possible label, as defined by Johansson et.al. [8]:

a_i^k=p_i^k-?max?_(j=1…C:j≠ck) p_i^j Eq. 2

Shown in equation 2, a_i^kis the conformity score for class k in the ith case. p_i^k is the probability of class label k and ?max?_(j=1…C:j≠ck) p_i^j is the maximum probability from the remaining class labels for that case. Utilizing the calibration and testing conformity scores, we can calculate the p-values of the testing cases. This allows us to transform case conformity into our measures of reliability, confidence and credibility. To calculate the p-values, we compare each of the testing conformity scores for a case to the set of calibration conformity scores. It represents the ratio of conformity scores in the calibration set that are less than or equal to the conformity score of that label to the total number of instances in the calibration set. Using this p-value, we can calculate confidence and credibility for each prediction as both an output for the radiologist to consider, and as a method of choosing the best BBA during iterative classification. The p-value as defined by Johansson et.al. [8] is:

P_ik=|{j=1..l &ik:a_j≤ a_i^k }|/(l+1) Eq. 3

Equation 3 defines the p-value, P_ik, for class k of the ith case. P_ik is shown as a_j, the number of calibration conformity scores that are less than or equal to the case conformity score a_j^i, over the number of calibration conformity scores. This produces a vector of p-values for a case, which can be used to compute confidence (?Cf?_i) as one minus the second highest probability where p_j^i is the vector of p-values, and credibility (?Cr?_j) as the maximum probability of p_ij, as defined by Johansson et.al. [8]:

?Cf?_i=1-?secondMax?_(j=1…k) p_j^i Eq. 4

?Cr?_j=?max?_(j=1…k) p_ij Eq. 5

PRELIMINARY RESULTS

Our BDT with conformal prediction achieves 43.5% testing accuracy and 0.64 AUC on our mean-balanced dataset with 800 cases (514 proper training, 86 calibration, 200 testing). Its optimal settings were found to be np = 23, nc = 11, and dmax = 25, where np represents the minimum number of cases a parent node must have to split, nc represents the minimum number of cases a child node must have for its parent to split, and dmax represents the maximum tree depth. Accuracy was defined by taking the maximum probability label from the actual and predicted label distributions, and assuming these were the actual and predicted labels. The low accuracy values obtained are likely influenced by the small size of our dataset, and the necessity of splitting it into three even smaller subsets. Accuracy may also be lowered by forcing a consensus out of intentionally uncertain probability distributions, in which case accuracy is likely not the best measure of performance. To improve the accuracy of our tree, we will use k-fold cross validation with k = 4 for further testing [9].

To compare the actual and predicted distributions without forcing consensus, we currently calculate the Pearson correlation between the actual and predicted distributions, shown in Figure 1, which helps us assess the BDT's ability to predict the correct distribution. Pearson correlation for our sample size of 200 testing pairs is significant with $p < 0.05$ at any correlation above 0.139, meaning that 62% of our test instances have a statistically significant correlation between actual and predicted distributions. We plan to implement the Area under a Distance Threshold Curve (AUCdt) [10] measure to better compare the distributions. The iterative classification step has been implemented, and can be added in at any time, but we chose to remove it until our implementation of conformal prediction is ready, as the process depends on the confidence output from conformal prediction to choose a final BBA for a case.

As shown in Figure 2, our mean CP results show a nonlinear variability for confidence with respect to AUC, and little variation in credibility. We will investigate this phenomenon further to determine the relationships between our performance and reliability measures.

INNOVATION & CONCLUSIONS

By incorporating conformal prediction into the decision-making process of an iterative probabilistic classifier, we are proposing a CAD system that will provide more informative probabilistic predictions for new cases, which would include measures of confidence and credibility for those predictions. In so doing, we aim to generate results that give clinicians a better idea of the context surrounding the predictions, and build their trust in the viability CAD tools for clinical use.

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10134-142, Session PS9

Compression fracture detection on CT

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We present an automated method for detecting spine compression fractures in CT scans. The algorithm proposed is comprised of two main steps given a patient CT scan. First, sagittal patches are extracted along the vertebral column. We then binary classify these patches to detect whether one contains a compression fracture using a Convolutional Neural Network.

To deal with this task, we assembled a medical dataset of CT scans containing 1880 individuals. The results of the algorithm proposed proved efficient in 92.3% accuracy over a balanced validation set split from the dataset.

10134-143, Session PS9

Detection of a slow-flow component in contrast-enhanced ultrasound of the synovia for the differential diagnosis of arthritis

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Contrast Enhanced Ultrasound (CEUS) is a sensitive imaging technique to assess tissue vascularity, that can be useful in the quantification of different perfusion patterns. This can particularly important in the early detection and differentiation of different types of arthritis. A Gamma-variate can accurately quantify synovial perfusion and it is flexible enough to describe many heterogeneous patterns. However, in some cases the heterogeneity of the kinetics can be such that even the Gamma model does not properly describe the curve, especially in presence of recirculation or of an additional slow-flow component.

In this work we apply to CEUS data both the Gamma-variate and the single compartment recirculation model (SCR) which takes explicitly into account an additional component of slow flow. The models are solved within a Bayesian framework.

When dividing the patients into two groups (rheumatoid arthritis and polyarticular RA-like psoriatic arthritis vs. other arthritis types), the median value of the parameter indicating the presence of slow-flow is significantly different (0.12 vs 0.09, $p<0.002$), whereas when performing ANOVA to check the differences among each type of arthritis, the median is no more different, but the parameter distribution is ($p<0.05$).

10134-144, Session PS9

Automated analysis of whole skeletal muscle for early differential diagnosis of ALS in whole-body CT images: preliminary study

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Amyotrophic lateral sclerosis (ALS) causes functional disorders such as difficulty in breathing and swallowing through the atrophy of voluntary muscles. ALS in its early stages is difficult to diagnose because of the difficulty in differentiating it from other muscular diseases. In addition, image inspection methods for aggressive diagnosis for ALS have not yet been established. The purpose of this study is to develop an automatic analysis system of the whole skeletal muscle to support the early differential diagnosis of ALS using whole-body CT images. In this study, the muscular atrophy parts for ALS patients are automatically identified by recognizing and segmenting whole skeletal muscle in the preliminary steps. First, the skeleton is identified by its gray value information. Second, the initial area of the body cavity is recognized by the deformation of the thoracic cavity based on the anatomical segmented skeleton. Third, the abdominal cavity boundary is recognized using ABM for precisely recognizing the body cavity. The body cavity is precisely recognized by non-rigid registration method based on the reference points of the abdominal cavity boundary. Fourth, the whole skeletal muscle is recognized by excluding the skeleton, the body cavity, and the subcutaneous fat. Additionally, the areas of muscular atrophy in ALS patients are automatically identified by comparison of the muscle mass. The experiments were carried out for ten cases with abnormality in the skeletal muscle. Global recognition and segmentation of the whole skeletal muscle were well realized in eight cases. Moreover, the areas of muscular atrophy in ALS patients were well identified in the lower limbs. As a result, this study indicated the basic technology to differentiate early ALS. In the future, it will be necessary to consider methods to differentiate other kinds of muscular atrophy as well as the clinical application of this detection method for early ALS detection.

10134-145, Session PS9

Automated grading of lumbar disc degeneration via supervised distance metric learning

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Lumbar disc degeneration (LDD) is a commonly age-associated condition related to low back pain, while its consequences are responsible for over 90% of spine surgical procedures. In clinical practice, grading of LDD by inspecting MRI is a necessary step to make a suitable treatment plan. This step purely relies on physicians' manual inspection so that it brings the unbearable tediousness and inefficiency. An automated method for grading of LDD is highly desirable. However, the technical implementation faces a big challenge from class ambiguity, which is typical in medical image classification problems with a large number of classes. This typical challenge is derived from the complexity and diversity of medical images, which lead to a serious class overlapping and brings a great challenge in discriminating different classes. To solve this problem, we proposed an automated grading approach, which is based on supervised distance metric learning to classify the input discs into four class labels (0: normal, 1: slight, 2: marked, 3: severe). By learning distance metrics from labeled instances, an optimal distance metric is modeled and with two attractive advantages: (1) keeps images from the same classes close, and (2) keeps images from different classes far apart. The experiments, performed in 93 subjects, demonstrated the superiority of our method with accuracy 0.9226, sensitivity 0.9655, specificity 0.9083, F-score 0.8615. With our approach, physicians will be free from the tediousness and patients will be provided an effective treatment.

10134-146, Session PS9

Individual bone structure segmentation and labeling from low-dose chest CT

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The segmentation and labeling of the individual bones serve as the first step to the fully automated measurement of skeletal characteristics and the detection of abnormalities such as skeletal deformities, osteoporosis, and vertebral fractures. Moreover, the identified landmarks on the segmented bone structures can potentially provide relatively reliable location reference to other non-rigid human organs, such as breast, heart and lung, thereby facilitating the corresponding image analysis and registration. A fully automated anatomy-directed framework for the segmentation and labeling of the individual bone structures from low-dose chest CT is presented in this paper. The proposed system consists of four main stages: First, both clavicles are segmented and labeled by fitting a piecewise cylindrical envelope. Second, the sternum is segmented under the spatial constraints provided by the segmented clavicles. Third, all ribs are segmented and labeled based on 3D region growing within the volume of interest defined with reference to the spinal canal centerline and lungs. Fourth, the individual thoracic vertebrae are segmented and labeled by image intensity analysis in the spatial region constrained by previously segmented bone structures. The system performance was validated with 1270 low-dose chest CT scans through visual evaluation. Satisfactory performance was obtained in 97.1%, 97.3%, 94.2%, and 89.9% scans for clavicle, sternum, individual ribs and individual vertebrae segmentation and labeling respectively.

10134-147, Session PS9

Can multivariate models based on MOAKS predict OA knee pain? : data from the Osteoarthritis Initiative

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Osteoarthritis is the most common rheumatic disease in the world. Knee pain is the most disabling symptom in the disease, the prediction of pain is one of the targets in preventive medicine, this can be applied to new therapies or treatments. Using the magnetic resonance imaging and the grading scales, a multivariate model based on genetic algorithms is presented. Using a predictive model can be useful to associate minor structure changes in the joint with the future knee pain. Results suggest that multivariate models can be predictive with future knee chronic pain. All models; T0, T1 and T2, were statistically significant, all p values were < 0.05 and all AUC > 0.6.

10134-148, Session PS9

Automatic lumbar spine measurement in CT images

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Accurate lumbar spine measurement in CT images provides an essential way for quantitative spinal diseases analysis such as spondylolisthesis and scoliosis. In today's clinical workflow, the measurements are manually performed by radiologists and surgeons, which is time consuming and irreproducible. Therefore, automatic and accurate lumbar spine measurement algorithm becomes highly desirable. In this study, we propose a method to automatically calculate five different lumbar spine measurements in CT images. There are three main stages of the proposed method: First, a learning based spine labeling method, which integrates both the image appearance and spine geometry information, is used to detect lumbar and sacrum vertebrae in CT images. Then, a multi-atlases based image segmentation method is used to segment each lumbar vertebra and the sacrum based on the detection result. Finally, measurements are derived from the segmentation result of each vertebra. Our method has been evaluated on 138 spinal CT scans to automatically calculate five widely used clinical spine measurements. Experimental results show that our method can achieve more than 90% success rates across all the measurements. Our method also significantly improves the measurement efficiency compared to manual measurements. Besides benefiting the routine clinical diagnosis of spinal diseases, our method also enables the large scale data analytics for scientific and clinical researches.

10134-149, Session PS9

Automatic vertebral bodies detection of x-ray images using invariant multiscale template matching

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Lower back pain and pathologies related to it are one of the most common results for a referral to a neurosurgical clinic in the developed and the developing world. Quantitative evaluation of these pathologies is a challenge. Image based measurements of angles/vertebral heights and disks could provide a potential quantitative biomarker for tracking and measuring these pathologies. Detection of vertebral bodies is a key element and is the focus of the current work.

From the variety of medical imaging techniques, MRI and CT scans have been typically used for developing image segmentation methods. However, CT scans are known to give a large dose of x-rays, increasing cancer risk [8]. MRI can be substituted for CTs when the risk is high [8] but are difficult to obtain in smaller facilities due to cost and lack of expertise in the field [2]. X-rays provide another option with its ability to control the x-ray dosage, especially for young people, and its accessibility for smaller facilities. Hence, the ability to create quantitative biomarkers from x-ray data is especially valuable.

Here, we develop a multiscale template matching, inspired by [9], to detect centers of vertebral bodies from x-ray data. The immediate application of such detection lies in developing quantitative biomarkers and in querying similar images in a database. Previously, shape similarity classification methods have been used to address this problem, but these are challenging to use in the presence of variation due to gross pathology and even subtle effects [1].

10134-150, Session PS9

Automatic segmentation of lumbar vertebrae in CT images

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Lower back pain is one of the most prevalent disorders in the developed and developing world. However, its etiology is poorly understood and treatment is often determined subjectively. In order to quantitatively study the emergence and evolution of back pain, it is necessary to develop consistently measurable markers for pathology. Imaging based measures offer one solution to this problem. The development of imaging based on quantitative biomarkers for the lowerback, necessitates automated techniques to acquire this data. While the problem of segmenting lumbar vertebrae has been addressed repeatedly in literature, the associated problem of computing relevant biomarkers on the basis of the segmentation has not been addressed thoroughly. In this paper we propose a Random Forest based approach that learns to segment vertebral bodies in computed tomography (CT) images followed by a biomarker evaluation framework that extracts vertebral heights and widths from the segmentations obtained. Our dataset consists of 15 CT sagittal scans obtained from General Electric Healthcare. Our main approach is divided into three parts: the first stage is image preprocessing which is used to correct for variations in illumination across all the images in the dataset followed by preparing the foreground and background objects from the images; the next stage is Machine Learning using Random Forests, which distinguishes the interest point vectors between foreground or background; and the last step is the image post-processing, which is crucial to refine the results of classifier. The combination of these three steps yield image segmentation. We approximate the dimensions of the spinal vertebrae through the use of box dimensions that are computed by finding contours of the segmented lumbars

10134-151, Session PS10

Apply Radiomics Approach for Early Stage Prognostic Evaluation of Ovarian Cancer Patients: A Preliminary Study

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Predicting metastatic tumor response to chemotherapy at early stage is critically important for improving efficacy of clinical trials of testing new chemotherapy drugs. However, using current response evaluation criteria in solid tumors (RECIST) guidelines only yields a limited accuracy to predict tumor response. In order to address this clinical challenge, we applied Radiomics approach to develop a new computer aided diagnosis scheme, aiming to more accurately assess the tumor response to new chemotherapy treatment, for the advanced ovarian cancer patients. This new scheme uses two sets of CT images acquired before and 6 weeks after chemotherapy, and the scheme consists of three steps. First, the tumors depicted on the CT images were segmented by a hybrid tumor segmentation tool employing eight different algorithms. Then, a total of 56 features were computed from the segmented tumors, which can be grouped as 1) tumor volume based features; 2) tumor boundary based features; and 3) tumor texture based features. After that, a Radiomic feature signature was determined by selecting the best performing features among these three groups. Using this feature signature, the preliminary results demonstrated that an area under the receiver operating characteristic curve (AUC) of 0.902±0.057 was achieved by adopting an average feature fusing method, which is significantly higher than using RECIST guidelines. This study indicates that applying a Radiomics based CAD scheme has potential to significantly increase discriminatory power to predict chemotherapy response at an early stage.

10134-152, Session PS10

Prostate lesion detection and localization based on locality alignment discriminant analysis

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Prostatic adenocarcinoma is one of the most commonly occurring cancers among men in the world, and it also the most curable cancer when it is detected early. Multiparametric MRI (mpMRI) combines anatomic and functional prostate imaging techniques, which have been shown to produce high sensitivity and specificity in cancer localization, which is important in planning biopsies and focal therapies. However, in previous investigations, lesion localization was achieved mainly by manual segmentation, which is time-consuming and prone to observer variability. Here, we developed an algorithm based on locality alignment discriminant analysis (LADA) technique, which can be considered as a version of linear discriminant analysis (LDA) localized to patches in the feature space. Sensitivity, specificity and accuracy generated by the proposed algorithm in five

prostates by LADA were 51.3%, 87.8% and 85% respectively, compared to 36.9%, 83.4% and 80.9% generated by LDA. The sensitivity reaches 89% when the detected area was expanded by a margin of 5 mm. The delineation accuracy attainable by this tool has a potential in increasing the cancer detection rate in biopsies and in minimizing collateral damage of surrounding tissues in focal therapies.

10134-153, Session PS11

Comparison of classification methods for voxel-based prediction of acute ischemic stroke outcome following intra-arterial intervention

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Voxel-based tissue outcome prediction in acute ischemic stroke patients is highly relevant for both clinical routine and research. Previous research has shown that features extracted from baseline multi-parametric MRI datasets have a high predictive value and can be used for the training of classifiers, which can generate tissue outcome predictions for both intravenous and conservative treatments. However, with the recent advent and popularization of intra-arterial (IA) treatment methods, novel research specifically addressing the utility of predictive classifiers for IA intervention is necessary for a holistic understanding of current stroke treatment options. The aim of this work was to develop three clinically viable tissue outcome prediction models using approximate nearest-neighbor, generalized linear model, and random decision forest approaches and evaluate the accuracies of predicting tissue outcome after intra-arterial (IA) treatment. Therefore, the three machine learning models were trained, evaluated, and compared using datasets of 42 acute ischemic stroke patients treated with IA methods. Classifier training utilized eight voxel-based features extracted from the MRI datasets and five global features. Evaluation of classifier-based predictions was performed via comparison to the known tissue outcome using the Dice coefficient and leave-on-patient-out cross validation. The random decision forest prediction model led to the best tissue outcome predictions, leading to a mean Dice coefficient of 0.37. The approximate nearest-neighbor and generalized linear model performed equally sub-optimally with Dice coefficients of 0.28 and 0.27 respectively, suggesting that both non-linearity and machine learning are desirable properties of a classifier well-suited to the IA tissue outcome problem.

10134-154, Session PS11

A hybrid 3D region growing and 4D curvature analysis-based automatic abdominal blood vessel segmentation through contrast-enhanced CT

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In abdominal disease diagnosis and various surgeries planning, segmentation of abdominal blood vessel (ABVs) is a very imperative task. Automatic segmentation enables fast and accurate processing of ABVs. We proposed a fully automatic approach for segmenting ABVs through contrast enhanced CT images by a hybrid of 3D region growing and 4D curvature analysis. The proposed method comprises three stages. First, candidates of bone, kidneys, ABVs and heart are segmented by an auto-adapted threshold. Second, bone is auto-segmented and classified into spine, ribs and pelvis. Third, ABVs are auto-segmented and classified in three sub-steps: (1) kidneys and abdominal part of the heart are segmented, (2) ABVs are segmented by a hybrid approach that integrates a 3D region growing and 4D curvature analysis, and (3) subsequent classification of aorta, main portal vein, inferior vena cava and blood vessels of other organs are classified. Results are compared with two conventional methods. Results show that the proposed method is very promising in segmenting and classifying bone, segmenting and classifying whole ABVs and may have potential utility in clinical use.

10134-155, Session PS11

Classification of bifurcations regions in IVOCT images using support vector machine and artificial neural network models

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Studies in intravascular optical coherence tomography (IV-OCT) have demonstrated the importance of coronary bifurcation regions in intravascular medical imaging analysis, as plaques are more likely to accumulate in this region leading to coronary disease. A typical IV-OCT pullback acquires hundreds of frames, thus developing an automated tool to classify the OCT frames as bifurcation or non-bifurcation can be an important step to speed up OCT pullbacks analysis and assist automated methods for atherosclerotic plaque quantification. In this work, we evaluate the performance of two state-of-the-art classifiers, SVM and Neural Networks in the bifurcation classification task. The study included IV-OCT frames from 9 patients. In order to improve classification performance, we trained and tested the SVM with different parameters by means of a grid search and different stop criteria were applied to the Neural Network classifier: mean square error, early stop and regularization. Different sets of features were tested, using feature selection techniques: PCA, LDA and scalar feature selection with correlation. Training and test were performed in sets with a maximum of 1460 OCT frames. We quantified our results in terms of false positive rate, true positive rate, accuracy, specificity, precision, false alarm, f-measure and area under ROC curve. Neural networks obtained the best classification accuracy, 98.83%, overcoming the results found in literature. Our methods appear to offer a robust and reliable automated classification of OCT frames that might assist physicians indicating potential frames to analyze. Methods for improving neural networks generalization have increased the classification performance.

10134-156, Session PS11

Evaluation of a processing scheme for calcified atheromatous carotid artery detection in face/neck CBCT images

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Cone Beam Computed Tomography (CBCT), a kind of face and neck exams can be opportunity to identify, as an incidental finding, calcifications of the carotid artery (CACA). Given the similarity of the CACA with calcification found in several x-ray exams, this work suggests that a similar technique designed to detect breast calcifications in mammography images could be applied to detect such calcifications in CBCT. The method used a 3D version of the calcification detection technique [1], based on a signal enhancement using a convolution with a 3D Laplacian of Gaussian (LoG) function followed by removing the high contrast bone structure from the image. Initial promising results show a 74% sensitivity with 0.75 false positive per exam.

10134-54, Session 12

Estimation of retinal vessel caliber using model fitting and random forests

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The retinal vasculature is a unique window for non-invasive assessment of the health of the systemic vasculature. Changes in the retinal vessel caliber can be evaluated using eye fundus images and are associated with several major diseases. However, the clinical assessment is tiresome and prone to errors, motivating the need for automatic methods. The variability of vessel appearance and image quality and resolution hinders the process. An automatic method based on vessel intensity profile model fitting for the estimation of vessel caliber in retinal images is herein proposed. First, vessels are segmented from the image, vessel centerlines are detected and individual segments are extracted and smoothed. Intensity profiles are extracted perpendicularly to the vessel, and the profile lengths are determined. Then, model fitting is applied to the smoothed profiles. A novel parametric model (DoG-L7) is used, consisting in a Difference-of-Gaussians multiplied by a line which is able to describe profile asymmetry. Finally, the parameters of the best-fit model are used to determine the vessel width through regression using ensembles of bagged regression trees with random feature selection. The method is evaluated on a public dataset (REVIEW). Results of the DoG-L7 model are compared with a state-of-the-art Hermite model, using 10-fold cross-validation, and show that the new model returns lower measurement errors. A precision close to the observers is achieved, outperforming other state-of-the-art methods. The method is robust and reliable for width estimation in images with pathologies and artifacts, with performance independent of the range of diameters.

10134-55, Session 12

Automatic and semi-automatic approaches for arteriolar-to-venular computation in retinal photographs

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The Arteriolar-to-Venular Ratio (AVR) is a popular dimensionless measure which allows the assessment of patients' condition for the early diagnosis of different diseases, including hypertension and diabetic retinopathy. This paper presents two new approaches for AVR computation in retinal photographs which include a sequence of automated processing steps: vessel segmentation, caliber measurement, optic disc segmentation, artery/vein classification, region of interest delineation, and AVR calculation. Both approaches have been tested on the INSPIRE-AVR dataset, and compared with a ground-truth provided by two medical specialists. The obtained results demonstrate the reliability of the fully automatic approach which provides AVR ratios very similar to at least one of the observers. Furthermore, the semi-automatic approach, which includes the manual modification of the artery/vein classification if needed, allows to significantly reduce the error to a level below the human error.

10134-56, Session 12

Automatic detection of diabetic retinopathy features in ultra-wide field retinal images

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Diabetic retinopathy (DR) is a major cause of irreversible vision loss. DR screening relies on retinal clinical signs (features). Opportunities for computer-aided DR feature detection have emerged with the development of Ultra-Wide-Field (UWF) digital scanning laser technology. UWF imaging covers 82% greater retinal area (200°), against 45° in conventional cameras, allowing more clinically relevant retinopathy to be detected. UWF images also provide a high resolution of 3078 x 2702 pixels.

Currently DR screening uses 7 overlapping conventional fundus images, and the UWF images provide similar results. However, in 40% of cases, more retinopathy was found outside the 7-field ETDRS fields by UWF and in 10% of cases, retinopathy was reclassified as more severe. This is because UWF imaging allows examination of both the central retina and more peripheral regions, with the latter implicated in DR. We have developed an algorithm for automatic recognition of DR features, including bright (cotton wool spots and exudates) and dark lesions (microaneurysms and blot, dot and flame haemorrhages) in UWF images.

The algorithm extracts features from grayscale (green "red-free" laser light) and colour-composite UWF images, including intensity, Histogram-of-Gradient and Local binary patterns. Pixel-based classification is performed with three different classifiers.

The main contribution is automatic detection of DR features in the peripheral retina. The method is evaluated by leave-one-out cross-validation on 25 UWF retinal images with 167 bright lesions and 61 other images with 1089 dark lesions. The SVM classifier performs best with AUC of 94.4%/95.31% for bright /dark lesions.

10134-57, Session 12

Retinal health information and notification system (RHINO)

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The retinal vasculature is the only part of the blood circulation system that can be observed non-invasively using fundus cameras. Changes in the dynamic properties of retinal blood vessels are associated with many systemic and vascular diseases, such as hypertension, coronary heart disease and diabetes. The assessment of the characteristics of the retinal vascular network provides important information for an early diagnosis and prognosis of many systemic and vascular diseases. The manual analysis of the retinal vessels and measurement of quantitative biomarkers in large-scale screening programs is a tedious task, time-consuming and costly.

This paper describes a reliable, automated, and efficient retinal health information and notification system (acronym 'RHINO') which can extract a wealth of geometric biomarkers in large volumes of fundus images. The fully automated software presented in this paper includes vessel enhancement and segmentation, artery/vein classification, optic disc, fovea, and vessel junction detection, and bifurcation/crossing discrimination. Pipelining these tools allows the assessment of several quantitative vascular biomarkers:

width, curvature, bifurcation geometry features and fractal dimension. The brain-inspired algorithms outperform most of the state-of-the-art techniques. Moreover, several annotation tools are implemented in RHINO for the manual labeling of arteries and veins, marking optic disc and fovea, and delineating vessel centerlines. The validation phase is ongoing and the software is currently being used for the analysis of retinal images from the Maastricht study (the Netherlands) which includes over 10,000 subjects (healthy and diabetic) with a broad spectrum of clinical measurements.

10134-58, Session 12

Joint deep shape and appearance learning: application to optic pathway glioma segmentation

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Automated tissue characterization is one of the major applications of computer-aided diagnosis systems. Deep learning techniques have recently demonstrated impressive performance for the image patch-based tissue characterization. However, existing patch-based tissue classification techniques struggle to exploit the useful shape information. Local and global shape knowledge such as the regional boundary changes, diameter, and volumetrics can be useful in classifying the tissues especially in scenarios where the appearance signature does not provide significant classification information. In this work, we present a deep neural network-based method for the automated segmentation of the tumors referred to as optic pathway gliomas (OPG) located within the anterior visual pathway (AVP; optic nerve, chiasm or tracts) using joint shape and appearance learning. To be considered an OPG, current clinical practice dictates that some portion of AVP must demonstrate shape enlargement. The method proposed in this work integrates multiple sequence magnetic resonance image (T1, T2, and FLAIR) along with local boundary changes to train a deep neural network. For training and evaluation purposes, we used a dataset of multiple sequences MRI obtained from 20 subjects (10 controls, 10 NF1+OPG). To our best knowledge, this is the first deep representation learning-based approach designed to merge shape and multi-channel appearance data for the glioma detection. In our experiments, mean misclassification errors of 2.39% and 0.48% were observed respectively for glioma and control patches extracted from the AVP. Moreover, an overall dice similarity coefficient of 0.87pm 0.13 (0.93pm 0.06 for healthy tissue, 0.78pm 0.18 for glioma tissue) demonstrates the potential of the proposed method in the accurate localization and early detection of OPG.

10134-59, Session 13

Multi-threshold white matter structural networks fusion for accurate diagnosis of early Tourette Syndrome children

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Tourette syndrome (TS) is a childhood-onset neurobehavioral disorder. Tic generation has been linked to disturbed structural networks. Recently, machine learning techniques have been developed to assist clinical diagnosis by extracting useful information provided by brain functional or structural networks. However, few studies were related to TS and some drawbacks still existed in them. Therefore, we propose a novel classification framework integrating a multi-threshold strategy and a network fusion scheme to address the preexisting drawbacks. Here we used diffusion MRI probabilistic tractography to construct the structural networks in 45 TS children and 48 healthy children. We ameliorated the Similarity Network Fusion (SNF) algorithm specially to fuse the multi-threshold structural networks. Graph theoretical analysis was then implemented, and nodal degree, nodal efficiency and nodal betweenness centrality were selected as features. Finally, support vector machine recursive feature extraction (SVM-RFE) algorithm was used for feature selection, and then features are fed into SVM for TS diagnosis. Compared to the previous methods, our proposed framework can greatly improve TS classification performance with an accuracy of 93.76% evaluated by a nested cross validation. The experimental results demonstrate the superior performance of our classification framework over other comparison methods, indicating our framework is an appealing assistance for clinical TS diagnosis.

10134-60, Session 13

Pairwise mixture model for unmixing partial volume effect in multi-voxel MR spectroscopy of brain tumour patients

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Multi-Voxel Magnetic Resonance Spectroscopy (MV-MRS) provides an important and insightful technique for the examination of the chemical composition of brain tissue. Within MRS the issue of the Partial Volume Effect (PVE), where the signals of multiple tissue types can be found within a single voxel, provides an obstacle to the interpretation of the data. The PVE results from the low resolution achieved in MV-MRS images relating to the signal to noise ratio. To counteract the PVE this paper proposes a novel Pairwise Mixture Model (PMM), that extends a recently reported Signal Mixture Model (SMM) for representing the MV-MRS signal as normal, low or high grade tissue types. The PMM, inspired by conditional random fields and their continuous variant, incorporates the surrounding voxel neighbourhood into an optimisation problem, the solution of which provides an estimation to a set of coefficients. The value of the estimated coefficients represents the amount of each tissue type (normal, low or high) found within a voxel. These coefficients can then be visualised as a nosological graph using a coloured grid representing the MV-MRS image overlaid on top of a structural image. Experimental results show an accuracy of 90.94%, in classifying patient scans tumours as either low or high grade compared against the histopathology. Compared to 86.40% achieved by the SMM, the proposed PMM method demonstrates the importance of incorporating spatial coherence into the estimation and its potential clinical usage.

10134-61, Session 13

IDH Mutation Assessment of Glioma Using Texture features of multimodal MR images

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Objective: IDH mutant status are significant for treatment strategy and prognosis prediction of patients with glioma. We aimed to verify the hypothesis that appropriate texture features derived from multimodal MR images may be used for noninvasive and well-repeatable detection of IDH mutant status. Method: 144 patients with glioma were enrolled (52 and 92 with and without IDH mutation, respectively). For each patient, volumes of interest (VOIs) were delineated on multimodal MRI. 3D gray-level co-occurrence and curvature co-occurrence matrix (GLCM and GLGCM) textural features were extracted from each VOI. Then sample augmentation method and the support vector machine (SVM) based feature selection and classification strategies were proposed to firstly obtain an optimal feature subset and then verify and improve its capacity to differentiating IDH mutant status. Results: Total 410 3D GLCM and GLGCM textural features were extracted from ten MRI modalities/parameter maps for each of the 144 patients. With the sample augmentation, feature selection steps included, the optimal accuracy and AUC reached to 88.04% and 0.9416, respectively. In optimal subset, features derived from diffusion and perfusion modalities/parameter maps contributed more in detecting IDH mutant status of glioma, comparing with those derived from structure modalities. Conclusion: In this study, 410 3D GLCM and GLGCM textural features extracted from 10 MRI can reflect the difference between gliomas with and without IDH mutation. With sample augmentation and feature selection, an optimal subset of 42 features was selected and its AUC for mutation detection reached to 0.9416, indicated that it may be a potential imaging biomarkers for predicting IDH mutant status.

10134-62, Session 13

Radiogenomic analysis of lower grade glioma: a pilot multi-institutional study shows an association between quantitative image features and tumor genomics

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Recent studies showed that genomic analysis of lower grade gliomas can be very effective for stratification of patients into groups with different prognosis and proposed specific genomic classifications. In this study we explore the association of one of those genomic classifications with imaging parameters to determine whether imaging could serve a similar role to genomics in cancer patient treatment. Specifically, we analyzed imaging and genomics data for 110 patients from 5 institutions from The Cancer Genome Atlas and The Cancer Imaging Archive datasets. The analyzed imaging data contained preoperative FLAIR sequence for each patient. The images were analyzed using the in-house algorithms which quantify 2D and 3D aspects of the tumor shape. Genomic data consisted of a cluster of clusters classification proposed in a very recent and leading publication in the field of lower grade glioma genomics. Our statistical analysis showed that there is a strong association between the tumor cluster-of-clusters subtype and two imaging features: bounding ellipsoid volume ratio and angular standard deviation. This result shows high promise for the potential use of imaging as a surrogate measure for genomics in the decision process regarding treatment of lower grade glioma patients.

10134-63, Session 13

Radiogenomic analysis of hypoxia pathway reveals computerized MRI descriptors predictive of overall survival in glioblastoma

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Glioblastoma Multiforme (GBM) is a highly aggressive brain tumor with a median survival of 14 months.Hypoxia is a predominant feature in GBM, and is known to be associated with tumor growth, and resistance to conventional therapy. In this study, we hypothesized that radiomic descriptors can capture molecular variations of tumor hypoxia on routine MRI that are otherwise not appreciable; and can discriminate patients with short-term survival(STS, overall survival (OS) < 7 months), mid-term (MTS) (7 months< OS<16 months), and long-term survival (LTS) (OS>16 months). 97 studies (25 STS, 36 MTS, 36 LTS) with Gd-T1c, T2w, and FLAIR protocols and the corresponding gene expression profiles were obtained from the cancer genome atlas (TCGA) database. For each MRI study, necrotic, enhancing tumor, and edematous regions were segmented by an expert. 30 radiomic descriptors (i.e.Haralick, Laws energy, Gabor) were extracted from every region across all three MRI protocols. Using the gene expression profile involved in the hypoxia pathway, a ”low”, ”medium”, or ”high” average hypoxia index was defined for every study. Spearmans correlation was used to identify the most significantly correlated MRI features with the hypoxia index for every study. These features were further used to categorize each study as STS, MTS, and LTS using Kaplan-Meier (KM) analysis. The most correlated features (p<0.05) were identified as Haralick features (capture image heterogeneity) from the enhancing lesion on Gd-T1c, T2w, and FLAIR sequences. These features were also found to be significantly associated with survival, distinguishing MTS from LTS (p=.005) and STS from LTS (p=.0008).

10134-64, Session 13

Effective user guidance in an online interactive semantic segmentation

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With the recent success of machine learning based solutions for automatic image annotation, the availability of reference image annotations for algorithm training is one of the major bottlenecks in medical image segmentation. We are interested in interactive semantic segmentation workflows that can be used in an online fashion to generate expert segmentations. These can be used for quick and accurate tumor progression monitoring or to train automated segmentation techniques. Using simulated user interactions in a MRI glioblastoma segmentation task, we show that if the user possesses knowledge of the correct segmentation it is significantly ($p \leq 0.009$) better to present data and current segmentation to the user in such a manner that they can easily identify falsely classified regions compared to guiding the user to regions where the classifier exhibits high uncertainty, resulting in differences of Dice scores between +0.070 (Whole tumor) and +0.136 (Tumor Core) after 20 iterations. The annotation process should cover all classes equally, which results in a significant ($p \leq 0.031$) improvement compared to random annotation anywhere in falsely classified

regions for small tumor regions such as tumor core (Dice +0.151 after 20 it.), non-enhancing abnormalities (Dice +0.069 after 20 it.) and enhancing tumor (Dice +0.063 after 20 it.). These findings provide important insights needed for the development of efficient interactive segmentation workflows and user interfaces.

10134-65, Session 14

Cephalometric landmark detection in dental X-ray images using convolutional neural networks

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In dental X-ray images, an accurate detection of cephalometric landmarks plays an important role in clinical diagnosis, treatment and surgical decisions for dental problems. In this work, we propose an end-to-end deep learning system for cephalometric landmark detection in dental X-ray images, using convolutional neural networks (CNN). For detecting 19 cephalometric landmarks in dental X-ray images, we develop a detection system using CNN-based coordinate-wise regression systems. By viewing x- and y-coordinates of all landmarks as 38 independent variables, multiple CNN-based regression systems are constructed to predict the coordinate variables from input X-ray images. First, each coordinate variable is normalized by the length of either height or width of an image. For each normalized coordinate variable, a CNN-based regression system is trained on training images and corresponding coordinate variable, which is a variable to be regressed. We train 38 regression systems with the same CNN structure on coordinate variables, respectively. Finally, we compute 38 coordinate variables with these trained systems from unseen images and extract 19 landmarks by pairing the regressed coordinates. In experiments, the public database from the Grand Challenges in Dental X-ray Image Analysis in ISBI 2015 was used and the proposed system showed promising performance by successfully locating the cephalometric landmarks within considerable margins from the ground truths.

10134-66, Session 14

Autoscope - otoscopy image analysis to diagnose ear pathology: use of clinically motivated eardrum features

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In this study, we propose an automated otoscopy image analysis system called Autoscope. To the best of our knowledge, Autoscope is the first study designed to detect a wide range of eardrum abnormalities by using high-resolution otoscope images and report the condition of the eardrum as “normal” or “abnormal.” In order to achieve this goal, first, we developed a preprocessing step to reduce camera-specific problems, detect the region of interest in the image, and prepare the image for the further analysis. Subsequently, we designed a new set of clinically motivated eardrum features (CMEF). Furthermore, we evaluated the potential of the visual MPEG-7 descriptors for the task of tympanic membrane image classification. Then, we fused the information extracted from the CMEF and state-of-the-art computer vision features (CVF), which included MPEG-7 descriptors and two additional features together, using a state of the art classifier. We have been developing a centralized database of high resolution adult and pediatric images, captured via a digital otoscope from inpatient and ambulatory patients. In our preliminary experiments, we used 247 tympanic membrane images with 14 different types of abnormality and observed that the Autoscope was able to classify the given tympanic membrane images as a normal or abnormal with 84.6% accuracy.

10134-67, Session 14

Examining in vivo tympanic membrane mobility using smart phone video-otoscopy and phase-based Eulerian video magnification

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The tympanic membrane (TM) is the bridging element between the pressure waves of sound in air and the ossicular chain. It allows for sound to be conducted into the inner ear, achieving the human sense of hearing. Otitis media with effusion (OME, commonly referred to as ‘glue ear’) is a typical condition in infants that prevents the vibration of the TM and causes conductive hearing loss, this can lead to stunting early stage development if undiagnosed. Furthermore, OME is hard to identify in this age group; as they cannot respond to typical audiometry tests. Tympanometry allows for the mobility of the TM to be examined without patient response, but requires expensive apparatus and specialist training. By combining a smartphone equipped with a 240 frames per second video recording capability with an otoscopic clip-on accessory, this paper presents a novel application of Eulerian Video Magnification to video-otology, that could provide an alternative to diagnosing OME to tympanometry. A spatial-temporal slice taken from an exaggerated video visualization of the TM being excited in vivo on a healthy ear is presented, demonstrating a potential means of diagnosing OME under visual inspection remotely and as an alternative to tympanometry.

10134-68, Session 14

Radiomics biomarkers for accurate tumor progression prediction of oropharyngeal cancer

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Accurate tumor progression prediction for oropharyngeal cancers is crucial for identifying patients who would best be treated with optimized treatment and therefore minimize the risk of under- or over-treatment. An objective decision support system that can merge the available radiomics, histopathologic and molecular biomarkers in a predictive model based on statistical outcomes of previous cases and machine learning may assist clinicians in making more accurate assessment of oropharyngeal tumor progression. In this study, we evaluated the feasibility of developing individual and combined predictive models based on quantitative image analysis from radiomics, histopathology and molecular biomarkers for oropharyngeal tumor progression prediction. With IRB approval 31, 84, and 127 patients with head and neck CT (CT-HN), tumor tissue microarrays (TMAs) and molecular biomarker expressions, respectively, were collected. For 8 of the patients all 3 types of biomarkers were available and they were sequestered in a test set. The CT-HN lesions were automatically segmented using our level sets based method. Morphological, texture and molecular based features were extracted from CT-HN and TMA images, and selected features were merged by a neural network. The classification accuracy was quantified using the area under the ROC curve (AUC). Test AUCs of

0.87, 0.74, and 0.71 were obtained with the individual predictive models based on radiomics, histopathologic, and molecular features, respectively. Combining the radiomics and molecular models increased the test AUC to 0.90. Combining all 3 models increased the test AUC further to 0.94. This preliminary study demonstrates that the individual domains of biomarkers are useful and the integrated multi-domain approach is most promising for tumor progression prediction.

10134-69, Session 14

Automatic cerebrospinal fluid segmentation in non-contrast CT images using a 3D convolutional network

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Segmentation of anatomical structures is fundamental in the development of computer aided diagnosis systems for cerebral pathologies. Manual annotations are laborious, time consuming and subject to human error and observer variability. Accurate quantification of cerebrospinal fluid (CSF) can be employed as a morphometric measure for diagnosis and patient outcome prediction. However, segmenting CSF in non-contrast CT images is complicated by low soft tissue contrast and image noise. In this paper we propose a state-of-the-art method using a multi-scale three-dimensional (3D) fully convolutional neural network (CNN) to automatically segment all CSF within the cranial cavity. The method is trained on a small dataset comprised of four manually annotated cerebral CT images. Quantitative evaluation of a separate test dataset of four images shows a mean Dice similarity coefficient of 0.87 ± 0.01 and mean absolute volume difference of 4.77 ± 2.70%. The average prediction time was 68 seconds. Our method allows for fast and fully automated 3D segmentation of cerebral CSF in non-contrast CT images, and shows promising results despite a limited amount of training data.

10134-70, Session 15

Automated assessment of imaging biomarkers for the PanCan lung cancer risk prediction model with validation on NLST data

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The imaging biomarkers NoduleSpiculation and EmphysemaPresence are required for several models aiming to predict the risk of indeterminate pulmonary nodules detected at baseline screening using low dose CT. To increase reproducibility and to accelerate screening workflow it is desirable to assess these biomarkers automatically. Validation on NLST image volumes indicates that standard histogram measures are not sufficient to assess EmphysemaPresence in screenees. However, automatic scoring of approximately spherical low attenuation areas can achieve agreement with experts with close to 80% sensitivity and specificity. NoduleSpiculation can be automatically assessed with similar accuracy. We find a dedicated spiculi tracing score to slightly outperform generic combinations of texture features with classifiers.

10134-71, Session 15

Quantitative analysis of CT attenuation distribution patterns of nodule components for pathologic categorization of lung nodules

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We investigated the feasibility of classifying pathologic invasive nodules and pre-invasive or benign nodules by quantitative analysis of the CT attenuation distribution patterns and other radiomics features of lung nodule components. We developed a new 3D adaptive multi-component Expectation-Maximization (EM) analysis method to segment the solid and non-sold nodule components, and the surrounding lung parenchymal region. Features were extracted to characterize the size, shape, and the CT attenuation distribution of the entire nodule as well as the individual regions. With permission of National Lung Screening Trial (NLST) project, a data set containing the baseline low dose CT scans of 103 cases and pathologic tumor type classification was obtained, of which 53 cases contain 45 invasive nodules (group 1) and 42 pre-invasive nodules (group 2), and 50 cases contain 79 benign nodules (group 3). Three logistic regression models (LRM) were built using leave-one-case-out resampling and receiver operating characteristic (ROC) analysis: (1) LRM-1 for classification of group 1 and group 2, (2) LRM-2 for differentiating group1 from group 3, and (3) LRM-3 for differentiating group 1 from group 2 and group 3, using the pathologic categorization as ground truth. With the same 4 selected features, LRM-1 achieved a test area under the curve (AUC) value of 0.877±0.036, LRM-2 achieved a test AUC of 0.811±0.041, and LRM-3 achieved a test AUC of 0.833±0.037. The results demonstrated that the pathologic invasiveness of lung adenocarcinomas could be categorized according to the CT attenuation distribution patterns of the nodule components manifested on LDCT images.

10134-72, Session 15

Contextual convolutional neural networks for lung nodule classification using Gaussian-weighted average image patches

Haeil Lee, Hansang Lee, Minseok Park, Junmo Kim, KAIST (Korea, Republic of)

Lung cancer is the most common cause of cancer-related death. To diagnose lung cancers in early stages, numerous studies and approaches have been developed for cancer screening with computed tomography (CT) imaging. In recent years, convolutional neural networks (CNN) have become one of the most common and reliable techniques in computer aided detection (CADe) and diagnosis (CADx) by achieving state-of-the-art-level performances for various tasks. In this study, we propose a CNN classification system for false positive reduction of initially detected lung nodule candidates. First, image patches of lung nodule candidates are extracted from CT scans to train a CNN classifier. To reflect the volumetric contextual information of lung nodules to 2D image patch, we propose a weighted average image patch (WAIP) generation by averaging multiple slice images of lung nodule candidates. Moreover, to emphasize central slices of lung nodules, slice images are locally weighted according to Gaussian distribution and averaged to generate the 2D WAIP. With these extracted patches, 2D CNN is trained to achieve the classification of WAIPs of lung nodule candidates into positive and negative labels. We used LUNA 2016 public challenge database to validate the performance of our approach for false positive reduction in lung CT nodule classification. Experiments show our approach improves the classification accuracy of lung nodules compared to the baseline 2D CNN with patches from single slice image.

10134-73, Session 15

Lung nodule malignancy prediction using multi-task convolutional neural network

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In this paper, we investigated the problem of diagnostic lung nodule malignancy prediction using thoracic Computed Tomography (CT) screening. Unlike most existing studies classify the nodules into two types benign and malignancy, we interpreted the nodule malignancy prediction as a regression problem to predict continuous malignancy level. We proposed a joint multi-task learning algorithm using Convolutional Neural Network (CNN) to capture nodule heterogeneity by extracting discriminative features from alternatingly stacked layers. We trained a CNN regression model to predict the nodule malignancy, and designed a multi-task learning mechanism to simultaneously share knowledge among 9 different nodule characteristics (Subtlety, Calcification, Sphericity, Margin, Lobulation, Spiculation, Texture, Diameter and Malignancy), and improved the final prediction result. Each CNN would generate characteristic-specific feature representations, and then we applied multi-task learning on the features to predict the corresponding likelihood for that characteristic. We evaluated the proposed method on 2620 nodules CT scans from LIDC-IDRI dataset with the 5-fold cross validation strategy. The multi-task CNN regression result for regression RMSE and mapped classification ACC were 0.830 and 83.03%, while the results for single task regression RMSE 0.894 and mapped classification ACC 74.9%. Experiments show that the proposed method could predict the lung nodule malignancy likelihood effectively and outperforms the state-of-the-art methods. The learning framework could easily be applied in other anomaly likelihood prediction problem, such as skin cancer and breast cancer. It demonstrated the possibility of our method facilitating the radiologists for nodule staging assessment and individual therapeutic planning.

10134-74, Session 15

Predictive capabilities of statistical learning methods for lung nodule malignancy classification using diagnostic image features: an investigation using the Lung Image Database Consortium dataset

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In the assessment of nodules in CT scans of the lungs, a number of image-derived features are considered to be diagnostically relevant. Currently, many of these features are defined only qualitatively, and hence, are difficult to quantify from first principles. Nevertheless, these features (through their qualitative definitions and interpretation thereof) are often quantified via a variety of mathematical methods for the purpose of computer-aided diagnosis (CAD). To determine the potential usefulness of quantified diagnostic image features as inputs to a CAD system, we investigate the predictive capability of statistical learning methods for classifying nodule malignancy, utilizing the Lung Image Database Consortium (LIDC) dataset, and only employ the radiologist-assigned diagnostic feature values for the lung nodules therein, as well as our derived estimates of the diameter and volume of the nodules from the radiologists' annotations. We analyze how the classification accuracy, obtained with both a linear and nonlinear statistical learning method, depends on the features and feature subsets. We also calculate theoretical upper bounds on the classification accuracy that is achievable from only the radiologist-assigned feature values, and rank the features according to their predictive power. By including the diameter and volume of the nodules, we significantly improve the classification accuracy.

10134-75, Session 15

Developing a radiomics framework for classifying non-small cell lung carcinoma subtypes

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Patient-targeted treatment of non-small cell lung carcinoma (NSCLC) has been well documented according to the histologic subtypes over the past decade. In parallel, recent development of quantitative image biomarkers has recently been highlighted as important diagnostic tools to facilitate histological subtype classification. In this study, we present a radiomics analysis that classifies the adenocarcinoma (ADC) and squamous cell carcinoma (SqCC). We extract 52-dimensional, CT-based features (7 statistical features and 45 image texture features) to represent each nodule. We evaluate our approach on a clinical dataset including 324 ADCs and 110 SqCCs patients with CT image scans. Classification of these features is performed with four different machine-learning classifiers including Support Vector Machines with Radial Basis Function kernel (RBF-SVM), Random forest (RF), K-nearest neighbor (KNN), and RUSBoost algorithms. To improve the classifiers' performance, optimal feature subset is selected from the original feature set by using an iterative forward inclusion and backward eliminating algorithm. Extensive experimental results demonstrate that radiomics features achieve encouraging classification results on both complete feature set (AUC=0.89) and optimal feature subset (AUC=0.91).

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10135-1, Session 1

Towards quantitative quasi-static elastography with a gravity-induced deformation source

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Biomechanical breast models have been employed for applications in image registration and analysis, breast augmentation simulation, and for surgical and biopsy guidance. Accurate applications of stress-strain relationships of tissue within the breast can improve the accuracy of biomechanical models that attempt to simulate breast deformations. Reported stiffness values for adipose, glandular, and cancerous tissue types vary greatly. Variations in reported stiffness properties are mainly due to differences in testing methodologies, continuum assumptions, measurement errors, and natural inter patient differences in tissue elasticity. Therefore, quantitative determination of patient specific, in vivo breast tissue properties would be highly desirable. Many in vivo elastography methods are not quantitative and/or do not measure material properties under deformation conditions that are representative of the procedure being simulated in the model. In this study, we developed an elastic property estimation method that is performed using deformations representative of supine therapeutic procedures. Reconstruction of material properties was performed by iteratively fitting two anatomical images before and after tissue deformation due to gravitational-induced loading. The method proposed is workflow friendly, quantitative, and uses a non-contact, gravity-induced deformation source. A simulation study was performed to measure the performance of the method under varying initial conditions, discretization levels of the breast for elastic property value reconstruction, and model-data fit metrics. The method is then applied in a clinical context to human subjects. Overall, simulation studies reflect an accurate quantitative methodology for breast tissue elasticity assessment, with percent errors of less than 10%. In a preliminary clinical study, the elastography method was shown to be promising for use in biomechanical model assisted supine procedures.

10135-2, Session 1

Validation of model-based brain shift correction in neurosurgery via intraoperative magnetic resonance imaging: preliminary results

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Brain shift during neurosurgery can compromise the spatial validity of preoperative imaging data, potentially leading to worse outcomes compared to intraoperative magnetic resonance (iMR) assisted procedures. Although iMR provides an enhanced understanding of brain shift intraoperatively, its cost-effectiveness is a consideration for medical centers. Hence a model-based and workflow-friendly shift compensation method could serve as a complementary technology for standard resections while intensive cases could be referred to iMR centers. Briefly, our deformation correction strategy pre-computes hundreds of possible deformation solutions via a biphasic biomechanical model, accounting for a myriad of dynamic variabilities in surgery such as head orientation, cerebrospinal fluid drainage, and swelling. The optimal deformation solution is then obtained via an inverse approach that combines precomputed solutions to best match cortical surface shift measurements. Subsequently, preoperative image is deformed accordingly for a more accurate presentation of intraoperative anatomy, thereby enhancing surgical navigation and execution. This study is a continuing effort to validate our methodology with iMR, the only clinically approved method for monitoring brain shift. Preoperative and intraoperative MR images of 2 patients were acquired. The preoperative image was updated based on corresponding brain surface points selected between preoperative and intraoperative images, as cortical surface deformation is the driving force of our brain shift correction method to update preoperative image volume. For validation, homologous subsurface points were determined among preoperative, intraoperative and updated preoperative images. When considering moderate-to-high levels of subsurface shift (>3 mm), the model-correction strategy provides an average correction of 52% across the two cases presented.

10135-3, Session 1

Mapping 3D breast lesions from full-field digital mammograms using subject-specific finite element models

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Patient-specific finite element (FE) models of the breast have received increasing attention due to the potential capability of fusing images from different modalities. During the Magnetic Resonance Imaging (MRI) to X-ray mammography registration procedure, the FE model is compressed mimicking the mammographic acquisition. Subsequently, suspicious lesions in MR images can be projected into the 2D mammographic space. However, most of the registration algorithms do not provide the reverse information, avoiding to obtain the 3D geometrical information from the lesions localized in the mammograms.

In this work we introduce a fast method to localize the position of the lesion within the MR image, using both cranio-caudal (CC) and medio-lateral oblique (MLO) mammographic projections, indexing the tetrahedral elements of the biomechanical model by means of an uniform grid.

For each marked lesion in the Full-Field Digital Mammogram (FFDM), the X-ray path from source to the marker is calculated. Barycentric coordinates are computed in the tetrahedrons traversed by the ray. The list of elements and coordinates allows to localize two curves within the MR image and the closest point between both curves is taken as the 3D position of the lesion. The registration errors in the mammographic space correspond to 12.6 mm in CC- and 13.2 mm in MLO-projection and the error in the 3D MRI space is equal to 15.1 mm. Regarding the data structure, the uniform grid is computed spending between 0.1 and 0.3 seconds. The time spent to compute the 3D location of the lesion is about 5 ms.

10135-4, Session 1

A biomechanical approach for in vivo diaphragm muscle motion prediction during normal respiration

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Haddad, Western Univ. (Canada); Behzad Seify, Amirkabir Univ. of Technology (Iran, Islamic Republic of); Abbas Samani, Western Univ. (Canada)

Lung cancer is a leading cause of cancer death in men and women. External Beam Radiation Therapy (EBRT) is a commonly used primary treatment for the condition. A major challenge with such treatments is the delivery of sufficient radiation dose to the lung tumor while surrounding healthy lung parenchyma receives only minimal dose. This can be achieved by coupling EBRT with respiratory computer models which can predict the tumour location as a function of phase in breathing cycle. The diaphragm muscle contraction is mainly responsible for a large portion of the lung tumor motion during normal breathing, therefore the importance of accurately modelling the diaphragm is paramount in lung tumour motion prediction. The goal of this research is to develop a biomechanical model of the diaphragm, including its active and passive response, using detailed geometric, biomechanical and anatomical information that parallels the diaphragmatic behaviour in a patient specific manner. For this purpose, a Finite Element Model (FEM) of the diaphragm was developed in order to predict the in vivo motion of the diaphragm, paving the way for computer assisted lung cancer tumor tracking in EBRT. Preliminary results obtained from the proposed model are promising and they indicate that it can be used as a plausible tool for effective lung cancer EBRT.

10135-5, Session 1

Modeling patterns of anatomical deformations in prostate patients undergoing radiation therapy with an endorectal balloon

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External beam radiation therapy (EBRT) treats cancer by delivering daily fractions of radiation to a target volume. For prostate cancer, the target undergoes day-to-day variations in position, volume, and shape. For stereotactic photon and for proton EBRT, endorectal balloons (ERBs) can be used to limit variations. To date, patterns of non-rigid variations for patients with ERB have not been modeled. We extracted and modeled the patient-specific patterns of variations, using regularly acquired CT-images, non-rigid point cloud registration, and principal component analysis (PCA). For each patient, a non-rigid point-set registration method, called Coherent Point Drift, (CPD) was used to automatically generate landmark correspondences between all target shapes. To ensure accurate registrations, we tested and validated CPD by identifying parameter values leading to the smallest registration errors (surface matching error 0.13±0.09 mm). PCA demonstrated that 88±3.2% of the target motion could be explained using only 4 principal directions. The most dominant component of target motion is a squeezing and stretching in the anterior-posterior and superior-inferior directions. A PCA model of daily landmark displacements, generated using 6 to 10 CT-scans, could explain well the target motion for the CT-scans not included in the model (modeling error decreased from 1.83±0.8 mm for 6 CT-scans to 1.6±0.7 mm for 10 CT-scans). PCA modeling error was smaller than the naive approximation by the mean shape (approximation error 2.66±0.59 mm). Future work will investigate the use of the PCA-model to improve the accuracy of EBRT techniques that are highly susceptible to anatomical variations such as, proton therapy.

10135-6, Session 2

Panorama imaging for image-to-physical registration of narrow drill holes inside spongy bone

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Image-to-physical registration based on volumetric data like computed tomography on the one side and intraoperative endoscopic images on the other side is an important method for various surgical applications. In this contribution, we present methods to generate panoramic views from endoscopic recordings for image-to-physical registration of narrow drill holes inside spongy bone. One core application is registration of drill poses inside the mastoid during minimally invasive cochlear implantation. Besides the development of image processing software for registration, investigations are performed on a miniaturized optical system, achieving 360° radial imaging with one shot by extending a conventional, small, rigid, rod lens endoscope. A cone geometry is used to deflect radially incoming light rays into the endoscope optics. Therefore, a cone mirror is mounted in front of a conventional 0° endoscope. Furthermore, panoramic images of a drill hole surface in artificial bone material are created. Preceding drilling, cone beam computed tomography data is acquired from this artificial bone and equivalent simulated endoscopic views are generated from this data. A qualitative and quantitative image comparison of resulting views in terms of image-to-image registration is performed. First results show possible downsizing of panoramic optics to a diameter of 3 mm. Conventional rigid rod lens endoscopes can be extended to produce suitable panoramic one-shot image data. Using dewarping and stitching methods, images of the inner drill hole surface similar to computed tomography image data of the same surface were created. Registration results show suitability of this image data for image-to-image registration.

10135-7, Session 2

Fundamental limits of image registration performance:effects of image noise and resolution in CT-guided interventions

Michael D. Ketcha, Tharindu de Silva, Johns Hopkins Univ. (United States); Runze Han, The Johns Hopkins Univ. School of Medicine (United States); Ali Uneri, Sureerat Reaungamornrat, Joseph Goerres, Johns Hopkins Univ. (United States); Matthew Jacobson, Johns Hopkins Univ (United States); Sebastian Vogt, Gerhard Kleinszig, Siemens Healthineers (Germany); Jeffrey H. Siewerdsen, Johns Hopkins Univ. (United States)

For image-guided interventions, the imaging task is often tied to registration to a preoperative image and the world coordinate system. While image quality characteristics in CT and CBCT and the relationship to visualization tasks have been studied extensively, comparatively little has been accomplished to relate image quality characteristics (noise and resolution) to the performance of image registration. To establish such a framework, we derived Cramer-Rao lower bounds (CRLB) for registration accuracy in a manner that depends on image variance and gradient strength. The bound was analyzed as a function of image quality factors (esp. dose) and compared to registration accuracy for CT images of an anthropomorphic head phantom reconstructed at various simulated dose levels. Using 5 subpixel registration methods, performance was evaluated in terms of root mean square error (RMSE) of the registration parameters. Analysis of the CRLB reveals two primary dependencies: 1) noise variance (related to dose); and 2) sum of squared image gradients (related to resolution and image content). Comparison of the measured RMSE to the CRLB showed that in the best case, RMSE was able to achieve the CRLB within a factor of 2.2, and optimal estimators followed the predicted 1/dose behavior in performance. Analysis of the CRLB for image registration is an important step toward understanding and evaluating an intraoperative imaging system with respect to registration task. While the CRLB is optimistic in absolute performance, it reveals a basis for understanding relative performance of various estimators and can help guide selection of protocols in image-guided interventions.

10135-8, Session 2

Which point-line registration?

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Based on the Iterative Closest Point (ICP) framework, we present a generalized solution for the registration between homologous points and lines. The transformation we seek comprises an anisotropic scaling, followed by rotation and translation. This algorithm is demonstrated using the Perspective-n-Point (PnP) problem where lines form a bundle, and the Non-Perspective-n-Point (NPnP) problem where each line potentially has its own origin. Applications for these types of registration include ultrasound calibration, kinematics tracking under fluoroscopic video, and camera pose estimation. Simulation results suggest this ICP algorithm compares favorably to existing PnP and NPnP algorithms, and has an extremely compact implementation.

10135-9, Session 2

Deformable 3D-2D registration for guiding K-wire placements in pelvic trauma surgery

Joseph Goerres, Matthew Jacobson, Ali Uneri, Tharindu de Silva, Michael D. Ketcha, Sureerat Reaungamornrat, Johns Hopkins Univ. (United States); Sebastian Vogt, Gerhard Kleinszig, Siemens Healthineers (Germany); Jean-Paul Wolinsky, Greg Osgood, The Johns Hopkins Hospital (United States); Jeffrey H. Siewerdsen, Johns Hopkins Univ. (United States)

Pelvic Kirschner wire (K-wire) insertion is a challenging surgical task requiring interpretation of complex 3D anatomical shape from 2D projections (fluoroscopy) and delivery of device trajectories within fairly narrow bone corridors in proximity to adjacent nerves and vessels. Over long trajectories (~10-25 cm), K-wires tend to curve (deform), making conventional rigid navigation inaccurate at the tip location. A system is presented that provides accurate 3D localization and guidance of rigid or deformable surgical devices (“components” – e.g., K-wires) based on 3D-2D registration. The patient is registered to a preoperative CT image by virtually projecting digitally reconstructed radiographs (DRRs) and matching to two or more intraoperative x-ray projections. The K-wire is localized using an analogous procedure matching DRRs of a deformably parametrized model for the device component (deformable known-component registration, or dKC-Reg). A cadaver study was performed in which ten K-wire trajectories were delivered in the pelvis. The system demonstrated target registration error (TRE) of 2.10 ± 0.81 mm in location of the K-wire tip (median ± interquartile range, IQR) and 1.65 ± 2.69º in orientation at the tip (median ± IQR), providing functionality analogous to surgical tracking / navigation using imaging systems already in the surgical arsenal without reliance on a surgical tracker. The method offers quantitative 3D guidance using images (e.g., inlet / outlet views) already acquired in the standard of care, potentially extending the advantages of navigation to broader utilization in trauma surgery to improve surgical precision and safety.

10135-10, Session 2

3D/2D image registration method for joint motion analysis using low-quality images from mini C-arm machines

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A 3D kinematic measurement of joint movement is crucial for orthopedic surgery assessment and diagnosis. This is usually obtained through a frame-by-frame registration of the 3D bone volume to a fluoroscopy video of the joint movement. The high cost of a high-quality fluoroscopy imaging system has hindered the access of many labs to this application. This is while the more affordable and low-dosage version, the mini C-arm, is not commonly used for this application due to low image quality. In this paper, we introduce a novel method for kinematic analysis of joint movement using the mini C-arm. In this method the bone of interest is recovered and isolated from the rest of the image using a non-rigid registration of an atlas to each frame. The 3D/2D registration is then performed using the weighted histogram of image gradients as an image feature. In our experiments, the registration error was 0.89 mm and 2.36˚ for human C2 vertebra. While the precision is still lacking behind a high quality fluoroscopy machine, it is a good starting point facilitating the use of mini C-arms for motion analysis making this application available to lower-budget environments. Moreover, the registration was highly resistant to the initial distance from the true registration, converging to the answer from anywhere within 90 degrees of it.

10135-11, Session 2

Investigation of 3D histograms of oriented gradients for image-based registration of CT with interventional CBCT

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Image registration of preprocedural contrast-enhanced CTs to intraprocedual cone-beam computed tomography (CBCT) can provide additional information for interventional liver oncology procedures such as transcatheter arterial chemoembolisation (TACE). In this paper, a novel similarity metric for gradient-based image registration is proposed. The metric relies on the patch-based computation of histograms of oriented gradients (HOG) building the basis for a feature descriptor.

To evaluate the performance of the new metric, the capture range was estimated based on the calculation of the mean target registration error and compared to the results obtained with a normalized cross correlation metric. The results show that 3D HOG feature descriptors are suitable as image-similarity metric and that the novel metric can compete with established methods in terms of registration accuracy.

10135-12, Session 3

Toward real-time tumor margin identification in image-guided robotic brain tumor resection

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For patients with malignant brain tumors (glioblastomas), a safe maximal resection of tumor is critical for an increased survival rate. However, complete resection of the cancer is hard to achieve due to the invasive nature of these tumors, where the margins of the tumors become blurred from frank tumor to more normal brain tissue, but in which single cells or clusters of malignant cells may have invaded. Recent developments in fluorescence imaging techniques have shown great potential for improved surgical outcomes by providing surgeons intraoperative contrast-enhanced visual information of tumor in neurosurgery. The current near-infrared (NIR) fluorophores, such as indocyanine green (ICG), cyanine5.5 (Cy5.5), 5-aminolevulinic acid (5-ALA)-induced protoporphyrin IX (PpIX), are showing clinical potential to be useful in targeting and guiding resections of such tumors. Real-time tumor margin identification in NIR imaging could be helpful to both surgeons and patients by reducing the operation time and space required by other imaging modalities such as intraoperative MRI, and has the potential to integrate with robotically assisted surgery. In this paper, segmentation method based on the Chan-Vese algorithm was developed for identifying the tumor boundaries in an ex-vivo mouse brain from relatively noisy fluorescence images acquired by a multimodal scanning fiber endoscope (mmSFE). Tumor contours were achieved iteratively by minimizing an energy function formed by a level set function and the Mumford-Shah segmentation model. Quantitative segmentation metrics based on tumor-to-background (T/B) ratio were evaluated. Results demonstrated feasibility in detecting the brain tumor margins at quasi-real-time and has the potential to yield improved precision brain tumor resection techniques or even robotic interventions in the future.

10135-13, Session 3

Real-time phase recognition in novel needle-based intervention: multi-operator feasibility study

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Purpose. One of the goals of new navigation systems in the operating room and in outpatient clinics is to support the surgeon's decision making while minimizing the additional load on surrounding health personnel. To do so the system needs to use context-awareness to provide the surgeon with the most relevant visualization at all times. Such a system could also provide support for the surgical training of novices. The objective of this work is to assess the feasibility of an automatic surgical phase recognition using position data of a novel needle-based instrument.

Methods. An injection into the ganglion sphenopalatine planned on fused MRI and CT images is carried out using optical tracking of the instrument. The intervention is performed by 5 operators, each 5 times on a specially designed phantom. The coordinate information is processed into 7 features characterizing the intervention. Three classifiers, Hidden Markov Model (HMM), a Support Vector Machine (SVM), and a combination of these (SVM+HMM), are trained on manually annotated data, and cross-validated for intra- and inter-operator variability. Standard test metrics are used to compare the classifiers.

Results. HMM alone and SVM alone are comparable classifiers, but feeding the output of the SVM into an HMM results in significantly better classifications: accuracy of 97.8%, sensitivity of 93.1% and specificity of 98.4%.

Conclusion. The use of trajectory information only can provide a robust real-time phase recognition of surgical phases for needle-based interventions.

10135-14, Session 3

Development of a mechanics based model of brain deformations during intracerebral hemorrhage evacuation

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Intracerebral hemorrhages (ICHs) occur in 24 out of 100,000 people annually and have high morbidity and mortality rates. The standard treatment is conservative. We hypothesize that a patient-specific, mechanical model coupled with a robotic steerable needle, used to aspirate a hematoma, would result in minimally invasive approach to ICH management with a goal of improving outcomes. As a preliminary study, two mechanical models based on Biot's Consolidation Theory were developed to approximate brain tissue deformations during aspiration. Short-term transient effects were neglected in favor of a steady state formulation for both. The Galerkin Method of Weighted Residuals was used to solve coupled partial differential equations using linear basis functions, and assumptions of plane strain and homogeneous isotropic properties. The difference between models was how the aspiration effects were incorporated. Both began with aspiration treated as an evacuation pressure on a fixed non-uniform grid. Both models calculated the resulting pressures, displacements, and von Mises stress distributions. With respect to aspiration, both models depended on the von Mises stress criterion; however, one model employs an element-deletion strategy followed by suction redeployment, while the second uses principles of superposition on a fixed grid. While the element-deletion approach had some intuitive appeal, without incorporating a dynamic grid strategy, it evolved into a less realistic result. The superposition strategy overcame this, but the inability to accommodate the impact of continual removal of material limits its utility. While both models have aspects of promise, the superposition method's ability to incorporate the surgical plan makes it favorable.

10135-15, Session 3

The introduction of capillary structures in 4D simulated vascular tree for ART 3.5D algorithm further validation

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Many neurosurgical procedures, such as ArteroVenous Malformations (AVMs), aneurysm embolizations and StereoElectroencephalography (SEEG), require accurate reconstruction of the cerebral vascular tree, as well as the classification of arteries and veins, in order to increase the

precision of the intervention. In the current state of the art, segmentation of arteries and veins from 4D CT perfusion scans has already been proposed. Nonetheless, such procedures require long acquisition protocols and the radiation dose given to the patient is not negligible. Hence, space is open to approaches attempting to recover the dynamic information from standard Contrast Enhanced Cone Beam Computed Tomography (CE-CBCT) scans, which do not require any further data acquisition and patient exposure. The algorithm proposed by our team is called ART 3.5 D. It is a novel algorithm based on the post-processing of both the angiogram and the raw data of a standard Digital Subtraction Angiography from a CBCT (DSA-CBCT) allowing arteries and veins segmentation and labeling without requiring any additional radiation exposure for the patient and neither introducing any lowering in resolution. In addition, while in previous versions of the algorithm the distinction of arteries and veins was just considered, here the capillary phase simulation is inserted, in order to introduce information useful for more precise vasculature segmentation. Results showed classification performances up to 98%. The simulation of capillary structures improved the classification confirming that the capillary phase introduces a wide temporal gap between the arterial and the venous phase, resulting in a remarkable facilitation for arteries and veins distinction.

10135-16, Session 3

Integration of sparse electrophysiological measurements with preoperative MRI using 3D surface estimation in deep brain stimulation surgery

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Intraoperative microelectrode recordings (MER) have been used for several decades to guide neurosurgeons during the implantation of Deep Brain Stimulation (DBS) electrodes, especially when targeting the subthalamic nucleus (STN) to suppress the symptoms of Parkinson's Disease. The standard approach is to use an array of up to five MER electrodes in a fixed configuration. Interpretation of the recorded signals yields a spatially very sparse set of information about the morphology of the respective brain structures in the targeted area. However, no aid is currently available for surgeons to intraoperatively integrate this information with other data available on the patient's individual morphology (e.g. MR imaging data used for surgical planning). This integration might allow surgeons to better determine the most probable position of the electrodes within the target structure during surgery. This paper suggests a method for reconstructing a surface patch from the sparse MER dataset utilizing additional a-priori knowledge about the geometrical configuration of the measurement electrodes. The conventional representation of MER measurements as intervals of target region/non-target region is therefore transformed into an equivalent boundary set representation, allowing efficient point-based calculations. Subsequently, the problem is to integrate the resulting patch with a preoperative model of the target structure, which can be formulated as registration problem minimizing a distance measure between the two surfaces. When restricting this registration procedure to translations, which is reasonable given certain geometric considerations, the problem can be solved globally by employing an exhaustive search with arbitrary precision in polynomial time. The proposed method is demonstrated using bilateral STN/Substantia Nigra segmentation data from preoperative MRIs of 17 Patients with simulated MER electrode placement. When using simulated data of heavily perturbed electrodes and subsequent MER measurements, our optimization resulted in an improvement of the electrode position within 1 mm of the ground truth in 80.29% of the cases.

10135-17, Session 4

Localization of the transverse processes in ultrasound for spinal curvature measurement

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PURPOSE: In scoliosis monitoring, tracked ultrasound has been explored as a safer imaging alternative to traditional radiography. The use of ultrasound in spinal curvature measurement requires identification of vertebral landmarks such as transverse processes, but as bones have reduced visibility in ultrasound imaging, skeletal landmarks are typically segmented manually, which is an exceedingly laborious and long process. We propose an automatic algorithm to segment and localize the surface of bony areas in the transverse process for scoliosis in ultrasound. METHODS: The algorithm uses cascade of filters to remove low intensity pixels, smooth the image and detect bony edges. By applying first differentiation, candidate bony areas are classified. The average intensity under each area has a correlation with the possibility of a shadow, and areas with strong shadow are kept for bone segmentation. The segmented images are used to reconstruct a 3-D volume to represent the whole spinal structure around the transverse processes. RESULTS: A comparison between the manual ground truth segmentation and the automatic algorithm in 50 images showed 0.17 mm average difference. The time to process all 1,938 images was about 37 Sec. (0.0191 Sec. / Image), including reading the original sequence file. CONCLUSION: Initial experiments showed the algorithm to be sufficiently accurate and fast for segmentation transverse processes in ultrasound for spinal curvature measurement. An extensive evaluation of the method is currently underway on images from a larger patient cohort and using multiple observers in producing ground truth segmentation.

10135-18, Session 4

Toward dynamic lumbar punctures guidance based on single element synthetic tracked aperture ultrasound imaging

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Every year, neurologists and emergency medicine personnel perform over 700,000 diagnostic and therapeutic lumbar punctures (LPs) to collect cerebrospinal fluid (CSF). The procedures involve palpating a patient for anatomical landmarks and inserting the needle up to 14 cm into a 3-5 mm window between two spinous processes in the L3-L5 intervertebral space; though the procedure may seem simple, precise and accurate navigation and placement present major challenges, as the needle must be advanced through many tissue layers, without hitting nerves, blood vessels, or bone. The failure of the procedure will result in complications, including post-dural puncture headache, CSF leak, hematoma, and nerve damage. EchoSpine is a new ultrasound imaging system with a single element embedded at the needle tip that ameliorates the current issues with LPs by collecting high resolution images as the needle advances into the tissue. Combining accurate transducer location tracking and synthetic aperture focusing (SAF) techniques, EchoSpine can reconstruct deeply located targets without using conventional array-based ultrasound probe. As a proof the concept, a single element transducer was built in a 14G Quincke needle, and it was mounted on the holster with a rotation tracking encoder. Metal wires phantom mimicking high reflection bone structures were imaged, and the images before and after SAF were compared. As a result, the resolution improvement of 182% and 253% was seen at 30 and 60 mm depth targets, respectively. Those results indicate the EchoSpine has a substantial potential to be used as the ultrasound imaging system combined with the lumbar puncture procedures.

10135-19, Session 4

Identification and tracking of vertebrae in ultrasound using deep networks with unsupervised feature learning

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Percutaneous needle insertion procedures on the spine often require proper identification of the vertebral level in order to effectively deliver anesthetics and analgesic agents to achieve adequate block. For example, in obstetric epidurals, the target is at the L3-L4 intervertebral space. The current clinical method involves 'blind' identification of the vertebral level through manual palpation of the spine, which has only 30% accuracy. This implies the need for better anatomical identification prior to needle insertion. A system is proposed to identify the vertebrae, assigning them to their respective levels, and track them in a standard sequence of ultrasound images, when imaged in the paramedian plane. Machine learning techniques are developed to identify discriminative features of the laminae. In particular, a deep network is trained to automatically learn the anatomical features of the lamina peaks, and classify image patches, for pixel-level classification. The chosen network utilizes multiple connected auto-encoders to learn the anatomy. Pre-processing with ultrasound bone enhancement techniques is done to aid the pixel-level classification performance. Once the lamina are identified, vertebrae are assigned levels and tracked in sequential frames. Experimental results were evaluated against an expert sonographer. Based on data acquired from 15 subjects, vertebrae identification with sensitivity of 95% and precision of 95% was achieved within each frame. Between pairs of subsequently analyzed frames, matches of predicted vertebral level labels were correct in 94% of cases, when compared to matches of manually selected labels.

10135-20, Session 4

Visualization of scoliotic spine using ultrasound-accessible skeletal landmarks

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PURPOSE: Ultrasound imaging is an attractive alternative to X-ray for scoliosis diagnosis and monitoring due to its safety and inexpensiveness. The transverse processes as skeletal landmarks are accessible by means of ultrasound and are sufficient for quantifying scoliosis, but do not provide an intuitively comprehendible visualization of the spine. METHODS: We created a method for visualization of the scoliotic spine using a 3D transform field, resulting from thin-spline interpolation of a landmark-based registration between the transverse processes that we localized in both the patient's ultrasound and an average healthy spine model. Additional anchor points were computationally generated to control the thin-spline interpolation, in order to gain a transform field that accurately represents the deformation of the patient's spine. The transform field is applied to the average spine model, resulting in a 3D surface model depicting the patient's spine. We applied ground truth CT from pediatric scoliosis patients in which we reconstructed the bone surface and localized the transverse processes. We warped the average spine model and analyzed the match between the patient's bone surface and the warped spine. RESULTS: Visual inspection revealed accurate rendering of the scoliotic spine. Notable misalignments occurred mainly in the anterior-posterior direction at the first and last vertebra, which is immaterial for scoliosis quantification. The average Hausdorff distance computed for 4 patients was 2.4 mm. CONCLUSIONS: We achieved qualitatively accurate and intuitive visualization to depict the 3D deformation of the patient's spine when compared to ground truth CT.

10135-21, Session 5

Evaluation of a high-resolution patient-specific model of the electrically stimulated cochlea

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Cochlear implants (CIs) are considered standard treatment for patients who experience sensorineural 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. Our group has developed the first image-guided CI programming (IGCIP) technique where the position of the electrodes are found in CT images and used to estimate neural activation patterns, which is unique information that audiologists can use to define patient-specific processor settings. It has been shown that CI outcomes can be improved when using IGCIP. In our current system, neural activation is estimated using only the distance from each electrode to the neural activation sites. This approach might be less accurate than a highresolution electro-anatomical model (EAM) of the electrically stimulated cochlea to perform physics-based estimation of neural activation. In recent work, we have created preliminary high-resolution EAMs and have shown how they can be made patient-specific by registering them to patient CT images. In this work, we aim to evaluate the accuracy of our EAM approach by comparing intra-cochlear voltage distributions estimated by the model with direct measurements of those voltage distributions for N=5 patients. We found that with our preliminary model, the mean percent difference between direct and simulated measurements is 22%. Visual comparison shows the simulated and measured voltage distributions are qualitatively in good agreement.

10135-22, Session 5

A cochlear implant phantom for evaluating CT acquisition parameters

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Cochlear Implants (CIs) are surgically implantable neural prosthetic devices used to treat profound hearing loss. Recent literature indicates that there is a correlation between the positioning of the electrode array within the cochlea and the ultimate hearing outcome of the patient, indicating that further studies aimed at better understanding the relationship between electrode position and outcomes could have significant implications for future surgical techniques, array design, and processor programming methods. Post-implantation high resolution CT imaging is the best modality for localizing electrodes and provides the resolution necessary to visually identify electrode position, albeit with an unknown degree of accuracy depending on image acquisition parameters, like the HU range of reconstruction, radiation dose, and resolution of the image. In this paper, we report on the development of a phantom that will both permit studying which CT acquisition parameters are best for accurately identifying electrode position and serve as a ground truth for evaluating how different

electrode localization methods perform when using different CT scanners and acquisition parameters. We conclude based on our tests that image resolution and HU range of reconstruction strongly affect how accurately the true position of the electrode array can be found by both experts and automatic analysis techniques. The results presented in this paper demonstrate that our phantom is a versatile tool for assessing how CT acquisition parameters affect the localization of CIs.

10135-23, Session 5

An image guidance system for positioning robotic cochlear implant insertion tools

Trevor L. Bruns, Robert J. Webster III, Vanderbilt Univ. (United States)

Cochlear implants must be inserted carefully to avoid damaging the delicate anatomical structures of the inner ear. This has motivated several approaches to improve the safety and efficacy of electrode array insertion by automating the process with specialized robotic or manual insertion tools. When such tools are used, they must be positioned at the entry point to the cochlea and aligned with the desired entry vector. This paper presents an image-guided system capable of accurately positioning a cochlear implant insertion tool. An optical tracking system localizes the electrode insertion tool in physical space while a graphical user interface incorporates this with patient-specific anatomical data to provide error information to the surgeon in real-time.

10135-24, Session 5

Micro-stereotactic frame utilizing bone cement for individual fabrication. An initial investigation of its accuracy

Thomas S. Rau, G. Jakob Lexow, Denise Blume, Marcel Kluge, Thomas Lenarz, Omid Majdani, Medizinische Hochschule Hannover (Germany)

A new method for template-guided cochlear implantation surgery is proposed which is developed to create a minimally invasive access to the inner ear. A first design of the surgical template was drafted, built, and finally tested regarding its accuracy. For individual finalization of the micro-stereotactic frame bone cement is utilized as this well-known and well-established material suggest ease of use as well as high clinical acceptance and enables both sterile and rapid handling. The new concept includes an alignment device, based on a passive hexapod with manually adjustable legs, for temporary fixation of the separate parts in the patient-specific pose until the bone cement is spread and finally cured. Additionally, a corresponding evaluation method was developed to determine the accuracy of the micro-stereotactic frame in some initial experiments. In total 18 samples of the surgical template were fabricated based on previously planned trajectories. The mean target error was 0.30 mm with a standard deviation of 0.25 mm.

10135-25, Session 5

Selecting electrode configurations for image-guided cochlear implant programming using template matching

Dongqing Zhang, Yiyuan Zhao, Jack H. Noble, Benoit M. Dawant, Vanderbilt Univ. (United States)

Cochlear implants (CIs) are used to treat patients with severe-to-profound hearing loss. In surgery, an electrode array is implanted in the cochlea. After implantation, the CI processor is programmed by an audiologist. One factor that negatively impacts outcomes and can be addressed by programming is cross-electrode neural stimulation overlap (NSO). In the recent past, we have proposed a system to assist the audiologist in programming the CI that we call Image-Guided CI Programming (IGCIP). IGCIP permits using CT images to detect NSO and recommend which subset of electrodes should be active, aka the “electrode configuration,” to avoid NSO. In an ongoing clinical study, we have shown that IGCIP leads to significant improvement in hearing outcomes. Most of the IGCIP steps are robustly automated but electrode configuration selection still sometimes requires expert intervention. With expertise, Distance-Vs-Frequency (DVF) curves, which are a way to visualize the spatial relationship learned from CT between the electrodes and the nerves they stimulate, can be used to select the electrode configuration. In this work, we propose an automated technique for electrode configuration selection. It relies on matching new DVF curves to DVF curves for which electrode configurations are known. We compare this approach to one we have previously proposed. We show that our new method produces results that approach those obtained with our previous one while being generic and requiring fewer parameters. We postulate that because this method is exemplar-based it will improve over time as our library of DVF curves increases.

10135-26, Session 6

Innovations in surgical technology with oncologic application *(Keynote Presentation)*

William R. Jarnagin, Memorial Sloan-Kettering Cancer Ctr. (United States)

No Abstract Available

10135-27, Session 6

Enabling image fusion for a CT guided needle placement robot

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This study presents development and integration of hardware and software that enables ultrasound (US) and computer tomography (CT) fusion for a FDA-approved CT-guided needle placement robot. Having real-time US image registered to a priori-taken intraoperative CT image provides more anatomic information during needle insertion, in order to target hard-to-see lesions or avoid critical structures invisible to CT, track target motion, and to better monitor ablation treatment zone in relation to the tumor location. Method: A passive encoded mechanical arm is developed for the robot in order to hold and track an abdominal US transducer. This 4 degrees of freedom (DOF) arm is designed to attach to the robot end-effector. The arm is locked by default and is released by a press of button. The arm is designed such that the needle is always in plane with US image. The articulated arm is calibrated to improve its accuracy. Custom designed software (OncoNav, NIH) was developed to fuse real-time US image to a priori-taken CT. Results: The accuracy of the end effector before and after passive arm calibration was 7.07mm ± 4.14mm and 1.74mm ±1.60mm, respectively. The accuracy of the US image to the arm calibration was 5mm. The feasibility of US-CT fusion using the proposed hardware and software was demonstrated in an abdominal commercial phantom. Conclusions: Calibration significantly improved the accuracy of the arm in US image tracking. Fusion of US to CT using the proposed hardware and software was feasible.

10135-28, Session 6

Training with Perk Tutor improves ultrasound-guided in-plane needle insertion skill

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PURPOSE: The open-source Perk Tutor training platform has been shown to improve trainee performance in interventions that require ultrasound guidance. Our goal was to determine if distance and angle between the needle and the ultrasound plane can be used as proxies for trainees’ needle coordination competence. Using these measures, we sought to determine if training with the Perk Tutor improved trainees’ needle coordination skills. METHODS: Twenty participants with no previous experience were split into two groups; the Perk Tutor group or the Control group. The Perk Tutor group had access to the 3D visualization model while the Control group had only ultrasound during their training. Performance was analyzed and compared by the Perk Tutor with regards to four needle coordination metrics. RESULTS: The needle tracking measurements showed, for the Perk Tutor group, lower average distance between the needle tip and ultrasound (1.2 [0.9 – 2.8] mm vs 2.7 [2.3 – 4.0] mm, respectively; P = 0.023) and lower maximum distance between the needle tip and ultrasound (2.2 [1.9 – 3.2] mm vs 4.6 [3.9 – 6.2] mm, respectively; P = 0.013). There was no significant difference in average needle to ultrasound plane angle and maximum needle to ultrasound plane angle. All participants were successful in the procedure. CONCLUSION: The Perk Tutor group had significantly reduced distance from the needle tip to the ultrasound plane. Training with the Perk Tutor can improve trainees’ needle and ultrasound coordination.

10135-29, Session 6

Real-time MRI-guided needle intervention for nerve and tumor cryoablation: a phantom study

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MRI-guided needle intervention for cryoablation is a promising way to treat the cancer and relieve the pain for its low complication and high accuracy. However, the limited size of MRI bore make it not ergonomics for the clinicians to perform the operation in the bore throughout the procedure. The patients had to be moved into the bore for scanning to verify the position of the needle’s tip and out for adjusting the needle’s trajectory. Needle tracking and visualization is of importance for to guide the clinicians performing this operation more efficiently. In this paper, we have instrumented the cryotherapy needle with a MRI-safe electromagnetic (EM) sensor and optical sensor to measure the needle’s position and orientation. To overcome the limitation of line-of-sight for optical sensor and the poor dynamic performance of the EM sensor, Kalman filter based sensor fusion is developed. Further, we developed a navigation system in open-source software, 3D Slicer, to provide accurate visualization of the needle and the surrounding anatomy. Experiment of simulation the needle intervention was performed with a realistic spine phantom to quantify the accuracy of guiding the needle to the target using the retrospective analysis method. Eleven trials of needle insertion were performed independently. The target accuracy with the navigation using only EM sensor, only optical sensor and data fusion are 2.27±1.60mm, 4.11±1.77mm and 1.91±1.10mm, respectively. The proposed method shows a perspective in the application of MRI-guided needle intervention for cryoablation.

10135-30, Session 7

Image-guided smart laser system for precision implantation of cells in cartilage

Nitesh Katta, John A. Rector, Michael Gardner, Austin B. McElroy, Kevin C. Choy, Janet Zoldan, Thomas E. Milner, The Univ. of Texas at Austin (United States)

We describe a novel combination of high-resolution, rapid scan-rate optical coherence tomography (OCT) combined with a short-pulsed nanosecond thulium (Tm) laser for precise cell seeding in cartilage. The superior beam quality of thulium lasers and wavelength of operation 1940 nm contributes to high volumetric tissue removal rates with minimal residual thermal footprint. OCT imaging enables targeted micro-well placement and precise cell deposition. A bench-top system is constructed using a 15 W, 1940 nm, nanosecond-pulsed Tm fiber laser (500 µJ pulse energy, 100 ns pulse duration, 30kHz repetition rate) for removing tissue, and a swept source laser (1310 ± 70 nm, 100 kHz sweep rate) for OCT imaging, forming a combined Tm/OCT system – a “smart laser knife”. OCT enables the smart laser knife user to identify cartilage characteristics to inform micro-well placement. Gelatin (4:1, water:gelatin) phantoms are constructed to mimic cartilage optical properties and physiological structure. The Tm laser creates micro-wells (100 µm diameter, 150 µm deep) and micro-incisions (2 mm wide, 150 µm deep) while OCT image-guidance assists and demonstrates this precision cutting and cell deposition with real-time feedback. Cell viability is then assessed to illustrate the efficacy of the smart laser knife in enhancing cell growth. Automated OCT feedback is demonstrated for cutting procedures to avoid important surface/subsurface structures. State-of-the-art treatment for joint diseases like osteoarthritis focuses on articular cartilage repair/regeneration, and we believe this bench-top smart laser knife system is possible addition to the physician’s toolkit for stem cell replacement therapy.

10135-31, Session 7

Feature tracking for automated volume of interest stabilization on 4D-OCT images

Max-Heinrich Laves, Andreas Schoob, Lüder A. Kahrs, Leibniz Univ. Hannover (Germany); Robert A. Huber, Institut für Biomedizinische Optik, Univ. zu Lübeck (Germany) and Optores GmbH (Germany); Tobias Ortmaier, Leibniz Univ. Hannover (Germany)

A common representation of volumetric medical image data is the triplanar view (TV), in which the surgeon manually selects the slices showing the anatomical structure of interest. In addition to common medical imaging, such as MRI or computed tomography, recent advances in the field of optical coherence tomography have enabled live processing and volumetric rendering of four-dimensional images of the human body. Due to moving region of interest, it is challenging for the surgeon to keep track of an object by continuously adjusting the TV to desired slices. To select these slices in subsequent frames automatically, it is necessary to track movement of the volume of interest (VOI). This has not been addressed to 4D-OCT images yet. Therefore, this paper evaluates current state-of-the-art tracking schemes for use on maximum intensity projections (MIP) of 4D-OCT images. The estimated VOI location is used to conveniently show corresponding slices and to improve the MIPs by calculating thin-slab MIPs. The tracking performances are evaluated on an in-vivo sequence of human skin, captured at 26 volumes/s. From investigated tracking schemes, we expect our recently presented tracking scheme for soft tissue motion providing highest accuracy. The thin-slab MIP improves tracking in both accuracy and computational expense. A conducted user study reveals benefit of automated triplanar slice selection in terms of view comfort. Object tracking on 4D-OCT images enables its use for image-guided interventions.

10135-32, Session 7

Microscope integrated OCT based needle-type optical probe for anterior segment surgery

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Optical coherence tomography (OCT) is an emerging biomedical optical imaging technique that provides high-resolution, tomographic cross-sectional imaging of structures in tissue. Recently, the introduction of microscope integrated OCT (MIOCT) to the ophthalmic surgery enables real-time visualizing integrative display of tomographic information of anterior segment tissue in the intraoperative setting. Therefore, MIOCT allows augmented reality (AR) based surgical navigation by superimposing the OCT images onto the microscopic field through the eyepieces. Nevertheless, using only MIOCT is insufficient and complicated to fully understand the surgical maneuver or detect the location of the surgical tools under the tissue during the ophthalmic surgery. Here, we present MIOCT based needle-type optical probe as a surgical guidance tool with enhanced function for anterior segment surgery. Integration of needle-type optical probe and MIOCT shares the optical components in MIOCT, hence, allows visualizing the real-time tomographic information as well as location of the inserted needle probe simultaneously. We also demonstrated the deep anterior lamellar keratoplasty (DALK) procedure on the anterior segment of porcine eyes to evaluate the feasibility of our system. Real-time depth information achieved from the MIOCT based needle-type optical probe assists surgeon to perform more precise and efficient surgery compare to the existing surgical technique with a conventional method. We believe that our system is promising surgical guidance tool especially for anterior segment surgery with great potential for variety of application in surgical fields.

10135-33, Session 7

Don’t get burned: thermal monitoring of vessel sealing using a miniature infrared camera

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Recently miniature chip-tip infrared cameras have come to market for industrial applications that have a form factor that facilitates packaging in endoscopic or other minimally invasive surgical instruments. If absolute temperature measurements can be made with these cameras, they may be useful for non-contact monitoring electrocautery-based vessel sealing, or other thermal surgical processes like thermal ablation of tumors. As a first step in evaluating the feasibility of optical medical thermometry with these new chip tip cameras, in this paper we explore how well thermal measurements can be made with them. These cameras measure the raw flux of incoming IR radiation, and we perform a calibration procedure to map their readings to absolute temperature values in the range between 35 and 95 °C.

10135-34, Session 7

Imaging with a single-element forward-looking steerable IVUS catheter using optical shape sensing

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Complex intravascular lesions, such as chronic total occlusions (CTOs), require forward-looking imaging. We propose to use a 25 MHz single-element transducer and an optical shape sensing (OSS) fiber integrated into a steerable catheter to achieve intravascular imaging in a forward-looking approach.

A tissue-mimicking phantom with three hollow channels (3, 2 and 1 mm in diameter) and two steel spheres (1.5 mm in diameter) is used as imaging target. Ultrasound data and OSS data are simultaneously acquired while steering and rotating a 8.5 F catheter with bidirectional tip flexion. The obtained ultrasound data are reconstructed in 3D space using the position and direction information from the OSS data. Afterwards, the sparsely sampled ultrasound data are projected on a 2D plane and interpolated using normalized convolution (NC), which has been shown previously to perform well on irregularly sampled data [1].

The front surface of the phantom together with the location of two of the three channels and the two steel spheres are successfully reconstructed. The ability to reconstruct different components and their location in space is very important during CTOs crossing. This type of information can aid the crossing procedure providing insights about the best entry point, such as channels location, and helping in avoiding highly calcified areas, which usually are displayed in ultrasound imaging as highly scattering regions.

10135-35, Session 8

Co-robotic ultrasound imaging: a cooperative force control approach

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Ultrasound (US) imaging remains one of the most commonly used imaging modalities in medical practice. However, due to the physical effort required to perform US imaging tasks, 63-91% of ultrasonographers develop musculoskeletal disorders throughout their careers. The goal of this work is to provide ultrasonographers with a system that facilitates and reduces strain in US image acquisition. To this end, we propose a system for admittance force robot control that uses the six-degree-of-freedom UR5 industrial robot. A six-axis force sensor is used to measure the forces and torques applied by the sonographer on the probe. As the sonographer pushes against the US probe, the robot complies with these forces, following the user’s desired path. A one-axis load cell is used to measure contact forces between the patient and the probe in real time. When imaging, the robot augments the axial forces applied by the user, lessening the physical effort required. A user study showed an average 39.37% decrease in hand tremor while imaging at high forces, and a user-reported decrease in difficulty and strenuousness.

10135-36, Session 8

Concentric agonist-antagonist robots for minimally invasive surgeries

Kaitlin P. Oliver Butler, Zane Epps, Daniel C. Rucker, The Univ. of Tennessee Knoxville (United States)

We present a novel continuum robot design concept that functions on push-pull, agonist-antagonist action of a pair of concentric tubes with non-central neutral axes. Bending is induced in the assembly due to notches selectively cut into the profile of two tubes fixed together at their distal ends. The notches relocate the neutral bending plane of each tube to a thin backbone of original material. Dubbed the Concentric Agonist-Antagonist Robot (CAAR), this design attains the millimeter-scale sizes and large, open lumen of traditional precurved, counter-rotated concentric-tube robots but offers simpler kinematics and the avoidance of elastic stability issues, as well as a wider range of motion. The assembly can be used to create 3 degree-of-freedom (DOF), constant- and non-constant-curvature robot segments of a scale appropriate for minimally invasive surgery. Further degrees of freedom can be gained by a multi-segment approach, with additional pairs of tubes deployed from the distal ends of a prior segment in order to attain a higher-dexterity, minimally-invasive robot for surgical applications. Both additive manufacturing and traditional machining methods can create and customize the geometry and performance of the CAAR. The adaptability of this design paired with additive manufacturing enables quickly built, customized devices for patient-specific uses in precision medicine.

10135-37, Session 8

Robotically assisted ureteroscopy for kidney exploration

Hadi Fooladi, Reza Monfaredi, Emmanuel Wilson, Emily Blum, Christopher Bayne, Children's National Medical Ctr. (United States); Craig A. Peters, The Univ. of Texas Southwestern Medical Ctr. at Dallas (United States); Anlin Zhang, Tianjin Univ. (China); Kevin Cleary, Children's National Medical Ctr. (United States)

Ureteroscopy is a minimally invasive procedure for diagnosis and treatment of a wide range of upper urinary tract pathology. It is most commonly performed in the diagnostic work-up of hematuria and the diagnosis and treatment of upper urinary tract malignancies and calculi. Ergonomic and visualization challenges as well as radiation exposure are limitations to conventional ureteroscopy. For example, for diagnostic tumor inspection, the urologist has to maneuver the ureteroscope through each of the 6 to 12 calyces in the kidney under fluoroscopy to ensure complete surveillance. Therefore, we are developing a robotic system to "power drive" a flexible fiber-optic ureteroscope with 3D tip tracking and pre-operative image overlay. Our goal is to provide the urologist precise control of the ureteroscope tip with less radiation exposure.

We designed and implemented a prototype add-on module for robotically assisted ureteroscopy. This prototype allows control of the three degrees of freedom of the ureteroscope via brushless motors and a joystick interface. The robot provides a steady platform for controlling the ureteroscope. Furthermore, the robot design facilitates a quick "snap-in" of the ureteroscope, thus allowing the ureteroscope to be mounted midway through the procedure.

We have completed the mechanical system and the controlling software and begun evaluation using a kidney phantom. We put MRI-compatible fiducials on the phantoms and obtained MR images. We registered these images with the robot using an electromagnetic tracking system and paired-point registration. We are currently recruiting urology residents, fellows, and attendings to evaluate the system and compare it to the current manual procedure.

10135-38, Session 8

Optimized positioning of autonomous surgical lamps

Jörn Teuber, Rene Weller, Ron Kikinis, Gabriel Zachmann, Univ. Bremen (Germany); Karl-Jürgen Oldhafer, Michael J. Lipp, Asklepios Klinik Barmbek (Germany)

We propose a two-tiered optimization technique for the real-time autonomous positioning of surgical lamps. Typically, finding optimal positions for surgical lamps is a multi-dimensional problem with several, in part conflicting, objectives, such as optimal lighting conditions at every point in time while minimizing the movement of the lamps in order to avoid distractions of the surgeon. Consequently, we use multi-objective optimization (MOO) to find optimal positions in real-time during the entire surgery.

Due to the conflicting objectives, there is usually not a emph{single} optimal solution for such kinds of problems, but a set of solutions that realizes a pareto-front. The selection of a solution from this set has to consider the individual preferences of the surgeon. This is a highly non-trivial task because it is complicated to detect a relationship between the solution and the parameters. In addition to the runtime optimization mentioned above, we present a meta-optimization that considers exactly this challenge. It delivers an easy to understand set of presets for the parameters and allows a balance between the lamp movement and lamp obstruction. This meta-optimization can be pre-computed for different kinds of operations.

Both optimization approaches use data obtained by a depth camera that captures the environment around the operating table. We evaluated our algorithms with data recorded during a real open abdominal surgery. It is available for use for scientific purposes. The results show that our optimizations produce more expedient movement and bigger variability.

10135-39, Session 8

Analysis of a Concentric-Tube Robot Design and Feasibility for Endoscopic Deployment

Ryan Ponten, Caroline B. Black, Daniel C. Rucker, The Univ. of Tennessee Knoxville (United States); Andrew J Russ, University of Tennessee Medical Center (United States)

In this paper, we explore the capabilities of concentric-tube robots to work as dexterous tool manipulators at the tip of a dual-channel colonoscope to perform endoscopic submucosal dissection (ESD) and endoscopic full thickness resection (EFTR). To establish feasibility of this approach, we first quantify design requirements for these procedures in terms of manipulator workspace and force capacity. We then provide an overview of kinematic modeling and analyze manipulator workspace and force capacity of a particular concentric tube robot design when it is deployed through a colonoscope. Results show that the concept is feasible, but force capacity can be further improved through active stiffness control and mechanical improvements to the long, torsional transmission tubes. We also present design and resolution analysis of a prototype robotic system with simplified mechatronic design of an actuation module for rotating and translating the component tubes outside the patient.

10135-40, Session 8

Accuracy of registration between a robotic system and a medical imaging system

Abhinav Gulhar, Institue for Medical Engineering, Otto-von-Guericke-Univ. Magdeburg (Germany) and Siemens Healthcare GmbH (Germany); Philip W. Mewes, Siemens Healthineers (Germany); Georg Rose, Institue for Medical Engineering, Otto-von-Guericke-Univ. Magdeburg (Germany)

The presence of robots not only for industrial production but also in operative rooms is increasing rapidly with the advancement of technology. The combination of medical imaging modalities with robots enables them to be guided to anatomical structures in the human body provided the robot is registered to the medical imaging system. In this paper, we evaluate the accuracy of 6 degrees of freedom registration of a robotic system to a medical imaging system without the use of any tracking device. The registration is realized by a series of landmark transformations whose positions are already known in the coordinate system of the imaging system. Multiple factors affect the accuracy of registration between a robotic system and a medical imaging system, with accuracy of pose (AP) of the robot being one of the primary factors. This factor is investigated in this paper and incorporated in the registration accuracy. The AP of the robotic system is evaluated using a tracking system which results in a mean deviation of 0.24 ± 0.07 mm, 0.21 ± 0.08 mm, 0.25 ± 0.11 mm, 0.35 ± 0.15 mm from the desired position when the robot is driven by a relative distance of 10 cm, 20 cm, 30 cm, 40 cm. After incorporating the AP in registration accuracy of the robotic system with an imaging system, a mean norm translation error of 11.88 ± 0.40 mm and a mean rotational error of 1.71 degrees are obtained when compared to an X-ray based ground truth.

10135-60, Session PS1

Integration of myocardial scar identified by preoperative delayed-contrast enhanced MRI into a high-resolution mapping system for planning and guidance of VT ablation procedures

Maryam E. Rettmann, Atsushi Suzuki, Songyun Wang, Mayo Clinic (United States); Nathan Pottinger, Chapman Arter, Andrew Netzer, Boston Scientific Corp. (United States); Kay Parker, Kimberly Viker, Douglas Packer, Mayo Clinic (United States)

Myocardial scarring creates a substrate for reentrant circuits which can lead to ventricular tachycardia. In ventricular catheter ablation therapy, regions of myocardial scarring are targeted to interrupt arrhythmic electrical pathways. Low voltage regions are a surrogate for myocardial scar and are identified by generating an electroanatomic map at the start of the procedure. Recent efforts have focussed on integration of preoperative scar information generated from contrast-enhanced delayed enhancement MR imaging to augment intraprocedural information. In this work, we describe an initial feasibility study of integration of a preoperative MRI derived scar maps into a high-resolution mapping system to improve planning and guidance of VT ablation procedures.

10135-61, Session PS1

A system for endobronchial-video analysis

Patrick D Byrnes, William E. Higgins, The Pennsylvania State Univ. (United States)

Image-guided bronchoscopy is a critical component in the treatment of lung-cancer and other pulmonary disorders. During bronchoscopy, a high-resolution endobronchial-video stream facilitates guidance through the lungs and allows for visual inspection of a patient's airway mucosal surfaces. Despite the detailed information it contains, little effort has been made to incorporate recorded video into the clinical workflow. Follow-up procedures often required in asthma treatment or cancer assessment could significantly benefit from effectively parsed and summarized video. Tracking diagnostic regions of interest (ROIs) could potentially improve asthma treatments such as bronchial thermoplasty or better equip physicians to detect early airway-wall cancer. To address this need, we have developed a system for the postoperative analysis of recorded endobronchial video. The system first parses an input video stream into endoscopic shots, derives motion information, and selects salient representative key frames. Next, a semi-automatic method for CT-video registration creates data linkages between a CT-derived airway-tree model and the input video. These data linkages then enable the construction of a {CT}-video chest model comprised of a bronchoscopy path history (BPH) --- defining all airway locations visited during a procedure --- and texture-mapping information for rendering registered video frames onto the airway-tree model. A suite of analysis tools is included to visualize and manipulate the extracted data. Video browsing and retrieval is facilitated through a video table of contents (TOC) and a search query interface. The system provides a variety of operational modes and additional functionality, including the ability to define ROIs. We demonstrate the potential of our system using two human case study examples.

10135-62, Session PS1

Evaluation of lung tumor motion management in radiation therapy with dynamic MRI

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Surrogate-based tumor motion estimation and tracing methods are commonly used in radiotherapy despite the lack of in-depth understanding of the underlying uncertainty. In this study, we propose a method to simultaneously track the tumor and external surrogates with dynamic MRI, which allows us to evaluate their correlation. Four MRI-compatible fiducials are placed on the patient's chest and upper abdomen, and multi-slice 2D cine MRIs are acquired to capture the lung and whole tumor, followed by two-slice 2D cine MRIs to simultaneously track the tumor and fiducials, all in sagittal orientation. A phase-binned 4D-MRI is first reconstructed from multi-slice MR images using body area as a respiratory surrogate and groupwise registration. The 4D-MRI provides 3D template volumes for different breathing phases. 3D tumor position is calculated by 3D-2D template matching in which 3D tumor templates in 4D-MRI reconstruction and the 2D cine MRIs from the two-slice tracking dataset are registered. 3D trajectories of the external surrogates are derived via matching a 3D geometrical model to the fiducial segmentations on the 2D cine MRIs. We tested our method on five lung cancer patients. Internal target volume from 4D-CT showed average sensitivity of 86.5% compared to the actual tumor motion for 5 min. 3D tumor motion correlated with the external surrogate signal, but showed a noticeable phase mismatch. The 3D tumor trajectory showed significant cycle-to-cycle variation, while the external surrogate was not sensitive enough to capture such variations. Additionally, there was significant phase mismatch between surrogate signals obtained from fiducials at different locations.

10135-63, Session PS1

Automatic detection of measurement points for non-contact vibrometer-based diagnosis of cardiac arrhythmias

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Monitoring of the heart's rhythm is the cornerstone of the diagnosis of cardiac arrhythmias. The current technologies are all based on the electrocardiogram (ECG). Major limitation of the ECG is the need of special electrodes attached to the body. We introduce a new technique that allows a non-contact registration of the heart rhythm. Because of the contactless principle, the technique offers potential application advantages in medical fields like emergency medicine (burn patient) or neonatal care where adhesive electrodes are not easily applicable.

A laser-based, mobile, contactless vibrometer for on-site diagnostics that works with the principle of laser Doppler vibrometry allows the acquisition of vital functions in form of a vibrocardiogram. Preliminary clinical studies at the Klinikum Karlsruhe have shown that the region around the carotid artery and the thoracic region are appropriate therefor. However, the challenge is to find a suitable measurement point in these parts of the body that differs from person to person.

Therefore, we propose a new Kinect-based approach. After several measurement points on the appropriate parts of the body are detected by processing the Kinect data, the vibrometer automatically moves to these points and acquires successively vibrocardiograms until a sufficient measurement quality is achieved. This is verified by analysis methods based on statistical features and structural signal models that identify structures that corresponding to e.g. P-wave or the QRS-complex of the electrocardiogram.

10135-64, Session PS1

Physiology informed virtual surgical planning: a case study with a virtual airway surgical planner and BioGears

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Impacts of tracheal stenosis in adults and infants include shortness of breath, lowered respiratory volumes, and cyanosis. Its treatment is often dictated by institutional factors, namely the clinician's experience or preference. Virtual Pediatric Airway Workbench (VPAW) is a surgical planner for upper airway stenosis. It incorporates CFD simulation and geometric authoring with objective metrics from both that help in informed evaluation and planning. However, this planner currently lacks physiological information which could impact the surgical planning outcomes. In this work we integrate a lumped parameter, model based physiological engine called BioGears with VPAW. It additionally offers some demonstrations of BioGears' functionality, and elucidates the uses of using patient-specific, systemic modeling software for clinical use.

10135-65, Session PS1

Is pose-based pivot calibration superior to sphere fitting?

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Calibrating a pointing stylus tracked via a dynamic reference frame (DRF)

is often performed by pivoting the stylus on its tip in a divot located at a fixed position in the tracking system coordinate frame. The calibration problem is solved by estimating the location of the fixed divot position. Recent work (Yaniv, Which pivot calibration?, Proceedings of SPIE Vol. 941527, 2015) provided evidence that solving the calibration problem using the measured poses of the stylus during pivoting is superior to fitting the measured position of the DRF during pivoting to a sphere. We constructed apparatus to acquire very high quality pivoting measurements over a much wider range of pivoting angles than could be obtained by pivoting in a divot. We tested pose-based calibration and sphere fitting and found that sphere fitting was as precise as (if not better than) pose-based calibration when using high-quality pivoting data. We performed a simple simulation where the stylus tip location deviated by a small amount during pivoting and found that the precision of sphere fitting degraded much more than pose-based calibration which suggests that pose-based calibration should be favored over sphere fitting when non-perfect pivoting is not possible.

10135-66, Session PS1

Online C-arm calibration using a marked guide wire for 3D reconstruction of pulmonary arteries

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3D reconstruction of vessels from 2D X-ray angiography is highly relevant to improve the visualization and the assessment of vascular structures such as pulmonary arteries by interventional cardiologists. However, to ensure a robust and accurate reconstruction, C-arm gantry parameters must be properly calibrated to provide clinically acceptable results. Calibration procedures often rely on calibration objects and complex protocol which is not adapted to an intervention context. In this study, a novel calibration algorithm for C-arm gantry is presented using the instrumentation such as catheters and guide wire. This ensures the availability of a minimum set of correspondences and implies minimal changes to the clinical workflow. The method was evaluated on simulated data and on retrospective patient datasets. Experimental results on simulated datasets demonstrate a calibration that allows a 3D reconstruction of the guide wire up to a geometric transformation. Experiments with patients datasets show a significant decrease of the retro projection error to 0.17 mm 2D RMS. Consequently, such procedure might contribute to identify any calibration drift during the intervention.

10135-67, Session PS1

On pattern selection for laparoscope calibration

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Camera calibration is a key requirement for augmented reality in surgery. Calibration of laparoscopes provides two challenges that are not sufficiently addressed in the literature. In the case of stereo laparoscopes the small distance (less than 6mm) between the channels means that the calibration pattern is an order of magnitude more distant than the stereo separation. For laparoscopes in general, if an external tracking system is used, hand-eye calibration is difficult due to the long length of the laparoscope.

We present a comparison of methods to perform laparoscope intrinsic and hand-eye calibration, focusing on the type of calibration pattern to use. We compare 3 calibration patterns, chessboard, rings, and AprilTags, along with a commercially available laparoscope calibration package (P3D). We measure the error in estimating the camera intrinsic parameters and the camera poses. Accuracy of camera pose estimation will determine the accuracy with which subsequent stereo or hand-eye calibration can be done. We compare the results of repeated real calibrations and simulations using idealised noise, to determine the expected accuracy of different methods and the sources of error. In this case we find that a chessboard grid outperforms the tested alternatives. We intend to make the software and data used freely available to allow others to determine the optimum approach for their application.

10135-68, Session PS1

A robot-assisted bone reposition system for orthognathic surgery: an immediate registration and evaluation

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Orthognathic surgery is a corrective jaw procedure that requires careful planning and accurate execution of a surgical plan. Image-guided navigation systems are currently used to help surgeons in the procedure. However, the systems have human limitations such as limited accuracy and dexterity. To solve these problems, we developed a robot-assisted bone reposition system for orthognathic surgery integrated with image-guided navigation. Our system consisted of a robot with six degrees of freedom, robot motion controller, optical tracking system (OTS) and workstation. A computed tomography (CT) image of a phantom was obtained and three-dimensional surface models were constructed from the CT image. Using the model, postoperative models were generated according to a translational and rotational surgical plan. The preoperative registration between a robot and a CT image was performed and the data was stored before surgery. In the operating room, we loaded the data from preoperative registration, which allowed an immediate task than the conventional method. When the surgeon commanded the robot to move to the final position after cutting the bone, the robot arm was moved according to the surgical plan. We evaluated the root mean square error of the robot movement measured by the navigation system. Experimental results were below 0.25mm in translational movement and below 0.6mm in rotational movement. The results showed that our system was feasible for surgical use, which was acceptable for a clinical tolerance of 2mm. We expect that our system can help surgeons to improve clinical outcomes and to overcome limitations in conventional surgery.

10135-69, Session PS1

On the nature of data collection for soft-tissue image-to-physical organ registration: a noise characterization study

Jarrod A. Collins, Jon S. Heiselman, Jared A. Weis, Logan W. Clements, Vanderbilt Univ. (United States); Amber L. Simpson, William R. Jarnagin, Memorial Sloan-Kettering Cancer Ctr. (United States); Michael I. Miga, Vanderbilt Univ. (United States)

In image-guided liver surgery (IGLS), sparse representations of the anterior organ surface may be collected intraoperatively to drive image-to-physical space registration. Soft tissue deformation represents a significant source of error for IGLS techniques. This work investigates the impact of data collection on a recently reported “state-of-the-art” IGLS registration method that is comprised of an initial rigid registration followed by a combined rigid & nonrigid approach. In this work, we characterize the robustness of our IGLS registration method to noise in organ surface digitization. We introduce a novel human-to-phantom data framework that allows a rapid evaluation of clinically realistic data and noise patterns on a fully characterized hepatic deformation phantom. Additionally, we implement a surface data resampling strategy that is designed to decrease the impact of differences in surface acquisition. For this analysis, N=13 cases of clinical intraoperative data consisting of organ surface and salient feature digitizations from open liver resection were collected and analyzed within our human-to-phantom data analysis methodology. As expected, preliminary results indicate that noise in surface acquisition causes registration fidelity to deteriorate. With respect to nonrigid registration using the raw data, target registration error (TRE) increased quite dramatically, ~97%, with up to 40% added noise. Interestingly, the resampled data outperformed the raw data result and was less susceptible to noise, experiencing only a ~57% increase in TRE when subjected to 40% noise. These results demonstrate the types of analyses our novel human-to-phantom analysis methodology can provide and indicate the considerable benefits of resampling strategies.

10135-70, Session PS1

Using an android application to assess registration strategies in open hepatic procedures: a planning and simulation tool

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Surface digitization with an optically tracked stylus for use in an organ-based image-to-physical registration is an approved approach for open image guided liver surgery procedures. Variability in swab data during open hepatic procedures can introduce error in alignment. While patterns of appropriate swabbing have been established in neurosurgical procedures, the application to soft tissue surgery, such as hepatic procedures, is more complex with no obvious marking procedure. Furthermore, unlike facial features that reside on a rigid cranium, there is considerable deformation during point capture due to the inherent soft-tissue contact as well as tendencies to lose contact given the swabbing coverage needed. These factors could potentially have a confounding effect on registration.

As opposed to neurosurgical procedures with nearly four decades of registration experience, soft-tissue image guided liver surgery is in its infancy. As a result, we have developed an application to allow surgeons to study the performance of surface digitization patterns on registration. In addition, given the intrinsic nature of soft-tissue, we also incorporate the realism of deformation when assessing fidelity. This also has impact on training technicians who are often tasked with demarking preoperative salient features in the case of image guided liver surgery. In this preliminary investigation, we report on the construction of our application and preliminary results. The preliminary data using a mock liver phantom registration shows that different swabbing techniques do cause surface error to be distributed differently across the mock liver. Target error between registered intraoperative and preoperative targets will be assessed in the new work to be presented.

10135-71, Session PS1

Slice-to-volume parametric image registration models with applications to cardiac MRI

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We propose a mathematical formulation aimed at intensity-based registration of a 3D volume to a 2D slice, aligning a cross-sectional slice of the 3D volume to the 2D image. The approach is flexible and can accommodate various regularization schemes, similarity measures, and optimizers. We evaluate the framework by registering 2D and 3D cardiac magnetic resonance (MR) images obtained in vivo, aimed at image-guided surgery applications that use real-time magnetic resonance imaging (MRI) as a visualization tool. Rigid-body and affine transformations are used to validate the parametric model. Target registration error (TRE), Jaccard, and Dice indices are used to validate the algorithm and demonstrate the accuracy of the registration scheme on both simulated and clinical data. Registration with the affine model appeared to be more robust than the rigid model in controlled registration experiments. By simply extending the rigid model to an affine model, alignment of the cardiac region generally improved.

10135-72, Session PS1

Virtual landmarks

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Much has been published on finding landmarks on object surfaces in the context of shape modeling. While this is still an open problem, many of the challenges of past approaches can be overcome by removing the restriction that landmarks must be on the object surface. The virtual landmarks we propose may reside inside, on the boundary of, or outside the object and are tethered to the object. Our solution is straightforward, simple, and is recursive in nature, proceeding from global features initially to local features in later levels to detect landmarks. Principal component analysis (PCA) is used as an engine to recursively subdivide the object. The object itself may be represented in binary form or with gray values. The method is illustrated in 3D space (although it generalizes readily to spaces of any dimensionality) on four objects (liver, trachea and bronchi, the outer boundary of the left and right lungs along the pleura) derived from 5 patient CT image data sets of the thorax and abdomen. We illustrate that the virtual landmark identification approach works well on different structures in different subjects and seems to detect landmarks that are homologously located in different samples of the same object. The approach guarantees that virtual landmarks are invariant to translation, scaling, and rotation of the object/image. Landmarking techniques are fundamental for many computer vision and image processing applications, and we are currently exploring their use in automatic anatomy recognition and object analytics.

10135-73, Session PS1

Skull registration for prone patient position using tracked ultrasound

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PURPOSE: Tracked navigation has become prevalent in neurosurgery. Problems with registration of a patient and a pre-operative image arise when the patient is in a prone position. Surfaces accessible to optical tracking on the back of the head are unreliable for registration. We investigated the accuracy of surface-based registration using points accessible through tracked ultrasound. Using ultrasound allows access to bone surfaces that are not available through optical tracking. Tracked ultrasound could eliminate the need to work (i) under the table for registration and (ii) adjust the tracker between surgery and registration. In addition, tracked ultrasound could provide a non-invasive method in comparison to an alternative method of registration involving screw implantation. METHODS: A phantom study was performed to test the feasibility of tracked ultrasound for registration. An initial registration was performed to partially align the pre-operative computer tomography data and skull phantom. The initial registration was performed by an anatomical landmark registration. Surface points accessible by tracked ultrasound were collected and used to perform an Iterative Closest Point Algorithm. RESULTS: When the surface registration was compared to a ground truth landmark registration, the average TRE was found to be 1.59±0.12mm The average distance of points off the skull surface was 0.59±0.07mm. CONCLUSION: The use of tracked ultrasound is feasible for registration of patients in prone position and eliminates the need to perform registration under the table. The translational component of error found was minimal. Therefore, the amount of TRE in registration is due to a rotational component of error.

10135-74, Session PS1

Comparison of Texture Synthesis Methods for Content Generation in Ultrasound Simulation for Training

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Navigation and interpretation of ultrasound (US) images require substantial expertise, the training of which can be aided by virtual-reality simulators. However, a major challenge in creating plausible simulated US images is the generation of realistic ultrasound speckle. Since typical ultrasound speckle exhibits many properties of Markov Random Fields, it is conceivable to use texture synthesis for generating plausible US appearance. In this work, we investigate popular classes of texture synthesis methods for generating realistic US content. In a user study, we evaluate their performance for reproducing homogeneous tissue regions in B-mode US images from small image samples of similar tissue and report the best-performing synthesis methods. We further show that regression trees can be used on given image texture features to learn a predictor based on these results.

10135-75, Session PS1

Consistent evaluation of an ultrasound-guided surgical navigation system by utilizing an active validation platform

Younsu Kim, Sungmin Kim, Emad M. Boctor, Johns Hopkins Univ. (United States)

Ultrasound-guided needle tracking systems have been widely used due to its cost-effectiveness and non-ionizing radiation properties. Various surgical navigation systems have been developed by utilizing state-of-the-art sensor technologies. Ultrasound transmission beam thickness causes unfair initial evaluation conditions due to inconsistent placement of the target with respect to the ultrasound probe. This inconsistency also brings high uncertainty and results in large standard deviations for each measurement when we compare accuracy with and without the guidance. We designed a complete evaluation platform by utilizing our mid-plane detection and time of flight measurement systems. The system uses a PZT element target and an ultrasound transmitting needle. We evaluated an optical tracker-based surgical ultrasound-guided navigation system. The optical tracker tracks optical fiducials attached on the ultrasound probe and the needle. We performed ten needle guidance experiment trials with mid-plane adjustment algorithm and with B-mode segmentation method. With mid-plane adjustment, the result showed a mean error of 1.62±0.72mm. The mean error increased to 3.58±2.07mm without mid-plane adjustment. Our evaluation system can identify the effect of beam-thickness problem, and measure ultrasound-guided technologies consistently with minimal standard deviation. Using our novel evaluation system, ultrasound-guided technologies can be compared under equal initial conditions. The error can be evaluated more accurately and provide better analysis on the error sources such as ultrasound beam thickness.

10135-76, Session PS1

Computational modeling of radiofrequency ablation: evaluation on ex vivo data using ultrasound monitoring

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Radiofrequency ablation (RFA) is the most widely used minimally invasive ablative therapy for liver cancer, but it is challenged by a lack of patient-specific monitoring. Inter-patient tissue variability and the presence of blood vessels make the prediction of the RFA difficult. A monitoring tool which can be personalized for a given patient during the intervention would be helpful to achieve a complete tumor ablation. However, the clinicians do not have access to such a tool, which results in incomplete treatment and a large number of recurrences.

Computational models can simulate the phenomena and mechanisms governing this therapy. The temperature evolution as well as the resulted ablation can be modeled. When combined together with intra-operative measurements, computational modeling becomes an accurate and powerful tool to gain quantitative understanding and to enable improvements in the ongoing clinical settings.

This paper shows how computational models of RFA can be evaluated using intra-operative measurements.

First, simulations are used to demonstrate the feasibility of the method, which is then evaluated on ex-vivo data. RFA is simulated on a simplified geometry to generate realistic longitudinal temperature maps and the resulted necrosis. Computed temperatures are compared with the temperature evolution recorded using thermometers, and with temperatures monitored by ultrasound (US) in a 2D plane containing the ablation tip.

One ablation is performed on one cadaveric bovine liver, and we achieve error of 3.7°C on average between the computed and the thermistors's temperature and 1.6°C on average between the computed and monitored by US temperature during the ablation.

10135-77, Session PS1

Needle tip visibility in 3D ultrasound images

Muhammad Arif, Adriaan Moelker, Theo van Walsum, Erasmus MC (Netherlands)

Needle visibility is of crucial importance for ultrasound guided interventional procedures. However, several factors, such as shadowing by bone or gas and tissue echogenic properties similar to needles, may compromise needle visibility. Additionally, small angle between the ultrasound beam and the needle, as well as small gauged needles may reduce visibility. Variety in needle tips design may also affect needle visibility. Whereas several studies have investigated needle visibility in 2D ultrasound imaging, no data is available for 3D ultrasound imaging, a modality that has great potential for image guidance interventions (1). In this study, we evaluated needle visibility using a 3D ultrasound transducer. We examined different needles in a tissue mimicking liver phantom at three angles (?20?^0,?55?^0 and ?90?^0) and quantify their visibility. The liver phantom was made by 5% polyvinyl alcohol solution containing 1% Silica gel particles to act as ultrasound scattering particles. We used four needles; two biopsy needles (Quick core 14G and 18G), one Ablation needle (Radiofrequency Ablation 17G), and Initial puncture needle (IP needle 17G). The needle visibility was quantified by calculating contrast to noise ratio. The results showed that the visibility for all needles were almost similar at large angles. However the difference in visibility at lower angles is more prominent. Furthermore, the visibility increases with the increase in angle of ultrasound beam with needles.

10135-78, Session PS1

Catheter tracking in an interventional photoacoustic surgical system

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In laparoscopic medical procedures, accurate tracking of interventional tools such as catheters are necessary. Photoacoustic imaging is an emerging imaging modality that does not currently have a general tool tracking solution. Photoacoustic-based catheter tracking would increase its attractiveness, by providing both an imaging and tracking solution. We present a catheter tracking method based on the photoacoustic effect. Photoacoustic markers are simultaneously observed by a stereo camera as well as a piezoelectric element attached to the tip of a catheter. The signals received by the piezoelectric element can be used to triangulate its position relative to the photoacoustic markers. This combined information can be processed to localize the position of the piezoelectric element with respect to the stereo camera system. We presented the methods to enable this work and demonstrated precisions of 1.60±1.13mm, 1.46±0.94mm, 2.14±1.46mm, and 3.12±2.43mm in four independent locations, which are comparable to conventional systems. We also demonstrated a relative accuracy of less than 4%. Future work will explore how the photoacoustic marker positions affect the localization errors as well as extensions to improve the practicality of this method.

10135-79, Session PS1

Study into needle displacement during navigated breast cancer surgery

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PURPOSE: Early stage breast cancer is typically treated with lumpectomy. During lumpectomy, electromagnetic tracking can be used to monitor tumor position using a localization needle with an electromagnetic sensor fixed on the needle shaft. This needle is stabilized in the tumor with tissue locking wire hooks, which are deployed once the needle is inserted. The localization needle can displace from its initial position of insertion due to mechanical forces, providing false spatial information about the tumor position and increasing the probability of an incomplete resection. This study investigates whether gravitational and mechanical forces affected the magnitude of needle displacement. METHODS: A physician evaluated 10 ultrasound scans to measure needle displacement in vivo. Needle position was approximated by the distance between the needle tip and the tumor boundary on a 2D ultrasound image, and needle displacement was defined by the change in position. The angle between the localization needle and the coronal plane was computed in an open-source platform (www.slicerigt.org). RESULTS: A significant relationship ($p = 0.04$) was found between the needle to coronal plane angle and increased needle displacement. Needles inserted vertically, pointing towards the operating room ceiling, tended to exhibit greater needle displacement. Average needle displacement was 1.7 ±1.2 mm. CONCLUSION: Needle to coronal plane angle has been shown to affect needle displacement, and should be taken into consideration when inserting the localization needle. Future works can be directed towards improving the clinical workflow and mechanical design of the localization needle to reduce slippage during surgery.

10135-80, Session PS1

An accurate detection method for biopsy needle in ultrasound images based on fuzzy enhancement and Hough transform

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Biopsy needle detection in ultrasound images plays an important role in prostate biopsy. The precise positioning of biopsy needle is vital for reducing the number of insertion failures and it still remains a challenging problem. Existing needle detection methods cannot provide accurate detection results or cannot meet the demand of real-time biopsy. To address this problem, we have proposed a fast and accurate biopsy needle detection method based on fuzzy enhancement and Hough Transform (HT). This method uses the fuzzy enhancement to improve the visibility of biopsy needle in ultrasound images. Based on the enhanced ultrasound images, Hough transform combined with edge thinning have been used to detect the biopsy needle. To ensure the detection accuracy in the case where the appearance of needle in ultrasound images is discontinuous, the intensity correlation based tracking algorithm is adopted to locate the tip of the needle. The proposed algorithm was tested on the prostate video sequences including 32 frames in total. Experimental results demonstrate that the needles in the sequences can be detected with 6.7% mis-detection rate. The mean length and angle errors are 8.8 pixels and 0.98 degree, respectively. The needle detection time is 25ms for one frame of size 800?600. Indeed, the proposed method will facilitate the reduction of insertion failures during ultrasound-guided needle procedures due to its high needle detection accuracy.

10135-81, Session PS1

Ultrasound guidance system for prostate biopsy

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We designed a guidance system for prostate biopsy based on PET/MR images and 3D ultrasound (US) With our proposed method the common inter-modal MR-US (or CT-US in case of PET/CTs) registration can be replaced by an intra-modal 3D/3D-US/US registration and the use of an optical tracking system (OTS). On the pre-operative site, a PET/MR calibration allows to link both hybrid modalities with an abdominal 3D-US. On the interventional site, another abdominal 3D US is taken to merge the pre-operative images with the real-time 3D-US via 3D/3D-US/US registration. Finally, the images of the tracked trans-rectal US (TRUS) probe can be displayed with the pre-operative images by overlay.

We found an fiducial registration error of 0.9 mm with respect to the PET/MR calibration. A target registration error between MR and 3D US amounted to 1.4 mm. The registration error for the 3D/3D-US/US registration was found to be 3.7 mm. Furthermore, we have shown that ultrasound is applicable in an MR environment.

10135-82, Session PS1

Motorized fusion guided prostate biopsy: phantom study

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Purpose: Fusion of Magnetic Resonance Imaging (MRI) with intraoperative real-time Ultrasound (US) during prostate biopsy has significantly improved the sensitivity of transrectal ultrasound (TRUS) guided cancer detection. Currently, sweeping of the TRUS probe to build a 3D volume and the TRUS manipulation for needle guidance are both done manually. A motorized, joystick controlled, probe holder was custom fabricated that can potentially reduce inter-operator variability, improve repeatability and uniformity of needle placement, which may have impacts upon the learning curve. Method: a 2DOF motorized probe holder was designed to provide translation and rotation of a tri-plane TRUS end firing probe for prostate biopsy. The probe holder was joystick controlled and can assist manipulation of the probe during needle insertion as well as in acquiring a smoother US 2D to 3D. A commercial MRI-US fusion platform was used. Three targets were specified on MRI of a commercial prostate phantom. After performing the registration, two operators performed targeting, once manually and once with the assistance of the motorized probe holder. They repeated these tasks 5 times, resulting in a total of 30 targeting events. Time of completion and mechanical error (i.e. distance of the target from the needle trajectory in the software user interface) were measured. Repeatability in reaching a given target (in a systematic and consistent way) was measured using a scatter plot showing the foci of targets. Pearson product-moment correlation coefficient (PPMCC) between the image frames was used to demonstrate probe steadiness during targeting. Results: The mechanical error was 0.75±0.4 mm, 0.45±0.4 mm, and 0.55±0.4 mm, for free hand approach while it was 1.0±0.57 mm, 0.45±0.4 mm, and 0.35±0.25 mm, for motorized approach, for target 1, 2, and 3, respectively. PPMCC remained almost at 1 for the motorized approach while having a variation between 0.9 and 1 for the free hand approach showing the higher steadiness in motorized approach. Conclusions: motorized fusion guided prostate biopsy in a phantom study was feasible and non-inferior to the free hand manual approach in terms of accuracy and speed of targeting, while being superior in terms of repeatability and steadiness.

10135-83, Session PS1

Safe electrode trajectory planning in SEEG via MIP-based vessel segmentation

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Stereo-ElectroEncephaloGraphy (SEEG) is a surgical procedure that allows brain's exploration of patients affected by focal epilepsy by placing intra-cerebral electrodes. The electrodes trajectory planning is challenging and time consuming. Various constraints have to be taken into account simultaneously, such as absence of vessels at the electrode Entry Point (EP), where bleeding is more likely to occur. In this paper, we propose a novel framework to help clinicians in defining a safe EP. For each electrode, a Maximum Intensity Projection (MIP) image was obtained from Computer Tomography Angiography (CTA) slices of the brain first centimeter measured along the electrode trajectory. A Gaussian Mixture Model (GMM) modified to include neighborhood prior through Markov Random Fields (GMM-MRF) was used to robustly segment vessels while dealing with the noisy nature of MIP images. Results were compared with simple GMM and manual global Thresholding (Th). GMM and GMM-MRF showed comparable and superior performance with respect to Th in terms of specificity (Th = 0.5030, GMM = 0.8909, MRF = 0.9528) and dice similarity coefficient (Th = 0.6690, GMM = 0.8205, GMM-MRF = 0.7876). GMM-MRF qualitatively showed better performance over GMM in reproducing the connected nature of brain vessels also in presence of noise and image intensity drops typical of MIP images.

10135-84, Session PS1

Automated location detection of injection site for preclinical stereotactic neurosurgery procedure

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Stereotactic neurosurgical procedure is a common practice in both preclinical and clinical settings. In animal studies, researchers use it to intervene specific regions of the brain to carry out various experiments of different aims. One example is the use of optogenetics to investigate functions of different brain regions, which involves stereotactic injection of virus and stereotactic implantation of optic fiber. It is also widely used clinically as a diagnostic tool for brain tumor biopsy, and for treatment of various neurologic disorders, including pain, movement disorders (e.g. Parkinson's Disease), epilepsy, and psychiatric disorders.

The current state-of-the-art stereotactic procedure in rodents involves many steps of calculation and human estimation, and is not error-free. For example, one of the key step is the identification of the Bregma, an anatomical point on the skull at which the coronal suture is intersected perpendicularly by the sagittal suture, which is used as the main reference point. In theory, it is a point which researchers can pinpoint with high accuracy, but in practice, that is seldom the case (Figure 1a, b). The sagittal suture, another important landmark, is also never a straight line. Identification of the Bregma and the sagittal suture, for example, is a part that requires repetitive checking, is laborious and time-consuming, and can benefit substantially from automation.

10135-85, Session PS1

Straight trajectory planning for keyhole neurosurgery in sheep with automatic brain structure segmentation

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Automatic planning systems for safe keyhole neurosurgery have already been proposed in literature. In general, they optimize straight trajectory planning maximizing the distance from vessels and risky structures. The work consists in the development of a linear trajectories planner for the placement of catheters going to be used to explore the drug diffusivity mechanisms in the brain. In a translational neuroscience perspective, sheep are considered good candidates to undergo such a study because of the similarity between their brain and the human one. The system takes the advantage of an online sheep brain atlas to execute a registration process with the Magnetic Resonance (MR) data obtained from ovine subjects. The surgeon selects a target point in the white matter to be reached by the probe and defines a possible entry area on the cortex.

To mitigate the risk of haemorrhage during the insertion process, which can prevent the success of the procedure, the trajectory planner wipes out from the poll of possible entry points all those constituting the part of brain cortex where blood vessels are normally located: the sulci. Subtracting to the original brain model one having undergone a smoothing process, a new sulci-free model is obtained where only the cortical gyri are preserved.

10135-86, Session PS1

Association between hemodynamic modifications and clinical outcome of intracranial aneurysms treated using flow diverters

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Treatment of intracranial aneurysms (IAs) has been revolutionized by the advent of endovascular Flow Diverters (FDs), which disrupt blood flow within the aneurysm to induce pro-thrombotic conditions, and serves as a scaffold for endothelial ingrowth and arterial remodeling. Despite good clinical success of FDs, complications like incomplete occlusion and post-treatment rupture leading to subarachnoid hemorrhage have been reported. In silico computational fluid dynamic analysis of the pre- and post-treated geometries of IA patients can shed light on the contrasting blood hemodynamics associated with different clinical outcomes. In this study, we analyzed hemodynamic modifications in 15 IA patients treated using a single FD; 10 IAs were completely occluded (successful) and 5 were partially occluded (unsuccessful) at 12-month follow-up. An in-house virtual stenting workflow was used to recapitulate the clinical intervention on these cases, followed by CFD to obtain pre- and post-treatment hemodynamics. Bulk hemodynamic parameters showed comparable reductions in both groups with average inflow rate and aneurysmal velocity reduction of 40.3% and 52.4% in successful cases, and 34.4% and 49.2% in unsuccessful cases. There was a substantial reduction in localized parameter like vortex coreline length and Energy Loss for successful cases, 38.2% and 42.9% compared to 10.1% and 10.5% for unsuccessful cases. This suggest that for successfully treated IAs, the localized complex blood flow is disrupted more prominently by the FD as compared to unsuccessful cases. These localized hemodynamic parameters can be used to prospectively predict the treatment outcome, thus aiding the clinicians in a priori assessment of different treatment strategies.

10135-87, Session PS1

Integrated system for point cloud reconstruction and simulated brain shift validation using tracked surgical microscope

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Intra-operative soft tissue deformation, referred to as brain shift, compromises the application of current image-guided surgery (IGS) navigation systems in neurosurgery. A computational model driven by sparse data has been used as a cost effective method to compensate for cortical surface and volumetric displacements. Stereoscopic microscopes and laser range scanners (LRS) are the two most investigated sparse intra-operative imaging modalities for driving these systems. However, integrating these devices in the clinical workflow to facilitate development and evaluation requires developing systems that easily permit data acquisition and processing. In this work we present a mock environment developed to acquire stereo images from a tracked operating microscope and to reconstruct 3D point clouds from these images. A reconstruction error of 1 mm is estimated by using a phantom with a known geometry and independently measured deformation extent. The microscope is tracked via an attached tracking rigid body that facilitates the recording of the position of the microscope via a commercial optical tracking system as it moves during the procedure. Point clouds, reconstructed under different microscope positions, are registered into the same space in order to compute the feature displacements. Using our mock craniotomy device, realistic cortical deformations are generated. Our experimental results report approximately 2mm average displacement error compared with the optical tracking system. These results demonstrate the practicality of using tracked stereoscopic microscope as an alternative to LRS to collect sufficient intraoperative information for brain shift correction.

Keywords: Brain shift, stereoscopic microscope, intra-operative imaging, stereopsis, reconstruction, tracking, accuracy

10135-88, Session PS1

Face-based smoothed finite element method for real-time simulation of soft tissue

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In brain surgery, a tumor and other anatomical structures are usually located using the preoperative CT or MR images. However, due to the deformation of the brain tissue known as the brain shift, this information suffers from inaccuracy when employed directly during the surgery. In order to account for the brain shift in the planning process, several authors propose using a bio-mechanical model of brain. Such models are often designed using the finite element method (FEM), which is, however, computationally expensive, in particular when a high accuracy of the simulation is required.

In our work, we propose to use a smoothed finite element method (S-FEM) in the context of modeling of the brain tissue deformation. This numerical technique has been introduced recently to overcome the overly stiff behavior of the standard FEM and to improve the solution accuracy and the convergence rate in solid mechanics problems. In this paper, a face-based smoothed finite element method (FS-FEM) using 4-node tetrahedral elements is presented. We show that the method allows for reducing the number of elements, while preserving the accuracy of the discretization.

The method is evaluated on a simulation of a cantilever beam loaded at the free end. Further, it is applied to the simulation of the brain shift. The results demonstrate that while being simpler to implement than quadratic FEM, the method seems to be well-suited for real-time applications requiring high accuracy.

10135-89, Session PS1

Automatic intraoperative fiducial-less patient registration using cortical surface

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In image-guided neurosurgery, patient registration is typically performed in the operating room (OR) at the beginning of the procedure to establish the patient-to-image transformation. The accuracy and efficiency of patient registration are crucial as they are associated with surgical outcome, workflow, and healthcare costs. In this paper, we present an automatic fiducial-less patient registration (FLR) by directly registering the cortical surface acquired from intraoperative stereovision (iSV) with preoperative MR (pMR) images without incorporating any prior information, and illustrate the method using one patient example. T1-weighted MR images were acquired prior to surgery and the brain was segmented. After dural opening, a pair of images of the exposed cortical surface was acquired using an intraoperative stereovision (iSV) system, and a three-dimensional (3D) texture-encoded profile of the cortical surface was reconstructed. The 3D surface was registered with pMR using a multi-start binary registration method to determine the location and orientation of the iSV patch with respect to the segmented brain. The total computational time was ~30 min using 12 CPUs, and can be significantly improved through code optimization and parallel computing with more CPUs. The results show that the iSV texture map aligned well with pMR using the FLR transformation, while misalignment was evident with fiducial-based registration (FBR). The difference between FLR and FBR was calculated at the focal point and the resulting distance was 4.34 mm. The results presented in this paper suggest potential for clinical application in the future.

10135-90, Session PS1

Real-time interactive tractography analysis for multimodal brain visualization tool: MultiXplore

Saeed Mahdizadeh Bakhshmand, Sandrine de Ribaupierre, Roy Eagleson, Western Univ. (Canada)

Most debilitating neurological disorders can have anatomical origins. Yet unlike other body organs, the anatomy alone cannot easily provide an understanding of brain functionality. In fact, addressing the challenge of linking structural and functional connectivity remains in the frontiers of Neuroscience. Aggregating multimodal neuroimaging datasets may turn out critical for developing theories that span brain functionality, global neuroanatomy and internal microstructures. Functional MRI (fMRI) and Diffusion Tensor Imaging (DTI) are main such techniques that are employed to investigate the brain under normal conditions, as well as pathological situations. fMRI records blood oxygenation level of the Grey Matter (GM) while DTI is able to reveal underlying structure of the White Matter (WM). Brain global activity is assumed to be an integration of GM functional hubs and WM neural pathways that serve to connect them. In this study we develop and evaluate a two-phase algorithm that helps to accelerate generating clusters of deterministic fiber bundles. This algorithm is employed in a 3D interactive connectivity visualization framework. In this paper, we will detail an algorithm, which makes use of an index-based membership array formed for a whole brain tractography file and corresponding parcellated brain atlas. Next, we demonstrate its efficiency by experimenting required times for generating a range of tract clusters. This combination of regions is chosen in such a way to resemble all sizes of actual outputs that algorithm will be assigned to generate. The proposed algorithm facilitates real time visual inspection of neuroimaging data to further discoveries in structure-function relationship.

10135-91, Session PS1

C-arm positioning using virtual fluoroscopy for image-guided surgery

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Introduction: Repeated radiographic acquisitions due to suboptimal C-arm positioning is common in operating rooms, costing time and radiation exposure. A virtual fluoroscopy system is reported that could dramatically reduce dose and time spent “fluoro hunting,” leveraging three advances: robust 3D-2D registration to a preoperative CT; real-time forward projection on GPU; and a motorized mobile C-arm with encoder feedback on C-arm orientation. Method: Geometric calibration of the C-arm was performed offline in two rotational directions (orbit ?, orbit ?). Patient registration was performed using image-based 3D-2D registration with an initially acquired radiograph of the patient. This approach for patient registration eliminated the requirement for external tracking devices inside the operating

room, allowing virtual fluoroscopy using commonly available systems in fluoroscopically guided procedures within standard surgical workflow. Geometric accuracy was evaluated in terms of projection distance error (PDE) in anatomical fiducials. A pilot study was conducted to evaluate the utility of virtual fluoroscopy to aid C-arm positioning in image guided surgery, assessing potential improvements in time, dose, and agreement between the virtual and desired view. Results: The overall accuracy of generating DRRs in comparison to the actual radiographs at various C-arm positions was PDE (mean ± std) = 1.59 ± 1.10 mm. The conventional approach required on average 8.0 ± 4.5 radiographs spent “fluoro hunting” to obtain the desired view. Positioning accuracy improved from 2.6o ± 2.3o (in ?) and 4.1o ± 5.1o (in ?) in the conventional approach to 1.5o ± 1.3o and 1.8o ± 1.7o, respectively, with the virtual fluoroscopy approach. Conclusion: Virtual fluoroscopy could improve accuracy of C-arm positioning and save time and radiation dose in the operating room.

10135-92, Session PS1

Patient identification using a near-infrared laser scanner

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We propose a new biometric approach where the tissue thickness of the forehead is used as a biometric feature. Given that the spatial registration of two 3D laser scans of the human face usually produces a low error value, the principle of point cloud registration – and its error metric – can be applied to human classification techniques. However, by only considering the spatial error, it is not possible to reliably verify a person’s identity. We propose to use a novel NIR laser-based head tracking system to determine an additional feature, the tissue thickness, and include this in the error metric. Using MRI as a ground truth, data from the foreheads of 30 subjects was collected from which 4D reference point clouds were created. The measurements from the NIR system were registered to all reference point clouds using the ICP algorithm. Afterwards, the spatial and tissue thickness errors were extracted, forming a 2D feature space. For all subjects, the lowest feature distance (average 0.70) resulted from the registration of a measurement and the reference point cloud of the same person. The average of the second-closest feature (always from a different person) was 1.31.

The combined registration error yielded two clusters in the feature space, one from the same subject and another from the other subjects. When only the tissue thickness error was considered, these clusters were less distinct but still present. These findings could raise safety standards for head-and-neck cancer patients and lay the foundation for a future human identification technique.

10135-93, Session PS1

Interactive planning of miniplates

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In this contribution, a novel method for computer aided surgery planning of facial defects by using models of purchasable MedArtis Modus 2.0 miniplates is proposed. Implants of this kind, which belong to the osteosynthetic material, are commonly used for treating defects in the facial area. By placing them perpendicular on the defect, the miniplates are fixed on the healthy bone, bent with respect to the surface, to stabilize the defective area. Our software is able to fit a selection of the most common implant models to the surgeon’s desired position in a 3D computer model. The fitting respects the local surface curvature and adjusts direction and position in any desired way. Conventional methods use Computed Tomography (CT) scans to generate STereoLithic (STL) models serving as bending template for the implants or use a bending tool during the surgery for readjusting the implant several times. Both approaches lead to undesirable expenses in time. With our visual planning tool, surgeons are able to pre-plan the final implant within just a few minutes. The resulting model can be stored in STL format, which is the commonly used format for 3D printing. With this technology, surgeons are able to print the implant just in time or use it for generating a bending tool, both leading to an exactly bent miniplate.

10135-94, Session PS1

Phantom-based evaluation method for surgical assistance devices in minimally-invasive cochlear implantation

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Several research groups have proposed individual solutions for surgical assistance devices to perform a minimally invasive cochlear implantation. Each group tested the accuracy of their device in their respective test bench or in a small number of temporal bone specimens. This complicates the comparison of the different approaches. Thus, the authors propose a simple and cheap phantom based evaluation method using commercial half skull models in a setting which resembles clinical conditions.

Clinical segmentations of temporal bone structures are registered into a computer tomographic scan of the skull phantom and used for the planning of the drill trajectory. Drilling is performed with the respective system under conditions close to the intraoperative setting.. Evaluation of accuracy can either be performed through postoperative imaging or by means of added targets on the inside of the skull model. Two different targets are proposed: a simple grid only for measuring the accuracy and a target containing a scala tympani model for evaluation of the complete work-flow including the insertion of the electrode carrier.

Experiments using the presented method take place under reproducible conditions thus allowing the comparison of the different approaches. In addition, artificial phantoms are easier to obtain and handle than human specimens.

10135-95, Session PS1

Temporal bone dissection simulator for training pediatric otolaryngology surgeons

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Cochlear implantation is the standard of care for infants born with severe hearing loss. Current FDA guidelines approve the surgical placement of implants as early as 12 months of age. Implantation at a younger age poses a greater surgical challenge since the underdeveloped mastoid tip, along with thin calvarial bone, creates less room for surgical navigation and can result in increased surgical risk. We have been developing a temporal bone dissection simulator based on actual clinical cases for training surgeons in this delicate procedure. The simulator system is based on pre-procedure CT images from pediatric infant cases (<12 months old) at our hospital. The simulator includes segmentation of the key structures, an algorithm for converting the current position of the surgical drill to a simulated force, a newly developed haptic interface for providing force feedback, and a virtual reality display that will simulate the microscope views from the procedure. A custom haptic device has been designed to hold the surgical drill. The device has been designed and built and testing will begin shortly. We have also collected 10 representative CT data sets and segmented the anatomy. Key structures, such as the round window position and bony overhang, have been identified. The simulator will present these key structures to the user and provide force feedback as the drill is advanced. By the time of the conference we anticipate having evaluation results from the first tests of the simulator.

10135-96, Session PS1

Planning acetabular fracture reduction using patient-specific multibody simulation of the hip

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Acetabular fractures are a challenge in orthopaedic surgery. Computer-aided solutions were proposed to segment bone fragments, simulate the fracture reduction or design the osteosynthesis fixation plates. This paper adresses the simulation part, which is usually carried out by freely moving bone fragments with six degrees of freedom to reproduce the pre-fracture state. Instead we propose a different paradigm, closer to actual surgeon's requirements: to simulate the surgical procedure itself rather than the desired result.

A simple, patient-specific, biomechanical multibody model is proposed, integrating the main ligaments and muscles of the hip joint while accounting for contacts between bone fragments. Main surgical tools and actions can be simulated, such as clamps, Schanz screws or traction of the femur. Simulations are computed interactively, which enables clinicians to evaluate different strategies for an optimal surgical planning.

Six retrospective cases are presented, with simple and complex fracture patterns. After interatively building the models from preoperative CT, gestures from the surgical reports were reproduced. Results of the simulations could then be compared with postoperative CT data. A qualitative study shows the model behavior is excellent and the simulated reductions fit the observed data. A more quantitative analysis is currently being completed.

Two cases are particularly significant, for which the surgical reduction actually failed. Simulations show it was indeed not possible to reduce these fractures with the chosen approach. Had our simulator being used, a better planning may have avoided a second surgery to these patients.

10135-97, Session PS1

Statistical shape modeling based renal volume measurement using tracked ultrasound

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Autosomal dominant polycystic kidney disease (ADPKD) is the fourth most common cause of kidney transplant worldwide accounting for 7-10% of all cases. Although ADPKD usually progresses over many decades, accurate risk prediction is an important task. Identifying patients with progressive disease is vital to providing new treatments being developed and enable them to enter clinical trials for new therapy. Among other factors total kidney volume (TKV) is a major biomarker predicting the progression of ADPKD. Consortium for Radiologic Imaging Studies in Polycystic Kidney Disease (CRISP) have shown that TKV is an early, and accurate measure of cystic burden and likely growth rate. It is strongly associated with loss of renal function. While ultrasound (US) has proven as an excellent tool for diagnosing the disease; monitoring short-term changes using ultrasound has been shown to not be accurate. This is attributed to high operator variability and reproducibility as compared to tomographic modalities such as CT and MR (Gold standard). Ultrasound has emerged as one of the standout modality for intra-procedural imaging and with methods for spatial localization has afforded us the ability to track 2D ultrasound in physical space which it is being used. In addition to this, the vast amount of recorded tomographic data can be used to generate statistical shape models that allow us to extract clinical value from archived image sets. In this work, we aim at improving the prognostic value of US in managing ADPKD by assessing the accuracy of using statistical shape model augmented US data, to predict TKV, with the end goal of monitoring short-term changes.

10135-98, Session PS1

Monitoring electromagnetic tracking error using redundant sensors

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PURPOSE: The intraoperative measurement of tracking error is crucial to ensure the reliability of electromagnetically navigated procedures. For intraoperative use, methods need to be quick to set-up, easy to interpret, and not interfere with the ongoing procedure. Our goal was to evaluate the feasibility of using redundant electromagnetic sensors to alert users to tracking error in a navigated intervention set-up. METHODS: Electromagnetic sensors were fixed to a rigid frame around a region of interest and on surgical tools. A software module was designed to compare real?time measurements of the differences between inter-sensor distances and angles to baseline measurements, as a detector of tracking error. Once these measurements were collected, a linear support vector machine?based classifier was used to predict tracking errors from redundant sensor readings. RESULTS: Measuring the deviation in the reported inter?sensor distance and angle on the needle and cautery served as a valid indicator for electromagnetic tracking error. The highest classification accuracy, 86%, was achieved based on readings from the cautery when the two sensors on the cautery were close together. The specificity of this classifier was 93% and the sensitivity was 82%. CONCLUSION: Placing redundant electromagnetic sensors in a workspace seems to be feasible for the intraoperative detection of electromagnetic tracking error in controlled environments. Further testing should be performed to optimize the measurement error threshold used for classification in the support vector machine, and improve the sensitivity of our method before application in real procedures.

10135-99, Session PS1

Visual tracking for multi-modality computer-assisted image guidance

Ehsan Basafa, Pezhman Foroughi, Martin Hossbach, Jasmine Bhanushali, Clear Guide Medical (United States); Philipp J. Stolka, Johns Hopkins Outpatient Ctr. (United States) and Clear Guide Medical (United States)

With optical cameras, many navigation tasks previously relying on EM, optical, or mechanical guidance can be performed robustly, quickly, and conveniently. We developed a family of novel guidance systems based on wide-spectrum cameras and vision algorithms for real-time tracking of interventional instruments and skin-attached multi-modality markers. These navigation systems support localization of anatomical targets, support of imaging probe and instruments placement, monitoring of treatment

progress, and fusion imaging. However, the unique architecture – low-cost, miniature, in-hand stereo vision cameras that can be fitted directly to the imaging probes – allows for an intuitive workflow that fits a wide variety of specialties such as anesthesiology, interventional radiology, interventional oncology, emergency medicine, urology, and others, many of which see increasing pressure to utilize medical imaging, but have yet to develop the requisite experience or skills for reliable success. Specifically, we developed a modular toolbox, consisting of hardware (the Optical Head containing the mini cameras) and software (including components for fully-automated marker segmentation from a variety of 3D imaging modalities, visual observation of meshes of widely-separated markers, instant automatic registration, visual instrument tracking with or without specialized visual features, and target tracking and guidance on real-time multi-modality fusion views). Using these components, we implemented a family of distinct clinical systems (for combinations of ultrasound, CT, CBCT, MRI, or image-free, and for different instrument types), several of which have international regulatory clearance for clinical use and are commercially available. We present technical and clinical results on phantoms, ex- and in-vivo animals, and patients.

10135-100, Session PS1

Usability of a real-time tracked augmented reality display system in musculoskeletal injections

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PURPOSE: Image-guided needle interventions are seldom performed with augmented reality guidance in clinical practice due to many workspace and usability restrictions. We propose a real-time optically tracked image overlay system to make image-guided musculoskeletal injections more efficient and assess its usability in a bed-side clinical environment.

METHODS: An image overlay system consisting of an optically tracked viewbox, tablet computer, and semi-transparent mirror allows users to navigate scanned patient volumetric images in real-time using software built on the open-source 3D Slicer application platform. A series of experiments were conducted to evaluate the latency and screen refresh rate of the system using different image resolutions. To assess the usability of the system and software, five medical professionals were asked to navigate patient images while using the overlay and completed a questionnaire to assess the system.

RESULTS: In assessing the latency of the system with scanned images of varying size, screen refresh rates were approximately 5 FPS. The study showed that participants found using the image overlay system easy, and found the table-mounted system was significantly more usable and effective than the handheld system.

CONCLUSION: It was determined that the system performs comparably with scanned images of varying size when assessing the latency of the system. During our usability study, participants preferred the table-mounted system over the handheld. The participants also felt that the system itself was simple to use and understand. With these results, the image overlay system show promise for use in a clinical environment.

10135-101, Session PS1

Real- time liver tumour tracking with low contrast radiopaque markers

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An improved auto segmentation methodology that will identify the position of a low contrast radiopaque fiducial marker has been investigated in this study. The developed methodology has been implemented in an in-house developed real-time 3D position monitoring system, SeedTracker, for liver Stereotactic Body Radio Therapy (SBRT). The SeedTracker system estimates the 3D position of the markers, and thereby tumour, using monoscopic kV x-ray images acquired during the treatment based on the seeds position in the projection image and 3D position information learned from Cone Beam Computed Tomography (CBCT) projections. The overall performance of SeedTracker software was evaluated using a retrospective analysis of CBCT images, acquired with the Elekta-XVI system, of five liver cancer patients implanted with embolization coils. For the evaluation of SeedTracker the 3D CBCT projection images acquired for patient position verification was used for 3D position learning of the SeedTracker system. The 4D CBCT projection images acquired during the same treatment session was processed in SeedTracker to estimate the 3D position of the seeds and isocentre at different phases of the breathing cycle. The SeedTracker estimated 3D positions were compared with the seed and isocentre positions in XVI reconstructed 4D CBCT image datasets. The system showed an auto seed segmentation True Positive Rate (TPR) of 96%. The 3D seed and plan isocentre positions estimated by SeedTracker agreed with the XVI 4D reconstructed data with a mean (?) difference of 0.2(1.8) mm. The developed system has a potential application of monitoring target position during treatment delivery in liver SBRT.

10135-102, Session PS1

Breathing motion compensated registration of laparoscopic liver ultrasound to CT

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Laparoscopic Ultrasound (LUS) is regularly used during laparoscopic liver resection to locate critical vascular structures. Many tumours are iso-echoic, and registration to pre-operative CT or MR has been proposed as a method of image guidance. However, factors such as abdominal insufflation, LUS probe compression and breathing motion deform the liver, making this task far from trivial. Fortunately, within a smaller local region of interest a rigid solution can suffice and the respiratory cycle expected to be consistent. Therefore, in this paper we propose a feature-based local rigid registration method to align tracked LUS data with CT while compensating for breathing motion. The method employs the Levenberg-Marquardt Iterative Closest Point (LMICP) algorithm, registers both on liver surface and vessels and requires two LUS datasets, one for registration and another for breathing estimation. Surface points are acquired through LUS probe digitisation and vessel contours are segmented from the images. Breathing compensation is achieved by fitting a 1D breathing model to the vessel points. We evaluate the algorithm by measuring the Target Registration Error (TRE) of three manually set landmarks of a single porcine subject. Breathing compensation improves accuracy in 72% of the measurements. In the best case, TRE values below 3mm are obtained. We conclude that our method can potentially correct for breathing motion without gated acquisition of LUS and be integrated in the surgical workflow with an appropriate segmentation.

10135-103, Session PS1

Emulation of the laparoscopic environment for image-guided liver surgery via an abdominal phantom system with anatomical ligamenture

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In order to correctly validate techniques for image-guided liver surgery (IGLS), an accurate mock representation of the intraoperative surgical scene would be highly desirable. However, many attempts to reproduce the laparoscopic environment have encountered limited success due to neglect of several crucial design aspects. The laparoscopic setting is complicated by factors such as gas insufflation of the abdomen, changes in patient orientation, incomplete organ mobilization from ligamenture, and limited access to organ surface data. The ability to accurately represent the influences of anatomical changes and procedural limitations is critical for appropriate evaluation of IGLS methodologies such as registration and deformation correction. However, these influences have not yet been comprehensively integrated into a platform usable for assessment of laparoscopic IGLS procedures. In this work, a mock laparoscopic liver simulator was created with realistic ligamenture to emulate the complexities of this constrained surgical environment for the purposes of realizing laparoscopic IGLS. The mock surgical system reproduces an insufflated abdominal cavity with dissectible ligamenture, variable levels of incline matching intraoperative patient positioning, and port locations in accordance with surgical protocol. Using this laparoscopic setup, image-to-physical registration accuracy was evaluated for simulations of both right and left lobe hepatectomy to assess registration performance under more representative conditions. Intraoperative surface digitization was performed using a trocar-compatible tracked stylus and a non-contact method of tracked conoscopic holography. Preliminary results suggest that nonrigid organ deformation and the extent of organ surface data available through ports are limiting factors towards attaining highly accurate registrations in laparoscopic applications.

10135-104, Session PS1

Automatic transperineal ultrasound probe positioning based on CT scan for image guided radiotherapy

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Image interpretation is crucial during ultrasound image acquisition. A skilled operator is typically needed to verify if the correct anatomical structures are all visualized and with sufficient quality. The need for this operator is one of the major reasons why presently ultrasound is not widely used in radiotherapy workflows.

To solve this issue, we introduce an algorithm that uses anatomical information derived from a CT scan to automatically provide the operator with a patient-specific ultrasound probe setup. The first application we investigated, for its relevance to radiotherapy, is 4D transperineal ultrasound image acquisition for prostate cancer patients.

As initial test, the algorithm was applied on a CIRS multi-modality pelvic phantom. Probe setups were calculated in order to allow visualization of the prostate and adjacent edges of bladder and rectum, as clinically required. Five of the proposed setups were reproduced using a precision robotic arm and ultrasound volumes were acquired. A gel-filled probe cover was used to ensure proper acoustic coupling, while taking into account possible tilted positions of the probe with respect to the flat phantom surface.

Visual inspection of the acquired volumes revealed that clinical requirements were fulfilled. Preliminary quantitative evaluation was also performed. The mean absolute distance (MAD) was calculated between actual anatomical structure positions and positions predicted by the CT-based algorithm. This resulted in a MAD of (2.8±0.4) mm for prostate, (2.5±0.6) mm for bladder and (2.8±0.6) mm for rectum. These results show that no large systemic errors due to e.g. probe misplacement were introduced.

10135-105, Session PS1

Fractional labelmaps for computing accurate dose volume histograms

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PURPOSE: In radiation therapy treatment planning systems structures are represented as parallel 2D contours. To be used in treatment planning algorithms, structures must be converted into labelmap (i.e. 3D image denoting structure inside/outside) representations. This is often done by constructing a triangulated surface from contours, which is converted into a binary labelmap. This surface to binary labelmap conversion can cause large errors in small structures. Binary labelmaps are often represented using one byte per voxel, meaning a large amount of unused memory is allocated. Our goal is to develop a fractional labelmap representation that contains continuous, non-binary values, which allows more information to be stored in the same amount of memory. METHODS: We propose an algorithm, which is implemented in the SlicerRT toolkit, to convert surfaces to fractional labelmaps by creating 216 binary labelmaps from the surface, temporarily changing the volume origin on each iteration. The binary labelmap values are summed together to create the fractional labelmap. In addition, an algorithm is implemented that calculates dose volume histograms (DVH) using fractional labelmaps. RESULTS: We found fractional labelmaps represent structure volume up to 20.68% more accurately than binary labelmaps, while occupying the same amount of memory. When compared to baseline DVH from treatment planning software, DVH from fractional labelmaps had an agreement acceptance percent (1% ?D, 1% ?V) up to 57.45% higher than DVH from binary labelmaps. CONCLUSION: Fractional labelmaps promise to be an effective method for structure representation, allowing more information to be stored in the same amount of memory.

10135-106, Session PS1

Evaluation of the Intel RealSense SR300 camera for image-guided interventions and application in vertebral level localization

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PURPOSE: Optical tracking of medical instruments is often used in image-guided interventions. Unfortunately, compared to modern computing devices, they tend to be large, heavy, and expensive. The Intel RealSense SR300 camera costs 1% of conventional trackers, and weighs less than

10 grams. We propose the SR300 is suitable for applications where it is not practical or feasible to use conventional trackers. We also put forward a vertebral level localization application utilizing the SR300 to reduce the risk of wrong-level surgery. METHODS: The SR300 was utilized as an object tracker by extending the PLUS toolkit to support data collection from RealSense cameras. Accuracy of the camera was tested by comparing to a high-accuracy optical tracker. CT images of a lumbar spine phantom were obtained and used to create a 3D model in 3D Slicer. The SR300 was used to obtain a surface model of the phantom and Slicer was used to register and overlay it with the CT image. RESULTS: The accuracy of the camera yielded a median position error of 3.3mm (95th percentile 6.7mm) and orientation error of 1.6 (95th percentile 4.3) in a 20x16x10cm workspace constantly maintaining proper marker orientation. The model and surface correctly aligned demonstrating the vertebral level localization application. CONCLUSION: The SR300 could be used for object tracking in medical procedures where limited accuracy is acceptable. Initial results suggest the SR300 is suitable for vertebral level localization. Further testing should be performed to assess the limitations of the camera and its robustness in other applications.

10135-41, Session 9

Patient-specific pediatric silicone heart valve models based on 3D ultrasound

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PURPOSE: Patient-specific heart and valve models have shown promise as training and planning tools for heart surgery, but physically realistic valve models remain elusive. Available proprietary, simulation-focused heart valve models are generic adult mitral valves and do not allow for patient-specific modeling as may be needed for rare diseases such as congenitally abnormal valves. We propose creating silicone valve models from a 3D-printed plastic mold as a solution that can be adapted to any individual patient and heart valve at a fraction of the cost of direct 3D printing using soft materials.

METHODS: The leaflets of a pediatric mitral valve, a tricuspid valve in a patient with hypoplastic left heart syndrome, and a complete atrioventricular canal valve were segmented from ultrasound images. A plastic mold was designed and 3D-printed for each valve based on the segmentation, and the molds were used to make silicone valve models. Pediatric cardiac surgeons practiced suturing on the models and evaluated them for use as surgical planning and training tools.

RESULTS: Five out of six surgeons reported that the valve models would be very useful as training tools for cardiac surgery. Leaflets in the valve model were felt to be unrealistically thick or stiff compared to real pediatric leaflets. A thin tube rim was preferred for valve flexibility.

CONCLUSION: The valve models were well received and considered to be valuable accessible tools for heart valve surgery training. Further improvements will be made based on surgeons' feedback.

10135-42, Session 9

Patient-specific indirectly 3D printed mitral valves for pre-operative surgical modelling

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Significant mitral valve regurgitation affects approximately two percent of the population [1]. Approximately five percent of mitral valve repair surgeries have non-trivial mitral regurgitation (MR grade 2 or higher) post-surgery [2, 3]. Recently, 3D printing has been used in numerous scenarios to assist surgeons in planning optimal treatments for difficult pathologies. However, while commercially available 3D printers are capable of printing soft, tissue-like materials, they cannot replicate the demanding combination of echogenicity, physical flexibility and strength of the mitral valve. In this work, we propose the use of diagnostic trans-esophageal (TEE) 3D image data and 3D printing technology to create patient specific mitral valve models. Patient specific diagnostic 3D TEE (one systolic, one diastolic) was segmented and used to generate a profile of the mitral valve leaflets. This profile was 3D printed and integrated into a mold to generate a silicone valve model that were placed in a dynamic heart phantom [4]. Our goal is to use silicone models to assess different repair options prior to surgery, in the hope of optimizing patient outcomes. The current work reports preliminary results comparing systolic and diastolic modelling. The models are assessed using 3D TEE images, as well as 2D and 3D Doppler image data for comparison to the original patient diagnostic ultrasound data. Initial findings suggest models based on diastolic image data create more accurate dynamic models.

10135-43, Session 9

Real-time catheter localization and visualization using three-dimensional echocardiography

Pawel Kozlowski, GE Vingmed Ultrasound (Norway); Raja Sekhar Bandaru, GE Vingmed Ultrasound (Norway) and KU Leuven (Belgium); Jan D'hooge, KU Leuven (Belgium); Eigil Samset, GE Vingmed Ultrasound (Norway) and Univ. I Oslo (Norway) and Ctr. for Cardiological Innovation (Norway)

Real-time three-dimensional transesophageal echocardiography (RT3D-TEE) is increasingly used during minimally invasive cardiac surgeries (MICS). In many cath labs, RT3D-TEE is already one of the requisite tool for image guidance during MICS. However, the visualization of the catheter is not satisfactory in many orientations due to the obstructing tissue. This makes 3D-TEE challenging use as the only modality for guidance. For this reason, TEE has been used by allowing registration of preoperative models of CT, Fluoroscopy or Magnetic tracking. However, this technique is challenging due to registration errors and complexity of imaging. Therefore, we propose a novel technique for better visualization of the catheter along with the cardiac anatomy using TEE alone - exploiting both beamforming and post processing methods. We extended our earlier method called Delay and Standard Deviation (DASD) beamforming to 3D in order to enhance the specular reflections. The beamformed image was further post-processed by the Frangi filter to segment the catheter. Multi-variate visualization techniques enabled us to render both the standard tissue and the DASD beamformed image on the scanner simultaneously. The transmit/receive frame rate using 6VT TEE probe (GE Vingmed, Horten, Norway) with a volume size of 33x25 degrees and a depth of 10 cm was limited to ~6 FPS. However, a frame rate of up to 15 FPS can be achieved with our post processing.

10135-44, Session 9

integrating atlas and graph cut methods for right ventricle segmentation from cardiac cine MRI

Shusil Dangi, Nathan D. Cahill, Cristian A. Linte, Rochester Institute of Technology (United States)

Right heart functional parameters such as right ventricular volume, ejection fraction, and wall thickness can be assessed by segmenting the right ventricle myocardium from cardiac MRI images. In addition to the diagnosis and functional assessment, segmented images can be used to build pre-operative anatomical heart models used to precisely identify regions of interest during minimally invasive therapy. Hence, the use of accurate and computationally efficient segmentation techniques is critical, especially for intra-procedural guidance applications that entail segmentation of peri- or intra-operative subject-specific datasets without delaying the procedure workflow. We formulate the segmentation procedure as an energy minimization problem in a graph subject to the shape prior obtained by label propagation from an average atlas using affine registration. The labeling corresponding to the minimum energy configuration of the graph is obtained via graph-cuts, yielding the optimal segmentation, which is iteratively refined to produce final RV blood pool segmentation. We quantitatively compare the segmentation results obtained from our algorithm to the provided gold-standard expert manual segmentation for 16 cine-MRI datasets available through the MICCAI 2012 Cardiac MR Right Ventricle Segmentation Challenge according to several similarity metrics, including Dice coefficient, Jaccard coefficient, Hausdorff distance, and Mean absolute distance error.

10135-45, Session 9

Patient Specific Atria Models for Training and Pre-Procedure Surgical Planning

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Minimally invasive cardiac procedures requiring a trans-septal puncture such as atrial ablation and MitraClip© mitral valve repair are becoming increasingly common. These procedures are performed on the beating heart, and require surgeons to rely on image-guided techniques. For cases of complex or diseased anatomy, in which the image guidance can be difficult to interpret, surgical teams may benefit from patient-specific atrial models that can be used for training and surgical planning.

A patient-specific atrial model was generated from computed tomography (CT) images of a patient's heart that were segmented and used to generate geometric models. Using rapid prototyping, the geometric models were converted into physical representations and used to build a mold. The atria were then molded using tissue-mimicking materials and imaged using CT. The resulting images were segmented and used to generate a point cloud data set that could be registered to the original patient data. The absolute distance of the two point clouds was compared and evaluated to determine the model's accuracy.

The outcome of the initial trial, when comparing the molded model point cloud to the original data set, resulted in a maximum distance of 4.5 mm, a Euclidean distance average of 0.7 mm and a standard deviation of 0.9 mm

Using our workflow for creating atrial models, potential complications, particularly for complex repairs, may be accounted for in pre-operative planning. The information gained by the clinicians involved in planning and performing the surgery should lead to shorter surgical times and better outcomes for patients.

10135-46, Session 10

Intraoperative 3D ultrasound guidance system for permanent breast seed implantation

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Permanent breast seed implantation (PBSI) is a single-visit technique for accelerated partial breast irradiation that uses a template and needles to implant 'seeds' of Pd-103 under 2D ultrasound (US) guidance. The short treatment time is advantageous given the widely hypothesized link between treatment burden and mastectomy use. However, limitations of 2D US contribute to high operator dependence. Our goal is to develop a 3D US guidance system to reduce operator dependence and increase implantation accuracy.

A 3D US scanner for PBSI has been developed and validated, with a mechanism for template localization under development. The 3D US system mechatronically moves and tracks a 2D US transducer over 5 cm translation and 60° tilt. A connected laptop captures the 2D images, reconstructing them into a 3D volume as they are acquired. A mechanical localizing arm was mounted to the scanner that uses encoders to track the location of its spherical tip. The tip is placed into conical divots on a modified needle template, localizing the template relative to the scanner.

Volume reconstruction was validated using linear measurements of a grid phantom and volumetric measurements of two surgical cavity phantoms. Additionally, volunteer scans were conducted to demonstrate clinical applicability. Localizing arm measurement accuracy was established using a testing jig with divots at known positions.

Median linear and average volumetric measurements were within ±1.5% of nominal and ±5% of water displacement measurements, respectively. Volunteer scans produced clinical quality images with positive user feedback. Median measurement accuracy of the localizing arm was 0.475mm.

10135-47, Session 10

Evaluation of an interactive ultrasound-based breast tumor contouring workflow

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Purpose: Computer-navigated breast tumor excision using tracked ultrasound is a viable technique for performing lumpectomies during early-stage breast cancer. An interactive method is used to contour tumors intra-operatively for excision. We evaluated this method's effectiveness in contouring the entire tumor with minimal inclusion of healthy tissue in the excision volume. Additionally, we investigated the possibility of adding a safety margin to the contoured volume to ensure that the entire tumor is contained by the contour. Methods: We conducted a study in which 10 participants contoured 5 tumors each using the intra-operative breast tumor contouring system. We analyzed their interactions with the system and their opinions of the contouring workflow. Results: We found that only 0.19% of the tumor volume was not contained by the contour on average. The addition of a 0.4 mm safety margin to the final tumor contour guaranteed that the entire tumor would be contained. We also found a correlation between the amount of time spent on contour verification and excess healthy tissue included in the contour. Users' perceptions of how well they excluded excess healthy tissue strongly correlated with reality. Conclusions: This workflow ensures that only a small amount of tumor volume is not

contained by the contour and allows the radiologist confidence that they have contained the entire tumor in their contour. With the addition of a safety margin to the resulting tumor contour, the tumor can be completely contained.

10135-48, Session 10

Models of Temporal Enhanced Ultrasound Data for Prostate Cancer Diagnosis: The Impact of Time-Series Order

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Recent studies have shown the potential of Temporal Enhance Ultrasound (TeUS) imaging for tissue characterization in transrectal ultrasound-guided prostate biopsies. In this paper, we present the results of experiments designed to study the significance of the temporal order of the data in TeUS signals. We assess the impact of temporal order on differentiating between benign and malignant prostate-tissues. We have previously used Hidden Markov Models (HMMs) to model TeUS data as HMMs are known to incorporate the order of time points, when modeling time series. Here we use HMMs to generate models of malignant and benign tissues trained and tested on TeUS signals in their original temporal order and signals with shuffled time points. We compare the performance of models learned from order-preserved signals and from order-altered signals for tissue characterization. Our results show that models built from order-preserved signals perform significantly better in capturing the difference between malignant and normal tissue compared to those built with order-altered signals. The performance degrades as more time points are shuffled in the signals used for training and testing the models. The accuracy of tissue characterization decreases from 85% using models of order-preserved signals to 62% using models trained and tested on completely shuffled signals. These results can offer an insight to understanding the physical interaction of TeUS with tissue.

10135-49, Session 11

Interpolation of 3D slice volume data for visualisation and 3D printing

Irina D. Voiculescu, Samuel Littley, Univ. of Oxford (United Kingdom)

Medical imaging from CT and MRI scans has become essential to clinicians for diagnosis, treatment planning and even prevention of a wide array of conditions. The presentation of image data volumes as 2D slice series provides some challenges with visualising internal structures. 3D reconstructions of organs and other tissue samples from data with low scan resolution leads to a `stepped' appearance. This paper demonstrates how to improve 3D visualisation of features and automated preparation for 3D printing from such low resolution data, using novel techniques for morphing from one slice to the next. The boundary of the starting contour is grown until it matches the boundary of the ending contour by adapting a variant of the Fast Marching Method-(FMM). Our spoke based approach generates scalar speed field for FMM by estimating distances to boundaries with line segments connecting the two boundaries. These can be regularly spaced radial spokes or spokes at radial extrema. We introduce clamped FMM by running the algorithm outwards from the smaller boundary and inwards from the larger boundary and combining the two runs to achieve FMM growth stability near the two region boundaries. Our method inserts a series of uniformly distributed intermediate contours between each pair of consecutive slices from the scan volume thus creating smoother feature boundaries. Whilst hard to quantify, our overall results give clinicians an evidently improved tangible and tactile representation of the tissues, that they can examine more easily and even handle.

10135-50, Session 11

Optimization of real-time rigid registration motion compensation for prostate biopsies using 2D/3D ultrasound

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The second highest incidence of cancer in men is found in the prostate aside from skin cancer.1 Needle biopsy of the prostate is the current clinical standard for definitive diagnosis for cancer, typically guided by two-dimensional transrectal ultrasound (2D TRUS). We have previously developed a system,2 which can provide 3D TRUS/MR fusion images intraoperatively, intended to increase needle guidance accuracy and improve diagnoses by augmenting the conventional 2D TRUS procedure. Unfortunately, prostate motion during a biopsy can cause misalignment between the preoperative fused images and planned targets within the live 2D image.

To correct for these misalignments, we have developed a motion compensation algorithm, which aligns 2D and 3D US images with computation speeds approaching the frame rate of the US system. 2D/3D US rigid registration was performed using normalized cross-correlation and a variation of the Powell search algorithm on previously acquired prostate images from seven biopsy patients. Image reduction techniques, including downsampling and region-of-interest minimization, were investigated to reduce the computation time of the algorithm. In addition, error in the algorithm was quantified though target registration errors computed from manually chosen fiducials observed in the images.

After optimization, the algorithm performed with a mean time and error of 57 ± 20 ms and 1.6 ± 0.6 mm respectively. The registration algorithm performed with a clinically acceptable error and had computation speeds applicable for a real-time implementation. Current and future work involves validating this algorithm in real-time on prostate phantoms and patients undergoing biopsy procedures.

10135-51, Session 11

Open-source software for collision detection in external beam radiation therapy

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PURPOSE: Collision detection for external beam radiation therapy (RT) is important for eliminating the need for dry-runs that aim to ensure patient safety. Commercial treatment planning systems (TPS) offer this feature but they are expensive and proprietary. Cobalt-60 RT machines are a viable solution to RT practice in low-budget scenarios. However, such clinics are hesitant to invest in these machines due to a lack of affordable treatment planning software. We propose the creation of an open-source room's eye view visualization module with automated collision detection as part of the development of an open-source TPS. METHODS: An openly accessible linac 3D geometry model is sliced into the different components of the treatment machine. The model's movements are based on the International Electrotechnical Commission standard. Automated collision detection is implemented between the treatment machine's components. RESULTS: The room's eye view module was built in C++ as part of SlicerRT, an RT research toolkit built on 3D Slicer. The module was tested using head and neck and prostate RT plans. These tests verified that the module accurately modeled the movements of the treatment machine and radiation beam. Automated collision detection was verified using tests where geometric parameters of the machine's components were changed, demonstrating accurate collision detection. CONCLUSION: Room's eye view visualization and automated collision detection are essential in a Cobalt-60 treatment planning system. Development of these features will advance the creation of an open-source TPS that will potentially help increase the feasibility of adopting Cobalt-60 RT.

10135-52, Session 11

Feature-based respiratory motion tracking in native fluoroscopic sequences for dynamic roadmaps during minimally invasive procedures in the thorax and abdomen

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For many minimally invasive procedures in the thorax and abdomen, conventional roadmap imaging is difficult to use since, due to respiratory motion, the position of the vessels changes constantly. Instead, a static contrast enhanced image is often shown on a separate monitor, while the physician is manipulating the device until its shape is similar to the desired vessel path. This technique is time consuming and requires an experienced physician. We propose a novel technique to track breathing motion in patients and create a motion model for the vasculature. This allows creating a dynamic overlay, which changes with the respiratory motion. The breathing motion is tracked based on edge features extracted from the native fluoroscopic images, using Canny edge detection followed by topology preserving thinning and centerline extraction. The dynamic vessel mask is created from two fluoroscopic sequences (native and contrast enhanced) using diffeomorphic displacement vector field estimation. A digital 4D phantom (XCAT) was used to evaluate the algorithm. Virtual projection sequences with additional noise and varying breathing parameters were created. The similarity between the estimated vessel mask and the ground truth was quantified with the Sørensen–Dice coefficient. The coefficient measured 0.94 ± 0.01 (mean ± standard deviation). The algorithm characterizes the current breathing state of the patient with a value between 0 (maximum exhalation) and 1 (maximum inhalation). The average error of the estimated state was less than 0.02. The proposed method could be used to create dynamic roadmaps, which could considerably improve the workflow of minimally invasive procedures.

10135-53, Session 11

Upper ankle joint space detection on low contrast intraoperative fluoroscopic C-arm projections

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Intraoperative mobile C-arm fluoroscopy is widely used for interventional verification in trauma surgery, high flexibility combined with low cost being the main advantages of the method. However, the lack of global device-to-patient orientation is challenging, when comparing the acquired data to other intra-patient datasets. In upper ankle joint fracture reduction accompanied with an unstable syndesmosis, a comparison to the unfractured contralateral anatomical site is helpful for verification of the reduction result. To reduce dose and operation time, our approach aims at the comparison of single projections of the unfractured ankle with volumetric images of the reduced fracture. For precise assessment, a pre-alignment of both datasets is a crucial step. We propose a contour extraction pipeline to estimate the joint space location for a pre-alignment of fluoroscopic C-arm projections containing the upper ankle joint. A quadtree-based hierarchical variance comparison extracts potential feature points and a Hough transform

is applied to identify bone shaft lines together with the tibiotalar joint space. By using this information we can define the coarse orientation of the projections independent from the ankle pose during acquisition in order to align those images to the volume of the fractured ankle. The proposed method was evaluated on thirteen cadaveric datasets consisting of 100 projections each with manually adjusted image planes by three trauma surgeons. The results show that the method can robustly detect the joint space orientation and the correlation between angle deviation and anatomical projection direction gives valuable input on the acquisition direction for future clinical experiments.

10135-54, Session 12

Boundary overlap for medical image segmentation evaluation

Varduhi Yeghiazaryan, Irina D. Voiculescu, Univ. of Oxford (United Kingdom)

All medical image segmentation algorithms need to be validated and compared, and yet no evaluation framework is widely accepted within the imaging community. Collections of segmentation results often need to be compared and ranked by their effectiveness. Evaluation measures which are popular in the literature are based on region overlap or boundary distance. None of these are consistent in the way they rank segmentation results: they tend to be sensitive to one or another type of segmentation error (size, location, shape) but no single measure covers all error types.

We introduce a new family of measures, with hybrid characteristics. These measures quantify similarity/difference of segmented regions by considering their overlap around the region boundaries. This family is more sensitive than other measures in the literature to combinations of segmentation error types. We compare measure performance on collections of segmentation results sourced from carefully compiled 2D synthetic data, and also on 3D medical image volumes. We show that our new measure (1)~penalises errors successfully, especially those around region boundaries; (2)~gives a low similarity score when existing measures disagree, thus avoiding overly inflated scores; and (3)~scores segmentation results over a wider range of values.

We consider a representative measure from this family and the effect of its only free parameter on error sensitivity, typical value range, and running time.

10135-55, Session 12

DeepInfer: open-source deep learning deployment toolkit for image-guided therapy

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Deep learning models have outperformed some of the previous state-of-the-art approaches in medical image analysis. Instead of using hand-engineered features, deep models attempt to automatically extract hierarchical representations at multiple levels of abstraction from the data. However, utilizing deep models during image-guided therapy procedures requires integration of several software components which is often a tedious task for clinical researchers. Hence, there is a gap between the state-of-the-art machine learning research and its application in clinical setup. In this paper, we propose an open-source toolkit for medical image analysis with deep learning models in 3D Slicer, called "DeepInfer". DeepInfer enables 3D Slicer to connect to a powerful processing back-end either on the local machine or a remote processing server via the OpenIGTLink protocol. Utilizing a repository of pre-trained, task-specific models, DeepInfer allows clinical researchers and biomedical engineers to choose and deploy a model on new data without the need for software development or configuration. As a practical use case, we demonstrate the application of DeepInfer in prostate segmentation for targeted MRI-guided biopsy.

10135-56, Session 12

Deep convolutional neural network for prostate MR segmentation

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Automatic segmentation of the prostate in magnetic resonance imaging (MRI) is a critical step in the targeted biopsy of the prostate. We propose a deep fully convolutional neural network (CNN) to extract the prostate contour automatically. Our deep CNN model is trained end-to-end in a single learning stage based on prostate MR images and the corresponding ground truths, and learns to make inference for pixel-wise segmentation. Experiments were performed on our in-house dataset, which contains 20 prostate MR images. The proposed CNN model could get a mean Dice similarity coefficient of 86.2%±3.2%. Experimental results show that our deep CNN model could yield satisfactory segmentation of the prostate.

10135-57, Session 12

Deep residual networks for automatic segmentation of laparoscopic videos of the liver

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Motivation: For primary and metastatic liver cancer patients undergoing liver resection, a laparoscopic approach can reduce recovery times and morbidity while offering equivalent curative results; however, only about 10% of tumours reside in anatomical locations that are accessible for laparoscopic resection. Augmenting laparoscopic video with registered vascular anatomical models from pre-procedure imaging could support using laparoscopy in a wider population. Segmentation of liver tissue on laparoscopic video supports the robust registration of anatomical liver models by filtering out false anatomical correspondences between pre-procedure and intra-procedure images. In this paper, we present a convolutional neural network (CNN) approach to liver segmentation in laparoscopic liver procedure videos. Method: We defined a CNN architecture comprising fully-convolutional deep residual networks with multi-resolution loss functions. The CNN was trained in a leave-one-patient-out cross-validation on 2050 video frames from 6 liver resections and 7 laparoscopic staging procedures, and evaluated using the Dice score. Results: The CNN yielded segmentations with Dice scores ≥0.95 for the majority of images; however, the inter-patient variability in median Dice score was substantial. Four failure modes were identified from low scoring segmentations: minimal visible liver tissue, inter-patient variability in liver appearance, automatic exposure correction, and pathological liver tissue that mimics non-liver tissue appearance. Conclusion: CNNs offer a feasible approach for accurately segmenting liver from other anatomy on laparoscopic video, but additional data or computational advances are necessary to address challenges due to the high inter-patient variability in liver appearance.

10135-58, Session 12

Spine segmentation from C-arm CT data sets: application to region-of-interest volumes for spinal interventions

Christian Buerger, Cristian Lorenz, Philips Research (Germany); Drazenko Babic, Jurgen Hoppenbrouwers, Robert Homan, Rami Nachabe, Philips Healthcare (Netherlands); John M. Racadio, Cincinnati Children's Hospital Medical Ctr. (United States); Michael Grass, Philips Research (Germany)

Spinal fusion is a common procedure to stabilize the spinal column by fixating parts of the spine. In such procedures, metal screws are inserted through the patients back into a vertebra, and the screws of adjacent vertebrae are connected by metal rods to generate a fixed bridge. In these procedures, 3D image guidance for intervention planning and outcome control is required. Here, for anatomical guidance, an automated approach for vertebra segmentation from C-arm CT images of the spine is introduced and evaluated.

As a prerequisite, 3D C-arm CT images are acquired covering the vertebrae of interest. An automatic model-based segmentation approach is applied to delineate the outline of the vertebrae of interest. The segmentation

approach is based on 24 partial spine models of the cervical, thoracic and lumbar vertebrae which aggregate information about (i) the basic shape itself, (ii) trained features for image based adaptation, and (iii) potential shape variations. Since the volume data sets generated by the C-arm system are limited to a certain region of the spine the target vertebra and hence initial model position is assigned interactively.

The approach was trained and tested on 21 human cadaver scans. A 3-fold cross validation of the segmentation results with respect to ground truth annotations yields an overall mean segmentation errors of 0.5 mm for T1 to 1.1 mm for C6. The results are promising and show potential to support the clinician in pedicle screw path and rod planning to allow accurate and reproducible insertions.

10135-59, Session 12

Liver segmentation in color images

Burton Ma, York Univ. (Canada); T. Peter Kingham, Memorial Sloan-Kettering Cancer Ctr. (United States); Michael I. Miga, Vanderbilt Univ. (United States); William R. Jarnagin, Amber L. Simpson, Memorial Sloan-Kettering Cancer Ctr. (United States)

We describe the use of a deep learning method for semantic segmentation of the liver from color images. Our intent is to eventually embed a semantic segmentation method into a stereo-vision based navigation system for open liver surgery. Semantic segmentation of the stereo images will allow us to reconstruct a point cloud containing the liver surfaces and excluding all other non-liver structures. We trained a deep learning algorithm using 136 images and 272 augmented images computed by rotating the original images. We tested the trained algorithm on 27 images that were not used for training purposes. The method achieves an 88% median pixel labeling accuracy over the test images.

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10136-1, Session 1

Perception in multi-modality breast imaging: a radiologist's perspective *(Keynote Presentation)*

Margarita L. Zuley, Univ. of Pittsburgh (United States)

No Abstract Available.

10136-2, Session 1

The effect of prevalence of disease on performance of residents and fellows during training for interpreting digital breast tomosynthesis (DBT) in a test-train-test observer study

Christiane M. Hakim, Magee-Womens Hospital (United States); Lauren Chang Sen, Andrew Degnan, Joseph Delic, Sarah Pai, Hersh Sagreiya, Mark C. Sparrow, Ernestine Thomas, Michael Yannes, Univ. of Pittsburgh Medical Ctr. (United States); David Gur, Univ. of Pittsburgh (United States)

There are no data on the effect of disease prevalence during training for interpreting digital breast tomosynthesis (DBT) based screening examinations on the performance of residents and fellows. We assessed the performance of six residents (four after one breast imaging rotation and two after two rotations) and two fellows in breast imaging when interpreting DBT screening examinations in a multi-case, mode balanced, test- train-test retrospective reader study (127 training and 160 testing cases). Half were trained with feedback of verified truth after reviewing each case with low prevalence of disease (13/127) and half with high prevalence (52/128). The pre- and post- training dataset was the same. Performance measures were compared (sensitivity, specificity and AUC). Readers trained with the low prevalence set decreased the overall recall rate of non-cancer cases (FPF from 0.21 to 0.13, $p<0.001$), and of cases with known malignancies (TPF from 0.70 to 0.61, $p=0.004$, due primarily to one clearly outlier reader). Readers trained with the high prevalence increased the overall recall rate (albeit, not statistically significant) of non-cancer cases (FPF from 0.16 to 0.18, $p=0.07$), and a borderline significant increase of cancer cases (TPF from 0.61 to 0.66, $p=0.04$). Fellows post six months of specialty training in each group had no significant changes in sensitivity, specificity or AUC after training (smallest $p>0.07$). Both residents with two rotations experience had significant changes in sensitivity and specificity (highest $p<0.028$), but not in AUC. Early training with low disease prevalence of "what not to recall" should be included during training.

10136-3, Session 1

The implementation of an AR (augmented reality) approach to support mammographic interpretation training - an initial feasibility study

Qiang Tang, Yan Chen, Alastair G. Gale, Loughborough Univ. (United Kingdom)

According to the radiology interpretation process model (Noumeir 2006) feedback plays an important role in optimising mammographic interpretation training while also ensuring good interpretation performance. The traditional 'keyboard and workstation' technical approach has a critical limitation in providing supplementary image-related information and providing complex feedback in real time. Augmented Reality (AR) provides a possible superior approach in this situation as feedback can be provided out with the mammographic workstation so making a generic approach which is vendor neutral. In this study radiological feedback was dynamically remapped virtually into the real world, using perspective transformation, in order to provide richer user experience in mammographic interpretation training. This is the first attempt of an AR approach to dynamically superimpose pre-defined marks of a DICOM image on top of a radiologist's view whilst the radiologist is examining information on a clinical workstation. The study demonstrates the feasibility of the approach although there are limitations on interactive operations which are due to the hardware used. The experimental results of this fully functional approach claim a high accuracy in a simulated mammographic interpretation environment. Thus, it is argued that employing AR is a feasible way to provide rich feedback in the delivery of mammographic interpretation training.

10136-4, Session 2

Does fatigue have any impact on satisfaction of search?

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Previous studies have demonstrated that fatigue impacts diagnostic accuracy, especially for those in training. We continued this line of investigation to determine if fatigue has any impact on a common source of errors – satisfaction of search (SOS). SOS requires subjects to participate in 2 sessions (SOS and non-SOS) and so does fatigue (fatigued and not fatigued) so we did 2 studies one SOS and not SOS not fatigued and then fatigued with new observers. We used 64 chest computed radiographs half demonstrating various "test" abnormalities were read twice by 20 radiologists, once with and once without the addition of a simulated pulmonary nodule. Receiver-operating characteristic detection accuracy and decision thresholds were analyzed to study the effects of adding the nodule on detecting the test abnormalities. Adding nodules did not influence detection accuracy for the other abnormalities ($P = 0.93$), but did induce a reluctance to report them ($P < 0.001$). Adding nodules did not affect inspection time ($P = 0.58$) so the reluctance to report was not associated with reduced search. Fatigue did not appear to exacerbate the SOS effect. A second study with fractures revealed the same shift in performance but did reduce viewing times when fatigued. The results of these two studies suggest that the impact of fatigue on SOS is more complicated than expected and thus may require more investigation to fully understand its impact in the clinic.

10136-5, Session 2

A model based on temporal dynamics of fixations for distinguishing expert radiologists' scanpaths

Ziba Gandomkar, The Univ. of Sydney (Australia); Kevin Tay, Prince of Wales Hospital (Australia); Claudia R. Mello-Thoms, Patrick C. Brennan, The Univ. of Sydney (Australia)

This study investigated a model which distinguishes expert radiologists from less experienced radiologists based on features describing spatio-temporal dynamics of their eye movement during interpretation of digital mammograms. Eye movements of four expert and four less experienced radiologists were recorded during interpretation of 120 two-view digital mammograms of which 59 had biopsy proven cancers. For each scanpath, a two-dimensional recurrence plot, which represents the radiologist's refixation pattern, was generated. From each plot, six features indicating the spatio-temporal dynamics of fixations were extracted. The first feature measured the percentage of recurrent fixations; the second indicated the percentage of recurrent fixations which was fixated later in several consecutive fixations; the third measured the percentage of recurrent fixations that form a repeated sequence of fixation and the fourth assessed whether the recurrent fixations were occurring sequentially close together. The number of switches between the two mammographic views was also measured as was the average number of consecutive fixations in each view before switching. These six features were fed into a support vector machine whose performance was evaluated using 10-fold cross validation. The model achieved a sensitivity of 86.3% and a specificity of 85.2% for distinguishing experts' scanpaths. The obtained result suggests that spatio-temporal dynamics of eye movements can characterize expertise level and has potential applications for monitoring the development of expertise among radiologists as a result of different training regimes and continuing education schemes.

10136-6, Session 2

On image texture parameters in digital breast tomosynthesis and their influence in detection tasks

William H. Nissbett, Amar Kavuri, Nathaniel R. Fredette, Mini Das, Univ. of Houston (United States)

Understanding factors that influence search and localization of signals in tomographic breast imaging can allow efficient system design and image displays. Several acquisition, reconstruction and display parameters can influence the signal detection. In this abstract we will examine variation of image texture features with varying digital breast tomosynthesis (DBT) acquisition parameters. We will analyze the influence of these parameters in human observer detection studies using results from localization ROC (LROC) studies. Our methods included calculation and analysis of these texture features at randomly samples ROIs in select image sets. Preliminary results that show gaze tracking studies performed on some of these images and evaluation of texture features on regions that attracted observer's attention are also presented. A complete study will include a more thorough analysis of multiple data sets to understand image texture feature that shows significant influence in detection process. This will further be correlated to influence in image acquisition/reconstruction methods.

10136-7, Session 2

Visual assessment of breast density using visual analogue scales: observer variability, reader attributes and reading time

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Background: Breast density is a strong risk factor for breast cancer and has potential use in breast cancer risk prediction, with subjective methods of density assessment providing a strong relationship with the development of breast cancer.

Objectives: This study aims to assess intra- and inter-observer variability in visual density assessment recorded on Visual Analogue Scales (VAS) among 11 trained readers, and examine whether reader age, gender and experience are associated with inter-observer variability.

Methods: 11 readers estimated the breast density of 120 mammograms on two occasions 3 years apart using VAS. Intra- and inter-observer agreement was assessed with intraclass correlation coefficient (ICC) and variation between readers visualised on Bland-Altman plots. The mean score of all mammograms per reader were used to analyse the effect of reader factors on inter-observer variability.

Results: Excellent intra-observer agreement (ICC>0.81) was found in majority of the readers. All but one reader had a mean difference <10 percentage points from the first to second reading. Inter-observer agreement was excellent for consistency (ICC 0.82) and substantial for absolute agreement (ICC 0.69). However, the 95% limits of agreement for pairwise differences were -6.8 to 15.7 at the narrowest and 0.8 to 62.3 at the widest. No significant associations between reader factors and inter-observer variability were found.

Conclusion: Overall, the readers were consistent in their scores, although some large variations were observed. Reader evaluation and targeted training may alleviate this problem.

10136-8, Session 2

Development of a discordant likelihood metrics for use in evaluation of 'double reviewer' performance in blinded independent central review (BICR) RECIST imaging studies

J. Michael O'Connor, Univ. of Massachusetts Medical School (United States) and PAREXEL International Corp. (United States); Manish Sharma, Anitha Singareddy, PAREXEL International Corp. (India); Annette Schmid, PAREXEL International Corp. (United States)

Purpose: Perform a systematic review of a number studies (n=9) for the purpose of proposing basic likelihood metrics for evaluation of discordance between two reviewers performing RECIST (Response Evaluation Criteria in Solid Tumors) assessments in a Blinded Independent Central Review (BICR)

Methods: Retrospective data analysis using R programming scripts to determine discordance subsets of interest.

Results: We present a basic time point discordant ratio and a likelihood of cases discordance ratio based on the number of time points per case for RECIST datasets.

New or Breakthrough Work: While this straightforward analysis of RECIST BICR data sets should not be characterized as a 'breakthrough', to our knowledge these are results have not been published elsewhere and they are of interest within the clinical research community that utilizes imaging to determine trial outcomes.

Conclusions: We propose basic ratios that that can be useful in improvement of reviewer performance models

10136-9, Session 2

Impact of different study populations on reader behavior and performance metrics: initial results

Brandon D. Gallas, U.S. Food and Drug Administration (United States); Etta Pisano, Beth Israel Deaconess Medical Ctr. (United States) and Harvard Medical School (United States); Elodia B. Cole, Beth Israel Deaconess Medical Ctr. (United States); Kyle J. Myers, U.S. Food and Drug Administration (United States)

The FDA recently completed a study on design methodologies surrounding the validation of imaging premarket evaluation and regulation called VIPER. VIPER consisted of five large reader sub-studies to compare the impact of different study populations on reader behavior as seen by sensitivity, specificity, and AUC, the area under the ROC curve (receiver operating characteristic curve). The study investigated different prevalence levels and two kinds of sampling of non-cancer patients: a screening population and a challenge population. The VIPER study compared full-field digital mammography (FFDM) to screen-film mammography (SFM) for women with heterogeneously dense or extremely dense breasts. All cases and corresponding images were sampled from DMIST archives. There were 20 readers (American Board Certified radiologists) for each sub-study, and instead of every reader reading every case (fully-crossed study), readers and cases were split into groups to reduce reader workload and the total number of observations (split-plot study). For data collection, readers first decided whether or not they would recall a patient. Following that decision, they provided an ROC score for how close or far that patient was from the recall decision threshold. Performance results for FFDM show that as prevalence increases to 50%, there is a moderate increase in sensitivity and decrease in specificity, whereas AUC is mainly flat. Regarding precision, the statistical efficiency (ratio of variances) of sensitivity and specificity relative to AUC are 0.66 at best and decrease with prevalence. Analyses comparing modalities and the study populations (screening vs. challenge) are still ongoing.

10136-10, Session 3

Does time of day influence cancer detection and recall rates in mammography?

Chris Stinton, David Jenkinson, Victor Adekanmbi, Aileen Clarke, Sian Taylor-Phillips, The Univ. of Warwick (United Kingdom)

Background: The interpretation of screening mammograms is influenced by factors such as reader experience and their annual interpretative volume. There is some evidence that time of day can also have an effect, with better diagnostic accuracy for readings conducted early in the day. This is not a consistent finding, however. The aim of our study is to provide further evidence on whether there is an effect of time of day on recall- and breast cancer detection rates.

Method: We analysed breast screening data from 1,191,451 women, with data split into three eight hour periods: 0900-1700, 1700-0100, 0100-0900. Differences in recall- and cancer detection rates were analysed using multilevel logistic regression models.

Results: There was no significant effect of time of day on cancer detection rates. Compared to the 0900-1700 period, recall rates were significantly higher during the 1700-0100 period but not the 0100 – 0900 period.

Conclusions: As demand increases, delivery of radiology services will likely extend beyond the traditional 0900-1700 office hours. Our finding that a greater proportion of women are recalled when mammogram interpretation is conducted in the evening suggest that increasing service capacity into this time period could lead to an increase in the number of women undergoing additional procedures and experiencing the associated emotional and financial costs, without increasing cancer detection. Future research should consider the influence of variables that might mediate time of day effects, including reader- (e.g. different readers reading at different times) and centre-level factors (e.g. staffing).

10136-11, Session 3

Changing behaviour and accuracy with time on task in mammography screening

Sian Taylor-Phillips, David Jenkinson, Chris Stinton, The Univ. of Warwick (United Kingdom); Matthew Wallis, Addenbrooke's Hospital (United Kingdom); Aileen Clarke, The Univ. of Warwick (United Kingdom)

Background: The vigilance decrement and prevalence effect both describe changes to speed and accuracy with time on task. Whilst there is much laboratory based research on these effects, little is known about whether they occur in real world mammography practice.

Methods: The Changing Case Order to Optimise Patterns of Performance in Screening (CO-OPS) trial randomised 37,724 batches containing 1.2 million women attending breast screening to intervention or control (222,208 from the Midlands of England). In the control arm the batch was examined in the same order by both readers, in the intervention arm it was examined in a different order by both readers. Time taken, recall decision by both readers, and cancers detected were recorded for each case, and used to examine patterns of performance with time on task.

Results: 49,575 women were recalled and 10,484 had cancer detected. Median time taken to examine each case was 35 seconds (out of cases where time taken was 10 minutes or less). The intervention did not affect overall cancer detection rates or recall rates. A more detailed analysis of the Midlands data indicates cancer detection rate did not change when reading up to 60 cases in a batch, but recall rate reduced. Time taken per case reduced with time on task, from a median 41 seconds when examining the second case in the batch to 28.5 seconds examining the 60th case.

Conclusion: Reader behavior and performance systematically changes with time on task in breast screening

10136-12, Session 3

How quickly do breast screeners learn their skills?

Hossein Nevisi, Yan Chen, Leng Dong, Alastair G. Gale, Loughborough Univ. (United Kingdom)

The UK's Breast Screening Programme is 27 years old and many experienced breast radiologists are now retiring, coupled with an influx of new screening personnel. It is important to the ongoing Programme that new mammography readers are quickly up to the skill level of experienced readers. How quickly are necessary cancer detection skills learnt? All breast screening radiologists in the UK read educational training sets of challenging FFDM images (the PERFORMS scheme) yearly to maintain and improve their performance in real life screening. Data were examined from the PERFORMS annual scheme for 61 new screeners, 58 screeners who have been screening for one year and also for more experienced screeners (>600). Not surprisingly, significant differences in cancer detection rate were found between new readers and both of the other groups. Additionally the performance of 58 new readers who have now been screening for about a year and have taken part twice in the PERFORMS scheme were further examined were again a significant difference in cancer detection was found. These data imply that cancer detection skills are learnt quickly in the first year of screening. Information was also examined concerning the volume of cases participants read and other factors.

10136-13, Session 3

The role of extra-foveal processing in 3D imaging

Miguel P. Eckstein, Miguel Angel Lago Angel, Craig K. Abbey, Univ. of California, Santa Barbara (United States)

The field of medical image quality has relied on the assumption that metrics of image quality for simple visual detection tasks are a reliable proxy for the more clinically realistic visual search tasks. Studies have shown that although search degrades performance due to the higher spatial uncertainty, methods allow to quantitatively relate performance across both tasks (Bochud, Abbey, & Eckstein, 2004; He, Samuelson, Zeng, & Sahiner, 2014). In addition, rank order of signal detectability across conditions often generalizes from detection to search tasks. In recent years, investigators have motivated the need to model the visual search process (Gifford, Liang, & Das, 2016). Here, we argue that search in 3D images represents a paradigm shift in medical imaging: radiologists typically cannot exhaustively scrutinize all regions of interest with the high acuity fovea requiring detection of signals with extra-foveal areas of the human retina. We hypothesize that extra-foveal processing can alter the detectability of certain types of signals in noise. We compare visual search of two different types of signals in 2D vs. 3D. We show that a small microcalcification-like signal is more highly detectable than a larger mass-like signal in 2D search but its detectability largely decreases (relative to the larger signal) in the 3D search task. Utilizing measurements of observer detectability as a function retinal eccentricity we can predict the experimental results in the 2D and 3D search studies. Together, our findings suggest that clinical tasks with 3D images might require taking into consideration the extra-foveal properties of human vision to develop accurate metrics of medical image quality.

10136-14, Session 3

Applying a social network analysis (SNA) approach to understanding radiologists' performance in reading mammograms

Seyedamir Tavakoli Taba, The Univ. of Sydney (Australia); Liaquat Hossain, The Univ. of Hong Kong (Hong Kong, China); Robert Heard, Patrick C. Brennan, Warwick B. Lee, Sarah J. Lewis, The Univ. of Sydney (Australia)

Rationale and objectives:

Observer performance has been widely studied through examining the characteristics of individuals. Applying a systems perspective, while understanding of the system's output, requires a study of the interactions between observers. This research explains a mixed methods approach to applying a social network analysis (SNA), together with a more traditional approach of examining personal/ individual characteristics in understanding observer performance in mammography.

Materials and Methods:

Using social networks theories and measures in order to understand observer performance, we designed a social networks survey instrument for collecting personal and network data about observers involved in mammography performance studies. We present the results of a study by our group where 31 Australian breast radiologists originally reviewed 60 mammographic cases (comprising of 20 abnormal and 40 normal cases) and then completed an online questionnaire about their social networks and personal characteristics. A jackknife free response operating characteristic (JAFROC) method was used to measure performance of radiologists. JAFROC was tested against various personal and network measures to verify the theoretical model.

Results:

The results from this study suggest a strong association between social networks and observer performance for Australian radiologists. Network factors accounted for 48% of variance in observer performance, in comparison to 15.5% for the personal characteristics for this study group.

Conclusion:

This study suggest a strong new direction for research into improving observer performance. Future studies in observer performance should consider social networks' influence as part of their research paradigm, with equal or greater vigour than traditional constructs of personal characteristics.

10136-15, Session 4

Comparison of two classifiers when the data sets are imbalanced: the power of area under the precision-recall curve as the figure of merit versus the area under the ROC curve

Berkman Sahiner, Weijie Chen, Aria X. Pezeshk, Nicholas A. Petrick, U.S. Food and Drug Administration (United States)

In many two-class problems in automated classification and information retrieval, the classes are imbalanced. This includes classification problems in which the positive class is rare (e.g., one diseased case per many undiseased cases) and information retrieval problems in which a small set of relevant cases exists in a large data set. The area under the precision-recall curve (AUCPR) has been suggested as an alternative performance measure to the area under the ROC curve (AUCROC) under such circumstances. AUCPR and AUCROC are distinct measures of performance, even though the relationship between the precision-recall and ROC curves is well-known. Whether (or under which conditions) the AUCPR offers a statistical advantage in comparison to the AUCROC is an open problem. In this study, we developed a statistical method for the comparison of two classifiers using the AUCPR as the figure of merit, and compared the statistical power of the AUCPR to that of the AUCROC. Our method extends the technique that we recently introduced for the semi-parametric estimation of the precision-recall curve to the comparison of two classifiers. We first performed a simulation study to investigate the type I error rate of the newly-developed method. We then extended the simulation study to compare the power of the AUCPR and AUCROC. Under the simulation study conditions, the AUCPR was more powerful than the AUCROC, especially when the data set was imbalanced. Our results indicate that, despite its dependence on the prevalence, the AUCPR can be a useful figure of merit when used judiciously.

10136-16, Session 4

Re-use of pilot data and interim analysisp of pivotal data in MRMC studies: a simulation study

Weijie Chen, Frank W. Samuelson, Berkman Sahiner, Nicholas A. Petrick, U.S. Food and Drug Administration (United States)

Novel medical imaging devices are often evaluated with multi-reader multi-case (MRMC) studies in which radiologists read images of patient cases for a specified clinical task (e.g., cancer detection). A pilot study is often used to measure the effect size and variance parameters that are necessary for sizing a pivotal study (including sizing readers, non-diseased and diseased cases). Due to practical difficulty of collecting patient cases or recruiting clinical readers, some investigators attempt to include the pilot data as part of their pivotal study. Moreover, the pilot data is often quite limited and there is enormous uncertainty in the estimate of sample sizes. Some investigators attempt to perform an interim analysis of their pivotal study data based upon which the sample sizes may be re-estimated. Re-use of the pilot data and/or interim analyses of the pivotal data may inflate the type I error of the pivotal study. In this work, we use the Roe and Metz model to simulate MRMC data under the null hypothesis (i.e., two devices have equal diagnostic performance) and investigate the type I error rate for several practical designs involving data re-use or interim analysis. Our preliminary results indicate that, under the simulation conditions we investigated, the inflation of type I error is only marginal for some design strategies, e.g., re-use of patient data without re-using readers, size re-estimation without using the effect-size estimated in the interim analysis.

10136-17, Session 4

Exploring the potential of analyse visual search behaviour data using FROC (free-response receiver operating characteristic) method: an initial study

Leng Dong, Yan Chen, Alastair G. Gale, Loughborough Univ. (United Kingdom); Sarah Dias, William Stone, The Univ. of Birmingham (United Kingdom); Joseph Dias, Univ. of Leicester (United Kingdom); John Rout, Birmingham Dental Hospital (United Kingdom)

Dental surgeons (dentists) read dental radiographs to aid diagnosis and treatment for patients. So it is important to identify the gap between trainee and experienced dentists in interpretation of these images. In this study, the eye-movement data of 17 dentists with different experience levels were recorded while they reviewed 20 dental radiographs. Additionally, they were asked to rate the severity of each case using a seven point scale. Each case had one abnormality and the area of interest (AOI) was delineated for every lesion. Various eye movement measurements were obtained based on image AOI information. FROC analysis was then carried out by using those eye movement measurements as a direct input source. Also expert dental surgeons' difficulty ratings of each image were used to assign each case with a different weight. The performance of FROC methods using different input parameters were tested and compared. The results found that there were significant differences in two out of the three eye movement parameters between groups with different experience levels. Also the score of area under the curve (AUC) shows higher values as experience increases. It is argued that FROC analysis using eye movement measurements as input parameters can act as a potential performance indicator to deliver assessment in medical imaging interpretation training procedures. Additionally, the data analyses lead to new ways of combining eye movement data and FROC methods and provide alternative dimension to assess performance and visual search behaviour in the area of medical imaging perceptual tasks.

10136-18, Session 4

A comparison of methods to evaluate gray scale response of tomosynthesis systems using a software breast phantom

Maria Angelica Z. Sousa, Univ. de São Paulo (Brazil); Predrag R. Bakic, The Univ. of Pennsylvania Health System (United States); Homero Schiabel, Univ. de São Paulo (Brazil); Andrew D. A. Maidment Sr., The Univ. of Pennsylvania Health System (United States)

Digital breast tomosynthesis (DBT) has been shown to be an effective imaging tool for breast cancer diagnosis as it provides three-dimensional images of the breast with minimal tissue overlap. The quality of the reconstructed image depends on many factors that can be assessed using uniform or realistic phantoms. In this paper, we used an anthropomorphic software breast phantom to compare four methods to evaluate the gray scale response in terms of the contrast, noise and detectability of adipose and glandular tissues binarized according to the phantom ground truth. For each method, circular regions of interest (ROIs) were selected in different size, quantity and the position inside a square area in the phantom. We also estimated the percent density of the simulated breast and the capability of distinguishing both tissues by receiver operating characteristic (ROC) analysis. Results shows a high sensitivity of the methods to the size, placement and slices considered.

10136-19, Session 4

Regression without truth with Markov chain Monte-Carlo

Hennadii Madan, Franjo Pernuš, Univ. of Ljubljana (Slovenia); Boštjan Likar, Univ of Ljubljana (Slovenia); Žiga Špiclin, Univ. of Ljubljana (Slovenia)

Regression without truth (RWT) is a statistical technique for estimation of error model parameters of each method in a group of methods used for measurement of a certain quantity. The main advantage of RWT is that it does not rely on a "gold standard" reference method. RWT was initially used for left-ventricular ejection fraction (EF) measurement method comparison, and has been applied for a variety of other medical imaging tasks.

In this work, we show how Markov chain Monte-Carlo (MCMC) can be used to augment RWT to achieve a number of benefits not present in the original approach. MCMC is a computational technique for drawing samples from a statistical distribution with probability density or mass function known only up to a normalizing coefficient. Compared to original RWT it allows joint posterior distribution estimation with natural marginalization of nuisance parameters, straightforward confidence interval (CI) estimation, estimation of true value of the measurand (with CI), does not require finite support for prior distribution of the measurand and has improved robustness against convergence to non-global maxima.

The approach is validated using synthetic data that emulate EF data for 45 patients measured with 8 methods from one of the latest paper on RWT [1]. The true values of all error model parameters and measurand all lie within 90% confidence interval of estimates produced using the proposed technique.

The proposed approach has a potential for application to more complex error models with more general assumptions.

10136-20, Session 4

No-gold-standard evaluation of image-acquisition methods using patient data

Abhinav K. Jha, Eric C. Frey, Johns Hopkins Univ. (United States)

Several new and improved modalities, scanners, and protocols, together referred to as image-acquisition methods (IAMs), are being developed to provide reliable quantitative imaging. Objective evaluation of these IAMs on the clinically relevant quantitative tasks is highly desirable. Such evaluation is most reliable and clinically decisive when performed with patient data, but that requires the availability of a gold standard, which is often rare. While no-gold-standard (NGS) techniques have been developed to clinically evaluate quantitative imaging methods, these techniques require that each of the patients be scanned using all the IAMs, which is expensive, time consuming, and could lead to increased radiation dose. A more clinically practical scenario is where different set of patients are scanned using different IAMs. Recognizing this practical limitation, we have developed an NGS technique that uses such patient data to compare the different IAMs. The technique posits a linear relationship, characterized by a slope, bias, and noise standard-deviation term, between the true and measured quantitative values. Under the assumption that the true quantitative values have been sampled from a unimodal distribution, a maximum-likelihood procedure was developed that estimates these linear relationship parameters for the different IAMs. Figures of merit can be estimated using these linear relationship parameters to evaluate the IAMs on the basis of accuracy, precision, and overall reliability. In realistic simulations conducted in the

context of evaluating IAMs for quantitative SPECT, the proposed technique accurately predicted the ranking of different IAMs in 90% of the cases. The proposed technique has several potential applications such as in protocol optimization, quantifying difference in system performance, and system harmonization using patient data.

10136-21, Session 5

Signal template generation from acquired mammographic images for the non-prewhitening model observer with eye-filter

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In this work, we studied the formulation of signal templates for the non-prewhitening model observer (MO) with eye filter (NPWE) using acquired full-field digital mammography (FFDM) images to assess image quality. We generated a signal template from acquired images by averaging multiple exposures resulting in a low background noise template. We investigated elimination of the noise while preserving the signal and propose a methodology which results in a noise-free template. In order to deal with signal location uncertainty, template shifting was implemented. We evaluated the procedure on images of an anthropomorphic breast phantom containing microcalcification-related signals. Optimal reduction of the background noise was achieved without changing the signal and dealt with the limitation that the exact signal location is not exactly known by template shifting. This method facilitates the use of the NPWE MO in acquired images and has potential for assessing image quality in FFDM.

10136-22, Session 5

Real space channelization for generic DBT system image quality evaluation with channelized Hotelling observer

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Digital breast tomosynthesis (DBT) is a relatively new 3D mammography technique that promises better visualization of low contrast lesions than conventional 2D mammography. The parameter space for DBT is large and finding an optimal balance between dose and image quality is challenging. Given the enormous number of conditions and images required in optimization studies, the use of human observers is time consuming and certainly not feasible for every condition. Our goal was to develop a model observer (MO) that could predict human detectability for clinically relevant details embedded within a structured phantom. This is formed from an acrylic semi-circular vessel containing acrylic spheres of different sizes with the remaining space filled by water. There are three types of lesions within the phantom: 3D printed spiculated and non-spiculated mass lesions along with calcification clusters. DBT series on Siemens Inspiration, Hologic Dimensions and Giotto Class systems were acquired at different dose levels and reconstructed with different algorithms. A channelized Hotelling observer (CHO) with Gabor channels was developed. The channels were designed to account for pixel size differences between the different systems, so by a single tuning session, the tuning factors can be used across all of the systems. Linear regression lines between MO and human observer scores were calculated, giving correlation coefficients between 0.912 and 0.995 for all of the reading sessions.

10136-23, Session 5

An observer model for quantifying panning artifacts in digital pathology

Ali R. N. Avanaki, Barco Healthcare (United States)

Typically, pathologists pan from one region of a slide to another, choosing areas of interest for closer inspection. Due to finite frame rate and imperfect zero-order hold reconstruction (i.e., when pixel drive changes, it takes non-zero time to reach the target brightness), panning in whole slide images (WSI) causes visual artifacts. It is important to study the impact of such artifacts since research suggests that 49% of navigation is conducted in low-power/overview with digital pathology (Molin et al., Histopathology 2015). In this paper, we explain what types of medical information may be harmed by panning artifacts, propose methods to simulate panning artifacts, and design an observer model to predict the impact of panning artifacts on typical human observers' performance in basic diagnostically relevant visual tasks. The proposed observer model is based on derivation of perceived object border maps from luminance and chrominance information and may be tuned to account for visual acuity of the human observer to be modeled. Our early results suggest that increasing the contrast (e.g., using a wide gamut display) with a slow response panel may not mitigate the panning artifacts which mostly affect visual tasks involving spatial discrimination of objects (e.g., normal vs abnormal structure, cell type and spatial relationships between them, and low-power nuclear morphology). Proposed methods can be used as building blocks in an automatic WSI quality assessment framework.

10136-24, Session 5

Foveated model observers to predict human performance in 3D images

Miguel A. Lago , Craig K. Abbey, Miguel P. Eckstein, Univ. of California, Santa Barbara (United States)

Medical Imaging is moving towards more and more complex image modalities. 3D images (e.g., computed tomography, CT and digital breast tomosynthesis, DBT) are becoming the standard for lesion diagnosis and treatment assessment. The large number of slices in each 3D case and the limited reading times prevent radiologists from scrutinizing all regions of each slice with their high resolution fovea. Thus, unlike 2D images, much of the image-data is processed with the visual periphery. Here we show that two different 3D tasks, search and detection, influence the relative human visual detectability of two signals of different sizes. One of the signals resembled a microcalcification (a small and bright sphere), while the other one was designed to look like a mass (a larger Gaussian blob). We evaluated current standard models observers (Hotelling; Channelized Hotelling; non-prewhitening matched filter with an eye filter, NPWE; non-prewhitening matched filter model, NPW) and showed that they incorrectly predicted the relative detectability of the two signals in 3D search. We propose a new model observer that incorporates the properties of the visual system over a large visual field (fovea and periphery). We show that foveated model observer can accurately predict the rank order of detectability of the signals in 3D images. Together, these results motivate the utilization of a new class of foveated model observers for predicting image quality for search tasks in 3D imaging modalities.

10136-25, Session 5

Evaluation of CNN as anthropomorphic model observer

Francesc Massanes, Jovan G. Brankov, Illinois Institute of Technology (United States)

Model observers (MO) are widely used in medical imaging to act as surrogates of human observers in task-based image quality evaluation, frequently towards optimization of reconstruction algorithms. In this paper, we explore the use of convolutional neural networks (CNN) to be used as MO. We will compare CNN MO to alternative MO currently being proposed and used such as the channelized Hotelling observer (CHO) and relevance vector machine based MO. As the success of the CNN, and other deep learning approaches, is rooted in large data sets availability, which is rarely the case in medical imaging systems task-performance evaluation, we will evaluate CNN performance on both large and small training data sets.

10136-26, Session 6

Interpretation of the rainbow color scale for quantitative medical imaging: perceptually linear color calibration (CSDF) versus DICOM GSDF

Frédérique Chesterman, Barco N.V. (Belgium); Hannah Manssens, Barco NV (Belgium); Céline Morel, Guillaume Serrell, Bastian Piepers, Tom R. L. Kimpe, Barco N.V. (Belgium)

Medical displays for primary diagnosis are calibrated to the DICOM GSDF but there is no accepted standard today that describes how display systems for medical modalities involving color should be calibrated. Recently CSDF [1] [2], a calibration using the CIEDE2000 color difference metric to make a display as perceptually linear as possible has been proposed. In this work we present the results of an observer study set up to investigate the difference in interpretation accuracy of a rainbow color scale when a medical display is calibrated to CSDF versus sRGB.

Colors are randomly sampled from a rainbow color scale and sequentially presented on the screen of a medical display. The observer is asked to translate the color stimulus into a numerical value using the rainbow color scale shown next to the stimulus. The interpretation accuracy is measured as the difference between the numerical value of the presented color stimulus and the numerical value entered by the user. Analysis of the results indicates that the error when interpreting a rainbow color scale is lower for CSDF than for sRGB with statistically significant difference (Mann-Whitney U test) for four out of six observers.

To our knowledge this is the first work that shows the added value of a perceptual color calibration method (CSDF) in interpreting color scales. Improved interpretation of the rainbow color scale may be beneficial in the area of quantitative medical imaging such as PET SUV, MRI, quantitative CT and doppler US, where a medical specialist needs to interpret quantitative medical data based on a color scale and where improved interpretation accuracy may contribute to a better diagnosis.

10136-27, Session 6

Low contrast detection in anatomical and uniform backgrounds in abdominal CT

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The role of texture when scrolling through CT images is not well known. We propose to evaluate human observer performance in detection of low contrast signals in CT images with uniform and anatomical texture when readers have access to single or multiple image slices. We collected real abdominal CT images from patient and a uniform abdominal phantom. We generated signal present and signal absent datasets by splitting the collected images in two equal parts. The signal present dataset contained hybrid CT images created by inserting 8 mm low contrast spherical signal mimicking hypodense focal liver lesion. ROC experiments were conducted to evaluate the presence of the lesion in the different backgrounds. The signal intensity was set in order to provide a performance of 0.85 in terms of AUC with the single slice uniform images. The ROC experiment resulted in differences between single and multiple slice viewing modes regardless of the type of texture. Small differences could be noted between uniform and anatomic textures.

10136-28, Session 6

Effects of increased compression with an ultrasound transducer on the conspicuity of breast lesions in a phantom

Katy Szczepura, Tahreem Faqir, David J. Manning, Univ. of Salford (United Kingdom)

Ultrasound imaging of the breast is highly operator dependant. The amount of pressure applied with the transducer has a direct impact on the lesion visibility in breast ultrasound.

The conspicuity index is a quantitative measure of lesion visibility, taking into account more parameters than standard measures that impact on lesion detection.

This study assessed the conspicuity of lesions within a breast phantom using increased transducer compression in breast ultrasound.

Methods

A phantom was constructed of gelatine to represent adipose tissue, steel wool for glandular/blood vessels and silicone spheres to represent lesions, this meant that the lesions were also compressible, but less than the surrounding tissue.

The phantom was imaged under increasing transducer compression.

The conspicuity index was measured using the Conspicuity Index Software. The distance between the transducer surface and lesion surface was measured as an indication of increased compression.

Results

When moderate compression (17mm) was applied, the conspicuity index increased resulting in better visualisation of the silicone lesions. However, with increased compression the conspicuity index decreased.

New work to be presented

The conspicuity index has never been demonstrated in ultrasound imaging before. This is preliminary phantom work to demonstrate the impact of increased transducer compression on quantitative lesion visibility assessment.

Conclusion

The compression applied should be considered for optimum visualisation, as excessive pressure decreases conspicuity. However, further work needs to be conducted in order to consider other factors, such as density of the breast and lesion location, for a better understanding of the effect of compression on the visualisation of the lesion. A human study is planned.

10136-29, Session 6

Assessment of the automatic exposure control performance in digital mammography using a no-reference anisotropic quality index

Bruno Barufaldi, Univ. of Pennsylvania (United States) and Univ. de São Paulo (Brazil); Lucas R. Borges, Univ. de São Paulo (Brazil); Predrag R. Bakic, Univ. of Pennsylvania (United States); Marcelo A. C. Vieira, Homero Schiabel, Univ. de São Paulo (Brazil); Andrew D. A. Maidment Sr., Univ. of Pennsylvania (United States)

Automatic exposure control (AEC) is implemented in mammography to achieve feasible radiation doses and adequate image quality regardless of the breast thickness and composition. Although there are consistent methods for assessing the AEC mode, it is not clear whether mammography systems operate with optimal dose and quality in clinical practice. In this work, we propose the use of a no-reference anisotropic quality index (NAQI), validated in previous studies, to evaluate the quality of mammograms acquired using AEC. The authors used a clinical dataset that consists of 559 patients and 1041 mammograms (CC views). Preliminary results show that image quality is often maintained, even at different radiation levels (0.11 ± 0.2). However, a more careful analysis of NAQI reveals that the image quality decreases as breast thickness increases. NAQI is reduced 28% when the breast thickness increases from 31 to 80 mm. Further results show that image quality also changes with breast density. Thus, this work highlights limitations on the automatic exposure control mode for some breast profiles.

10136-30, Session 6

Digital breast tomosynthesis for detecting multifocal and multicentric breast cancer: influence of acquisition geometry on model observer performance in breast phantom images

Gezheng Wen, The Univ. of Texas at Austin (United States) and The Univ. of Texas M.D. Anderson Cancer Ctr. (United States); Subok Park, U.S. Food and Drug Administration (United States); Mia K. Markey, The Univ. of Texas at Austin (United States) and The Univ. of Texas M.D. Anderson Cancer Ctr. (United States)

Multifocal and multicentric breast cancer (MMBC), i.e., the presence of two or more tumor foci within the same breast, has an immense clinical impact on treatment planning and survival outcomes. Detecting multiple breast tumors is challenging as the prevalence of tumors varies across breast regions, and human observers do not know the number or locations of tumors a priori. Digital breast tomosynthesis (DBT), in which an x-ray beam sweeps over a limited angular range across the breast, has the potential to improve the detection of multiple tumors. However, prior efforts to optimize DBT image quality only considered unifocal scenarios, so the recommended geometries may not necessarily yield images that are informative for the task of diagnosing MMBC. Hence, the goal of this study is to employ a 3D multi-signal model observer to identify optimal DBT acquisition geometries for MMBC. Digital breast phantoms were scanned by simulated scanners of different geometries (e.g., wide-arc or narrow-arc, number of projections in each scan). Multiple lesions were inserted into different regions to simulate multifocal cases and multicentric cases. 3D partial least squares channels and decision templates were estimated directly from the images to capture discriminant information and interactions among signals, enabling the model observer to make both image-level and location-specific detection decisions. The results show that multicentric cases may be more difficult to accurately detect than multifocal cases, and the optimal design of DBT may vary as the tasks of clinical interest change (i.e., find at least lesion versus count the number of lesions).

10136-31, Session 6

Lesion detectability in stereoscopically viewed digital breast tomosynthesis projection images: a model observer study with anthropomorphic computational breast phantoms

Jacob Reinhold, The Univ. of Texas at Austin (United States); Gezheng Wen, The Univ. of Texas at Austin (United States) and The Univ. of Texas M.D. Anderson Cancer Ctr. (United States); Joseph Y. Lo, Duke Univ. (United States); Mia K. Markey, The Univ. of Texas at Austin (United States) and The Univ. of Texas M.D. Anderson Cancer Ctr. (United States)

Stereoscopic views of 3D breast imaging data may better reveal the 3D structures of breasts, and potentially improve the detection of breast lesions. The imaging geometry of digital breast tomosynthesis (DBT) lends itself naturally to stereo viewing because a stereo pair can be easily formed by two projection images with a reasonable separation angle for perceiving depth. This simulation study attempts to mimic breast lesion detection on the stereo viewing of a sequence of stereo pairs of DBT projection images. 3D anthropomorphic computational breast phantoms were scanned by a simulated DBT system, and spherical signals were inserted into different breast regions (i.e., lower outer region, and near the nipple) to imitate the presence of breast lesions. The regions of interest (ROI) had different local anatomical structures and consequently different background statistics. The projection images were combined into a sequence of stereo pairs, and then presented to a stereo matching model observer for determining lesion presence. The signal-to-noise ratio (SNR) was used as the figure of merit in evaluation, and the SNR from the stack of reconstructed slices (i.e., most common viewing mode of DBT imaging data) was considered as the benchmark. We have shown that: 1) incorporating local anatomical backgrounds may improve lesion detectability relative to ignoring location-dependent image characteristics. The SNR was lower for the ROI with the higher local power-law-noise coefficient ?. 2) Stereo viewing may underperform viewing reconstructed slices, but further studies are needed to confirm this observation.

10136-32, Session 7

Development of local complexity metrics to quantify the effect of anatomical noise on detectability of lung nodules in chest CT imaging

Justin B. Solomon, Geoffrey D. Rubin, Taylor B. Smith, Brian Harrawood, Kingshuk R. Choudhury, Ehsan Samei, Duke Health (United States)

The purpose of this study was to develop metrics of local anatomical complexity and compare them with detectability of lung nodules in CT. Data were drawn retrospectively from a published perception experiment in which detectability was assessed in cases enriched with virtual nodules (13 radiologists x 157 total nodules = 2041 responses). A local anatomical complexity metric called the distractor index was developed, defined as the Gaussian weighted proportion (i.e., average) of distracting local voxels (50 voxels in-plane, 5 slices). A distracting voxel was classified by thresholding image data that had been selectively filtered to enhance nodule-like features. The distractor index was measured for each nodule location in

the nodule-free images. The local pixel standard deviation (STD) was also measured for each nodule. Other confounding factors of search fraction (proportion of lung voxels to total voxels in the given slice) and peripheral distance (defined as the 3D distance of the nodule from the trachea bifurcation) were measured. A generalized linear mixed-effects statistical model (no interaction terms, probit link function, random reader term) was fit to the data to determine the influence of each metric on detectability. In order of decreasing effect size: distractor index, STD, and search fraction all significantly affected detectability ($P < 0.001$). Distance to the trachea did not have a significant effect ($P > 0.05$). These data demonstrate that local lung complexity degrades detection of lung nodules and the distractor index could serve as a good surrogate metric of such complexity.

10136-33, Session 7

Task-based image quality assessment in radiation therapy: initial characterization and demonstration with CT simulation images

Steven Dolly, Mark A. Anastasio, Washington Univ. in St. Louis (United States); Lifeng Yu, Mayo Clinic (United States); Hua Li, Washington Univ. in St. Louis (United States)

We present a comprehensive implementation and evaluation of a new methodology for objective task-based image quality (IQ) assessment in radiation therapy. A modular simulation framework was designed to perform an automated, computer-simulated end-to-end radiation therapy treatment. The framework was created that utilizes new learning-based stochastic object models (SOM) to obtain known organ boundaries, generates a set of images directly from the numerical phantoms created with the SOM, and automates the image segmentation and treatment planning steps of a radiation therapy workflow. Therefore, therapeutic operating characteristic (TOC) curves can be utilized to guide optimization of the treatment planning process.

10136-34, Session 7

Task-based data-acquisition optimization for sparse image reconstruction systems

Yujia Chen, Yang Lou, Mark A. Anastasio, Washington Univ. in St. Louis (United States)

Conventional wisdom dictates that imaging hardware should be optimized by use of an ideal observer (IO) that exploits full statistical knowledge of the class of objects to-be-imaged, without consideration of the reconstruction method to-be-employed. However, accurate and tractable models of the complete object statistics are often difficult to determine in practice. Moreover, in imaging systems that employ compressive sensing concepts, imaging hardware and (sparse) image reconstruction are innately coupled technologies. We have previously proposed a sparsity-driven ideal observer (SDIO) that can be employed to optimize hardware by use of a stochastic object model that describes object sparsity. The SDIO and sparse reconstruction method can therefore be 'matched' in the sense that they both utilize the same statistical information regarding the class of objects to be imaged. To efficiently compute SDIO performance, the posterior distribution is estimated by use of computational tools developed recently for variational Bayesian inference. Subsequently, the SDIO test statistic can be computed semi-analytically. The advantages of employing the SDIO instead of a Hotelling observer are systematically demonstrated in case studies in which magnetic resonance imaging (MRI) data acquisition schemes are optimized for signal detection tasks.

10136-35, Session PS1

Inconsistencies between the ideal and human observers in imaging system optimization: theoretical explanations and evidence

Xin He, . (United States)

The ideal observer is widely used in imaging system optimization. One practical question remains open: is an ideal-observer optimized system necessarily an optimal one for the humans? Based on the ideal observer's mathematical properties proposed by Barrett et. al. and the human observers' empirical properties investigated by Myers et. al., I attempt to pursue general rules regarding the applicability of the ideal observer in system optimization. Particularly, in software optimization, the ideal observer pursues data conservation while the humans may pursue data presentation or perception. In hardware optimization, the ideal observer pursues a system with the maximum total information, while the humans may pursue a system with the maximum selected (e.g., certain frequency band) information. These different objectives may result in different system optimizations between the human and the ideal observers. Thus, an ideal observer optimized system is not necessarily desirable for the humans. I cite empirical evidence in search and detection tasks, in hardware and software evaluation, in X-ray CT, pinhole imaging, as well as emission computed tomography to corroborate the claims. (Disclaimer: the views expressed in this work do not necessarily represent those of the FDA)

10136-36, Session PS1

Improving the consistency of the ideal human observers in imaging system optimization: theory and examples

Xin He, . (United States)

While computational modeling techniques of the ideal observer make it "can-be-used" in system optimization, its "usefulness" depends on whether it serves the empirical purpose for which it is used: to identify desirable imaging systems to be used by human observers. In a separate SPIE study, I have shown that the ideal and the human observers do not necessarily prefer the same system as the optimal or better one due to their different objectives in both hardware and software system optimization. The general empirical validity of the ideal observer is in question. In this work, I attempt to identify a necessary but insufficient condition under which the human and the ideal observer may rank systems consistently. A well formulated condition allows a numerical test on the "usefulness" of the ideal observer for a particular application without routine human observer studies. I reproduced data from Abbey et al. JOSA 2001 to verify the proposed condition (i.e., not a rigorous corroboration/falsification due to the lack of specific falsifiability in the proposed conjecture. A roadmap for more falsification conditions is proposed). Via this work, I would like to emphasize the reality of practical decision making more than the realism in mathematical modeling. (Disclaimer: the views expressed in this work do not necessarily represent those of the FDA.)

10136-37, Session PS1

Visual-search models for location-known detection tasks

Howard C. Gifford, Zohreh Karbaschi, Kheya Banerjee, Mini Das, Univ. of Houston (United States)

Human-observer performance in lesion-detection studies is of interest for optimizing the data acquisition and processing for many types of oncologic imaging. These studies often combine humans and statistical discriminants

(model observers) for basic tasks involving a known target at a fixed target location in simulated images. Past comparisons with ideal observers suggest that humans can partially decorrelate (prewhiten) statistical noise as part of the detection process. A two-alternative forced-choice study was conducted with synthetic nuclear medicine images to investigate if model observers based on a visual-search paradigm allow an alternative interpretation.

10136-38, Session PS1

Visual-search model observer for assessing mass detection in CT

Zohreh Karbaschi, Howard C. Gifford, Univ. of Houston (United States)

Mathematical model observers (MO) have been extensively used in diagnostic image-quality assessments through different stages of imaging system development. Of particular interest are MOs that can closely predict human performance. Due to the need for prior statistical information, commonly used MOs are limited to simple detection tasks. This study compared a general form of scanning observer which depends highly on prior statistical information with visual-search (VS) MOs which require less prior statistical information and can be used in more clinically realistic tasks. We investigated the performances of three VS observers and a scanning observer in a mass detection-localization study in computer tomography (CT).

Tumor detection-localization accuracy was tested for two sampling parameters: 1) the number of acquired projections P and the number of imaging detectors N. Data acquisition and reconstruction for parallel hole CT images were simulated. Tumors were added to the acquired projections in random locations within the lung regions. The observer task was defined to be the detection-localization of the tumors within the reconstructed images. The observers were tested in the presence and absence of quantum noise. Our results indicated that VS observers illustrate more sensitivity to imaging artifacts that are caused by the low number of P and better match with human performance compared to scanning observers. Preliminary human results were collected for comparison, however not reported at this time. We plan to report complete human results as well as the performance of the channelized Hoteling (CH) observer for the same parameters in a location-known study.

10136-39, Session PS2

Hologram placement and stability evaluation for Microsoft HoloLens

Reid Vassallo, Adam Rankin, Elvis C. S. Chen, Terry M. Peters, Robarts Research Institute (Canada) and Western Univ. (Canada)

Augmented reality (AR) has an increasing presence in the world of image-guided interventions. This is amplified with the availability of consumer-grade head-mounted display (HMD) technology. The Microsoft® HoloLens™ optical pass-through display looks to be at the forefront of this sector. It shows promise of effectiveness in increasing patient safety during clinical interventions, however its accuracy and stability must still be evaluated for the clinical environment. We have developed an evaluative protocol for the HoloLens™ using an optical measurement device to digitize the perceived location of the hologram. This is compared against an expected location determined outside of the HoloLens™ system. This evaluates the HMD's ability to accurately place holograms in their desired location and the stability of these holograms once placed. The stability is measured both over time and when actions are performed that may cause a shift in the hologram's location due to its use of spatial mapping for location and pose tracking. An emphasis is placed on actions that are more likely to be performed in a clinical setting. This will be used to determine the most applicable use cases for this technology in the future and how to increase its abilities when it is in use. Preliminary results do not show a high degree of accuracy in this system, although this could be due to confounding variables such as the environment used for testing and scripts used to create the application.

10136-40, Session PS2

Perceived image quality for autostereoscopic holograms in healthcare training

Brian F. Goldiez, Julian Abich IV, Austin Carter, Univ. of Central Florida (United States); Matthew Hackett, U.S Army Research Lab. (United States)

Holographic displays are autostereoscopic and demonstrate high levels of parallax. In other words, users can view the image in 3D without glasses, and from multiple viewpoints. Dynamic holographic displays are presently technologically immature, with limited resolution and refresh rate. Introducing dynamics, where the image can be manipulated in real time, into holographic imagery is a challenge in order to maintain scene quality (color, contrast, scene density, etc.). The challenge for technology developers is determining the most important scene parameters for users. The approach describes the generation of a high quality 3D model of a simulated traumatic amputation above the knee using 3D scanning. Using that model, a set of static holographic prints were created with degraded quality characteristics including: monochrome, limited color palette, contrast ratio, display resolution, and polygon density. Clinicians and medical students then compared image quality during a forced choice pairwise comparison. The accumulated data from participants was statistically evaluated. Based on this data, the most important attributes related to image quality were determined for holographic prints, providing a unique data point and begins to address the topic of image quality in 3D. This data also guides future development of the next generation of dynamic and static holographic displays.

10136-88, Session PS2

On analyzing free-response data on location level

Andriy I. Bandos, Univ. of Pittsburgh (United States); Nancy A. Obuchowski, Cleveland Clinic Foundation (United States)

No Abstract Available

10136-41, Session PS3

Colorimetric calibration of wound photography with off-the-shelf devices

Subhankar Bala, National Institute of Technology, Warangal (India); Ekaterina Sirazitdinova, Thomas M. Deserno, Uniklinik RWTH Aachen (Germany)

Digital cameras are often used in recent days for photographic documentation in medical sciences. However, color reproducibility of same objects suffers from different illuminations and lighting conditions. This variation in color representation is problematic when the images are used for segmentation and measurements based on color thresholds. In this paper, motivated by photographic follow-up of chronic wounds, we assess the impact of (i) gamma correction, (ii) white balancing, (iii) background unification, and (iv) reference card-based color correction. and white balancing , where gamma correction is a non-linear color transform. In the last step, we apply colorimetric calibration using a reference color card of 24 patches with known colors. A lattice detection algorithm is used for locating the card. The least squares algorithm is applied for affine color calibration in the RGB model. We have tested the algorithm on images with 7 different types of illumination: with and without flash using 3 different off-the-shelf cameras including smartphones. We analysed the spread of resulting color value of selected color patch before and after applying the calibration. Additionally, we checked the individual contribution of different steps of the whole calibration process. Using all steps, the variance of same colors is significantly reduced, supporting manual as well as automatic quantitative wound assessments with off-the-shelf devices.

10136-42, Session PS3

Color image enhancement of medical images using alpha-rooting and zonal alpha-rooting methods on 2D-QDFT

Aparna John, Artyom M. Grigoryan, The Univ. of Texas at San Antonio (United States)

Image processing is a great tool of enhancing the visual perception of the images either by improving the contrast of the images or by filtering out the noises of the images. One of the most effective and the most popular frequency domain method of image enhancements are the algorithms based on Discrete Fourier transform. The Quaternion Discrete Fourier transform (2D-QDFT) is the Fourier transform applied to color images, when the color images are considered as a quaternion number. The quaternion numbers are four dimensional hyper-complex numbers. The color images can be seen as the components of a hyper-complex numbers because most of the color images are images that contain three or four channels. This allows us to see the color of the color image as a single unit. This quaternion approach see the color image as a vector, so this permits us to see the merging effect of the color due to the combination of the primary colors. Till recently, the color images were processed by applying the respective algorithm onto each channels separately, and then, composing the color image from these processed channels. The quaternion approach is a much better method for color images. The alpha-rooting is a method that takes the alpha-root of the transformed frequency values of 2D-QDFT, before taking the inverse transform. In zonal alpha-rooting, the alpha-rooting method is done on different zones of frequency spectrum, with different alpha values for different zones. The optimization of the choice of alpha is done with the genetic algorithm method.

10136-43, Session PS3

Do quantitative metrics derived from standard fluoroscopy phantoms used for quality control assess vendor-specific advancements in interventional fluoroscopy systems?

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Approximately 9 million fluoroscopically-guided interventional procedures are performed annually in the USA. Recent technological advancements for interventional fluoroscopy systems have focused towards vendor-specific real-time image and signal processing. Therefore the purpose of this study was to evaluate if quantitative metrics derived from standard image quality phantoms, routinely used for quality control, are able to distinguish vendor-specific processing features for interventional fluoroscopy systems. Six standard image quality phantoms were used to measure contrast-to-noise ratio (CNR), full-width-at-half-maximum (for determining edge blurring) and modulation transfer function, to analyze contrast detail characteristics, and to assess digital subtraction angiography (DSA) performance of six flat-panel detector based interventional fluoroscopy systems from Philips (with and without ClarityIQ) and Siemens. Phantom data were acquired with different dose modes and field-of-view settings. Fluoroscopy loops and digital subtraction acquisitions were saved (duration 3 seconds; repeated 3 times). Images were analyzed offline in ImageJ. The CNR measurements showed no differences between systems, the contrast-detail analysis and edge blurring characterization showed relatively low performance of Philips Clarity systems as compared to Siemens and Philips non-Clarity systems, whereas the modulation transfer function showed that the limiting spatial resolution was higher for the Philips systems as compared to the Siemens system. However, with the DSA phantom the performance of Siemens and Philips Clarity-systems was similar. In conclusion, depending on the image quality phantom used for comparing different systems, the performance results differ and therefore, quantitative metrics derived from standard fluoroscopy phantoms lack the discriminatory ability to assess vendor-specific advancements in interventional fluoroscopy systems.

10136-44, Session PS4

Impact of tube current modulation on lesion conspicuity index in hi-resolution chest computed tomography

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Introduction

Tube current modulation in CT is used to optimise radiation dose to the patient. The acceptable noise (noise index) can be varied, based on the level of optimisation required; higher accepted noise reduces the patient dose.

Recent research suggests that measuring the conspicuity index (C.I.) of focal lesions within an image is more reflective of a clinical reader's ability to perceive focal lesions. Software has been developed and validated to calculate the C.I. in DICOM images.

This work focuses on comparing conspicuity index for varying noise indices.

Method

A anthropomorphic chest phantom was used "Lungman" with inserted lesions of varying size and HU.

The phantom was scanned using the standard protocol for high-resolution helical chest. Three repeated images were performed on each noise index (standard deviation SD) available. CTDIvol was recorded for each scan.

The conspicuity index of the three lesions was calculated using the Conspicuity Index software.

Results

Conspicuity index vs CTDI was plotted.

Conspicuity index values increased with a positive logarithmic relationship with CTDIvol. Improvements in C.I. can be seen at low CTDIvol values, with less impact at higher dose levels. A dose reduction of 95% was witnessed using a high noise index SD without impacting on lung lesion conspicuity for lesions of low contrast. For lesions of high contrast (lesion 1), 51% reduction in dose was seen from a noise index SD of 5 to 7.5 with only a 10% reduction in conspicuity.

Conclusion

Increasing noise index offers dose reductions without significant reduction in Conspicuity Index.

10136-45, Session PS4

Hounsfield unit inaccuracy in computed tomography: lesion size and density, diagnostic quality vs. attenuation correction

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Purpose

In computed tomography the Hounsfield Units (HU) are used as an indicator of the tissue type based on the linear attenuation coefficients of the tissue. HU accuracy is essential when this metric is used in any form to support diagnosis. In hybrid imaging, such as SPECT/CT and PET/CT, the information is used for attenuation correction (AC) of the emission images.

This work investigates the HU accuracy of nodules of known size and HU, comparing diagnostic quality (DQ) images with images used for AC.

Method

AC and DQ images were acquired on a 64-slice PET/CT system. Images were acquired using an anthropomorphic phantom and simulated nodules. Five different configurations of nodule position were imaged and HU recorded using regions of interest in ImageJ. Measurements were compared to the known HU of the nodules.

Standard imaging protocols were used.

Results and Discussion

HU accuracy is reduced in AC images when compared to DQ, with smaller lesions having greater variance. Also, there is less accuracy for lesions closer to 0HU. These factors are, in part, due to the higher noise and poorer contrast within the image, but mainly due to the partial volume effect owing to the larger slice thickness used with AC.

Conclusion

HU accuracy needs to be taken into account when selecting imaging parameters, if accuracy is required for diagnosis or attenuation correction, then thinner imaging slices should be selected to overcome the partial volume effect.

10136-46, Session PS4

Characterization of a CT unit for the detection of low contrast structures

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Major technological advances in CT enabled the acquisition of high quality images while minimizing patient exposure. The goal of this study was to present a strategy to optimize abdominal protocols on two recent CT units from one manufacturer while keeping a comparable level of low-contrast detectability (LCD).

An abdominal phantom (QRM, Germany), containing 5mm-diameter spheres (20 HU nominal contrast relative to background) was scanned using our standard clinical noise index settings on two GE CTs: “750 HD” and “Revolution”. Two additional rings (2.5 and 5 cm) were also added to the phantom. On “750 HD”, images were reconstructed using FBP, ASIR 50% and VEO (Model Based Iterative Reconstruction, MBIR). On “Revolution”, ASIR-V0% (FBP being not available) and ASIR-V50% were used. The reconstructed slice thickness was 2.5 mm except 0.625 mm with VEO. To assess LCD, the Channelized Hotelling Observer (CHO) with 10 DDoG channels was used with the area under the curve (AUC) as a figure of merit. Image contrast and noise properties were also studied.

AUC decreased by 25% with the increase of phantom size for “750 HD” using FBP but only by 15% for “Revolution” CT using ASIR-V0%. The contrast of the spheres decreased up to 20% on “750 HD” but remained constant on “Revolution”. In spite of the lower performance of “HD 750” when compared to “Revolution”, the use of VEO for the largest-sized phantom significantly improved AUC while providing slices thinner by a factor of 4. VEO is particularly interesting for LCD when dealing with large patients.

10136-47, Session PS4

Investigation on location dependent detectability in cone beam CT images with uniform and anatomical backgrounds

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The cone beam CT imaging system produces different noise structures in different local regions, and the difference is significant along the longitudinal direction due to the large cone angle. In this work, we investigate location dependent lesion detectability for different background types (i.e., uniform and anatomical backgrounds) and image planes (i.e., transverse and longitudinal). Anatomical backgrounds are generated using a power law spectrum of breast anatomy, 1/f^?, with ?=3. Spherical object with a 5mm diameter is used as a signal. CT projection data are acquired by the forward projection of uniform and anatomical backgrounds with and without the signal. Then, projection data are reconstructed using FDK algorithm. Detectability of transverse and longitudinal planes with different slice thicknesses of reconstructed images is evaluated by a channelized Hotelling observer with Laguerre-Gauss channels. Optimal slice thickness is 3.8mm for uniform background images and 1.9mm for anatomical background images. With the optimal slice thickness, the task SNR of each plane for different signal locations show similar values within uniform and anatomical backgrounds. For uniform background, transverse plane yields higher task SNR than longitudinal plane. For anatomical background, longitudinal plane yields higher task SNR than transverse plane at iso-center, but both planes show similar task SNR at off-center

10136-48, Session PS4

A phantom design and assessment of lesion detectability in PET imaging

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The early detection of abnormal regions with increased tracer uptake in positron emission tomography (PET) is a key driver of imaging system design and optimization as well as choice of imaging protocols. Fillable phantoms, with tradeoffs between complexity and utility, provide a means to test and compare these systems under truth-known conditions. This work presents a novel phantom design and analysis techniques to evaluate detectability in the context of realistic, non-piecewise constant backgrounds. The design consists of a phantom filled with small solid plastic balls and a radionuclide solution to mimic heterogeneous background uptake. A set of 3D-printed regular dodecahedral ‘features’ were included at user-defined locations within the phantom to create ‘holes’ within the matrix of chaotically-packed balls. These features fill at approximately 3:1 contrast to the lumpy background. A series of signal-known-present (SP) and signal-known-absent (SA) sub-images were generated and used as input for observer studies. This design was imaged in a head-like 20 cm diameter, 20 cm long cylinder and in a body-like 36 cm wide by 21 cm tall by 40 cm long tank. A series of model observer detectability indices were compared across scan conditions (count levels, number of scan replicates), PET image reconstruction methods (with/without TOF and PSF) and between PET/CT scanner system designs using the same phantom imaged on multiple systems. The detectability index was further compared to the noise-equivalent count (NEC) level to characterize the relationship between NEC and observer SNR.

10136-49, Session PS4

Fractal dimension metric for quantifying noise texture of computed tomography images

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This study investigated a fractal dimension algorithm for noise texture quantification in CT images. Quantifying noise in CT images is important for assessing image quality. Noise is typically quantified by calculating noise standard deviation and noise power spectrum (NPS). Different reconstruction kernels and iterative reconstruction approaches affect both the noise magnitude and noise texture. The shape of the NPS can be used as a noise texture descriptor. However, the NPS calculation requires numerous images and NPS is a vector quantity. This study proposes the metric of fractal dimension to quantify noise texture, because fractal dimension is a single scalar metric calculated from a small number of images. Fractal dimension measures the complexity of a pattern. . In this study, the ACR CT phantom was scanned and images were reconstructed using filtered back-projection with three reconstruction kernels: bone, soft and standard. Regions of interest were extracted from the uniform section of the phantom for NPS and fractal dimension calculation. The results demonstrated a mean fractal dimension of 2.03 for soft kernel, 2.13 for standard kernel, and 2.33 the bone kernel. Increasing fractal dimension was seen as NPS shifted towards the higher spatial frequency and as the noise became visually grainier. Stable fractal dimension was calculated from five images compared to 80 images needed for NPS calculation. The scalar fractal dimension metric may be a useful noise texture descriptor for evaluating or tuning reconstruction algorithms

10136-50, Session PS4

Effects of window width and window level adjustment on the detectability index in computed tomography images

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This study experimentally evaluated the effect of window width (WW) and window level (WL) on the task based detectability index (d’). Window-level transformation is frequently performed on CT images to improve visualization. Numerous model observers and metrics have been used to assess CT image quality. However, objective assessment is typically performed on the reconstructed CT image without considering the WW and WL settings used by the reader. In this study, the ACR CT phantom was scanned at two different dose levels and images were reconstructed using filtered back projection. The bone and acrylic contrast objects from module one of the ACR phantom were selected for calculating the effect of the WW/WL on the detectability index (d’). The d’ for each object and dose level was calculated for a range of WW and WL values. The results demonstrated that the d’ values were affected by the WW and WL settings. For example, at one dose level used in this study, a WL setting of 10 HU and window width of 150 HU resulted in a 46% increase in d’ compared to the d’ of the untransformed image. For the high contrast object, the investigated WW and WL settings did not improve d’. A WL of 100 and WW of 1250 resulted in a 19% decrease in the d’ value for the high contrast object. The results suggest that observer studies should consider the displayed window width and level settings.

10136-51, Session PS4

An interactive, stereoscopic virtual environment for medical imaging visualization, simulation and training

Erik Messier, Evan Krueger, Gabriel Diaz, Cristian A. Linte, Rochester Institute of Technology (United States)

Despite recent advancements in medical image acquisition that allow for the reconstruction of anatomies with 3D, 4D, and 5D renderings, the standard for anatomical and medical data visualization still relies heavily on the use of traditional 2D didactic tools (i.e., textbooks and slides) or, at best, the visualization of the native images in their 2D slice format. While these approaches have their merit in being cost effective and easy-to-disseminate, anatomy is implicitly 3D and when using 2D visualizations of more complex morphologies, interactions between structures are often missed. In medical practice, such as in the planning and execution of surgical interventions, professionals require an intricate knowledge of anatomical complexities, which are more easily, or only can be, elucidated with more natural, intuitive method of interacting with complex 3D volumetric datasets extracted from high-resolution CT or MRI images. Leveraging open source, high quality, 3D medical imaging datasets and the emerging popularity of 3D display technologies; affordable, consistent, and widely available 3D anatomical visualizations can be achieved. In this study we describe the design, implementation, and evaluation of a 3D visualization paradigm for human anatomy extracted from 3D medical images using an interactive stereoscopic table-top display. Using a Northern Digital Polaris Spectra tracking system, and a reverse projection screen, a multiple-viewing-angle interactive stereoscopic display was created. While this paradigm is sufficiently versatile to enable a wide variety of applications in need of 3D visualization, we designed our study in the context of an interactive game that allows users to explore the anatomy of various organs and systems by manipulating 3D virtual data. In analysis we aim to quantify and qualify users visual and motor interactions with virtual environments, as well as quantify their learning capabilities when employing this interactive display as a 3D didactic tool.

10136-52, Session PS4

A new method to quantify fiber orientation similarity in registered volumes

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Differences in fiber orientations between registered image volumes can be difficult to quantify. Errors between diffusion tensor imaging (DTI) volumes are often a combination of image registration errors and fluctuations of diffusion values used to determine the fiber orientations. In order to properly quantify the similarity between two images containing fiber orientation information, both displacement and angular fluctuation should be considered. We present a method to quantify fiber orientation similarity between registered images by allowing small pixel displacements in conjunction with minor angle differences. Adjustments to the allowed pixel displacement and degree of angle difference can help identify the major factor contributing to fiber estimation error. The proposed method can provide a new metric for the evaluation of the fiber orientation difference.

10136-53, Session PS5

Automatic breast tissue density estimation scheme in digital mammography images

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Cases of breast cancer have increased substantially each year. However, radiologists are subject to subjectivity and failures of interpretation which may affect the final diagnosis in this examination. The high density features in breast tissue are important factors related to these failures. Thus, among many functions some CADx (Computer-Aided Diagnosis) schemes are classifying breasts according to the predominant density. In order to aid in such a procedure, this work attempts to describe an automatic software for classification and statistical information on the percentage change in breast tissue density, through analysis of sub regions (ROIs) from the whole mammography image. Once the breast is segmented, the image is divided into regions from which texture features are extracted. Then an artificial neural network MLP was used to categorize ROIs. Experienced radiologists have previously determined the ROIs density classification, which was the reference to the software evaluation. From tests results its average accuracy was 88.7% in ROIs classification, and 83.25% in the classification of the whole breast density in the 4 BI-RADS® density classes – taking into account a set of 400 images. Furthermore, when considering only a simplified two classes division (high and low densities) the classifier accuracy reached 93.5%, with a AUC = 0.95.

10136-54, Session PS5

Characterization of breast density in Vietnam and its association with demographic, reproductive and lifestyle factors

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In Vietnam breast cancer is the most common cancer amongst women with incidence levels rapidly increasing. Whilst mammographic density is currently used as a predictor of breast cancer risk amongst westernized women, epidemiological evidence suggests that the Vietnamese population may have a unique stratification of breast density distribution. Previous studies have consistently suggested a need to develop alternative models based on ethnicity to better understand mammographic characteristics. This study therefore aims to investigate pattern of breast density of women in Vietnam and its association with demographic, reproductive and lifestyle features.

A cross-sectional study was conducted in the two largest cities in the northern and southern of Vietnam (Ha Noi and Ho Chi Minh city) using 1,651 digital mammograms collected in 2015. Mammographic breast density was collated in the form of Breast Imaging Reporting and Data System (BIRADS) scores from radiology reports. Suspected factors associated with breast density were obtained from questionnaires, which considered demographic, reproductive and lifestyle features provided by women who attended mammography examinations. The association of high and low breast density with these features was investigated by t-test for continuous variables and chi-square test for categorical variables. Logistic regression was used to derive odds ratios (OR) for factors demonstrating statistically significant associations with high breast density. Two-tailed tests were employed and a P value ≤ 0.05 was considered to be significant

Our results showed that a large proportion of Vietnamese women (78.4%) had a high breast density. Significant associations of high breast density were evident with women less than 55 years old (OR=3.0; P<0.0001) and having a BMI<23 (OR=2.2; P<0.0001), pre-menopausal status (OR=2.9; P<0.0001), less than 3 babies (OR=2.9; P=0.001), or being less than 32 years old when having their last child (OR=1.8; P<0.0001). Smokers (OR=3.8; P=0.04) and individuals who consumed more than two serves of vegetable daily (OR=2.6; P<0.0001) were also linked to higher density.

The findings suggest some unique features regarding levels of mammographic density and causal agents for increased density amongst Vietnamese compared with westernized women. The data emphasizes the importance of ethnically-dependent strategies to minimise the incidence of breast cancer.

10136-55, Session PS5

The development and testing of a unique and flexible training module for residents and fellows using digital breast tomosythesis (DBT)

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The transition from FFDM to digital breast tomosynthesis (DBT) necessitates new approaches for training radiology residents and fellows that highlight the differences between depictions of the same abnormalities on these modalities. We developed a unique, flexible training module that enables training with complete feedback, as well as testing performance before and after training. Currently, we included 219 examinations, with priors and other relevant information. Using a special interface to the SecurView workstation (Hologic), we developed a management program that displays in a randomized manner each case in a sequential mode (FFDM first followed by FFDM+DBT) and allows the reader to rate the case followed by viewing the images side by side with results of the full imaging based history (reporting) by the screening interpreter, the diagnostic workup interpreter (when applicable), and the actual pathology (biopsy and/or surgical). This allows the reader to review their correct and/or incorrect interpretation at each step of the management decision making. The module also has sets of pre- and post-training cases, allowing for a test-train-test study to be performed. Two observer studies using 18 radiologists, residents, and fellows have been performed using this module, to date. The training module was assembled, tested, and implemented. We found it to be extremely flexible and useful in training. After completing two observer performance studies, the module was installed in our clinical facility and is currently being used to train residents and fellows at their own pace. All users found this module to be useful and extremely informative.

10136-56, Session PS5

Developing a visual sensitive image Features based CAD scheme to assist classification of mammographic masses

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Computer-aided diagnosis (CAD) schemes of mammograms have been previously developed and tested. However, due to using "black-box" approaches with a large number of complicated features, radiologists have lower confidence to accept or consider CAD-cued results. In order to help solve this issue, this study aims to develop and evaluate a new CAD scheme that uses visual sensitive image features to classify between malignant and benign mammographic masses. A dataset of 301 masses detected on both craniocaudal (CC) and mediolateral-oblique (MLO) view images was retrospectively assembled. Among them, 152 were malignant and 149 were benign. An iterative region-growing algorithm was applied to the special Gaussian-kernel filtered images to segment mass regions. Total 13 Image features were computed to mimic 5 categories of visually sensitive features that are commonly used by radiologists in classifying suspicious mammographic masses namely, mass size, shape factor, contrast, homogeneity and spiculation. We then selected one optimal feature in each of 5 feature categories by using a student t-test, and applied two logistic regression classifiers using either CC or MLO view images to distinguish between malignant and benign masses. Last, a fusion method of combining two classification scores was applied and tested. By applying a 10-fold cross-validation method, the area under receiver operating characteristic curves was 0.806±0.025. This study demonstrated a new approach to develop CAD scheme based on 5 visually sensitive image features. Combining with a "visual-aid" interface, CAD results are much more easily explainable to the observers and may increase their confidence to consider CAD-cued results.

10136-57, Session PS5

Can BI-RADS features on mammography be used as a surrogate for expensive genomic testing in breast cancer patients?

Michael R. Harowicz, Jeffrey Marks, P. Kelly Marcom, Duke Univ. School of Medicine (United States); Maciej A. Mazurowski, Duke Univ. School of Engineering (United States)

Medical oncologists increasingly rely on expensive genomic analysis to stratify patients for different treatment. The genomic markers are able to divide patients into groups that behave differently in terms of tumor presentation, likelihood of metastatic spread, and response to chemotherapy and radiation therapy. In recent years there has been a rapid increase in the number of genomic tests available, like the Oncotype Dx test, which provides the risk of cancer recurrence for a subset of patients. Radiogenomics, a new field that investigates the relationship between imaging phenotypes and genomic characteristics, may offer a less expensive and less invasive imaging surrogate for molecular subtype and Oncotype Dx recurrence score (ODRS). This retrospective study analyzes the relationship between Breast imaging-reporting and data system (BI-RADS) features as assessed by radiologists on mammograms with molecular subtype and ODRS. We used data from patients with BI-RADS features (shape or margin) and a genomic feature (subtype or ODRS) for the following cohort: shape vs. subtype (n=69), margin vs. subtype (n=78), shape vs. ODRS (n=20), and margin vs. ODRS (n=18). The association between features was assessed using a Fisher's exact test. Our results show that shape assessed by radiologists according to the BI-RADS lexicon is associated with molecular subtype (p=0.0171), while BI-RADS features of shape and margin were not significantly associated with ODRS (p=0.7839, p=0.6047 respectively). These preliminary findings suggest that an imaging-based surrogate of molecular subtype using BI-RADS shape features on mammography may be a valid and less expensive alternative to genomic testing.

10136-58, Session PS5

Statistical aspects of radiogenomics: Can radiogenomics models be used to aid prediction of outcomes in cancer patients?

Boya Ren, Maciej A. Mazurowski, Duke Univ. (United States)

Radiogenomics is a new direction in cancer research that aims at identifying the relationship between tumor genomics and its appearance in imaging. One of the general applications of radiogenomics is to generate imaging-based models for prediction of outcomes through modeling the relationship between imaging and genomics. We show a preliminary simulation study evaluation whether such approach results in improved models. Our experiments indicated what parameters have impact on usefulness of the radiogenomic approach. Overall, there are some situations in which radiogenomics approach is beneficial but only when the radiogenomic relationship is strong and low number of imaging cases are available.

10136-59, Session PS5

Exploring a new bilateral focal density asymmetry based image marker to predict breast cancer risk

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Since an important prerequisite to establish a new personalized mammographic screening paradigm requires a short-term risk factor or stratification model that can identify which women have high risk of developing cancer in a short-term after a negative screening of interest (e.g., 2 to 5 years), we recently have built a unique short-term breast cancer risk stratification model based on the bilateral mammographic image feature asymmetry. The purpose of this study is to evaluate performance of our new risk model using an independent image dataset and demonstrate a new graphic user interface platform that allows users to interactively apply this new risk model to process and analyze the selected negative screening mammograms. A new independent image dataset of "prior" images was retrospectively assembled and used. The dataset includes 100 high risk cases (in which the subtle cancers were detected in "current" images) and 100 low-risk cases (which maintained negative in "current" images). Applying to this dataset, the risk model yielded a risk stratification performance as measured by the area under a ROC curve of 0.726±0.035. Our testing results demonstrated that applying this new risk model could yield significantly higher discriminatory power in predicting short-term breast cancer risk than using other existing breast cancer risk factors and/or epidemiology study based risk prediction models. In addition, our interactive risk model platform increases the transparency of image feature computation and risk assessment process, which may also help increase the confidence of the women and/or healthcare providers to better determine the interval of mammographic screening.

Conference 10137: Biomedical Applications in Molecular, Structural, and Functional Imaging

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10137-1, Session 1

Evaluation of the anti-neoplastic effect of sorafenib on liver cancer through bioluminescence tomography

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Hepatocellular carcinoma (HCC) is one of the most important leading causes of cancer-related deaths worldwide. In this study, we evaluated the efficacy of sorafenib on hepatocellular carcinoma through bioluminescence tomography (BLT) based on Micro-CT/BLT multi-modal system.

Initially, the human hepatocellular carcinoma cell line HepG2-Red-FLuc, which was transfected with luciferase gene, was cultured. And then, the orthotopic liver tumor mouse model was established on 4~5 weeks old athymic male Balb/c nude mice by inoculating the HepG2-Red-FLuc cell suspension into the liver lobe under isoflurane anesthesia. 15~20 days after tumor cells implantation, the mice were divided into two groups including the sorafenib treatment group and the control group. The mice in the treatment group were treated with sorafenib with dosage of 62 mg/kg/day by oral gavage for continuous 14 days, and the mice in the control group were treated with sterile water at equal volume. The tumor growth and drug treatment efficacy were dynamically monitored through bioluminescence tomography.

The results in this study showed that the growth of liver cancer can be dynamically monitored from very early stage, and also the sorafenib treatment efficacy can be reliably and objectively assessed using BLT imaging method. Our data demonstrated sorafenib can inhibit the tumor growth effectively . BLT enabled the non-invasive and reliable assessment of anti-neoplastic drug efficacy on liver cancer.

10137-2, Session 1

Enhanced imaging resolution in dynamic fluorescence molecular tomography by multispectral excitation method

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Dynamic fluorescence molecular tomography (DFMT) is a promising method for the quantitative evaluation of the metabolic process of fluorescent agents in body. However, the resolution is limited due to the ill-posed nature of fluorescence molecular tomography (FMT) and the high absorption and scattering of the fluorescent light in biological tissues. In this paper, the resolution of DFMT is improved by multispectral excitation method. Firstly, the imaged object with varied fluorescent concentrations at different time points is excited by several excitation lights with different wavelengths, and the fluorescent images are collected. Secondly, the individual FMT images at different time points are respectively reconstructed, and independent component analysis (ICA) is employed to decompose the fluorescent targets. The independent components (ICs) and corresponding spectrum courses (SCs) which obtained from ICA represent the spatial structures and spectral variations of the fluorescent targets, respectively. Thirdly, the ICs and SCs are combined to quantitatively recover the concentrations of individual fluorescent targets. Finally, the metabolic parameters and DFMT images are obtained by fitting the FMT images of each fluorescent targets at different time points into a two compartment model. Numerical simulations are carried out to validate the feasibility of the proposed method. The results demonstrate that the resolution of DFMT is significantly improved. The metabolic curves can be correctly recovered even when the edge-edge-distance of the fluorescent targets is less than 0.1 cm.

10137-3, Session 1

X-ray luminescence computed tomography: a sensitivity study

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X-ray luminescence computed tomography (XLCT) is a hybrid molecular imaging modality that uses x-ray beams to excite deeply embedded phosphor based nanoparticles (e.g. Europium doped Gadolinium Oxysulfide – GOS: Eu3+) that will emit near-infrared (NIR) photons to be captured by a sensitive detector for optical image reconstruction. At the same time, an x-ray detector is used to detect the transmitted x-ray photons for possible simultaneous anatomical imaging. Due to the selective x-ray excitation of this modality, XLCT can obtain high spatial resolution. XLCT thus combines both the merits of x-ray imaging (high resolution) and optical imaging (high sensitivity), allowing for detection of deeply embedded targets with high spatial resolution. In this study, we compare the measurement sensitivity between XLCT and traditional x-ray computed tomography (CT) using phantom experiments. Cylindrical phantoms embedded with a cylindrical target with varying concentrations of GOS: Eu3+ (0.1, 1.0, 10 mg/mL, etc.) are scanned inside our lab made XLCT imaging system contained inside an x-ray shielding and light tight cabinet. After the XLCT scan, the phantoms were placed inside our lab made microCT scanner for CT imaging. After both imaging schemes are performed, the detected intensity contrast between the target region and background are compared between XLCT and CT images. The XLCT images demonstrated much higher contrast between target and the background compared to the microCT images. The microCT could not detect the target concentrations of 1.0 and 0.1 mg/mL, thus XLCT demonstrates much higher sensitivity than CT for phosphor targets.

10137-4, Session 1

A radiative transfer equation-based image-reconstruction method incorporating boundary conditions for diffuse optical imaging

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Developing reconstruction methods for transcranial optical imaging of brain network activity (BRAIN initiative effort) requires accurate modeling of photon propagation, including boundary conditions arising due to refractive index mismatch between different regions of the brain and between tissue and air. For this purpose, we developed an analytical Neumann-series radiative transport equation (RTE)-based approach. Each Neumann series term models different scattering, absorption, and boundary-reflection events. The reflection is modeled using the Fresnel equation. We use this approach to design a gradient-descent-based analytical reconstruction algorithm using a diffuse optical imaging (DOI) system. The algorithm was implemented for a three-dimensional DOI system consisting of a laser source, cuboidal scattering medium (refractive index > 1), and a pixelated detector at one cuboid face (setup similar to in Jha et al., JOSAA, 2012). The system was placed in air (refractive index of 1), thus modeling a scenario where photons propagate from tissue to air. In simulation experiments, the refractive index of the scattering medium was varied from 1.1 to 1.5 to test the robustness of the reconstruction algorithm over a wide range of refractive index mismatches. The experiments were repeated over multiple noise realizations. Results showed that by using the proposed algorithm, the absorption coefficient of the medium was estimated substantially more accurately (root mean square error (RMSE) of 20% +- 8%) in comparison

to when the boundary conditions were not modeled (RMSE of 152% +- 54%). These results demonstrated the importance of modeling boundary conditions in the photon-propagation model.

10137-5, Session 1

Image deblurring using a joint entropy prior in X-ray luminescence computed tomography

Chang Su, Tsinghua Univ. (China); Joyita Dutta, Massachusetts General Hospital (United States) and University of Massachusetts Lowell (United States); Hui Zhang, Tsinghua Univ. (China); Georges El Fakhri, Quanzheng Li, Massachusetts General Hospital (United States)

X-ray luminescence computed tomography (XLCT) is an emerging hybrid imaging modality that can provide functional and anatomical images at the same time. Traditional narrow beam XLCT can achieve high spatial resolution as well as high sensitivity. However, by treating the CCD camera as a single pixel detector, this kind of scheme resembles the first generation of CT scanner which results in a long scanning time and a high radiation dose. Although cone beam or fan beam XLCT has the ability to mitigate this problem with an optical propagation model introduced, image quality is affected because the inverse problem is ill-conditioned. Much effort has been done to improve the image quality through hardware improvements or by developing new reconstruction techniques for XLCT. The objective of this work is to further enhance the already reconstructed image by introducing anatomical information through retrospective processing. The deblurring process used a spatially variant point spread function (PSF) model and a joint entropy based anatomical prior derived from a CT image acquired using the same XLCT system. A numerical experiment was conducted with a real mouse CT image from the Digimouse phantom used as the anatomical prior. The resultant images of bone and lung regions showed sharp edges and good consistency with the CT image. Activity error was reduced by 52.3% even for nanophosphor lesion size as small as 0.8mm.

10137-6, Session 2

An image processing framework for automated analysis of swimming behavior in tadpoles with vestibular alterations

Kasra Zarei, Bernd Fritzsch, James Buchholz, The Univ. of Iowa (United States)

Prolonged space flight, specifically microgravity, presents a problem for space exploration. Animal models with altered connections of the vestibular ear, and thus altered gravity sensation, would allow the examination of the effects of microgravity and how various countermeasures can establish normal function. We describe a novel image acquisition and segmentation framework to monitor the effects of ear manipulations to generate asymmetric gravity input on the frog embryo escape response. The motion of the animal was recorded using high-speed imaging followed by detailed movement pattern analysis, performed using a developed imaging apparatus that uses a high-speed camera to obtain real-time, high-resolution images of tadpole movements.

A general framework was established for performing image segmentation on tadpole bodies. The numerical framework developed in this work is based on a massively parallel Cartesian grid based Eulerian solver. A narrow band level set approach is used for sharp tracking of the tadpole body. Speckle Reducing Anisotropic Diffusion is used to smooth image signals by diffusing noise while retaining edges. The use of level set method for interface tracking provides an inherent advantage of using level set based image segmentation algorithm (active contouring) for the representation of tadpole bodies. The image processing approach allows performing simulation on real geometries rather than the idealized shapes.

The image acquisition and segmentation methods presented form an important element of a rigorous investigation into the response of the tadpole vestibular system to mechanical and biochemical manipulations, and can ultimately contribute to a better understanding of the effects of altered gravity perception on humans.

10137-7, Session 2

Automated boundary segmentation and wound analysis for longitudinal corneal OCT images

Fei Wang, Fei Shi, Soochow Univ. (China); Weifang Zhu, Lingjiao Pan, Soochow University (China); Haoyu Chen, Joint Shantou International Eye Ctr. of Shantou Univ. and the Chinese Univ. of Hong Kong (China); Haifan Huang, Kangkeng Zheng, Joint Shantou International Eye Center of Shantou University and The Chinese University of Hong Kong (China); Xinjian Chen, Soochow Univ. (China)

The optical coherence tomography (OCT) has been widely applied in the examination and diagnosis of corneal diseases, but the information we can directly achieve from the OCT images is limited. We propose an automatic processing method to assist ophthalmologists in locating the boundary of longitudinal corneal OCT images and judge the recovery of corneal wounds after treatment. It includes the following steps: epithelium and endothelium boundary segmentation and correction, wound region classification using random forest, corneal boundary fitting and wound analysis. The method was tested on a data set with longitudinal corneal OCT images from 20 subjects; each subject has five images acquired after corneal operation over a period of time. The algorithm's segmentation and classification accuracy is high and can be used for analyzing recovery after corneal surgery.

10137-8, Session 2

Characterizing the lung tissue mechanical properties using a micromechanical model of alveolar sac

Elham Karami, Western Univ. (Canada) and Robarts Research Institute (Canada); Behzad Seify, Amirkabir Univ. of Technology (Iran, Islamic Republic of); Hadi Moghadas, Isfahan Univ. of Technology (Iran, Islamic Republic of); Masoomeh Sabsalinejad, National Institute of Genetic Engineering and Biotechnology (Iran, Islamic Republic of); Ting-Yim Lee, Robarts Research Institute (Canada) and Western Univ. (Canada); Abbas Samani, Western Univ. (Canada) and Robarts Research Institute (Canada)

According to statistics, lung disease is among the leading causes of death worldwide. As such, many research groups are developing powerful tools for understanding, diagnosis and treatment of different lung diseases. Recently, biomechanical modeling has emerged as an effective tool for better understanding of human physiology, disease diagnosis and computer assisted treatment. Mechanical properties of lung tissue are an important requirement for methods developed for lung disease diagnosis and treatment. As such, the main objective of this study is to develop an effective tool for estimating the mechanical properties of normal and pathological lung parenchyma tissue based on its microstructure. For such purpose, a micromechanical model of the lung tissue was developed using finite element method and demonstrated to have the capability of being used for creating regional maps of tissue stiffness. The proposed model was developed by assembling truncated octahedron tissue units resembling the alveoli. A compression test was simulated using finite element method on

the created geometry and the stiffness parameter was calculated for the alveoli wall using reported experimental data and an inverse optimization framework. Preliminary results indicate that the proposed model can be potentially used to reconstruct microstructural images of lung tissue using macro-scale tissue response for normal and different pathological conditions.

10137-9, Session 2

Registration pipeline for pulmonary free-breathing 1H MRI ventilation measurements

Fumin Guo, Dante P. I. Capaldi, Robert D. Cesare, Aaron Fenster, Grace Parraga, Robarts Research Institute (Canada)

Objective: Our aim was to develop a clinically-practical and physiologically-relevant approach for regional structure-function measurements of the lung using Fourier decomposition of free-breathing pulmonary magnetic resonance imaging (FDMRI).

Methods: Five non-small-cell lung cancer patients and five patients with chronic obstructive pulmonary disease provided written informed consent to study protocols approved by Health Canada and completed pulmonary function tests, 1H/hyperpolarized noble gas and free-breathing pulmonary magnetic resonance imaging (MRI) during a single 2-hour visit. Free-breathing 1H MRI was simultaneously segmented using a multi-region coupled continuous max-flow approach by exploring primal/dual analysis and convex optimization techniques. The segmented free-breathing 1H MRI lung was registered using a deformable registration approach that was developed using dual and convex optimization methods to compensate for respiratory/cardiac motion. Fourier decomposition of the co-registered lung was used to generate pulmonary functional information that was quantified as ventilation-defect-percent (VDP). The pipeline was implemented on a GPU for speed-up. Lung segmentation accuracy was measured by comparing algorithm and manual lung masks using Dice-similarity-coefficient (DSC). FD-VDP was compared to noble gas VDP using Pearson correlation coefficient and the reproducibility was measured using coefficient of variation (CoV) and intraclass correlation coefficient (ICC).

Results: The pipeline yielded a whole lung DSC of 94.0±2.6% and FD-VDP that correlated with noble gas VDP (r = 0.87, p = 0.001). CoV (ICC) were 0.8% (0.97) and 1.0% (0.95) for whole lung DSC and FD-VDP, respectively. The proposed approach requires ?30 min for parallel implementation with minimal user interaction.

Conclusion: The proposed approach provides a clinically-practical pipeline to generate regional pulmonary structure-function measurements using free-breathing pulmonary 1H MRI with promising potential for widespread clinical translation.

10137-10, Session 2

Development of a semi-automated combined PET and CT lung lesion segmentation framework

Farli Rossi, Siti Salasiah Mokri, Ashrani Aizzuddin Abd. Rahni, Univ. Kebangsaan Malaysia (Malaysia)

Segmentation is one of the most important steps in automated medical diagnosis applications, which affects the accuracy of the overall system. In this paper, we propose a semi-automated segmentation method for extracting lung lesions from thoracic PET/CT images by combining low level processing and active contour techniques. The lesions are first segmented in PET images which are first converted to standardised uptake values (SUVs). The segmented PET images then serve as an initial contour for subsequent active contour segmentation of corresponding CT images. To evaluate its accuracy, the Jaccard Index (JI) was used as a measure of the accuracy of the segmented lesion compared to alternative segmentations from the QIN lung CT segmentation challenge, which is possible by registering the whole body PET/CT images to the corresponding thoracic CT images. The results show that our proposed technique has acceptable accuracy in lung lesion segmentation with JI values of around 0.8, especially when considering the variability of the alternative segmentations.

10137-11, Session 2

Algorithmic evaluation of lower jawbone segmentations

Jan Egger, Technische Univ. Graz (Austria) and BioTechMed (Austria); Kerstin M. Hochegger, Markus Gall, Technische Univ. Graz (Austria); Xiaojun Chen, Shanghai Jiao Tong Univ. (China); Knut Reinbacher, Katja Schwenzer-Zimmerer, Medizinischen Univ. Graz (Austria); Dieter Schmalstieg, Technische Univ. Graz (Austria); Jürgen Wallner, Medizinischen Univ. Graz (Austria)

The lower jawbone (or mandible), is due to its exposure to complex biomechanical forces the largest and strongest facial bone in humans. In this publication, an algorithmic evaluation of lower jawbone segmentation with a cellular automata algorithm called GrowCut is presented. For an evaluation, the algorithmic segmentation results were compared with slice-by-slice segmentations from two specialized physicians, which is considered to assess the given ground truth. As a result, pure manual slice-by-slice outlining took on average 39 minutes (minimum 35 minutes and maximum 46 minutes). This stands in strong contrast to an algorithmic segmentation which needed only about one minute for an initialization, hence needing just a fraction of the manual contouring time. At the same time, the algorithmic segmentations could achieve an acceptable Dice Similarity Score (DSC) of nearly ninety percent when compared to the ground truth slice-by-slice segmentations generated by the physicians. This stands in direct comparison to somewhat above ninety percent Dice Score between the two manual segmentations of the jawbones. In summary, this contribution shows that an algorithmic GrowCut segmentation can be an alternative to the very time consuming manual slice-by-slice outlining in the clinical practice.

10137-12, Session 3

Advances in neuroimaging *(Keynote Presentation)*

Bruce Rosen, Massachusetts General Hospital (United States)

No Abstract Available

10137-13, Session 4

Atlas-based automatic measurements of the morphology of the tibiofemoral joint

Michael Brehler, Gaurav Thawait, William Shyr, Johns Hopkins Univ. (United States); John Ramsay, U.S. Army Natick Soldier Research, Development and Engineering Ctr. (United States); Jeffrey H. Siewerdsen, Wojciech Zbijewski, Johns Hopkins Univ. (United States)

Purpose: Anatomical metrics of the tibiofemoral joint support assessment of joint stability and surgical planning. We propose an automated, atlas-based algorithm to streamline the measurements in 3D images of the joint and reduce user-dependence of the metrics arising from manual identification of the anatomical landmarks.

Methods: The method is initialized with coarse registrations of a set of atlas images to the fixed input image. The initial registrations are then refined separately for the tibia and femur and the best matching atlas is selected. Finally, the anatomical landmarks of the best matching atlas are transformed onto the input image by deforming a surface model of the atlas to fit the shape of the tibial plateau in the input image (a mesh-to-volume registration). We apply the method to weight-bearing volumetric images of the knee obtained from 23 subjects using an extremity cone-beam CT system. Results of the automated algorithm were compared to an expert radiologist for measurements of Static Alignment (SA), Medial Tibial Slope (MTS) and Lateral Tibial Slope (LTS).

Results: Intra-reader variability as high as ~10% for LTS and 7% for MTS (ratio of standard deviation to the mean in repeated measurements) was found for expert radiologist, illustrating the potential benefits of an automated approach in improving the precision of the metrics. The proposed method achieved excellent registration of the atlas mesh to the input volumes. The resulting automated measurements yielded high correlations with expert radiologist, as indicated by correlation coefficients of 0.72 for MTS, 0.8 for LTS, and 0.89 for SA.

Conclusions: The automated method for measurement of anatomical metrics of the tibiofemoral joint achieves high correlation with expert radiologist without the need for time consuming and error prone manual selection of landmarks.

10137-14, Session 4

Real-time live-cell microscopy during dynamic multimodal mechanostimulation

Daniel Lorusso, Hristo N. Nikolov, Ryan Beach, Stephen M. Sims, Samuel J. Dixon, David W. Holdsworth, Western Univ. (Canada)

Mechanotransduction is the process by which cells sense local mechanical stimuli and respond via biochemical signaling pathways. Mechanotransduction is essential for a number of physiological processes including skeletal homeostasis. Cells are thought to be sensitive to different modes of mechanical stimuli, including vibration and fluid shear. Little is known concerning the molecular mechanisms underlying mechanotransduction. Here, we describe the development and validation of devices for high-frequency mechanostimulation (vibration and fluid shear) of live cells that can be integrated with real-time optical microscopy. A custom microfluidic chamber was prepared from polydimethylsiloxane on a glass-bottom cell culture dish. Fluid flow was applied with a syringe pump to induce shear stress. This device is compatible with a custom-designed motion control vibration system. A voice coil actuates the system's moving parts that are suspended on linear air bushings. The integrated system is capable of delivering 1–3 Pa of fluid shear and sinusoidal vibration with 0.1–1 g peak acceleration at 15–500 Hz. Stimuli can be applied simultaneously or independently to cells during real-time microscopic imaging. Fluid shear magnitude was calculated from flow velocities using computational fluid dynamics, and validated using particle-imaging velocimetry. Magnitude and frequency of acceleration were determined using an on-board accelerometer and validated optically. We have developed and validated a system to deliver physiologically relevant vibrations and fluid shear to live-cells during real-time imaging and photometry. Monitoring the behavior of live cells loaded with appropriate fluorescent probes will enable characterization of the initial transient signals activated by mechanical stimuli.

10137-15, Session 4

A FSI-Based Structural Approach for Micromechanical Characterization of Adipose Tissue

Behzad Seyfi, Amirkabir Univ. of Technology (Iran, Islamic Republic of); Masoumeh Sabzalinejad, National Institute of Genetic Engineering and Biotechnology (Iran, Islamic Republic of); Seyed Haddad, Western Univ. (Canada); Nasser Fatouraee, Amirkabir Univ. of Technology (Iran, Islamic Republic of); Abbas Samani, Western Univ. (Canada)

This paper presents a novel structural method which accounts for both solid and fluid components and mechanical interaction between them. In the model, the lipid droplets and extracellular matrix were considered as the fluid and solid phases, respectively. As such, the developed fluid-structure interaction (FSI) problem was solved using finite element method. The developed model can be regarded as the first step for developing an inversion based framework for that uses adipose stiffness data obtained from elastography to determine its microstructural alterations. Such information can be used as biomarkers for diseases associated with adipose tissue microstructure alteration.

10137-16, Session 4

Anatomical based registration of multi-sector x-ray images for long limb panorama generation

Yehuda K. Ben Zikri, Rochester Institute of Technology (United States); Stacy Mendez, Fairfield Univ. (United States); Cristian A. Linte, Rochester Institute of Technology (United States)

An accurate measurement of the long limb alignment is an essential stage of the pre-operative planning of realignment surgery. This alignment is quantified according to the hip-knee-ankle (HKA) angle of the mechanical axis of the lower extremity and is measured based on a full-length weight-bearing X-ray image of the patient in standing position. Due to the digital X-ray imaging system's limited field of view, several sector images are required to capture the posture of a standing individual. These sector images are then stitched together to reconstruct the standing posture. To eliminate the user variability and time constraints associated with the traditional manual stitching, we have created an image processing application that automates the stitching protocol which only relies on anatomical features. The application begins with detecting a mask along the medial bone edge. The sector images are then registered by maximizing the DICE overlap between the medial edge masks of the tibia. The identified registration transformations are used to register the original sector images into the panoramic image. To ensure robustness, our method utilizes only on the most reliable anatomical content of the image. To test the robustness of our method, we randomly selected 40 datasets from a variant database consisting of nearly 100 patient X-ray images constructed from screening patients as part of a multi-site clinical trial. The resulting horizontal and vertical translation values from the automated registration were compared to the homologous translations recorded during the manual panorama generation conducted by a knowledgeable X-ray imaging technician. The mean and the standard deviation of the differences for the horizontal translation parameters were 0.04mm plus minus 0.89mm and -0.06 plus minus 0.79mm right and left limbs, respectively, while the vertical translation differences were 1.87 plus minus 5.6mm and 1.84 plus minus 5.3mm, for the right and left limbs, respectively. It is worthwhile noting that the expert radiologist reported no difference in the hip-knee-ankle angular measurements for translation differences of up to plus minus 15mm between two stitched images. In this abstract we show robust edge detection and subsequent registration for the lower image sectors (i.e., upper foot and lower knee) that use the tibia as the anatomical image marker, with the upper sector registration involving the femur to be described in the final version of the paper.

10137-17, Session 5

Use of patient specific 3D printed neurovascular phantoms to evaluate the clinical utility of a high resolution x-ray imager.

Swetadri Vasan Setlur Nagesh, Megan K. Russ, Ciprian N. Ionita, Daniel R. Bednarek, Stephen Rudin, Toshiba Stroke and Vascular Research Ctr. (United States)

Modern 3D printing technology can print vascular phantoms based on an actual human patient with a high degree of precision facilitating a realistic simulation environment for an intervention. We present two experimental setups using 3D printed patient-specific neurovasculature to simulate different disease anatomies.

To simulate the human neurovasculature in the Circle of Willis, patient-based phantoms with aneurysms were 3D printed using a Objet Eden 260V printer. Anthropomorphic head phantoms and a human skull combined with acrylic plates simulated human head bone anatomy and x-ray attenuation. For dynamic studies the 3D printed phantom was connected to a pulsatile flow loop with the anthropomorphic phantom underneath. By combining different 3D printed phantoms and the anthropomorphic phantoms, different patient pathologies can be simulated. For static studies a 3D printed neurovascular phantom was embedded inside a human skull and used as a positional reference treatment devices such as stents. To simulate tissue attenuation acrylic layers were added. Different combinations can simulate different patient treatment procedures.

The Complementary-Metal-Oxide-Semiconductor-based Micro-Angiographic-Fluoroscope (MAF-CMOS) with 75μm pixels offers an advantage over the state-of-the-art 200 μm pixel Flat Panel Detector (FPD) due to higher Nyquist frequency and better DQE performance. Whether this advantage is clinically useful during an actual clinical neurovascular intervention can be addressed by qualitatively evaluating images from a cohort of various cases performed using both detectors. The above-mentioned method can offer a realistic substitute to an actual clinical procedure. Also a large cohort of cases can be generated and used for a MAF-CMOS clinical utility determination study.

10137-18, Session 5

Blood flow measurement using digital subtraction angiography for assessing hemodialysis access function

Nischal Koirala, Cleveland State Univ. (United States) and The Cleveland Clinic (United States); Randolph M. Setser, Siemens Healthineers (United States); Jennifer Bullen, Gordon McLennan, The Cleveland Clinic (United States)

Blood flow rate is the critical parameter for diagnosing dialysis access function during fistulography where a flow rate of 600ml/min (grafts) or 400-500ml/min (fistula) is considered the clinical threshold for fully functioning access. The aim of this study is to validate a flow rate computation model in an in vitro set up using digital subtraction angiographic (DSA) images, and apply the model to evaluate the accuracy of flow estimation in clinical cases. An in vitro flow model was constructed using ?” silicone tubing connected to a peristaltic pump, power injector and in-line transonic flow meter in an open circuit arrangement with water as the circulating fluid. DSA images were acquired at flow rates from 400-1000ml/min using frame rates of 3, 6, 7.5 and 10 frames/s while 10ml of iodinated contrast agent was power injected for 3s duration. Each acquisition was repeated three times. Flow rates were computed by tracking the bolus through two regions of interest (ROI) using a cross correlation (XCOR) based algorithm and correlated versus an in-line transonic flow meter measurement. Lastly, the XCOR algorithm was applied to compute the blood flow rate in fistulagrams and the accuracy of flow computation was correlated with available clinical flow data. The mean difference (mean+/-SD) between XCOR and inline flow measurements for in vitro setup were 118+/-63; 52+/-43; 32+/-30; and 58+/-42 ml/min at 3, 6, 7.5 and 10 F/s respectively. For clinical cases, the differences were between 79+/-37ml/min to 214+/-43ml/min for flow rates of 617+/-68ml/min at 3F/s and 2F/s respectively.

10137-19, Session 5

Cerebral vessels segmentation for light-sheet microscopy image using convolutional neural networks

Chaoen Hu, Hui Hui, Shuo Wang, Di Dong, Key Lab. of Molecular Imaging, Institute of Automation (China); Xia Liu, School of Automation, Harbin Univ. of Science and Technology (China); Xin Yang, Jie Tian, Key Lab. of Molecular Imaging, Institute of Automation (China)

Blood vessel segmentation is an important step in image analysis for tumor angiogenesis study etc. With the purpose of extracting line structures of blood vessels, some filter-based methods are used to segment vessels. However, the design of accurate and automatic vessel segmentation algorithms is still challenging, due to the variety and complexity of images, especially in brain blood vessel segmentation. In this work, we address a problem of automatic segmentation of brain micro-vessels structures in light-sheet image stacks. To segment micro-vessels in large-scale image data, we propose a method using convolutional neural networks (CNN) as a pixel binary classifier. Three convolutional layers and one fully connected layer are used in the CNN model. We extract a patch of size 32x32 pixels in each acquired brain vessel image stack as training data set to feed into CNN for classification. This network is trained to output the probability that the center pixel of input patch belong to vessel structures. To build the CNN architecture, a series of mouse brain vascular images acquired from a commercial light sheet fluorescence microscopy (LSFM) system were used for training the model. The preliminary experimental results demonstrated that our approach is a promising method for effectively extracted micro-vessels structures in brain images.

10137-20, Session 5

Real-time myocardium segmentation for the assessment of cardiac function variation

Fabian Zöhrer, Markus Huellebrand, Fraunhofer MEVIS (Germany); Teodora Chitiboi, NYU Langone Medical Center (United States); Thekla Oechtering, Malte Sieren, Klinik fuer Radiologie und Nuklearmedizin UKSH (Germany); Jens Frahm, Max-Planck-Institute for Biophysical Chemistry (Germany); Horst K. Hahn, Anja Hennemuth, Fraunhofer MEVIS (Germany)

Recent developments in MRI enable the acquisition of image sequences with high spatio-temporal resolution. Cardiac motion can be captured without gating and triggering.

Image size and contrast relations differ from conventional cardiac MRI cine sequences requiring new adapted analysis methods.

We suggest a novel segmentation approach utilizing contrast invariant spiral scanning techniques.

It has been tested with 20 datasets of arrhythmia patients.

The results do not differ significantly more between automatic and manual segmentations than between observers.

This indicates that the presented solution could enable clinical applications

of real-time MRI for the examination of arrhythmic cardiac motion in the future.

10137-21, Session 5

Extracellular matrix directions estimation of the heart on micro-focus x-ray CT volumes

Hirohisa Oda, Masahiro Oda, Nagoya Univ. (Japan); Takayuki Kitasaka, Aichi Institute of Technology (Japan); Toshiaki Akita, Kanazawa Medical Univ. (Japan); Kensaku Mori, Nagoya Univ. (Japan)

In this paper we propose an estimation method of extracellular matrix directions of the heart. Myofiber are surrounded by the myocardial cell sheets whose directions have strong correspondence between heart failure. Estimation of the myocardial cell sheet directions is difficult since they are very thin. Therefore, we estimate the extracellular matrices which are touching to the sheets as if piled up. First, we perform a segmentation of the extracellular matrices by using the Hessian analysis. Each extracellular matrix region has sheet-like shape. We estimate the direction of each extracellular matrix region by the principal component analysis (PCA). In our experiment using the left ventricle of a dog which had not contracted the heart failure, mean inclination angle was 31.9 degree with standard deviation 20.7 degree.

10137-22, Session 6

Identifying cognitive impairment in type 2 diabetes with functional connectivity: a multivariate pattern analysis of resting state fMRI data

Jie Tian, Zhenyu Liu, Institute of Automation (China); Xinwei Cui, Zhengzhou Univ. (China); Zhenchao Tang, Shandong Univ. at Weihai (China); Di Dong, Yali Zang, Institute of Automation (China)

Previous researches have shown that type 2 diabetes mellitus (T2DM) is associated with an increased risk of cognitive impairment. Early detection of brain abnormalities at the preclinical stage can be useful for developing preventive interventions to abate cognitive decline. We aimed to investigate the whole-brain resting-state functional connectivity (RSFC) patterns of T2DM patients between 90 regions of interest (ROIs) based on the RS-fMRI data, which can be used to test the feasibility of identifying T2DM patients with cognitive impairment from other T2DM patients. 74 patients were recruited in this study and multivariate pattern analysis was utilized to assess the prediction performance. Elastic net was firstly used to select the key features for prediction, and then a linear discrimination model was constructed. 23 RSFCs were selected and it achieved the performance with classification accuracy of 90.54% and areas under the receiver operating characteristic curve (AUC) of 0.944 using ten-fold cross-validation. The results provide strong evidence that functional interactions of brain regions undergo notable alterations between T2DM patients with cognitive impairment or not. By analyzing the RSFCs that were selected as key features, we found that most of them involved the frontal or temporal. We speculated that cognitive impairment in T2DM patients mainly impacted these two lobes. Overall, the present study indicated that RSFCs undergo notable alterations associated with the cognitive impairment in T2DM patients, and it is possible to predicted cognitive impairment early with RSFCs.

10137-23, Session 6

Brain structure in sagittal craniosynostosis

Beatriz Paniagua, Sun Hyung Kim, Mahmoud Mostapha, Martin A. Styner, Heather Hazlett, Rachel Smith, The Univ. of North Carolina at Chapel Hill (United States); Ashley Rumple, The Univ. of North Carolina at Chapel Hill School of Medicine (United States); Joseph Piven, John Gilmore, The Univ. of North Carolina at Chapel Hill (United States); Gary Skolnick, Kamlesh Patel, Washington Univ. in St. Louis (United States)

Craniosynostosis, the premature fusion of one or more cranial sutures, leads to grossly abnormal head shapes and pressure elevations within the brain caused by these deformities. To date, accepted treatments for craniosynostosis involve improving surgical skull shape aesthetics. However, the relationship between improved head shape and brain structure after surgery has not been yet established. Typically, clinical standard care involves the collection of diagnostic medical computed tomography (CT) imaging to evaluate the fused sutures and plan the surgical treatment. CT is known to provide very good reconstructions of the hard tissues in the skull but it fails to acquire good soft brain tissue contrast. This study intends to use magnetic resonance imaging to evaluate brain structure in a small dataset of sagittal craniosynostosis patients and thus quantify the effects of surgical intervention in overall brain structure. Very importantly, these effects are to be contrasted with normative shape, volume and brain structure databases. The work presented here wants to address gaps in clinical knowledge in craniosynostosis focusing on understanding the changes in brain volume and shape secondary to surgery, and compare those with normally developing children. This initial pilot study has the potential to add significantquality to the surgical care of a vulnerable patient population in whom we currently have limited understanding of brain developmental outcomes.

10137-24, Session 6

A multivariate pattern analysis study of the HIV-related white matter anatomical structural connections alterations

Jie Tian, Institute of Automation (China); Zhenchao Tang, Shandong Univ. at Weihai (China); Zhenyu Liu, Institute of Automation (China); Ruili Li, Beijing YouAn Hospital, Capital Medical Univ. (China); Xinwei Cui, Zhengzhou Univ. (China); Hongjun Li, Beijing YouAn Hospital, Capital Medical Univ. (China); Enqing Dong, Shandong Univ. at Weihai (China)

It’s widely known that HIV infection would cause white matter integrity impairments. Nevertheless, it is still unclear that how the white matter anatomical structural connections are affected by HIV infection. In the current study, we employed a multivariate pattern analysis to explore the HIV-related white matter connections alterations. Forty antiretroviral-therapy-naïve HIV patients and thirty healthy controls were enrolled. Firstly, an Automatic Anatomical Label (AAL) atlas based white matter structural network, a 90 ? 90 FA-weighted matrix, was constructed for each subject. Then, the white matter connections deprived from the structural network were entered into a lasso-logistic regression model to perform HIV-control group classification. Using leave one out cross validation, a classification accuracy (ACC) of 90% (P=0.002) and areas under the receiver operating characteristic curve (AUC) of 0.96 was obtained by the classification model. This result indicated that the white matter anatomical structural connections contributed greatly to HIV-control group classification, providing solid evidence that the white matter connections were affected by HIV infection. Specially, 11 white matter connections were selected in the classification model, mainly crossing the regions of frontal lobe, Cingulum, Hippocampus,

and Thalamus, which were reported to be damaged in previous HIV studies. This might suggest that the white matter connections adjacent to the HIV-related impaired regions were prone to be damaged.

10137-25, Session 6

Decreased triple network connectivity in patients with post-traumatic stress disorder

Yang Liu, Liang Li, Baojuan Li, Xi Zhang, Hongbing Lu, Fourth Military Medical Univ. (China)

To explore the functional connectivity of triple network model in recent onset post-traumatic stress disorder (PTSD) induced by a single prolonged trauma exposure, we recruited 20 survivors experiencing the same coal mining flood disaster as the PTSD (n=10) and non-PTSD (n=10) group, respectively. Using pulsed arterial spin labeling (ASL) sequence, group independent component analysis was utilized to study functional connectivity within the triple network, i.e., default mode network (DMN), salience network (SN), and central executive network (CEN), in PTSD patients as compared to non-PTSD survivors. Comparing PTSD patients with healthy survivors, decreased connectivity in triple network model was identified, i.e., left middle frontal gyrus in CEN, left precuneus and bilateral superior frontal gyrus in DMN, and right anterior insula in SN. Furthermore, the decrease of connectivity in left middle frontal gyrus of CEN was identified to associate with clinical severity (r=?0.682, p=0.043). These results are in line with the observations of our cortical thickness and cerebral blood flow studies. Our multi-modality approach increases the credibility and provide the solid output of PTSD. The findings of this study indicate the disrupted pattern of triple network in this kind of PTSD, especially interplay between CEN and DMN, which may also provide the putative biomarker and therapeutic targets for this kind of PTSD.

10137-26, Session 6

CIVILITY: cloud based interactive visualization of tractography brain connectome

Juan C. Prieto, Danaele Puechmaille, Martin A. Styner, The Univ. of North Carolina at Chapel Hill (United States)

Cloud based Interactive Visualization of Tractography Brain Connectome (CIVILITY) is an interactive visualization tool of brain connectome in the cloud. This application submits tasks to remote computing grids were the CIVILITY-tractography pipeline is deployed. The application will list the running tasks for the user and once a task is completed the brain connectome is visualized using Hierarchical Edge Bundling. The analysis pipeline uses FSL tools (bedpostx and probtrackx2) to generate a triangular matrix indicating the connectivity strength between different regions in the brain. This work is motivated by medical applications in which expensive computational tasks such as brain connectivity is needed and to provide a state of the art visualization tool of Brain Connectome.

This work does not contribute any novelty with respect to the visualization methodology, is rather a new resource for the neuroimaging community. This work is submitted to the SPIE Biomedical Applications in Molecular, Structural, and Functional Imaging conference. The source code of this application is available in NITRC.

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10137-27, Session 6

Ex vivo tissue imaging of human glioblastoma using a small bore 7T MRI and correlation with digital pathology and proteomics profiling by multiplex tissue immunoblotting.

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Recent advancement in MRI established multiparametric imaging for in vivo characterization of pathologic changes in brain cancer, which is expected to play a role in imaging biomarker development. Diffusion Tensor Imaging (DTI) is a prime example, which has been deployed for assessment of therapeutic response via analysis of apparent diffusion coefficient (ADC) / mean diffusivity (MD) values. They have been speculated to reflect apoptosis/necrosis. As newer medical imaging emerges, it is essential to verify that apparent abnormal features in imaging correlate with histopathology. Furthermore, the feasibility of imaging correlation with molecular profile should be explored in order to enhance the potential of biomedical imaging as a reliable biomarker. We focus on glioblastoma, which is an aggressive brain cancer. Despite the increased number of studies involving DTI in glioblastoma; however, little has been explored to bridge the gap between the molecular biomarkers and DTI data. Due to spatial heterogeneity in, MRI signals, pathologic change and protein expression, precise correlation is required between DTI, pathology and proteomics data in a histoanatomically identical manner. The challenge is obtaining an identical plane from in vivo imaging data that exactly matches with histopathology section. Thus, we propose to incorporate ex vivo tissue imaging to bridge between in vivo imaging data and histopathology. With ex vivo scan of removed tissue, it is feasible to use high-field 7T MRI scanner, which can achieve microscopic resolution. Once histology section showing the identical plane, it is feasible to correlate protein expression by a unique technology, "multiplex tissue immunoblotting".

10137-28, Session 7

A fast image registration approach of neural activities in light-sheet fluorescence microscopy images

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The ability of fast and single-neuron resolution imaging of neural activities enables light-sheet fluorescence microscopy (LSFM) as a powerful imaging technique in functional neural connection applications. The state-of-art LSFM imaging system can record the neuronal activities of entire brain for small animal, such as zebrafish or C. elegans at single-neuron resolution. However, the stimulated and spontaneous movements in animal brain result in inconsistent neuron positions during recording process. In this work, we address the problem of real-time registration of neural positions in stacks of LSFM images. This is necessary to register brain structures and activities. To achieve real-time registration of neural activities, we present a fast rigid registration architecture by implementation of Graphics Processing Unit (GPU). In this approach, the image stack was preprocessed on GPU by mean stretching to reduce the computation effort. The present image was registered to the previous stack that considered as reference. A fast Fourier transform (FFT) algorithm was used for calculating the shift of the image stack. The calculations for image registration were performed in different

threads while the preparation functionality was refactored and called only once by the master thread. We implemented our registration algorithm on NVIDIA Quadro K4200 GPU under Compute Unified Device Architecture (CUDA) programming environment. The experimental results showed that the registration computation can speed-up to 550ms for a full high-resolution brain image. The registration can be accelerated using more GPUs in the architecture. Our approach also has potential to be used for other dynamic image registrations in biomedical applications.

10137-29, Session 7

Phenotypic feature quantification of patient derived 3D cancer spheroids in fluorescence microscopy image

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We present a cell image quantification method for predicting image-based drug responses in patient-derived glioblastoma cells. The drug response of each person differs at the cellular level. Therefore, quantification of a patient-derived cellular phenotype is important for drug response prediction. We performed fluorescence microscopy to understand the features of patient-derived 3D cancer spheroids. A 3D cell culture simulates the in vivo environment more closely than 2D adherent cultures and thus, allows more accurate cell analysis. Furthermore, it allows the assessment of cellular aggregates. Cohesion is an important feature of cancer cells. In this paper, we demonstrate image-based quantification of cellular area, fluorescence intensity, and cohesion. To this end, we first performed image stitching to create an image of each well of the plate with the same environment. This image shows colonies of various sizes and shapes. To automatically detect these colonies, we used a learning based classification algorithm. The nuclear intensity and morphological characteristics were used for the segmentation of individual nuclei; the fluorescence intensity and morphological features of each nucleus were measured. We then calculated the location correlation of each cell that is appeal of the cell density in the well environment. Finally, we compared the results obtained from drug-treated and untreated cells. This technique could potentially be applied for drug screening and quantification of drug effects.

10137-30, Session 7

Disease quantification on PET/CT images without object delineation

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The derivation of quantitative information from images to make Quantitative Radiology clinically practical continues to face a major image analysis hurdle because of image segmentation challenges. This paper presents a novel approach to disease quantification (DQ) via PET/CT images that explores how to decouple DQ methods from explicit dependence on object segmentation through the use of only object recognition results to quantify disease burden. The concept of an object-dependent disease map is introduced to express disease severity without performing explicit delineation of either the object or the lesions and partial volume correction. The parameters of the disease map are estimated from a set of training image data sets. The idea is illustrated on 20 lung lesions and 20 liver lesions derived from FDG-PET/CT scans of patients with various types of cancers and also on 20 NEMA PET/CT phantom data sets. Our preliminary results show that on phantom data “disease burden” can be estimated to within 2% of known absolute true activity. Notwithstanding the difficulty in establishing true quantification on patient PET images, our results achieve 8% deviation from “true” estimates, with slightly larger deviations for small and diffuse lesions where establishing ground truth becomes really questionable, and smaller deviations for larger lesions where ground truth set up becomes more reliable. We are currently exploring extensions of the approach to include fully automated body-wide DQ, extensions to just CT or MRI alone, to tracers other than FDG, and other functional forms of the disease maps.

10137-31, Session 7

An automatic cells detection and segmentation

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This paper presents an end-to-end framework for automatic detecting and segmenting the blood cells from peripheral blood smear images, which contains four phases:

-Blood cell color representation:

We first design a novel color representation to emphasize different components in images (red blood cell, RBC, and white blood cell, WBC). The color subspace is learned by Fisher linear discriminant analysis (LDA) with labels automatically estimated by the Gaussian mixture model (GMM) classifier.

-Template matching for detection:

Then the minimum average correlation energy (MACE) filter is introduced for cell detection in the proposed colorspace. The correlation is performed in prequency domain with high efficiency, upon which Mean-Shift algorithm is used to locate detected cell centroids. Note that our system is able to detect connected RBCs. A template matching and mask transfer stragety can be then used to separate connected RBCs.

-Adaptive level-set segmentation:

A modified Chan-Vese level-set method is developed for cell segmentation. The energy function has four terms: (1) a local fitting term, (2) a global fitting term, (3) a contour term, and (4) a regularization term.

-Shape matching:

Shape matching by shape context and inner distance is then used to classify the abnormal RBCs from the normal RBCs.

-Experiments:

Our proposed method has been tested and evaluated on different datasets including ALL-IDB, WebPath etc. The precision and recall of RBC detection are 98.43% and 94.99% respectively, and those of WBC detection are 99.12% and 99.12%. The F-measure of WBC segmentation gets up to 95.8%.

10137-32, Session 7

Partial volume morphology: eliminating precision loss in binary morphology

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Binary morphology has innumerable applications in biomedical imaging, from segmentation to denoising. However, it suffers from inherently low precision. This is most notably due to the limitation of image voxel resolution and imperfect shape approximations. Common workflows involving multiple binary morphology iterations, such as opening, closing, bottom-hat or top-hat, compound this error. Also, small structuring elements often cannot be applied to 3D anisotropic image volumes. This work describes an extension to the theory of binary morphology, dubbed

partial volume morphology, which allows the structuring element and/or image to hold fractional gray values accounting for partial volumes. Partial volume morphology enables arbitrary shaped structuring elements to be applied regardless of the underlying image resolution. This technique also extends to 3D anisotropic volumes, allowing high precision morphological operations in anisotropic datasets heretofore impossible with binary morphology. This technique can be applied to a binary segmentation, where its primary utility is to eliminate precision error in the intermediate steps of a multiple-operation workflow, but is is particularly suited for use on, e.g., level set segmentations, where the partial volume contribution at each edge voxel can be found, or `soft' segmentations which return the probability of each object. With both segmentation and structuring elements partial volume aware, partial volume morphology reaches its full potential as a high precision analytical tool. We present an open source reference implementation in Python/Cython, and discuss a number of potential applications for partial volume morphology.

10137-33, Session 7

Multi-frame Super Resolution Robust to Local and Global Motion

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Super resolution (SR) is to produce a higher resolution image from one or a sequence of low resolution images of a scene. It is essential in medical image analysis as a zooming of a specific area of interest is often required. This paper presents a new multi-frame super resolution (SR) method that is robust to both global and local motion. One of major challenges in multi-frame SR is concurrent global and local motion emergent in the sequence of low resolution images. It poses difficulties in aligning the low resolution images, resulting in artifacts or blurred pixels in the computed high resolution image. We solve the problem via a series of new methods. We first align the upscaled images from bicubic interpolation, and analyze the pixel distribution for the presence of local motion. If local motion is identified, we conduct the local image registration using dense SIFT features. Based on the local registration of images, we analyze pixel locations whose cross-frame variation is high and adaptively select subset of frame pixels in those locations. The adaptive selection of frame pixels is based on a clustering analysis of luminance values of pixels aligned at the same position, such that noise and motion biases are excluded. At the end, a median filter is applied for the selected pixels at each pixel location for super resolution image. We conduct experiments for multi-frame SR, where the proposed method deliver favorable results, especially better than state-of-the-art in dealing with concurrent local and global motions across frames.

10137-34, Session 7

An intelligent despeckling method for swept source optical coherence tomography images of skin

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Optical Coherence Optical coherence tomography is a powerful high-resolution imaging method with a broad biomedical applications. Nonetheless, OCT images suffer from a multiplicative artefacts so-called speckle, a result of coherent imaging of system. Digital filters become ubiquitous means for speckle reduction. Addressing the fact that there still a room for despeckling in OCT, we proposed an intelligent speckle reduction algorithm (INSR) based on OCT tissue morphological, textural and optical features that through a trained network selects the winner filter in which adaptively suppresses the speckle noise while preserves structural information of OCT signal. These parameters are calculated for different steps of the procedure to be used in designed Artificial Neural Network decider that select the best denoising technique for each segment of the image. Three different categories of despeckling filters including sliding window filters (Median, Mean and Symmetric Nearest Neighborhood (SNN)), adaptive statistical based ones consist of Wiener, enhanced LEE and Kuwahara and more highly edge preserving ones comprising of Non Local Mean, Total Variance and BM3D are used in methodology. A figure of merit comprise of a weighted combination of the quality assessment metrics (signal-to-noise ratio (SNR), contrast-to-noise ratio (CNR), equivalent number of looks (ENL), edge preservation index (EPI) and Mean structural similarity index (MSSI)) is employed in our devised Feed Forward Multilayer perceptron neural network. Results of training shows the dominant filter is BM3D from the last category.

10137-55, Session PS1

Spatially varying regularization based on retrieved support in diffuse optical tomography

Sohail Sabir, Sanghoon Cho, Seunryong Cho, KAIST (Korea, Republic of)

Diffuse optical tomography (DOT) is a promising noninvasive imaging modality capable of providing the functional characteristics (oxygen saturation and hemodynamic states) of thick biological tissue by quantifying the optical parameters. The parameter recovery problem in DOT is a nonlinear, ill-posed and ill conditioned inverse problem. The non-linear iterative methods are usually employed for image reconstruction in DOT by utilizing Tikhonov based regularization approach. These methods employ l2-norm based regularization where the constant regularization parameter is determined either empirically or through generalized cross validation methods or L curve method. The reconstructed images look smoother or noisy depending on the chosen value of the regularization constant. Moreover the edges information of the inclusions appeared to be blurred in such constant regularization methods. In this study we proposed a method to retrieve and utilized a non-zero support (possible tumor location) to generate a spatially varying regularization map. The inclusions locations were determined by considering the imaging problem as a multiple measurements vector (MMV) problem. Based on the recovered inclusion positions spatially regularization map was generated to be used in non-linear image reconstruction framework. The results retrieved with such spatially varying priors shows slightly improved image reconstruction in terms of better contrast recovery, reduction in background noise and preservation of edge information of inclusions compared with the constant regularization approach.

10137-56, Session PS1

Low-intensity calibration source for optical imaging systems

David W. Holdsworth, Robarts Research Institute (Canada)

Laboratory optical imaging systems for fluorescence and bioluminescence imaging have become widely available for research applications. These systems use an ultra sensitive CCD camera to produce quantitative measurements of very low light intensity, detecting signals from small-animal models labeled with optical fluorophores or luminescent emitters. Commercially available systems typically provide quantitative measurements of light output, in units of radiance (photons s-1 cm-2 SR-1) or intensity (photons s-1 cm-2). One limitation to current systems is that there is often no provision for routine quality assurance and performance

evaluation. We describe such a quality assurance system, based on an LED-illuminated thin-film transistor (TFT) display module. The light intensity is controlled by pulse-width modulation of the backlight, producing radiance values ranging from 1.8 x 106 photons s-1 cm-2 SR-1 to 4.2 x 1013 photons s-1 cm-2 SR-1. The lowest light intensity values are produced by very short backlight pulses (i.e. approximately 10 µs), repeated every 300 s. This very low duty cycle is appropriate for laboratory optical imaging systems, which typically operate with long-duration exposures (up to 5 minutes). The low-intensity light source provides a stable, traceable radiance standard that can be used for routine quality assurance of laboratory optical imaging systems.

10137-57, Session PS1

Improving graph-based OCT segmentation for severe pathology in retinitis pigmentosa patients

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3D segmentation of macular optical coherence tomography (OCT) data of subjects with retinitis pigmentosa (RP) is a challenging problem due to the disappearance of the photoreceptor layers. Which causes algorithms developed for segmentation of healthy data to perform poorly on RP patients. In this work, we present enhancements to a previously developed graph-based OCT segmentation pipeline to enable processing of RP data. The algorithm segments eight retinal layers in RP data by relaxing constraints on the thickness and smoothness of each layer learned from healthy data. Following from the prior work, a random forest classifier is first trained on the RP data to estimate boundary probabilities. Which are used by a graph search algorithm to find the optimal set of nine surfaces which fit the data. Due to the intensity disparity between healthy controls and RP patients, an additional intensity normalization step is introduced. Leave-one-out validation on data acquired from nine subjects showed an average overall boundary error of 4.22 microns as compared to 6.02 microns using the original algorithm.

10137-58, Session PS1

Anatomic optical coherence tomography for dynamic imaging of the upper airway

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Upper airway obstructive disorders (UAOD), characterized by the dynamic collapse of the airway, are associated with diseases like obstructive sleep apnea (OSA), subglottic stenosis (SGS) and Pierre Robin Sequence (PRS). To aid in diagnosis and treatment of UAOD, quantitative imaging to capture dynamic deformation of the upper airway during respiration is in urgent need.

Here we report an optical imaging technique, anatomic Optical Coherence Tomography (aOCT), to capture quantitative airway geometry during respiration. The system is equipped with a wavelength-swept laser source centered at 1310 nm. A fiber-based catheter, which rotates at 20Hz, providing 20 frames/s of the airway luminal cross-section, is used as a minimally invasive probe. The radial resolution of the system is 25.6 µm, and the circumferential and longitudinal resolutions range between 100-400 µm depending on the radius. The signal-to-noise ratio of the system is 98dB at a radial distance of 2mm.

To test the ability of the aOCT system for dynamic imaging, upper airway endoscopy was performed on swine in vivo. A ventilator was employed to provide dynamic pressure with different maximum inspiratory pressures (MIP). CT scans were also collected under the same conditions to view the position of the aOCT catheter in the airway. aOCT results revealed that, relative to 0 pressure, the cross-sectional area expanded by 8% when MIP was 18cmH2O, and by 36% when MIP was 35cmH2O. These results highlight the capability for aOCT to capture dynamic upper airway deformation, which can aid in detecting regions of highly compliant tissue where collapse is most likely to occur.

10137-59, Session PS1

Simulation of photoacoustic tomography (PAT) system in COMSOL(R) and comparison of two popular reconstruction techniques

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Photoacoustic imaging is a molecular cum functional imaging modality based on differential optical absorption of the incident laser pulse by the endogeneous tissue chromophores. Several numerical simulations and finite element models have been developed in the past to describe and study Photoacoustic (PA) signal generation principles and study the effect of variation in PA parameters. Most of these simulation work concentrate on analyzing extracted 1D PA signals and each of them mostly describe only few of the building blocks of a Photoacoustic Tomography (PAT) imaging system. Further, different simulation platforms have been used for the different blocks. Papers describing simulation of the entire PAT system in one simulation platform, along with reconstruction is seemingly rare. This study attempts to describe how a commercially available Finite Element software (COMSOL(R)), can serve as a single platform for simulating PAT that couples the electromagnetic, thermodynamic and acoustic pressure physics involved in PA phenomena. Further, an array of detector elements placed at the boundary in the FE model can provide acoustic pressure data that can be exported to Matlab® to perform tomographic image reconstruction. As an example, we describe the simulation of PA imaging of a breast tumor. In addition, the performance of two most commonly used image reconstruction techniques, namely, Filtered Backprojection(FBP) and Synthetic Aperture(SA) beamforming are analyzed and compared. Preliminary results obtained show that reconstruction using FBP has artifacts along the spherical shells on which the signal is backprojected, while this artifact was absent in the SA technique. A systematic parametric analysis is currently under-way.

10137-60, Session PS2

Automatic segmentation of vessels in in-vivo ultrasound scans

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Ultrasound scans of the carotid artery are becoming increasingly popular for screening of atherosclerosis. The screening involves measuring the thickness of the vessel wall and diameter of the lumen. In this paper we present a fully automatic segmentation algorithm, for robustly segmenting the vessel lumen in longitudinal B-mode ultrasound images. The automatic segmentation is computed using both B-mode and power Doppler images. The proposed algorithm combines a series of preprocessing steps, to produce a vessel segmentation by use of the marker-controlled watershed transform. The ultrasound images used in this study were acquired using the “bk5000” ultrasound scanner with two transducers “8L2 Linear” and “10L2w Wide Linear” from BK Ultrasound. The algorithm was evaluated empirically by applying it to an in-vivo dataset of 1770 images recorded from 8 subjects. The resulting segmentation was compared to a manual

delineation performed by two experienced users. The results showed a sensitivity and specificity of 90.41 ± 11.2 % and 97.93 ± 5.7 % (mean ± standard deviation), respectively. The amount of overlap of segmentation and manual segmentation, was measured by the Dice similarity coefficient, which was 91.25 ± 11.6 %. The empirical results demonstrate the feasibility of segmenting the vessel lumen in ultrasound scans by use of a fully automatic algorithm. This paper serves as an original contribution to real-time image guidance in procedure-driven ultrasound.

10137-61, Session PS2

Computerized method to compensate a breathing body motion in dynamic chest radiographs

Hirokai Matsuda, Rie Tanaka, Shigeru Sanada, Kanazawa Univ. (Japan)

Purpose: Dynamic chest radiography combined with computer analysis allows us quantitative analyses on pulmonary function and rib motion. The accuracy of kinematic analysis is directly linked to diagnostic accuracy, and thus body motion compensation is a major concern. Our purpose in this study was to develop a computerized method to reduce a breathing body motion in dynamic chest radiographs.

Methods and Materials: Dynamic chest radiographs of 30 patients were obtained using a dynamic flat-panel detector. The images were divided into a 1 cm-square and the squares on body counter were used to detect the body motion. Velocity vector was measured using cross-correlation method on the body counter and the body motion was then determined on the basis of the summation of motion vector. The body motion was then compensated by shifting or rotating the images based on the measured vector.

Results: By using our method, the body motion was accurately detected by the order of a few pixels in clinical cases, 73% and 78% in right and left directions, respectively. In addition, our method detected slight body motion which was not able to be identified by human observations. We confirmed our method effectively worked in kinetic analysis of rib motion (Fig. 2).

Conclusion: The body motion was detected based on vector analysis around the body counter. The detected motion was compensated based on the measured vector by shifting and rotating images. The present method would be useful for the reduction of a breathing body motion in dynamic chest radiography.

i) Description of purpose

Background: Dynamic chest radiography is a flat-panel detector (FPD)-based functional X-ray imaging, which is performed as an additional examination in chest radiography. The large field of view (FOV) of FPDs permits real-time observation of the entire lungs and simultaneous right-and-left evaluation of diaphragm kinetics. Most importantly, pulmonary function and rib motion can be assessed by measuring the pixel value and/or velocity vector in the local lung area. However, breathing body motion occasionally degrades functional analyses, and therefore, body motion compensation is a major concern. Global matching technique for preprocessing image warping has been developed for temporal subtraction between a current and prior image. However, an image registration method for a sequential and slight shift of the order of a few pixels is required for dynamic chest radiography.

Long-term goal: Development of a functional chest radiography based on vector analysis in the lungs, which enables to provide quantitative information related to pulmonary function.

Our purpose in this study was to develop a computerized method to detect and compensate for breathing body motion in dynamic chest radiographs.

ii) Methods

Image Acquisition: Dynamic chest radiographs of 30 patients (21-61 years old; mean, 36.8 years old; M:F=9:8) were obtained using a dynamic flat-panel detector (FPD) system with exposure conditions of 120 kV, 80 mA, 6.3 ms, SID of 2.0 m, and 3.0 fps in 10 s. Imaging was performed during respiration, in the standing position and posteroanterior (PA) direction. The total exposure dose was almost the same as that in conventional chest radiography in two projections (PA + LA).

Classification of breathing body motion:

Dynamic chest radiographs were observed on an LCD monitor and body motions were classified into 4 categories, such as right, left, up, and down directions (Table 1). The body motions in the left-right directions were often identified, whereas, those in the up and down directions were rarely found and most of them were limited to the shoulder part due to costal breathing. The primary body motions during a dynamic chest radiography were the body motions in the left-right directions and the physiological motions of the shoulder in the up and down directions that did not influence the analysis.

Image analysis: The images were divided into 1-cm squares, and the squares on the body counter were determined by edge detection using the first derivative technique. Velocity vector was measured using the cross-correlation method on the body counter and the body motion was then determined based on the summation of the motion vectors (Fig. 1). This method distinguished the accidental body motion from normal respiratory motion as below; The movement, where the shoulder goes and the abdomen shrinks, and the shoulder goes up and the abdomen widens, was normal movement during respiration, otherwise accidental body motion. The body motion was then compensated by shifting or rotating the images based on the measured vector.

iii) Results

By using our method, the body motion was accurately detected by the order of a few pixels in clinical cases, 73% and 78% accuracy in the right and left directions, respectively. (Table 1). Our method detected a slight body motion, which was not identified by human observations (5% of detected body motion). Such a slight body motion is critical for quantitative analysis of pulmonary function. We confirmed that our method effectively worked in the kinetic analysis of rib motion (Fig. 2).

iv) New or breaking work to be presented

Dynamic chest radiography is an emerging technique. The imaging is performed in an almost similar manner to that of conventional chest radiography, except during respiration. Our study was the first one to detect a breathing patient motion, compensate it based on the measured vector, and demonstrate its clinical usefulness in dynamic chest radiographs.

v) Conclusions

The body motion was detected based on the vector analysis around the body counter. The detected motion was compensated based on the measured vector by shifting and rotating the images. The present method would be useful for the reduction of a breathing body motion in dynamic chest radiographs. A further study is required to detect other types of body motion in all dimensions, such as rotation, anterior/posterior inclinations, etc.

vi) This work has not been published in any journal.

10137-62, Session PS2

Time-series analysis of the lung texture on bone-suppressed dynamic chest radiography for the evaluation of pulmonary function: a preliminary study

Rie Tanaka, Akihiro Matsuda, Shigeru Sanada, Kanazawa Univ. (Japan)

Purpose: Pulmonary ventilation on fluoroscopic images is represented as changes in radiograph translucency. Therefore, a time-series analysis of the lung texture can be used to evaluate relative pulmonary function. This study was performed to investigate a time-series analysis of the lung texture on dynamic chest radiographs during respiration, to demonstrate its usefulness in the diagnosis of pulmonary impairments.

Methods and Materials: Dynamic chest radiographs during respiration, consisting of 30 images collected over 10 seconds, were obtained using a dynamic FPD system. Thirteen patients with pulmonary diseases were included. Thirty-seven regions had ventilatory defects according to lung scintigraphy. The rib shadows were reduced by the bone suppression technique. Average pixel value, standard deviation (SD), kurtosis, and skewness were calculated based on density histogram analysis in manually determined regions of interest (ROIs) in the lungs by tracking the same ROIs during respiration.

Results: Respiratory-induced changes in pixel value effectively differentiated between ventilatory defects and normal lung tissues. The average pixel values in normal areas changed dynamically in synchronization with the respiratory phase, whereas those in ventilatory defect regions indicated reduced variations in pixel value. There were no significant differences between ventilatory defects and normal lung tissues in the other parameters.

Conclusion: Time-series analysis of the lung texture was useful for the evaluation of pulmonary function in dynamic chest radiography during respiration. Pulmonary impairments were detected as reduced changes in pixel value. This technique is a simple, cost-effective diagnostic tool for the evaluation of regional pulmonary function.

10137-63, Session PS2

Extraction of membrane structure in eyeball from MR volumes

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This paper presents an accurate extraction method of spherical shaped membrane structures in the eyeball from MR volumes. In ophthalmic surgery, operation field is limited to a small region. Patient specific surgical simulation is useful to reduce complications. Understanding of tissue structure in the eyeball of a patient is required to achieve patient specific surgical simulations. We propose an extraction method of spherical shaped membrane structures including the sclerotic coat, choroid, and retina. This method is applied to a T2 weighted MR volume of the head region. We roughly extract membrane structures by applying a sheet structure enhancement filter. Then, we apply the Hough transform to extract a sphere structure from the voxels set of the rough extraction result. An experimental result using a T2 weighted MR volume of the head region showed that the proposed method can segment spherical shaped membrane structures accurately.

10137-64, Session PS3

Robust segmentation of trabecular bone for in vivo CT imaging using anisotropic diffusion and multi-scale morphological reconstruction

Cheng Chen, Dakai Jin, Xiaoliu Zhang, Steven Levy, Punam K. Saha, The Univ. of Iowa (United States)

Osteoporosis is associated with an increased risk of fractures. Although, bone mineral density is used for clinical diagnosis of osteoporosis, there is evidence showing that trabecular bone (TB) microarchitecture is a key determinant of bone strength and fracture risk. TB segmentation is essential for quantitative assessment of TB microstructure. Here, we present a new method of TB segmentation for in vivo CT imaging. The method uses Hessian matrix-guided anisotropic diffusion to improve local separability of trabecular structures, followed by a new multi-scale morphological reconstruction algorithm for TB segmentation. The multi-scale morphological operation is designed to build a space-varying strategy to select bright peaks as trabecular structures that survive over a large scale range of morphological reconstruction. Ten human ankle CT scans were used to examine the accuracy, sensitivity, and specificity of the new method. TB segmentation using regional manual thresholding by expert users were used as ground truth. High accuracy (0.92), sensitivity (0.93), and specificity (0.93) were observed for the new method. Based on a cadaveric ankle specimen study (N = 13) using mechanical testing of specimen cores, it was observed that the new TB segmentation method improves TB microarchitectural measures' predictability of actual bone strength (R = 0.91).

10137-65, Session PS3

Direct biomechanical modeling of trabecular bone using a nonlinear manifold-based volumetric representation

Dakai Jin, Jia Lu, Erwei Bai, Xiaoliu Zhang, Punam K. Saha, The Univ. of Iowa (United States)

Osteoporosis is associated with increased fracture risk. Recent advancement in the area of in vivo imaging allows segmentation of trabecular bone (TB) microstructures, which is a known key determinant of bone strength and fracture risk. An accurate biomechanical modelling of TB microstructure provides a comprehensive summary measure of bone microartchitectural quality. In this paper, a new direct TB biomechanical modelling method is presented using nonlinear manifold-based volumetric reconstruction of trabecular network. It is accomplished in two sequential modules. The first module reconstructs a nonlinear manifold-based volumetric representation of TB networks from three-dimensional digital images. Specifically, it starts with the fuzzy digital segmentation of a TB network, and computes its surface and curve skeletons. An individual trabecula is identified as a topological segment in the curve skeleton. Using geometric analysis, smoothing and optimization techniques, it generates smooth, curved, and continuous representation of individual trabeculae glued at their junctions. Also, the method generates a geometrically consistent TB volume at junctions. Finally, in the second module, a direct computational biomechanical stress-strain analysis is applied on the reconstructed TB volume for global and regional measures under different loading conditions. Repeat scan reproducibility of computed biomechanical measures will be performed on multirow detector CT imaging of distal tibia specimens (N = 12) under in vivo conditions, and the results will be presented. Also, the results assessing the ability of the computed TB strength to predict the actual TB strength, determined experimentally, will be presented based on a cadaveric ankle study (N = 12).

10137-66, Session PS4

Subject-specific Left Ventricular Dysfunction Modeling using Composite Material Mechanics Approach

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Diverse cardiac conditions such as myocardial infarction and hypertension can lead to diastolic dysfunction as a prevalent cardiac condition. Diastolic dysfunction can be diagnosed through different adverse mechanisms such as abnormal left ventricle (LV) relaxation, filling, and diastolic stiffness. This paper is geared towards evaluating diastolic stiffness and measuring the LV blood pressure non-invasively. Diastolic stiffness is an important parameter which can be exploited for more accurate diagnosis of diastolic dysfunction. For this purpose, the finite element (FE) LV mechanical model, which works based on a novel composite material model of the cardiac tissue, was utilized. Here, this model was tested for inversion-based applications where it was applied for estimating the cardiac tissue passive stiffness mechanical properties as well as diastolic LV blood pressure. To this end, the model was applied to simulate diastolic inflation of the human LV. The start-diastolic LV geometry was obtained from MR image data segmentation of a healthy human volunteer. The obtained LV geometry was discretized into a FE mesh before FE simulation was conducted. The LV tissue stiffness and diastolic LV blood pressure were adjusted through optimization to achieve the best match between the calculated LV geometry and the one obtained from

imaging data. The performance of the LV mechanical simulations using the optimal values of tissue stiffness and blood pressure was validated by comparing the geometrical parameters of the dilated LV model as well as the stress and strain distributions through the LV model with available measurements reported on the LV dilation.

10137-67, Session PS4

Nonrigid 2D registration of fluoroscopic coronary artery image sequence with propagated deformation field

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We propose a novel method for nonrigid registration of whole coronary artery sequence models with periodic deformation field. 2D nonrigid registration method is proposed that periodic deformed information is applied into correspondence with whole fluoroscopic angiograms. The proposed methodology is divided into four parts: layered structures alignments, one phase's nonrigid registration, spreading periodic displacement information into other phases and, whole nonrigid registration. In the first part, a layered rigid transformation aligns layered motion information. In the second part, a nonrigid registration method of one phase is implemented and used to compensate for any local shape discrepancy. In the third part, periodic deformation field is spreading into images on other phases in order to roughly align the whole sequence. In the fourth part, whole nonrigid registration is conducted as the final registration. Experimental evaluation conducted on a set of 7 fluoroscopic angiograms with layered motions results in a reduced target registration error, which showed the effectiveness of the proposed methodology.

10137-68, Session PS4

Current source enhancements in Electrical Impedance Spectroscopy (EIS) to cancel unwanted capacitive effects

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Electrical Impedance Spectroscopy (EIS) has emerged as a new non-invasive testing modality to detect and quantify functional or molecular signals related to the suspicious tumours in cancer screening, diagnosis and prognosis assessment. However, both the output impedance and system performance depend on the total output resistance, capacitance at the electrode level, and crosstalk at the chip and PCB levels. There is high complexity in the design of stable current sources, with stray capacitance reducing the output impedance and bandwidth of the data acquisition system. To confront this, we have designed an EIS current source which eliminates the effect of stray capacitance and other impacts of the capacitance via a variable inductance. In this paper, we presented a combination of operational CCII based on a generalized impedance converter (OCCII-GIC) with a current source. The performance of two different structures of the current source i.e. voltage-based and current-based structure, which are commonly employed in EIS systems while combined with the OCCII-GIC, were compared. The aim of this study is to use the EIS system as a biomedical imaging technique, which is effective in the early detection of breast cancer. This research begins with the theoretical description of current source topologies and proposes a current conveyor in application of Gyrator to eliminate the current source limitations and its development followed by simulation and experimental results. We demonstrated that the new design could achieve a high output impedance over a 3MHz frequency range when compared to other types of GIC circuits with improved Howland topology.

10137-51, Session PS5

1H magnetic resonance spectroscopy metabolite profiles of neonatal rat hippocampus and brainstem regions following early postnatal exposure to intermittent hypoxia

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Most premature infants born at less than 30 weeks gestation are exposed to periods of mild intermittent hypoxia (IH) associated with apnea of prematurity and periodic breathing (1). In adults, IH associated with sleep apnea causes neurochemical and structural alterations in the brain (2, 3). However, it is unknown whether IH in the premature infant leads to neurodevelopmental impairment (4). Quantification of biochemical markers that can precisely identify infants at risk of adverse neurodevelopmental outcome is essential. In vivo 1H magnetic resonance spectroscopy (1H MRS) facilitates the quantification of metabolites from distinct regions of the developing brain (5). We report the changes in metabolite profiles in the brainstem and hippocampal regions of developing rat brains, resulting from exposure to IH. Rat pups were chosen for study because there is rapid postnatal hippocampal development that occurs during the first 4 weeks in the developing rat brain, which corresponds to the first 2–3 postnatal years of development in humans. Metabolite profiles were compared between hypoxia treated rat pups (n = 9) and normoxic controls (n = 6). Metabolite profiles were acquired using the Point-RESolved spectroscopy (PRESS) MRS sequence and were quantified using the TARQUIN software (6). There was a significant difference in the concentrations of creatine (p = 0.031), total creatine (creatine + phosphocreatine) (p = 0.028), and total choline (p = 0.001) in the brainstem, and glycine (p = 0.031) in the hippocampal region. The changes are consistent with altered cellular bioenergetics and metabolism associated with hypoxic insult (7, 8).

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10137-70, Session PS5

Automatic falx cerebri and tentorium cerebelli segmentation from magnetic resonance images

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The falx cerebri and tentorium cerebelli are dural structures found in the brain, both of which are required to create realistic finite element models of the head for predicting brain dynamics during injury events. To date there has been very little research work on automatically segmenting these two structures, which is understandable given that 1) their thin structure challenges the resolution limits of in vivo 3-d imaging, and 2) contrast with respect to surrounding tissue is low in standard magnetic resonance imaging. An automatic segmentation algorithm to find the falx and tentorium is proposed which uses the results of a multi-atlas segmentation and cortical reconstruction algorithm. Gray matter labels for certain regions are expanded and used to find the location of the falx and tentorium. 3D visualizations of the final result are provided.

10137-71, Session PS5

Quantitative analysis of structural variations in corpus callosum in adults with multiple system atrophy (MSA)

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Multiple system atrophy (MSA) is a rare, non-curable, progressive neurodegenerative disorder that affects nervous system and movement, poses a considerable diagnostic challenge to medical researchers. Corpus callosum (CC) being the largest white matter structure in brain, enabling inter-hemispheric communication, quantification of callosal atrophy may provide vital information at the earliest possible stages. The main objective is to identify the differences in CC structure for this disease, based on quantitative analysis on the pattern of callosal atrophy. We report results of quantification of structural changes in regional anatomical thickness, area and length of CC between patient-groups with MSA with respect to healthy controls. The method utilizes isolating and parcellating the mid-sagittal CC into 100 segments along the length - measuring the width of each segment. It also measures areas within geometrically defined five callosal compartments of the well-known Witelson, and Hofer-Frahma schemes. For quantification, statistical tests are performed on these different callosal measurements. From the statistical analysis, it is concluded that compared to healthy controls, width is reduced drastically throughout CC for MSA group and as well as changes in area and length are also significant for MSA. The study is further extended to check if any significant difference in thickness is found between the two variations of MSA, Parkinsonian MSA and Cerebellar MSA group, using the same methodology. However area and length of this two sub-MSA group, no substantial difference is obtained. The study is performed on twenty subjects for each control and MSA group, who had T1-weighted MRI.

10137-46, Session PS6

Correlation of BAT activity with the thyroid metabolic activity of patients with fibromyalgia

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The objective of this work was to correlate the brown fat activity (BAT) with the metabolic activity of thyroid in patients with fibromyalgia (FM) using thermal images. The BAT is an important regulator of energy balance and metabolism in animals, and the infrared thermography can register the BAT activation in patients with FM by the “mantle sign”, which are areas with hyper-radiation, corresponding to muscular painful regions. The thermogenic BAT activity is increased by the same conditions of FM, and patients may present a body temperature reduction and low metabolic rate. For the development of the research, it was selected a database containing 47 patients of a thermography laboratory, male and female, with age above 18 years. The images were captured by an infrared camera FLIR T650SC and it was selected the anteroposterior orthostatic top and anteroposterior in cervical extension. The Flir Report program was used to select the thyroid, the left and the right interscapular regions in the thermal images in order to evaluate the respective temperatures and to detect the hyper-radiation (“mantle sign”) in the interscapular. The temperatures were organized in table format and statistical analysis was performed using the Microcal Origin 6.0 program. The patients without FM showed mean thyroid (32.5°C) and BAT (30.0°C) temperatures higher than the temperatures for patients with FM (31.5°C and 29.8°C, respectively). Thus, it was possible to conclude that patients with FM have decreased body temperature and low metabolic rate, correlating the BAT with the thyroid function.

10137-72, Session PS6

A feasibility study on estimation of tissue mixture contributions in 3D arterial spin labeling sequence

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Arterial spin labeling (ASL) provides a noninvasive measurement of cerebral blood flow (CBF). Due to relatively low spatial resolution, the accuracy of CBF measurement is affected by the partial volume (PV) effect. To obtain accurate CBF estimation, the contribution of each tissue type in the mixture is desirable. In general, this can be obtained according to the registration of ASL and structural image in current ASL studies. This approach can obtain probability of each tissue type inside each voxel, but it also introduces error, which include error of registration algorithm and imaging itself error in scanning of ASL and structural image. Therefore, estimation of mixture percentage directly from ASL data is greatly needed. Under the assumption that ASL signal followed the Gaussian distribution and each tissue type is independent, a maximum a posteriori expectation-maximization (MAP-EM) algorithm was formulated to estimate the contribution of each tissue type to the observed perfusion signal at each voxel. Considering the sensitivity of MAP-EM to the initialization, an approximately accurate initialization was obtain using 3D Fuzzy c-means method. Our results showed a good estimation results of tissue mixture contribution in the voxel of ASL sequence based on simulated and in vivo data. As far as we know, no study investigated the tissue mixture contribution using only ASL sequence.

More importantly, the results may be further used in PV correction and CBF calculation study of ASL.

10137-73, Session PS6

Photothermal characterization of gold nanorods for superficial breast cancer therapy in an engineered 3 dimensional human decellularized adipose tissue platform

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Over the last decade, the use of gold nanoparticles has emerged to be highly promising photothermal cancer therapy, because plasmonic photothermal therapy (PPTT) provides a strong potential in localized and targeted treatment of tumors, selective cell death with high efficiency, reduced side effect, and improved patient quality of life, through the ability of gold nanoparticles to target destructive heat preferentially to tumor regions. And yet, clinical application of the thermal therapies has not accomplished due to insufficient processes of the heating methods and temperature measuring techniques leading to low reproducibility of such treatment. In this study, we demonstrate an engineered three dimensional human decellularized adipose tissue (hDAT) constructs is fabricated to characterize the heating method and to control the generated heat in the tissue used for a superficial breast cancer therapy using gold nanorods (GNRs, citrate-coated) irradiated near-infrared (NIR, 808 nm) laser. The hDAT was designed to mimic a localized tumor in the human breast tissue with a 2 mm wide hemisphere where defined GNRs exist at the center of the tissue platform and to measure temperature and heat distribution of the GNRs according to the variables on the cross-section of the tissue. The hDAT platform will provide an optimized condition for clinical treatment of photothermal cancer therapy.

10137-74, Session PS6

Interactive iterative relative fuzzy connectedness lung segmentation on thoracic 4D dynamic MR images

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Lung segmentation on dynamic 4D thoracic MRI images is necessary for quantitative analysis in the study of respiratory disease and for radiotherapy planning. Instead of using purely manual segmentation and registration based approaches, we propose an interactive IRFC-based approach as a potential practical solution to lung segmentation on 4D dynamic thoracic MR images. Manual segmentation costs much human labor and leads to low repeatability of the segmentation results. The registration-based approach to 4D images is somewhat inefficient and might not produce accurate results due to the accumulated registration error and complexity. The proposed approach works in a similar way as the livewire tool but uses IRFC as an image segmentation engine. Seeds are set up manually and can also be propagated to the following slices, decreasing human labor, and then a fuzzy connectedness map can be automatically calculated, leading to the final segmentation. Although human interactive labor is still involved the current procedure, the advantage from the interactive IRFC is the high-control ability on the final segmentation and almost no need to refine the segmentation results. 39 3D volume images from 5 subject dynamic MR sequences are used to evaluate the proposed approach. For comparison, another two IRFC-based 4D thoracic MR image segmentation approaches of pseudo 4D IRFC and 3D volume-independent IRFC are also evaluated. The preliminary experimental results show that the proposed interactive IRFC can effectively segment lung from 4D dynamic thoracic MR images with TPFV around 0.91, FPFV around 0.03, and Hausdorff distance (HD) around 2 mm.

10137-75, Session PS6

Noise reduction in OCT skin images

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Optical coherence tomography (OCT) has become a popular imaging modality in dermatology. Although OCT skin images reveal a great knowledge about the microstructures of the tissue morphology, they suffer from artifacts. Speckle is the main artifact, and the other one is background noise. In this study, we propose an algorithm that significantly reduces the background noise in the OCT images before applying the speckle reduction algorithm. A speckle reduction method based on subpixel weighted median filtering is then applied to the images. The edges in resultant images are preserved. The results show that, in this way the speckle reduction procedure is more efficient and that the diagnostically relevant features in the images become clearer. The results have been quantified using signal to noise ratio (SNR), contrast to noise ratio (CNR) and edge preserving index (EPI). We observed increase of 10.84%, 33%, and 34% in SNR, CNR and EPI in the OCT images of skin, respectively.

10137-77, Session PS6

A spatially variant deconvolution method based on total variation for optical coherence tomography images

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Optical Coherence Tomography (OCT) has a great potential to elicit clinically useful information from tissues due to its high axial and transversal resolution. In practice, an OCT setup cannot reach to its theoretical resolution due to imperfections of its components, which make its images blurry. The blurriness is different alongside regions of image, thus they cannot be modeled by a unique point spread function (PSF). In this paper, we investigate the use of solid phantoms to estimate the PSF of each sub-region of imaging system. We then utilize Lucy-Richardson, steepest descent (SD) and total variation (TV) based iterative deconvolution methods for mitigating occurred spatially variant blurriness. It is shown that the TV based method will suppress the so-called speckle noise in OCT images better than the two other approaches. The performance of proposed algorithm is tested on various samples, including several skin tissues besides the phantom itself, demonstrating qualitatively and quantitatively the advantage of TV based deconvolution method using spatially-variant PSF for enhancing image quality.

10137-78, Session PS6

Semi-automatic segmentation of the placenta into fetal and maternal compartments using intravoxel incoherent motion MRI

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Intravoxel incoherent motion (IVIM) magnetic resonance imaging is an emerging non-invasive technique that has been recently applied to quantify in vivo global placental perfusion. We propose a robust semi-automated method for segmenting the placenta into fetal and maternal compartments from IVIM data, using a multi-label image segmentation algorithm called 'GrowCut'. Placental IVIM data were acquired on a 1.5T scanner from 16 healthy pregnant women between 21-37 gestational weeks. The voxel-wise perfusion fraction was then estimated after non-rigid image registration. The seed regions of the fetal and maternal compartments were determined using structural T2-weighted reference images, and improved progressively through an iterative process to accurately encompass fetal and maternal compartments. We demonstrated that the placental perfusion fraction decreased in both fetal (-0.010/week) and maternal compartments (-0.013/week) while their relative difference (fetal-maternal) gradually increased with advancing gestational ages (+0.003/week, p=0.065). Our preliminary results show that the proposed method was effective in distinguishing placental compartments using IVIM.

10137-79, Session PS6

FADDTSter: accelerating hypothesis testing with functional analysis of diffusion tensor tract statistics

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FADTTS is a toolbox used to compute statistical analysis on fiber tracts.

FADTTS allows associating multiple diffusion properties with a set of covariates of interest such as age, diagnostic status etc.

However, to use this toolbox, the user is required to have an intermediate knowledge in scripting languages (MATLAB).

FADTTSter was created to overcome this issue and make the statistical analysis accessible to any non-technical researcher. FADTTSter is actively being used by researchers at the University of North Carolina.

FADTTSter guides non-technical users through a series of steps including quality control of subjects and fibers in order to setup the necessary parameters to run FADTTS.

Additionally, FADTTSter implements an interactive chart for FADTTS' outputs. This interactive chart enhances the researcher experience and facilitates the analysis of the results.

FADTTSter's motivation is to improve usability and provide a new analysis tool to the community that complements FADTTS.

Ultimately, by enabling FADTTS to a broader audience, FADTTSter seeks to accelerate hypothesis testing in neuroimaging studies involving heterogeneous clinical data and diffusion tensor imaging.

This work is submitted to the Biomedical Applications in Molecular, Structural, and Functional Imaging conference.

The source code of this application is available in NITRC.

10137-80, Session PS6

Monitoring of VX2 tumor growth in rabbit liver using T2-weighted and dynamic contrast-enhanced magnetic resonance imaging at 1.5T

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This study aimed to investigate the VX2 tumor growth in rabbit liver using T2-weighted imaging (T2WI) and dynamic contrast-enhanced magnetic resonance imaging (DCE-MRI). Five New Zealand white (NZW) rabbits were implanted with VX2 cell suspension in liver. Afterwards, MRI was performed on 7, 14, 21 and 28 days after tumor implantation. A 1.5 T whole-body clinical MRI scanner with a 15-channel high resolution knee coil was used to perform scans. After 3-plane localizer, T1 weighted imaging (T1WI) and T2WI, then DCE-MRI using a three-dimensional gradient echo pulse sequence was performed. After 4 pre-contrast images were acquired, each rabbit was injected with 0.1 mmole/kg Dotarem through a right ear vein. The total scan time after Dotarem administration was 30 minutes. All acquired images were analyzed using ImageJ software. Several regions of interest were selected from the rims of tumor, liver, and muscle. The enhancement ratio (ER) was calculated by dividing the MR signal after Dotarem injection to the MR signal before Dotarem injection. The maximum ER (ER_max) value of tumor for each rabbit was observed right after the Dotarem injection. The T2W MR signal intensities (T2W_SI) and the ER_max values obtained at 7, 14, 21 and 28 days after tumor implantation were analyzed with a linear regression algorithm. Both T2W_SI and ER_max of tumors increased with time. The changes for T2W_SI and ER_max of tumors between 7 and 28 days after tumor implantation were 32.66% and 18.14%. T2W_SI is more sensitive than ER_max for monitoring the growth of VX2 tumor in a rabbit liver model.

10137-81, Session PS6

Evaluation of a pulmonary strain model by registration of dynamic CT scans

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Idiopathic pulmonary fibrosis (IPF) is a chronic fibrotic lung disease that develops in adults without any known cause. It is an interstitial lung disease in which the lung tissue becomes scarred and stiffens, ultimately leading to respiratory failure. This disease currently has no cure with limited treatment options, leading to an average survival time of 3-5 years after diagnosis. As a continuation of our previous work, we employ a mathematical model simulating the lung parenchyma as hexagons with elastic forces applied to connecting vertices and opposing vertices. Using an image registration algorithm, we obtain trajectories of 4D-CT scans of a healthy patient, and one suffering from IPF. Converting the image trajectories into a hexagonal lattice, we fit the model parameters to match the respiratory motion seen for both patients across multiple image slices. We found the model could decently describe the healthy lung slices, with a minimum average error between corresponding vertices to be 1.66 mm. For the fibrotic lung slices the model was less accurate, maintaining a higher average error across all slices. Using the optimized parameters, we apply the forces predicted from the model using the image trajectory positions for each phase. Although the error is large, the spring constant values determined for the fibrotic patient were not as high as we expected, and more often than not determined to be lower than corresponding healthy lung slices. However, the net force distribution for some of those slices were still found to be greater than the healthy lung counterparts. With the limited sample size available, a clear distinction between the healthy and fibrotic lung cannot yet be made.

10137-82, Session PS6

A numerical finite element model to study the biomechanical behavior of abdominal aortic aneurysm

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Abstract: Abdominal aortic aneurysm (AAA) is a leading cause of death in the United States. AAA is an abnormal dilation of the aorta, which usually occurs below the renal arteries and causes an expansion at least 1.5 times its normal diameter. It has been shown that biomechanical parameters of the aortic tissue, coupled with a set of specific geometric parameters characterizing the vessel expansion, affect the risk of aneurysm rupture. Here, we developed a numerical model that incorporates both biomechanical and geometrical factors to study the behavior of abdominal aortic aneurysm. Our workflow enables the extraction of the aneurysm geometry from clinical-quality MR images. We used a two-parameter, hyper-elastic, isotropic, incompressible material approximation to model the vessel tissue. Our numerical model was tested using both synthetic and mouse data and we evaluated the effects of the geometrical and biomechanical properties according to the estimated peak wall stress, which confirmed previously disseminated results. In addition, we performed a series of parameter sensitivity analyses to investigate the effect of different factors affecting the AAA and its biomechanical behavior as a predictor for rupture. Lastly, relationships between different geometrical and biomechanical parameters and peak wall stress were determined. We believe these studies help us better understand vessel tissue response to various loading, geometry and biomechanics conditions, and we plan to further correlate these findings with the pathophysiological conditions from a patient population diagnosed with abdominal aortic aneurysms.

10137-83, Session PS7

An automated image processing method for classification of diabetic retinopathy stages from conjunctival microvasculature images

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We are presenting an automated method for classification of conjunctival microvasculature images at different stages of DR. Diabetic retinopathy (DR) is the most frequent cause of visual impairment and blindness among working adults. Blindness in DR is caused by retinal tissue ischemia and macular edema. DR is a microvascular disease; therefore, microvasculopathies can be expected to be present, at least partially, in other tissues such as conjunctiva. Conjunctiva is a vascularized mucous membrane covering scleral of the eye which provides direct visualization of human microvasculature. In the current study, an automated image processing method was applied to conjunctival microvascular images to classify different stages of DR. Pixels of each conjunctival image were shifted by 1 or 2 pixels row-wise, column-wise, and along the diagonal to yield 8 unique combinations of the original image. These images were vectorized by stacking columns of the 2D image into a 1D vector. Ordinary least square regression was employed to perform fine structural analysis of conjunctival microvasculature images. Fisher linear discriminant analysis was performed to classify images. The classification rates obtained by the automated method were constantly higher than those obtained by human observers. The automated classification rates for clinical and non-clinical DR were over 80% and 70%, respectively. The method allowed quick and sensitive classification of conjunctival microvasculature images at different stages of DR and can be potentially useful for DR screening and monitoring.

10137-84, Session PS7

Machine learning for cardiac ultrasound time series data

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We consider the problem of identifying frames in a cardiac ultrasound video associated with left ventricular chamber end-systolic (contraction) and end-diastolic (expansion) phases of the cardiac cycle. Our procedure involves a simple application of Non-negative matrix factorization (NMF) to a set of data corresponding to a series of frames of a video from a single patient. Binary topic modeling is performed to compute two end-members. The end members are shown to be close representations of the actual heart morphology at the end of each phase of the heart function. Moreover, the entire time series can be represented as a linear combination of these two end-member states thus providing a very low dimensional representation of the time dynamics of the heart. Unlike previous work, our methods do not require any electrocardiogram (ECG) information in order to select the end-diastolic frame. Results are presented for a data set of 100 patients including both healthy and diseased examples.

10137-85, Session PS7

Early classification of Alzheimer's disease using hippocampal texture from structural MRI

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Alzheimer's disease (AD) is the most common cause of dementia in older individuals. And the hippocampus is often considered the primary brain area because it is affected early in the AD pathological process(Bird and Burgess, 2008, Shi et al., 2009, Tahmasian et al., 2015). The altered hippocampal volume or connectivity features were proven to be effective markers in AD diagnosis. A recent study also highlights the possibility that hippocampal texture may serve as a prognostic neuroimaging biomarker of early cognitive impairment(Sorensen et al., 2016). In this study, we specifically to investigate if the proposed hippocampal texture can be served as an MRI biomarker of AD.

For this purpose, MRI data was obtained from 48 AD and 38 normal samples. The bilateral hippocampus were segmented using a local label learning method. Second, texture features were extracted for each side of hippocampus. The performance of the proposed features is tested using 10-fold cross-validation. All features of the training data are ranked using t-test ranking method; and Fisher criterion between AD and NC were introduced for selecting optimal parameters for classification.

The support vector machine(SVM) classifier with 10-fold cross-validation showed that the used hippocampal textures can be taken as potential MRI markers for early detection of AD with accuracy(87.74%) and specificity (87.42%) based on 1000 times repeating analysis. The present study highlights the presence of hippocampal texture abnormalities in AD, and the possibility that texture may serve as a neuroimaging biomarker for AD.

10137-87, Session PS8

Context-dependent astrocyte dynamics visualized with novel freely-moving imaging platform

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Determining how information is processed in cerebral cortex is a central goal in neuroscience, which requires in vivo assessments of circuit activities during different behaviors. Although much insight has been gained about the neurons, those of the non-neuronal cells and their interactions with neurons remain poorly understood. To incorporate astrocytes into the existing framework of cortical circuits, studies of astrocyte-neuron interactions in combination with defined behaviors are crucial.

To investigate astrocyte-neuron circuit in various behaviors, we developed a new imaging platform that enables visualization of Ca2+ levels in astrocytes in the CNS of freely moving animals. This system was based on an optic bundle containing 30K cores coupled to an achromatic lens pair, rendering cellular/subcellular resolution of <4 μm. The NA of 0.58 and working distance of 2.5 mm allowed the lens probe to be positioned outside a cranial window to minimize tissue injury. Astrocyte Ca2+ was monitored in GLAST-CreER; GCaMP3 transgenic mice, in which genetically-encoded Ca2+ indicators GCaMP3 was selectively expressed in cortical astrocytes. Fluorescence reflecting Ca2+ levels were obtained by coupling the imaging bundle to a 473 nm laser and a high resolution CCD camera. Animal behaviors were tracked in concert using a NIR camera and data acquisition was synchronized using custom programs written in C#. Our results indicated that astrocyte responses in freely moving mice were far more heterogeneous than in head fixed conditions, demonstrated bidirectional change in Ca2+ levels and were dependent on a variety of neuromodulators.

These studies reveal that astrocyte dynamics in vivo is modulated locally using diverse mechanisms depending on distinct behavioral contexts. The ability to monitor astrocyte network activity in freely-moving animals, when combined with in vivo cell specific manipulations, will help define the physiological significances of astrocytes-neurons in circuits and behaviors.

10137-88, Session PS8

Deep learning based classification for head and neck cancer detection with hyperspectral imaging in an animal model

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Hyperspectral imaging (HSI) is an emerging imaging modality that can provide a noninvasive tool for cancer detection and image-guided surgery. HSI acquires high-resolution images at hundreds of wavelength bands, providing big data to differentiating different type of tissues. We proposed a deep learning based detection method for head and neck cancer in hyperspectral images. Since the deep learning algorithm can learn the feature hierarchically, the learned features are more discriminative and concise than the handcrafted features. Hence, instead of handcrafted features, we adopt convolutional neural networks (CNN) to learn the deep feature of pixels for classifying them into tumor or normal tissue. We evaluated our proposed classification method on the dataset containing hyperspectral images of 12 tumor-bearing mice. Experimental results show that our method achieved an average accuracy of 91.36%. The preliminary study demonstrated that our deep learning method can be applied to hyperspectral images for detecting head and neck tumors in animal models.

10137-90, Session PS8

Diagnostic index: an open-source tool to classify TMJ OA condyles

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Osteoarthritis (OA) appears in a big number of patients with temporomandibular joint (TMJ) disorders. Despite its prevalence, OA diagnosis and treatment remain controversial since there are no clear symptoms of the disease, especially in early stages. We believe that quantitative tools based on 3D imaging of the TMJ condyle could help characterize and understand TMJ OA. This would ultimately lead to the design of more appropriate biomarkers and treatments. This work proposes to identify differences among asymptomatic controls and different clinical phenotypes of TMJ OA by means of Statistical Shape Modeling (SSM), obtained via clinical expert consensus. From three different grouping schemes (with 3, 5 and 7 groups), our best results reveal that that the majority (74.5%) of the classifications occur in agreement with the groups assigned by consensus between our clinical experts. This strongly suggests the existence of different disease-based phenotypic morphology in TMJ OA. It also reveals that statistical shape modeling based biomarkers can provide a quantitative staging of the disease. Finally and more importantly, the methodology used in this study is disseminated and included in an open source image analysis toolbox, to ensure reproducibility and appropriate distribution of the solution proposed.

10137-91, Session PS8

Undersampling strategies for compressed sensing accelerated magnetic resonance spectroscopic imaging

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Purpose: Compressed sensing (CS) can accelerate magnetic resonance spectroscopic imaging (MRSI) facilitating its clinical integration. The objective of this study was to assess the effect of different undersampling masks on CS-MRSI reconstruction quality.

Methods: Phantom data for the test simulations was acquired on a Philips 3 T Ingenia scanner. Four types of undersampling masks, namely, low resolution, variable density, iterative design, and a priori were simulated in Matlab and retrospectively applied to the test 1X MRSI data to generate undersampled datasets corresponding to the 2X – 5X, 7X, and 10X accelerations for each type of mask. Reconstruction parameters were kept the same across the board to ensure that any resulting differences can be attributed to the type of mask being employed. The reconstructed datasets

from each mask were statistically compared with the reference 1X, and assessed using metrics like the root mean square error and metabolite ratios.

Results: Simulation results indicate that both the a priori and variable density undersampling masks maintain high fidelity with the 1X up to five-fold acceleration. The low resolution reconstructions showed statistically significant differences from the 1X with the reconstruction failing at 3X, while the iterative design reconstructions maintained fidelity with the 1X till 4X acceleration.

Conclusion: A pilot study was conducted to identify an optimal sampling mask in CS-MRSI. Simulation results demonstrate that the a priori and variable density masks can provide statistically similar results to the fully sampled reference. Future work would involve implementing these two masks prospectively on a clinical scanner.

10137-92, Session PS8

Federating heterogeneous datasets to enhance data sharing and experiment reproducibility

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Recent studies have demonstrated the difficulties to replicate scientific findings and/or experiments published in past.

The effects seen in the replicated experiments were smaller than previously reported. Some of the explanations for these findings include the complexity of the experimental design and the pressure on researches to report positive findings.

The International Committee of Medical Journal Editors (ICMJE) suggests that every study considered for publication must submit a plan to share the de-identified patient data no later than 6 months after publication.

There is a growing demand to enhance the management of clinical data, facilitate data sharing across institutions and also to keep track of the data from previous experiments. The ultimate goal is to assure the reproducibility of experiments in the future.

This paper describes Shiny-tooth, a web based application created to improve clinical data acquisition during the clinical trial; data federation of such data as well as morphological data derived from medical images.

Currently, this application is being used to store clinical data from an osteoarthritis (OA) study.

10137-93, Session PS8

Exploring the use of optical flow for the study of functional NIRS signals

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Near infrared spectroscopy (NIRS) is an optical imaging technique that allows real-time measurements of Oxy- and Deoxy-hemoglobin concentrations in human body tissue. In functional NIRS (fNIRS), this technique is used to study cortical activation in response to external stimulation. However, analysis of brain activation regions using NIRS is a challenging task in the field of medical image analysis. For that reason, the aim of our present study is to report the use of an optical flow method for the analysis of cortical activation using near-infrared spectroscopy signals. We used real fNIRS data recorded from an acupuncture stimulation experiment as base of our implementation. To compute the optical flow algorithm, we first arrange NIRS signals (Oxy-Hemoglobin) following the 24 channels (12 channels per hemisphere) head-probe configuration. We then used two consecutive fNIRS images (samples) per hemisphere as input frames for the optical flow algorithm, making one computation per hemisphere. The output from these two computations is the velocity field for each hemisphere. The experimental results showed that the radial structure of flow vectors exhibited the origin of cortical activity, the development of stimulation as expansion or contraction of such flow vectors, and the flow of activation patterns may suggest prediction in cortical activity. In the present study, we have demonstrated that optical flow provides a power tool for the analysis of NIRS signals. Finally, we suggested a novel idea to identify pain status in nonverbal patients by using optical flow motion vectors; however, this idea will be study further in our future research.

10137-94, Session PS8

Silica coated gold nanoparticles as photoacoustic and ultrasonic contrast agents for biomedical imaging

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Many methods are being studied to increase the strength of photoacoustic signals, such as contrast agents, high quality transducers, advanced signal processing, etc. Photoacoustic (PA) and contrast enhanced ultrasound (CE-US) imaging have been used for tracking abnormal tumour microenvironment characteristics in vivo.

In this work, we performed an enhanced method to improve the resolution, contrast, and depth of detection by silica coated gold nanoparticles (SiAuNp) as Photoacoustic and Ultrasonic Contrast Agents.

We performed a comparative study of Photoacoustic (PA) and contrast enhanced ultrasound (CE-US) imaging as unmodified melanoma agents, silica coated gold nanoparticle (AuNP) tagged melanoma agents. Each sample was irradiated at 805 nm and 1064 nm. The transducer used to record the PA and (CE-US) signals consisted of three elements arranged in an annular array. Each melanoma sample was loaded into cylindrical tubes and placed at the focus of the ultrasonic transducer. the PA and (CE-US) signal strength (PSS) was computed as the integration of the Hilbert Transform of the PA and (CE-US) signal. The function generation and signal acquisition were performed in the PC using Labview software.

The comparison revealed that the silica coated gold nanoparticles could show their viability for pre-cancerous and malignant melanoma lesions at a very low concentration. The results of our study have the potential to not only better develop Photoacoustic (PA) and contrast enhanced ultrasound (CE-US) detection of melanoma, but also extend the viability and use of Photoacoustic (PA) and contrast enhanced ultrasound (CE-US) imaging into detection of otherwise unpigmented cancers.

10137-35, Session 8

Boosted learned kernels for data-driven vesselness measure

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Common vessel centerline extraction methods rely on the computation of a measure providing the likeness of the local appearance of the data to a curvilinear tube-like structure. The most popular techniques rely on empirically designed (hand crafted) measurements as the widely used Hessian vesselness, the recent oriented flux tubeness or filters (e.g. the Gaussian matched filter) that are developed to respond to local features, without exploiting any context information nor the rich structural information embedded in the data.

At variance with the previously proposed methods, we propose a completely data-driven approach for learning a vesselness measure from expert-annotated dataset. For each data point (voxel or pixel), we extract the intensity values in a neighborhood region, and estimate the discriminative convolutional kernel yielding a positive response for vessel data and negative response for non-vessel data. The process is iterated within a boosting framework, providing a set of linear filters, whose combined response is the learned vesselness measure.

We show the results of the general-use proposed method on the DRIVE retinal images dataset, comparing its performance against the hessian-based vesselness, oriented flux antisymmetry tubeness, and vesselness learned with a probabilistic boosting tree or with a regression tree. We demonstrate the superiority of our approach that yields a vessel detection accuracy of 0.95, with respect to 0.92 (hessian), 0.90 (oriented flux) and 0.85 (boosting tree) .

10137-36, Session 8

Deep learning for brain tumor classification

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Recent research has shown that deep learning methods have performed well on supervised machine learning, image classification tasks. The purpose of this study is to apply deep learning methods to classify brain images with different tumor types: meningioma, glioma, and pituitary. A dataset was publicly released containing 3,064 T1-weighted contrast enhanced MRI (CE-MRI) brain images from 233 patients with either meningioma, glioma, or pituitary tumors split across axial, coronal, or sagittal planes. This research focuses on the 989 axial images from 191 patients in order to avoid confusing the neural networks with three different planes containing the same diagnosis. Two types of neural networks were used in classification: fully connected and convolutional neural networks. Within these two categories, further tests were computed via the augmentation of the original 512x512 axial images. Through rotating, shifting, scaling, and mirroring, data sizes could be increased with the sacrifice of image clarity. Training neural networks over the axial data has proven to be accurate in its classifications with an average five-fold cross validation of 91.43% on the best trained neural network. This result demonstrates that a more general method (i.e. deep learning) can outperform specialized methods that require image dilation and ring-forming subregions on tumors.

10137-37, Session 8

Robust hepatic vessel segmentation using multi deep convolution network

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Extraction of blood vessels of the organ is a challenging task in the area of medical image processing. It is really difficult to get accurate vessel segmentation results even with manually labeling by human being. The difficulty of vessels segmentation is the complicated structure of blood vessels and its large variations that make them hard to recognize. In this paper, we present a deep artificial neural network architecture to automatically segment the hepatic vessels from computed tomography (CT) image. We proposed a novel deep neural network (DNN) architecture for vessel segmentation from a medical CT volume, which consists of three deep convolution neural networks to extract features from difference planes of CT data. The three networks have share features at the first convolution layer but will separately learn their own features in the second layer. All three networks will join again at the top layer. To validate effectiveness and efficiency of our proposed method, we conduct experiments on 10 CT volumes which training data are randomly generate from 3 CT volumes and 7 using for test. Our network can yield an average dice coefficient 0.830, while 3D deep convolution neural network can yield around 0.7 and multi-scale can yield only 0.6.

10137-38, Session 8

Automated diagnosis of Alzheimer's disease with multi-atlas based whole brain segmentations

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Voxel-based analysis is widely used in quantitative analysis of structural brain MRI and automated disease detection, such as Alzheimer's disease (AD). However, noise at the voxel level may cause low sensitivity to AD-induced structural abnormalities. This can be addressed with the use of a whole brain structural segmentation approach which greatly reduces the dimension of features (the number of voxels). In this paper, we propose an automatic AD diagnosis system that combines such whole brain segmentations with advanced machine learning methods. We used a multi-atlas segmentation technique to parcellate T1-weighted images and extract the structural volumes to serve as the features for principal-component-analysis-based dimension reduction and support-vector-machine-based classification. The relationship between the number of retained principal components (PCs) and the diagnosis accuracy was systematically evaluated, in a leave-one-out fashion, based on 28 AD subjects and 23 age-matched healthy subjects. Our approach yielded pretty good classification results with 96.08% overall accuracy being achieved using the three foremost PCs. In addition, our approach yielded 96.43% specificity, 100% sensitivity, and 0.9891 area under the receiver operating characteristic curve.

10137-39, Session 8

Towards an affordable deep learning system: automated intervertebral disc detection in x-ray images

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Adult Spinal Deformity is a prominent medical issue with about 68% of the healthy, elderly population suffering from the disease. Detailed biomechanical assessment is needed both in the presurgical planning of structural spinal deformity as well as in early functional biomechanical compensation in ambulatory spinal pain patients. When considering automation of this process, we have to look at photographic intervertebral disc detection technique as a way to produce a detailed model of the spine with appropriate measurements required to make efficient and accurate decisions on patient care. Deep convolutional neural network (CNN) has given remarkable results in object detection tasks in recent years. However, massive training data, computational resources and long training time is needed for both training a deep network from scratch or fine-tuning a network. Using pre-trained model as feature extractor has shown promising result for moderate sized medical data. However, most work have extracted features from the last layer and little has been explored in terms of the number of layers needed for best performance. In this work we trained

Support Vector Machine (SVM) classifiers on different layers of CaffeNet [3] features to show that “deeper the better” concept does not hold for intervertebral disc detection task. Furthermore, our experimental results show the potential of using very small training data to yield satisfactory classification performance with accuracy up to 97.2% using only 15 training data.

10137-40, Session 9

Implementation of material decomposition using an EMCCD and CMOS-based micro-CT system

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This project assessed the effectiveness of using a unique electron multiplying CCD based micro-CT system to carry out material decomposition on axial slices of a 3D printed phantom. Basis materials of the phantom included iodine contrast agent, water, background air, and the 3D printing material. At any instance, three basis materials were selected to make up the micro-CT phantom. Scans were performed using our micro-CT system setting the kVp of the x-ray tube first at 25 kVp, followed by 70 kVp to obtain the dual energy scan data needed for the decomposition. Using the projection data, slices of the scanned object were reconstructed using the FDK reconstruction algorithm. Following reconstruction, slices of the phantom were decomposed into the three basis materials selected for the trial. The success of the decomposition was assessed qualitatively through visual inspection of the resulting three reconstructions in each of the three basis material “spaces”, and quantitatively through the computation of normalized root-mean-square error (NRMSE). Our results indicate that the decomposition was successful when the difference in atomic number between the two basis materials was large, such as in the decomposition between the 3D printing material and iodine contrast agent. The regions of iodine contrast agent were differentiated consistently from the rest of the phantom. Worked supported by Toshiba America Medical Systems, and partially supported by NIH grant 2R01EB002873.

10137-41, Session 9

Ultrahigh resolution and brilliance laser wakefield betatron x-ray source for rapid in vivo tomographic microvasculature imaging in small animal models

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Purpose

To develop ultrahigh resolution (< 2 μm) high brilliance laser wakefield betatron radiation (LWBR) x-ray source for rapid in vivo tomographic microvasculature imaging in small animal models using micro-CT.

Method

Ultrashort (20-30 fs) high-intensity laser pulse interaction with a supersonic gas jet plasma generate burst of incoherent x-rays with characteristic duration time comparable to the laser pulse duration, continuous synchrotron-like spectral distribution, very high brilliance, very small focal spot and highly directional emission in the cone-beam geometry. This phenomenon is called the LWBR. We achieved 250 TW on target, 6 J, 25 fs pulse duration at 2.5 Hz repetition rate with the optical power density 3.5?1019 W/cm2.

Results

The LWBR x-ray source created in our lab produces mean ~1023 photons s-1 mrad-2mm-2/0.1% bw, mean critical energy at ~30 keV, x-ray source size for a single laser shot (FWHM) 1.7 μm, x-ray beam divergence 20– 30 mrad. We obtained projection images of mice using single laser shots. Therefore, ultrahigh resolution tomography requiring thousands of projection images could be accomplished in minutes.

Conclusions

The high-brilliance LWBR x-ray source might provide foundation for in vivo ultrahigh resolution tomographic imaging of microvascular fine structures in small animal models with suitable contrast agents using micro-CT setup and appropriate x-ray detectors. Such systems would achieve spatial resolution and acquisition speed not attainable today. The major challenges are stabilization of the x-ray photon flux and stabilization of critical energy over thousands of laser shots needed to obtain ultrahigh resolution tomographic data.

10137-42, Session 9

Spatial resolution properties of digital autoradiography systems for pre-clinical alpha particle imaging

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Attaching alpha-emitting radionuclides to cancer-targeting agents increases the anti-tumor effects of targeted cancer therapies. The success of alpha therapy for treating bone metastases has increased interest in using targeted alpha therapy (TAT) to treat a broad spectrum of metastatic cancers. Estimating radiation doses to targeted tumors, including small (<250μm) clusters of cancer cells, and to non-targeted tissues is critical in the pre-clinical development of TATs. However, accurate quantification of heterogeneous distributions of alpha-emitters in small metastases is not possible with existing pre-clinical in-vivo imaging systems. Ex-vivo digital autoradiography using a scintillator in combination with an image intensifier and a charged coupled device (CCD) has gained interest for pre-clinical ex-vivo alpha particle imaging. We present a simulation-based analysis of the fundamental spatial resolution limits of digital autoradiography systems. Spatial resolution was quantified in terms of the modulation transfer function (MTF) and Wagner’s equivalent aperture. We modeled systems operating in either particle-counting (PC) or energy-integrating (EI) mode using a cascaded systems approach that accounts for: 1) the stopping power of alpha particles; 2) the distance alpha particles travel within the scintillator; 3) optical blur, and; 4) binning in detector elements. We applied our analysis to imaging of astatine-211 using an LYSO scintillator with thickness ranging from 10 μm to 20μm. Our analysis demonstrates that when these systems are operated in particle-counting mode with a centroid-calculation algorithm, the effective apertures of ~35μm can be achieved, which suggests that digital autoradiography may enable quantifying the uptake of alpha emitters in tumors consisting of a few cancer cells. Future work will investigate the image noise and energy-resolution properties of digital autoradiography systems.

10137-45, Session 9

3D Histology of soft tissue samples using novel staining methods

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The application of X-ray imaging for biological samples (e.g. biopsies) is limited by the missing contrast of soft tissue, which is important to visualize microscopic structures. To overcome these challenges, we recently developed novel staining methods for X-ray imaging of soft tissue samples based on histological stains. The novel staining methods were explicitly developed in order to enhance the contrast in X-ray imaging, while the methods enable compatibility with conventional histological examinations, i.e. the possibility of counter staining by the histologist. Furthermore, the methods allow for a result within 24 h (time required for staining and X-ray imaging), and are therefore, much faster than currently available stains for X-ray imaging such as IKI, I2E or PTA and display the feasibility of integration of these methods into the clinical routine.

The stains were designed to improve the contrast in X-ray imaging, which is achieved by changing chemical parameters such as the addition of additives to the fixative, the increase of stain concentration within the sample, the introduction of elements with a higher atomic number Z and density.

We will show MicroCT and NanoCT slices and renderings of different soft tissue samples with resolutions ranging from several microns down to 200 nm. The results clearly show that the X-ray contrast in the samples is remarkably improved by our staining methods and detailed tissue substructures are visible that cannot be visualized without the staining. We will further present correlative data from electron and light microscopy to validate the X-ray data.

This work demonstrates the powerful potential of three-dimensional histology as a tool for modern histological and histopathological applications.

10137-86, Session 9

A simulation study of spectral Cerenkov luminescence imaging for tumour margin estimation

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Breast cancer is the most common cancer in women in the world. Breast-conserving surgery (BCS) is a standard surgical treatment for breast cancer with the key objective of removing breast tissue, maintaining a negative surgical margin and providing a good cosmetic outcome. A positive surgical margin, meaning the presence of cancerous tissues in the breast after surgery, is associated with local recurrence after therapy. In this study, we investigate a new imaging modality based on Cerenkov luminescence imaging (CLI) for the purpose of detecting positive surgical margins in situ during BCS. We develop Monte Carlo simulations using the Geant4 nuclear physics simulation toolbox to study the spectrum of photons emitted given F-18 and breast tissue properties. The resulting simulation spectra show that the CLI signal contains information that may be used for cancer margin evaluation given appropriate imaging system design and sensitivity, however this information varies significantly with breast optical parameters. While promising, further studies are needed to quantify the CLI response to more accurately incorporate tissue specific parameters and patient specific anatomical details.

10137-89, Session 9

Bipolar current injection methods for electrical impedance tomography: a comparative study

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Electrical Impedance Tomography (EIT) is one of the non-invasive medical imaging techniques that can be used for detecting abnormalities in the human tissues. In this method a high frequency, low amplitude current is injected into the tissues through a set of electrodes .The conductivity variations in the abnormalities are measured from the potential drop caused due to the injected current in the medium. Methodologies adopted to inject current into the medium and the electrode configuration used for voltage measurements play a vital role in the detection of any abnormal conductivity variations within the tissues. A comparative study of different bipolar current injection methods viz. adjacent method, cross method and opposite method using 16 electrodes EIT system is reported in this paper. Variations in the boundary voltages measured with respect to fixed electrode are higher than the variations in the voltages measured across adjacent electrode pairs. Optimal locations of the fixed electrode are determined to maximize the variation in the boundary voltage due to the inhomogeneity in the medium. Sensitivity of different current injection methods to inhomogeneity at different locations is examined. The effect of conductivity contrast on boundary voltages is studied by varying the conductivity of the inhomogeneity from 0.01mS/cm to 9.1mS/cm. Ill-posedness of the inverse problem is analyzed in terms of condition number for the aforementioned methods. Convergence of reconstruction error is used in this study to analyze which method yields faster convergence. Based on the simulation studies and experimental validations, cross method is found to be the optimal current injection method to attain better data acquisition and image reconstruction.

10137-52, Session 10

Using large-scale Granger causality to study changes in brain network properties in the Clinically Isolated Syndrome (CIS) stage of Multiple Sclerosis

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Clinically Isolated Syndrome (CIS) is often considered to be the first neurological episode associated with Multiple sclerosis (MS). At an early stage the inflammatory demyelination occurring in the CNS can manifest as a change in neuronal metabolism, with multiple asymptomatic white matter lesions detected in clinical MRI. Such damage may induce topological changes of brain networks, which can be captured by advanced functional MRI (fMRI) analysis techniques. We test this hypothesis by capturing the effective relationships of 90 brain regions, defined in the Automated Anatomic Labeling (AAL) atlas, using a large-scale Granger Causality (lsGC) framework. 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 study for differences in these properties in network graphs obtained for 18 subjects (10 male and 8 female, 9 with CIS and 9 healthy controls). Global network properties captured trending differences with modularity and clustering coefficient ($p<0.1$). Additionally, local network properties, such as local efficiency and the strength of connections, captured statistically significant ($p<0.01$) differences in some regions of the inferior frontal and parietal lobe. We conclude that multivariate analysis of fMRI time-series can reveal interesting information about changes occurring in the brain in early stages of MS.

10137-53, Session 10

Investigating changes in resting-state connectivity from functional MRI data in patients with HIV associated neurocognitive disorder using MCA and machine learning

Adora M. DSouza, Anas Z. Abidin, Axel Wismüller, Univ. of Rochester Medical Ctr. (United States)

Infection of the brain by the Human Immunodeficiency Virus (HIV) causes irreversible damage to the synaptic connections resulting in cognitive impairment. Patients with HIV infection, showing signs of impairment in multiple cognitive domains, as assessed by neuropsychological testing, are said to exhibit symptoms of HIV Associated Neurocognitive Disorder (HAND). In this study, we use resting-state functional MRI (fMRI) data to distinguish between healthy subjects and subjects with symptoms of HAND. To this end, we first establish a measure of interaction between pairs of regional time-series by quantifying their non-linear functional connectivity using Mutual Connectivity Analysis (MCA). Subsequently, we use a classifier to distinguish patterns of interaction between healthy and diseased individuals. Our results, quantified as the mean Area under the ROC curve (AUC) over 75 iterations, indicate that, using fMRI data, we can discriminate between the two cohorts well (AUC > 0.8). Specifically, we find that MCA (mean AUC = 0.89) based connectivity features perform significantly better ($p < 0.05$) when compared to cross correlation (mean AUC = 0.82) at the classification task. A higher AUC using our approach suggests that such a nonlinear approach is better able to capture connectivity changes between brain regions and has potential for the development of novel neuro-imaging biomarkers.

10137-54, Session 10

Diffusion tractography and graph theory analysis reveal the disrupted rich-club organization of white matter structural networks in early Tourette Syndrome children

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Tourette syndrome (TS) is a childhood-onset neurobehavioral disorder. At present, the topological disruptions of the whole brain white matter (WM) structural networks remain poorly understood in TS children. Considering the unique position of the topologically central role of densely interconnected brain hubs, especially the rich club regions, therefore, we aimed to investigate whether the rich club regions and their related connections would be particularly vulnerable in early TS children. In our study, we used diffusion tractography and graph theoretical analyses to explore the rich club structures in 44 TS children and 48 healthy children. The structural networks of TS children exhibited altered rich club organization with reorganization of rich club regions, as well as significantly increased density and decreased number in rich club and feeder connections, suggesting that TS is characterized by altered structural integrity of this centrally embedded rich club backbone, potentially resulting in altered global communication capacity. Furthermore, the rich club coefficients of patients were significantly increased, and the significant correlations between rich club coefficients and the network clustering coefficient, small-worldness exist in healthy children were disrupted in TS group. In all, our results suggest a disrupted rich club organization in TS children and provide structural insights into the brain networks of early TS children.

10137-95, Session 10

Learning discriminative functional network features of schizophrenia

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No Abstract Available

10137-47, Session 11

Test-suite for image-based motion estimation of the brain and tongue

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Noninvasive analysis of motion has important uses as qualitative markers for organ function, and to validate biomechanical computer simulations relative to experimental observations. Tagged MRI is considered the gold standard for non-invasive tissue motion estimation in the heart, and this has inspired multiple studies focusing on other organs including the brain under acceleration, and the tongue during speech. However, as with other estimation approaches, tracking of tagged MRI in 3D includes several preprocessing steps and parameters that affect the quality and accuracy of the estimation. These parameters are often tuned by comparing the results of motion estimation with a test suite that includes known benchmark geometry and displacements. In that way, different approaches can be used, and compared, in the same set of images. Although some cardiac motion databases do exist, comprehensive datasets in other organs is scarce or even nonexistent, and it is uncertain that the existent data is applicable in the novel applications given fundamental differences in the motion patterns that would be expected in these new organs compared the heart. Therefore, the objective of this research was to design and construct a motion estimation 4D test suite including realistic geometry, imaging parameters (such as acquisition inconsistency), and mechanically representative motion obtained via finite-element modeling. Finally, as a demonstration the applicability of the test suite, the effect of motion inconsistency on synthetic measurements of head rotation was evaluated. Preliminary results indicate that acquisition inconsistency is propagated, and roughly proportional, to head rotation estimation error.

10137-48, Session 11

Longitudinal analysis of mouse SDOCT volumes

Bhavna J. Antony, Aaron Carass, Andrew Lang, Byung-Jin Kim, Donald J. Zack, Jerry L. Prince, Johns Hopkins Univ. (United States)

Spectral-domain optical coherence tomography (SDOCT), in addition to its routine clinical use in the diagnosis of ocular diseases, has begun to find increasing use in animal studies. Animal models are frequently used to study disease mechanisms as well as to test drug efficacy. In particular, it provides the ability to non-invasively study animals longitudinally over longer periods of time. However, the lack of anatomical landmarks makes the longitudinal scan acquisition prone to inconsistencies in orientation. Here, we propose a method for the automated registration of mouse SDOCT volumes. The method begins by accurately segmenting the blood vessels and the optic nerve head region in the scans, and subsequently uses these landmarks to register the longitudinal scans. Consequently, layer thickness measurements can now be compared accurately and consistently, increasing the ability to discern localized changes.

10137-49, Session 11

A fully-automated multiscale kernel graph cuts based particle localization scheme for temporal focusing two-photon microscopy

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The temporal focusing two-photon microscope (TFM) is established to perform depth resolved wide field imaging by capturing frames sequentially. However, due to strong nonignorable noises and diffraction rings surrounded by scanned particles, further researches are extremely formidable without a precise particle localization technique. In this paper, we created a fully-automated scheme to locate particles with high noise tolerance. Our scheme includes the following procedures: noise reduction using a hybrid Kalman filter method, particle segmentation based on a multiscale kernel graph cuts global and local segmentation algorithm, and a kinematic estimation based particle tracking method. As a consequence, both isolated and partial-overlapped particles can be accurately identified with removal of unrelated pixels. Based on our quantitative analysis, 96.22% isolated particles and 84.19% partial-overlapped particles were successfully detected.

10137-50, Session 11

Inter-session repeatability of retinal layer thickness in optical coherence tomography

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Reliable retinal layer thickness measurements using optical coherence tomography (OCT) are important to track the subtle retinal changes in longitudinal studies. A total of 10 eyes (5 healthy subjects, 40±13 years old) were enrolled to study the inter-session repeatability and identify the pitfalls affecting the reliabilities. Each eye was scanned using spectral domain OCT (Spectralis SDOCT, Heidelberg Engineering) for 3 sessions with 30 seconds rest in between. The first and second sessions were scanned independently and the third one was scanned with the first one as the baseline visit. Each session consisted of a confocal scanning laser ophthalmoscopy (cSLO) image and 61 B-scans of 496x768 pixels. The first, second and third sessions were named as baseline, unregistered and registered sessions; respectively. Seven retinal layers labeled as RNFL, GCL+IPL, INL, OPL, ONL, IS and OS were segmented using a custom software (OCTRIMA3D) and measured in the ETDRS grid. Inter-session standard deviation (?), coefficient of repeatability (CR) and coefficient of variations (COV) were calculated to quantify the repeatability. Paired t-test of COVs was used to compare the repeatability and the level of significance was set at 5%. We obtained that values of the CR >5 μm and COV of 5%, were revealed only in the outer layers. The values of COV were not significantly different ($p<0.05$) in the unregistered scanning session. Our results show that the rotations in the unregistered scanning sessions do not cause significant change in repeatability.

10137-76, Session 11

Efficient multi-atlas registration using an intermediate template image

Blake E. Dewey, Aaron Carass, Ari M. Blitz, Jerry L. Prince, Johns Hopkins Univ. (United States)

Multi-atlas label fusion is an accurate but time-consuming method of labeling the human brain. Using an intermediate image as a registration target can allow researchers to reduce time constraints by storing the deformations required of the atlas images. In this paper, we investigate the effect of registration through an intermediate template image on multi-atlas label fusion and propose a novel registration technique to counteract the negative effects of through-template registration. We show that overall computation time can be decreased dramatically with minimal impact on final label accuracy and time can be exchanged for improved results in a predictable manner. We see almost complete recovery of Dice similarity over a simple through-template registration using the corrected method and still maintain a 3-4 times speed increase.

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10138-501, Session PL

Applying deep learning to medical imaging

Greg Corrado, Google (United States)

No Abstract Available

10138-1, Session 1

Active contours extension and similarity indicators for improved 3D segmentation of thyroid ultrasound images

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Thyroid segmentation in tracked 2D ultrasound using active contours creating a 3D model has low segmentation accuracy mainly due to the fact that smaller structures cannot be efficiently recognized and segmented. To address that issue, we propose an improved method to by extending an active contour model in 2D to generate a 3D segmented thyroid volume. First, a preprocessing step is carried out to suppress the noise present in US data. Histogram Equalization and Median Filter are used to suppress the noise and enhance the contrast in the image. In the second phase, active contours are used to segment the thyroid in each 2D image of the dataset. After performing the first segmentation, two similarity indicators (ratio of mean square error and correlation between histograms) are computed at each pixel around the segmented thyroid by comparing the inside and outside of the segmented thyroid. A threshold is used on these indicators to find the probable regions for further segmentation in the image, where active contours are used again to perform the segmentation. This process is repeated until any new segmentation regions are not identified by similarity indicators. This process is repeated in all the images of the dataset. Finally, all the segmented thyroid images are passed to a 3D reconstruction algorithm to obtain a 3D model of the thyroid.

10138-2, Session 1

Frequency-based similarity detection of structures in human brain

Dave I. Sims, Mohamad-Reza Siadat, Oakland Univ. (United States)

Advancements in 3D scanning and volumetric imaging methods have motivated researchers to tackle new challenges related to storing, retrieving and comparing 3D models, especially in medical domain. Comparing natural rigid shapes and detecting subtle changes in 3D models of brain structures is of great importance. Precision in capturing surface details and insensitivity to shape orientation are highly desirable properties of good shape descriptors. In this paper, we propose a new method, Spherical Harmonics Distance (SHD), which leverages the power of spherical harmonics to provide more accurate representation of surface details. At the same time, the proposed method incorporates the features of a shape distribution method (D2) and inherits its insensitivity to shape orientation. Comparing SHD to a spherical harmonics based method (SPHARM) shows that the performance of the proposed method is less sensitive to rotation. Also, comparing SHD to D2 shows that the proposed method is more accurate in detecting subtle changes. The performance of the proposed method is verified by calculating the Fisher measure (FM) of extracted feature vectors. The FM of the vectors generated by SHD on average shows 27 times higher values than that of D2. Our preliminary results show that SHD successfully combines desired features from two different methods and paves the way towards better detection of subtle dissimilarities among natural rigid shapes (e.g. structures of interest in human brain). Detecting these subtle changes can be instrumental in more accurate diagnosis, prognosis and treatment planning.

10138-3, Session 1

Implementation of a Computer-aided Detection Tool for Quantification of Intracranial Radiologic Markers on Brain CT Images

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Aneurysmal subarachnoid hemorrhage (aSAH) is a form of hemorrhagic stroke that affects middle-aged individuals and associated with significant morbidity and/or mortality especially those presenting with higher clinical and radiologic grades at the time of admission. Previous studies suggested that blood extravasated after aneurysmal rupture was a potentially clinical prognosis factor. But all such studies used qualitative scales to predict prognosis. The purpose of this study is to develop and test a new interactive computer-aided detection scheme to detect, segment and quantify brain hemorrhage and ventricular cerebrospinal fluid on non-contrasted brain CT images. First, scheme segments brain skull using a multilayer region growing algorithm with adaptively adjusted thresholds. Second, scheme assigns pixels inside the segmented brain region into one of three classes namely, normal brain tissue, blood and fluid. Third, to avoid a "black-box" approach and increase accuracy in quantification of these two image markers using CT images with large noise variation in different cases, scheme allows users to visually examine segmentation results. If a user likes to correct any errors (i.e., deleting clinically irrelevant blood or fluid regions, or fill in the holes inside the relevant blood or fluid regions), he/she manually defines the region and selects a corresponding correction function. Scheme will automatically perform the correction and update the computed data. The new scheme is now being used in clinical and research settings to estimate various quantitative radiological parameters to determine radiological severity of aSAH at presentation and correlate the estimation with various homeostatic/metabolic derangements and predict clinical outcome.

10138-4, Session 1

Optic disc segmentation: level set methods and blood vessels inpainting

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Segmenting the optic disc (OD) is an important and essential step in creating a frame of reference for diagnosing optic nerve head (ONH) pathology such as glaucoma. Therefore, a reliable OD segmentation technique is necessary for automatic screening of ONH abnormalities. The main contribution of this paper is in presenting a novel OD segmentation algorithm based on applying a level set method on a localized OD image. To prevent the blood vessels from interfering with the level set process, an inpainting technique is applied. The algorithm is evaluated using a new retinal fundus image dataset called RIGA (retinal images for glaucoma analysis). In the case of low quality images, a double level set was applied in which the first level set was considered to be a localization for the OD. Five hundred and fifty images are used to test the algorithm accuracy as well as the agreement among the manual markings of six ophthalmologists. The accuracy of the algorithm in marking the optic disc area and centroid is 83.9%, and the best agreement is observed between the results of the algorithm and manual markings in 379 images.

10138-5, Session 1

Automatic multi-label annotation of abdominal CT images using CBIR

Zhiyun Xue, Sameer K. Antani, Rodney Long, George R. Thoma, National Library of Medicine (United States)

We present a technique to annotate multiple organs shown in 2D abdominal/pelvic CT images using CBIR. This annotation task is motivated by our research interests in visual question-answering (VQA). We aim to apply results from this effort in Open-i, a multimodal biomedical search engine developed by the National Library of Medicine (NLM). Understanding visual content of biomedical images is a necessary step for VQA. Sometimes sufficient semantic information for the image is available in textual metadata related to the images. However, not all anatomical labels may be available. In this paper, we develop and evaluate a multi-label image annotation method using CBIR. We evaluate our method on two 2D CT image datasets we generated from 3D volumetric data obtained from a multi-organ segmentation challenge hosted in MICCAI 2015. Shape and spatial layout information is used to encode visual characteristics of the anatomy. We adapt a weighted voting scheme to assign multiple labels to the query image by combining the labels of the images identified as similar by the method. We examine the important parameters that may affect the annotation performance, such as the number of images used in the label voting and the threshold for excluding labels that have low weights. We propose a coarse-to-fine retrieval strategy which integrates the classification with the nearest-neighbor search. We carry out several experiments to assess our method.

10138-6, Session 2

Discriminating between benign and malignant breast tumors using 3D convolutional neural network in dynamic contrast enhanced MR images

Jing Li, Ming Fan, Hangzhou Dianzi Univ. (China); Juan Zhang, Zhejiang Cancer Hospital (China); Lihua Li, Hangzhou Dianzi Univ. (China)

Convolutional neural networks (CNNs) are the state-of-the-art deep learning network architectures that can be used in a range of applications, including computer vision and medical image analysis. It exhibits a powerful representation learning mechanism with an automated design to learn features directly from the data. However, the common 2D CNNs only use the two dimension spatial information without evaluating the correlation between the adjoin slices. In this study, we established a method of 3D CNNs to discriminate between malignant and benign breast tumors. To this end, 133 patients were enrolled which include 74 benign and 59 malignant instances. The MRI images were pre-processed for noise reduction, image registration and breast region segmentation. Data augmentation by spatial translation and rotation and vertical and horizontal flipping is applied to the cases to reduce possible over-fitting. A region-of-interest (ROI) and a volume-of-interest (VOI) were segmented in 2D and 3D DCE-MRI, respectively. The enhance rate for each MR series was calculated for the 2D and 3D images. The results for the enhance images in the two series are intergraded for classification. The results of accuracy, are 69.17% and 72.93% for 2D and 3D images, respectively. The results for CNN to combine 5 slices for each subtraction images achieved a high accuracy, sensitivity and specificity of 0.89, 0.81 and 0.95, respectively. This study indicates that 3D CNN deep learning methods can be a promising technology for breast tumor classification without manual feature extraction.

10138-7, Session 2

Making sense of large data sets without annotations: analyzing age-related correlations from lung CT scans

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The analysis of large datasets can help to gain knowledge about specific organs or on specific diseases, just as big data analysis does in many non-medical areas. This article aims to gain information from 3D volumes, so the visual content of lung CT scans of a large number of patients. In the case of the described dataset, only little annotation is available on the patients that were all part of an ongoing screening program and besides age and gender no information on the patient and the findings was available for this work. This is a scenario that can happen regularly as image datasets are produced and become available in increasingly large quantities but manual annotations are often not available and also clinical data such as text reports are often harder to share. We extracted a set of visual features from 12,414 CT scans of 9,348 patients that had CT scans of the lung taken in the context of a national lung screening program. Lung fields were segmented by two segmentation algorithms and only cases where both algorithms were able to find left and right lung and had a Dice coefficient above 0.95 were analyzed. Patients ranged in age between 0 and 106 years. Data analysis shows that age can be predicted with a fairly high accuracy for persons under 15 years. Relatively good results were also obtained between 30 and 65 years. For young adults and older people the results are not as good. The experiments allow learning the evolution of the lung and the gained results show that even with limited meta-data we can extract interesting information from large-scale visual data. These age-related changes (for example of the lung volume, density histogram of the tissue) can also be taken into account for the interpretation of new cases.

10138-8, Session 2

Local-global classifier fusion for screening chest radiographs

Meng Ding, Sameer K. Antani, Stefan R. Jaeger, Zhiyun Xue, Sema Candemir, National Library of Medicine (United States); Marc Kohli, Univ. of California, San Francisco (United States); George R. Thoma, National Library of Medicine (United States)

Tuberculosis (TB) is a severe comorbidity of HIV and chest x-ray (CXR) analysis is a necessary step in screening for the infective disease. Automatic

analysis of digital CXR images for detecting pulmonary abnormalities is critical for population screening, especially in medical resource constrained developing regions. In this article, we describe steps that improve previously reported performance of NLM's CXR screening algorithms and help advance the state of the art in the field. We propose a local-global classifier fusion method where two complementary classification systems are combined. The local classifier focuses on subtle and partial presentation of the disease leveraging information in radiology reports that roughly indicates locations of the abnormalities. In addition, the global classifier models the dominant spatial structure in the gestalt image using GIST descriptor for the semantic differentiation. Finally, the two complementary classifiers are combined using linear fusion, where the weight of each decision is calculated by the confidence probabilities from the two classifiers. We evaluated our method on three datasets in terms of the area under the Receiver Operating Characteristic (ROC) curve, sensitivity, specificity and accuracy. The evaluation demonstrates the superiority of our proposed local-global fusion method over any single classifier.

10138-9, Session 2

Theoretical and empirical comparison of big data image processing with Apache Hadoop and Sun Grid Engine

Shunxing Bao, Frederick D. Weitendorf, Andrew J. Plassard, Yuankai Huo, Aniruddha Gokhale, Bennett A. Landman, Vanderbilt Univ. (United States)

The field of big data is generally concerned with the scale of processing at which traditional computational paradigms break down. In medical imaging, traditional large scale processing uses a cluster computer that combines a group of workstation nodes into a functional unit that is controlled by a job scheduler. Typically, a shared-storage network file system (NFS) is used to host imaging data. However, data transfer from storage to processing nodes can saturate network bandwidth when data is frequently uploaded/retrieved from the NFS, e.g., "short" processing times and/or "large" datasets. Recently, an alternative approach using Hadoop and HBase was presented for medical imaging to enable co-location of data storage and computation while minimizing data transfer. The benefits of using such a framework must be formally evaluated against a traditional approach to characterize the point at which simply "large scale" processing transitions into "big data" and necessitates alternative computational frameworks. The proposed Hadoop system was implemented on a production lab-cluster alongside a standard Sun Grid Engine (SGE). Theoretical models for wall-clock time and resource time for both approaches are introduced and validated. To provide real example data, three T1 image archives were retrieved from a university secure, shared web database and used to empirically assess computational performance under three configurations of cluster hardware (using 72, 109, or 209 CPU cores) with differing job lengths. Empirical results match the theoretical models. Based on these data, a comparative analysis is presented for when the Hadoop framework will be relevant and non-relevant for medical imaging.

10138-10, Session 2

DAX - the next generation: towards one million processes on commodity hardware

Stephen Damon, Brian D. Boyd, Andrew J. Plassard, Warren Taylor, Bennett A. Landman, Vanderbilt Univ. (United States)

Large scale image processing demands a standardized way of not only storage but also a method for job distribution and scheduling. The eXtensible Neuroimaging Archive Toolkit (XNAT) is one of several platforms that seeks to solve the storage issues. Distribution Automation for XNAT (DAX) is a job control and distribution manager. Recent massive data projects have revealed several bottlenecks for projects with >100,000 assessors (i.e., data processing pipelines in XNAT). In order to address these concerns, we have developed a new API, which exposes a direct connection to the database rather than REST API calls to accomplish the generation of assessors. This method, consistent with XNAT, keeps a full history for auditing purposes. Additionally, we have optimized DAX to keep track of processing status on disk (called DISKQ) rather than on XNAT, which greatly reduces load on XNAT by vastly dropping the number of API calls. Finally, we have integrated DAX into a Docker container with the idea of using it as a Docker controller to launch Docker containers of image processing pipelines. Using our new API we reduced the time to create 1,000 assessors (a sub-cohort of our case project) from 65040 seconds to 229 seconds (a decrease of over 270 fold). DISKQ, using pyXnat, allows launching of 400 jobs in under 10 seconds which previously took 2,000 seconds. Together these updates position DAX to support projects with hundreds of thousands of scans and to run them in a time-efficient manner.

10138-11, Session 2

Digital pathology annotation data for improved deep neural network classification

Edward Kim, SaiLakshmiDeepika Mente, Villanova Univ. (United States); Andrew Keenan, Villanova University (United States); Vijay Gehlot, Villanova Univ. (United States)

In the field of digital pathology, there is an explosive amount of imaging data being generated. Thus, there is an ever growing need to create assistive or automatic methods to analyze collections of images for screening and classification. Deep learning architectures have demonstrated great success over existing classification models but require massive amounts of labeled training data that either do not exist or are cost and time prohibitive to obtain. In this project, we present a framework for representing, collecting, validating, and utilizing cytopathology features for improved neural network classification. Preliminary results show that online crowdsourcing of cytological image features is feasible and can greatly improve deep learning classification results.

10138-12, Session 3

Prediction of response to neoadjuvant chemotherapy in breast cancer: a radiomic study

Guolin Wu, Ming Fan, Hangzhou Dianzi Univ. (China); Juan Zhang, Guoliang Shao, Zhejiang Cancer Hospital (China); Lihua Li, Hangzhou Dianzi Univ. (China)

Breast cancer is one of the most malignancies among women worldwide. Neoadjuvant Chemotherapy (NACT) has gained interest and is increasingly used in treatment of breast cancer in recent years. Therefore, it is necessary to find a reliable non-invasive method which can predict the response of NACT in breast cancer. Recent studies have highlighted the use of magnetic resonance imaging (MRI) for prediction. In addition, molecular subtype could also effectively identify patients who are likely have better prognosis in breast cancer after treatment. In this study, a radiomic analysis was performed, by extracting features from dynamic contrast-enhanced MRI (DCE-MRI) and immunohistochemistry (IHC) determined subtypes. A dataset with fifty-seven breast cancer patients were included, all of whom received MRI examination before NACT. Among them, 47 patients of response who had complete response (CR) or partial response (PR) and 10 with non-response, i.e., stable disease (SD) to chemotherapy based on the RECIST criterion. A total of 135 imaging features including statistical characteristics, morphology, texture and dynamic enhancement were extracted from DCE-MRI. In multivariate analysis, the proposed imaging predictors achieved an AUC of 0.777 (P = 0.0004) in leave-one-out cross-validation. The performance of the classifier increased to 0.860 and 0.821 when status of HER2 and Luminal B subtypes were added into the classification model, respectively. The results of this study demonstrated that radiomic features from DCE-MRI combined with IHC determined molecular status could be used as promising clinical marker that could predict response to NACT in breast cancer.

10138-13, Session 3

Phenotype analysis of early risk factors from electronic medical records improves image-derived diagnostic classifiers for optic nerve pathology

Shikha Chaganti, Kunal P. Nabar, Katrina M. Nelson, Louise A. Mawn, Bennett A. Landman, Vanderbilt Univ. (United States)

We examine imaging and electronic medical records (EMR) of 392 subjects over five major disease groups that affect optic nerve function. An objective evaluation of the role of imaging and EMR data in diagnosis of these conditions would improve understanding of these diseases and help in early intervention. We developed an automated image-processing pipeline that identifies the orbital structures within the human eyes from computed tomography (CT) scans, and calculates structural size, and volume measurements. We customized the EMR-based phenome-wide association study (PheWAS) to derive diagnostic EMR phenotypes that occur at least two years prior to the onset of the conditions of interest from a cohort of 28,411 ophthalmology patients. We used random forest classifiers to evaluate the predictive power of image-derived markers, EMR phenotypes, and clinical visual assessments in identifying disease cohorts from a control group of 1,566 patients without optic nerve disease. Image-derived markers showed more predictive power than clinical visual assessments or EMR phenotypes. However, the addition of EMR phenotypes to the imaging markers improves the classification accuracy against controls: the AUC improved from 0.84 to 0.87 for glaucoma, 0.79 to 0.86 for intrinsic optic nerve disease, 0.82 to 0.87 for optic nerve edema, 0.84 to 0.86 for orbital inflammation, and 0.91 to 0.93 for thyroid eye disease. This study illustrates the importance of diagnostic context for interpretation of image-derived markers and the proposed PheWAS technique provides a flexible approach for learning salient features of patient history and incorporating these data into traditional machine learning analyses.

10138-14, Session 3

The development and implementation of MOSAIQ Integration Platform (MIP) based on the radiotherapy workflow

Xin Yang, Ying SUN, Sun Yat-Sen Univ. Cancer Ctr. (China)

To meet the special demands in China and the particular needs for the radiotherapy department, a MOSAIQ Integration Platform CHN (MIP) based on the workflow of radiation therapy (RT) has been developed, as a supplement system to the Elekta MOSAIQ.

The MIP adopts C/S (client-server) structure mode, and its database is based on the Treatment Planning System (TPS) and MOSAIQ SQL Server 2008, running on the hospital local network. Five network servers, as a core hardware, supply data storage and network service based on the cloud services. The core software, using C# programming language, is developed based on Microsoft Visual Studio Platform. The MIP server could offer network service, including entry, query, statistics and print information for about 200 workstations at the same time.

The MIP was implemented in the past one and a half years, and some practical patient-oriented functions were developed. And now the MIP is almost covering the whole workflow of radiation therapy. There are 15 function modules, such as: Notice, Appointment, Billing, Document Management (application/execution), System Management, and so on. By June of 2016, recorded data in the MIP are as following: 13546 patients, 13533 plan application, 15475 RT records, 14656 RT summaries, 567048 billing records and 506612 workload records, etc.

The MIP based on the RT workflow has been successfully developed and clinically implemented with real-time performance, data security, stable operation?And it is demonstrated to be user-friendly and is proven to significantly improve the efficiency of the department. It is a key to facilitate the information sharing and department management. More functions can be added or modified for further enhancement its potentials in research and clinical practice.

10138-15, Session 3

A low noise stenography method for medical images with QR encoding of patient information

Juan Carlos Martinez-Santos, Alberto Patiño-Vanegas, Sonia H. Contreras-Ortiz, Univ. Tecnológica de Bolívar (Colombia)

This paper proposes an approach to facilitate the process of individualization of patients from their medical images, without compromising the inherent confidentiality of medical data. The identification of a patient from a medical image is not often the goal of security methods applied to image records. Usually, any identification data is removed from shared records, and security features are applied to determine ownership. To be able to identify an individual patient keeping secure his information, we use steganography. It is the study and application of techniques to hide objects within others, called carriers, so that they are not perceived. This technique allows hiding an identification pattern into the clinical image for sharing, so that the extra information passes unnoticed by anyone who has access to the image. The main idea of steganography is to transmit information “hidden” in a seemingly innocuous message. Then, the information can be retrieved by using an inverse function. The proposed steganographic scheme starts with a genuine medical image (H), called carrier, that is slightly modified to embed the patient identification pattern (Q). The steganographic message (H’) is the result of embedding the information within the carrier. The QR-code is distributed in the image by changing several pixels according to a threshold value based on the average value of adjacent pixels surrounding the point of interest. The results show that the code can be embedded and later fully recovered with minimal changes in the UIQI index - less than 0.1% of different.

10138-16, Session 3

Exploring a New Quantitative Image Marker to Assess Benefit of Chemotherapy to Ovarian Cancer Patients

Seyedehnafiseh Mirniaharikandehei, Omkar Patil, Faranak Aghaei, Yunzhi Wang, Bin Zheng, The Univ. of Oklahoma (United States)

Accurately assessing the potential benefit of chemotherapy to cancer patients is an important prerequisite to developing precision medicine in cancer treatment. the Previous study has shown that total psoas area (TPA) measured on preoperative cross-section CT image might be a good image marker to predict long-term outcome of pancreatic cancer patients after surgery. However, accurate and automated segmentation of TPA from the CT image is difficult due to the fuzzy boundary or connection of TPA to other muscle areas. In this study, we developed a new interactive computer-aided detection (ICAD) scheme aiming to more accurately segment TPA from the abdominal CT images and assess the feasibility of using this new quantitative image marker to predict the benefit of ovarian cancer patients who receiving Bevacizumab-based chemotherapy. ICAD scheme was

applied to identify a CT image slice of interest, which locates at the level of L3 (vertebral spines). The cross-sections of the right and left TPA are segmented using a set of adaptively adjusted boundary conditions. TPA is then quantitatively measured. The scheme and TPA measurement task was applied to a large national clinical trial database involving 938 ovarian cancer patients. By comparing with manual segmentation results, we found that ICAD scheme could yield higher accuracy and consistency for this task. Using a new ICAD scheme can provide clinical researchers a useful tool to more efficiently and accurately extract TPA as a new image maker, and then investigate the discriminatory power of TPA to predict progression-free survival and/or overall survival of the cancer patients before taking chemotherapy.

10138-17, Session 4

Evaluation of a web based informatics system with data mining tool for predicting outcomes with quantitative imaging features in stroke rehabilitation clinical trials

Ximing Wang, Bokkyu Kim, Ji Hoon Park, Erik Wang, Sydney Forsyth, Cody Lim, Ragini Ravi, Sarkis Karibyan, Alexander Sanchez, Brent J. Liu, The Univ. of Southern California (United States)

Quantitative imaging biomarkers are used widely in clinical trials for tracking and evaluation of the medical interventions. Previously, we have presented a web based informatics system utilizing quantitative imaging features for predicting outcomes in stroke rehabilitation clinical trials. The system integrates imaging features extraction tools and a generalized linear mixed effects model (GLMM) module that can automatically investigate potential significance and correlation based on features extracted from clinical data and quantitative biomarkers. The imaging features extraction tools allow user to collect imaging features and the GLMM module allows user to select clinical data and imaging features such as stroke lesion characteristics from the database as regressors and regressands. The GLMM module will conveniently display the significance and correlations of selected variables. Once an accurate GLMM model is identified, the module can predict outcomes for new patients and can be utilized as a decision support tool for the treatment plans optimization.

This paper will discuss the application and evaluation results of the system in a stroke rehabilitation clinical trial - Dose optimization for Stroke Evaluation(DOSE) clinical trial. The DOSE clinical trial collects 44 subjects in a four year period. A baseline evaluation, three sessions of treatments, and six follow-ups are conducted for each patient. The data involved includes digital questionnaires, MRI and DTI images, videos, and motion sensor data. The system is utilized to manage clinical data and extract imaging biomarkers including stroke lesion volume, location and ventricle/brain ratio. The GLMM module will be used to investigate potential correlation within baseline information, outcome measurements, therapy information and imaging features. The GLMM module will be validated by the DOSE clinical trial and the efficiency of data analysis will also be evaluated.

10138-18, Session 4

Evaluation of longitudinal tracking and data mining for an imaging informatics-based multiple sclerosis e-folder

Kevin C. Ma, Sydney Forsyth, Lilyana Amezcua, Brent J. Liu, The Univ. of Southern California (United States)

We have designed and developed a multiple sclerosis eFolder system for patient data storage, image viewing, and automatic lesion quantification results to allow patient tracking. 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 quantifies lesion volumes, identify and register lesion locations to track shifts in volume and quantity of lesions in a longitudinal study. We aim to evaluate the two most important features of the system, data mining and longitudinal lesion tracking, to demonstrate the MS eFolder's capability in improving clinical workflow efficiency and outcome analysis for research. In order to evaluate data mining capabilities, we have collected radiological and neurological data from 72 patients, 36 Caucasian and 36 Hispanic matched by gender, disease duration, and age. Data analysis on those patients based on ethnicity is performed, and analysis results are displayed by the system's web-based user interface. The data mining module is able to successfully separate Hispanic and Caucasian patients and compare their disease profiles. For longitudinal lesion tracking, we have collected 4 longitudinal cases and simulated different lesion growths over the next year. As a result, the eFolder is able to detect changes in lesion volume and identifying lesions with the most changes. Data mining and lesion tracking evaluation results show high potential of eFolder's usefulness in patientcare and informatics research for multiple sclerosis.

10138-19, Session 4

Prediction of near-term breast cancer risk using local region-based bilateral asymmetry features in mammography

Yane Li, Ming Fan, Lihua Li, Hangzhou Dianzi Univ. (China); Bin Zheng, Hangzhou Dianzi Univ. (China) and The Univ. of Oklahoma (United States)

To predict near-term breast cancer risk, this study proposed a novel near-term risk assessment model based on local region bilateral asymmetry features in Mammography. The database includes 570 cases who underwent at least two sequential FFDM examinations. The "prior" examination in the two series all interpreted as negative (not recalled). In the "current" examination, 285 women were diagnosed cancers and 285 remained negative. Cancers and negative cases of age completely matches. These cases were divided into three subgroups according to age: 77 cases among the 37-49 age-bracket, 110 cases in the age-bracket 50-60, and 98 cases with the 61-86 age-bracket. Two local regions were obtained, including strip-based regions and difference-of-Gaussian basic element regions. After that, structural variations among pixel values and structural similarity indices were computed for strip regions. Meanwhile, positional information were extracted for basic element regions. The absolute subtraction value was computed between each feature of the left and right local-regions. Next, a multi-layer perception classifier was implemented to assess performance of features for prediction. Features were then selected according to their attribute and performance. The maximum AUC of the individual features were 0.611, 0.59 and 0.623 and the AUC of combined selected features were 0.708, 0.673 and 0.721 for the 3 age-based subgroups, respectively. The maximum adjustable odds ratios were 8, 3.1043 and 9.99 for the three groups, respectively. This study demonstrate that the local region-based bilateral asymmetry features extracted from CC-view mammography could provide useful information to predict near-term breast cancer risk.

10138-20, Session 4

The development of a decision support system with an interactive clinical user interface for estimating treatment parameters in radiation therapy in order to reduce radiation dose in head and neck patients.

Sneha K. Verma, Joseph Liu, Ruchi R. Deshpande, The Univ. of Southern California (United States); John J.

DeMarco, Cedars-Sinai Health System (United States); Brent J. Liu, The Univ. of Southern California (United States)

The primary goal in radiation therapy is to target the tumor with the maximum possible radiation dose while limiting the radiation exposure of the surrounding healthy tissues. However, in order to achieve an optimized treatment plan, many constraints, such as gender, age, tumor type, location, etc. need to be considered. The location of the malignant tumor with respect to the vital organs is another possible important factor for treatment planning process which can be quantified as a feature making it easier to analyze its effects. Incorporation of such features into the patient's medical history could provide additional knowledge that could lead to better treatment outcomes. To show the value of features such as relative locations of tumors and surrounding organs, the data is first processed in order to calculate the features and formulate a feature matrix. Then these feature are matched with retrospective cases with similar features to provide the clinician with insight on delivered dose in similar cases from past. This process provides a range of doses that can be delivered to the patient while limiting the radiation exposure of surrounding organs based on similar retrospective cases. As the number of patients increase, there will be an increase in computations needed for feature extraction as well as an increase in the workload for the physician to find the perfect dose amount. In order to show how such algorithms can be integrated we designed and developed a system with a streamlined workflow and interface as prototype for the clinician to test and explore. Integration of the tumor location feature with the clinician's experience and training could play a vital role in designing new treatment algorithms and better outcomes.

10138-36, Session PSWed

Using Deep Learning for Content-Based Medical Image Retrieval

Qinpei Sun, Yuanyuan Yang, Jianyong Sun, Shanghai Institute of Technical Physics of the Chinese Academy of Sciences (China); Zhiming Yang, Radiology Department of Huadong Hospital (China); Jianguo Zhang, Shanghai Institute of Technical Physics of the Chinese Academy of Sciences (China)

Medical imaging modalities generate huge amount of medical images daily, and there are urgent demands to search large scale image databases in an RIS-integrated PACS environment to support medical research and do decision support during diagnosis by using image visual content to find visually similar images. Content-based image retrieval (CBIR) is technique to retrieve similar images from image database based on extracted features. There are two major issues in CBIR research and applications. First one issue is "semantic gap" which exists between low-level image pixels captured by machines and high-level semantic concepts perceived by human; The second one is the "curse of dimensionality" which is a large number (hundreds even thousands) of dimensions of feature vectors were usually used to comparing the similarity of images and this would significantly decrease the performance of the CBIR. We had developed semantic based CBIR and high dimensional Imaging Database for CBIR Search and presented in SPIE Medical Imaging 2009 and 2016. In this presentation, we proposed a novel framework which uses deep learning technique to build CBIR and combine semantic information and image pixel features together in the CBIR and to retrieval the medical image from a simulated RIS-integrated PACS to improve the accuracy and speed of a CBIR.

10138-37, Session PSWed

Collaborative SDOCT segmentation and analysis software

Yeyi Yun, Aaron Carass, Andrew Lang, Jerry L. Prince, Bhavna J. Antony, Johns Hopkins Univ. (United States)

Spectral domain optical coherence tomography (SDOCT) is routinely used in the management and diagnosis of a variety of ocular diseases. This imaging modality also finds widespread use in research, where quantitative measurements obtained from the images are used to track disease progression. In recent years, the number of available scanners and imaging protocols have grown and there is a distinct absence of a unified tool that is capable of visualizing, segmenting, and analyzing the data. This is especially noteworthy in longitudinal studies, where data from older scanners and/or protocols may need to be analyzed. Here, we present a graphical user interface (GUI) that allows users to visualize and analyze SDOCT images obtained from two commonly used scanners. The retinal surfaces in the scans can be segmented using a previously described method, and the retinal layer thicknesses can be compared to a normative database. If necessary, the segmented surfaces can also be corrected and the changes applied. The interface also allows users to import and export retinal layer thickness data to an SQL database, thereby allowing for the collation of data from a number of collaborating sites.

10138-38, Session PSWed

DICOM Image quantification secondary capture (DICOM IQSC) integrated with numeric results, regions and curves: implementation and applications in nuclear medicine

Xinhua Cao, Boston Children's Hospital (United States) and Harvard Medical School (United States); Xiaoyin Xu, Brigham and Women's Hospital (United States) and Harvard Medical School (United States); Stephan Voss, Boston Children's Hospital (United States) and Harvard Medical School (United States)

Image quantification (IQ) of nuclear medicine provides more efficient and accurate diagnosis than subjective visual assessment of clinical images. In order to store IQ results, including numbers, regions of interest (ROIs) and time activity curves (TACs), one or multiple screen shots of an integrated IQ report, or said savescreens are created using a digital imaging and communications (DICOM) secondary capture (SC) object model. Such DICOM SC images can be archived into PACS and retrieved from any DICOM clients for review, but the numeric results, ROIs and TACs could not be reused in later clinical practice and research. DICOM structured report (SR) object provides an approach of integrating numeric IQ results, ROIs and TACs into PACS for archiving and retrieving based on IHE (Integrating the Healthcare Enterprise) workflow profiles, but it is too complete to implement with the existing PACS system under clinical environment. In this paper, we describe an enhanced DICOM SC that integrates IQ results, ROIs, and TACs with screen shots by embedding extra medical imaging information into a standard SC DICOM header. A software toolkit of DICOM IQSC has been developed to implement the SC-centered information integration of quantitative analysis for routine practice of nuclear medicine. Primary experiments show that the DICOM IQSC method is simple and easy to implement integrating seamlessly post-processing workstations with PACS for archiving and retrieving QI information. Further applications of DICOM IQSC in routine nuclear medicine and clinic research are also discussed.

10138-39, Session PSWed

High Precision Localization of Intracerebral Hemorrhage Based on 3D MPR on Head CT Images

Jianyong Sun, Xiaoshuai Hou, Shanghai Institute of Technical Physics of the Chinese Academy of Sciences (China); Shujie Sun, Clinical Medical Ctr. in Shanghai, Chinese Academy of Sciences (China); Jianguo Zhang, Shanghai Institute of Technical Physics of the Chinese Academy of Sciences (China)

The key step for minimally invasive cerebral hemorrhage surgery is precisely positioning the hematoma location in the brain before and during the hematoma surgery, which can significantly improves the success rate of puncture hematoma. We designed a 3D computerized surgical plan (CSP) workstation precisely to locate brain hematoma based on Multi-Planar Reconstruction (MPR) visualization technique. We used ten patients' CT/MR studies to verify our designed CSP cerebral hemorrhage localization method. With the doctor's assessment and comparing with the results of manual measurements, the output of CSP WS for hematoma surgery is more precise and reliable than manual procedure.

Purposes:

With the aged population becoming a serious problem in China, the cerebral hemorrhage causing the high morbidity and high mortality has been a major public health problem now. Compared to the traditional conservative treatment and surgical treatment, minimally invasive hematoma surgery has simple and less invasive characteristics, and it can significantly improve the patients' survival rate and life quality after surgery. Minimally invasive hematoma surgery has been gradually becoming an important clinical solution in the field of treatment of cerebral hemorrhage.

The key step for minimally invasive cerebral hemorrhage surgery is precisely positioning the hematoma location in the brain, which can significantly improves the success rate of puncture hematoma. It is important to have three-dimensional brain hematoma precisely positioning base on the reference plane in CT or MR imaging scanning. However, due to cerebral hemorrhage patients being usually conscious unclear or restlessness during brain CT/MR imaging, CT/MR slicing images are usually not strictly paralleled to the reference scan plane, so doctors have manually to determine the reference plane based on clinical experience, which will bring inconvenience and clinical measurement errors.

In order to resolve the above mentioned problems, we designed a 3D computerized surgical plan (CSP) workstation precisely to locate brain hematoma based on Multi-Planar Reconstruction (MPR) visualization technique. As a CSP tools, the workstation can be used to create hematoma minimally invasive surgical plan.

Materials and Methods:

The designed precision localization of brain hematoma uses the following parameters: ? scan reference plane Position, ? the distance between the puncture plane and the reference plane, ? the puncture plane which is the largest cross-sectional of Hematoma, ? brain radius of puncture plane, ? forehead distance which is the distance between the hematoma and the front coronal on puncture plane, and ? temporal distance which is the distance between the hematoma and the outer sagittal on puncture plane.

In our CSP workstation (WS) design, we first use MPR visualization method to reconstruct coronal plane (Coronal), sagittal plane (Sagittal) and the inclined plane (Oblique) plane, then based on the above three reconstruction plane with the designed positioning tools to move and rotate MPR cut line to search the reference plane; secondly combined with doctor's observation and using the designed positioning tools to find the puncture plane on sagittal planes. On the third step, we use crosshair tools to calculate brain radius, forehead distance, and temporal distance on puncture plane. Based on the parameters mentioned above and medical right-angle positioning rule designed in CSP WS, a neuro-surgeon can first create three-dimensional structure in hematoma puncture direction, then determine the puncture points, puncture direction and puncture depth, and finally perform hematoma surgery with the graphic surgical information generated in the CSP WS.

Results:

We used ten patients' CT/MR studies to verify our designed CSP cerebral hemorrhage localization method. With the doctor's assessment and comparing with the results of manual measurements, the output of CSP WS for hematoma surgery is more precise and reliable than manual procedure.

New Technologies and Results to be Presented:

This presentation presents a new cerebral hemorrhage localization method for hematoma surgery planning based on MPR visualization in PACS 3D workstation, which can calculate the reference plane and puncture plane more precisely than manual way.

Conclusions:

In this presentation, the new computerized cerebral hemorrhage surgical plan method precisely provides the localization of Cerebral Hemorrhage for neurosurgeons and can be easily to use before and during the hematoma surgery.

10138-40, Session PSWed

Computerized detection of breast cancer using resonance-frequency-based electrical impedance spectroscopy

Wei Gao, Ming Fan, Weijie Zhao, Hangzhou Dianzi Univ. (China); Bin Zheng, Hangzhou Dianzi Univ. (China) and The Univ. of Oklahoma (United States); Lihua Li, Hangzhou Dianzi Univ. (China)

This study developed and tested a multi-probe resonance-frequency-based electrical impedance spectroscopy (REIS) system aimed at detection of breast cancer. The REIS system consists of specially designed mechanical supporting device that can be easily lifted to fit women of different height, a seven probe sensor cup, and a computer providing software for system control and management. The sensor cup includes one central probe for direct contact with the nipple, and other six probes uniformly distributed at a distance of 35mm away from the center probe to enable contact with breast skin surface. It takes about 18 seconds for this system to complete a data acquisition process. We utilized this system for examination of breast cancer, collecting a dataset of 289 cases including biopsy verified 74 malignant and 215 benign tumors. After that, 22 REIS based features, including seven frequency and fifteen magnitude features were extracted. To reduce redundancy we selected 18 features using the support vector machine recursive feature elimination (SVM-RFE) for classification. The area under a receiver operating characteristic curve (AUC) was computed to assess classifier performance. A multivariate logistic regression method was performed for detection of the tumors. The results of our study showed AUC of 0.80 for the 18 REIS features, and AUC of 0.65 and 0.64 for the frequency and magnitude based REIS features, respectively. The results indicated the REIS system is a promising tool for detection of breast cancer and may be acceptable for clinical implementation.

10138-41, Session PSWed

Integration of the HTC Vive into the medical platform MeVisLab

Jan Egger, Technische Univ. Graz (Austria) and BioTechMed-Graz (Austria); Markus Gall, Technische Univ. Graz (Austria); Jürgen Wallner, Medizinischen Univ. Graz (Austria); Pedro de Almeida Germano Boechat, Techniche Univ. Graz (Austria); Alexander Hann, Univ. Ulm (Germany); Xing Li, Xiaojun Chen, Shanghai Jiao Tong Univ. (China); Dieter Schmalsteig, Techniche Univ. Gras (Austria)

No Abstract Available

10138-42, Session PSWed

Differentiating malignant from benign breast tumors on acoustic radiation force impulse imaging using fuzzy-based neural networks with principle component analysis

Hsiao-Chuan Liu, Univ. of Southern California (United States) and Children's Hospital Los Angeles (United States); Yi-Hong Chou, Chui-Mei Tiu, Taipei Veterans General Hospital (Taiwan); Chi-Wen Hsieh, National Chiayi Univ. (Taiwan); Brent J. Liu, K. Kirk Shung, The Univ. of Southern California (United States)

No Abstract Available

10138-43, Session PSWed

The design and integration of retinal CAD-SR to diabetes patient ePR system

Huiqun Wu, Yufang Wei, Univ. of Southern California, Los Angeles (United States); Yujuan Shang, Jiang Kui, Nantong Univ. (China); Jiancheng Dong, Nantong Univ. (China); Brent J. Liu, The Univ. of Southern California (United States)

No Abstract Available

10138-21, Session 5

Introduction to 3D printing *(Keynote Presentation)*

William Weadock, Univ. of Michigan (United States)

No Abstract Available

10138-22, Session 6

Feasibility of fabricating personalized 3D-printed bone grafts guided by high-resolution imaging

Chamith S. Rajapakse, Abigail Hong, Benjamin T. Newman, Arbab Khalid, Olivia M. Teter, Elizabeth A. Kobe, Malika Shukurova, Rohit S. Shinde, Daniel B. Sipzner, Univ. of Pennsylvania (United States); Robert J. Pignolo, Hospital of the Univ. of Pennsylvania (United States) and Presbyterian Medical Ctr. of Philadelphia (United States); Jayaram K. Udupa, Univ. of Pennsylvania (United States)

Current methods of bone graft treatment for critical size bone defects can give way to several clinical complications such as limited available bone for autografts, non-matching bone structure, lack of strength which can compromise a patient's skeletal system, and sterilization processes that can prevent osteogenesis in the case of allografts. We intend to overcome these disadvantages by generating a patient-specific 3D printed bone graft guided by high-resolution medical imaging. Our synthetic model allows us to customize the graft for the patients' macro- and microstructure and correct any structural deficiencies in the re-meshing process. These 3D-printed models can presumptively serve as the scaffolding for human mesenchymal stem cell (hMSC) engraftment in order to facilitate bone growth.

In this study, we performed high-resolution CT imaging of a cadaveric human proximal femur at 0.030-mm isotropic voxels. We used these images to generate a 3D computer model that mimics bone geometry from micro to macro scale represented by STereoLithography (STL) format. These models were then reformatted to a format that can be interpreted by the 3D printer. To assess how much of the microstructure was replicated, 3D-printed models were re-imaged using micro-CT at 0.025-mm isotropic voxels and compared to original high-resolution CT images used to generate the 3D model in 35 sub-regions. We found a strong correlation between 3D-printed bone volume and volume of bone in the original images used for 3D printing ($R2 = 0.97$). We expect to further refine our approach with additional testing to create a viable synthetic bone graft with clinical functionality.

10138-23, Session 6

3D printed Abdominal Aortic Aneurysm phantom for image guided surgical planning with a patient specific fenestrated endovascular graft system

Karen M. Meess, The Jacobs Institute, Inc. (United States) and CUBRC Inc. (United States) and Univ. at Buffalo (United States); Richard L. Izzo, The Jacobs Institute, Inc. (United States) and Univ. at Buffalo (United States) and Toshiba Stroke and Vascular Research Ctr. (United States); Maciej L. Dryjski, Richard E. Curl, Univ. at Buffalo (United States); Linda M Harris, Department of Vascular Surgery, University at Buffalo Jacobs School of Medicine and Biomedical Scien (United States); Michael E. Springer, The Jacobs Institute, Inc. (United States); Adnan H. Siddiqui, Univ. at Buffalo (United States); Stephen Rudin, Ciprian N. Ionita, Univ. at Buffalo (United States) and Toshiba Stroke and Vascular Research Ctr. (United States)

Purpose: Following the new trends in precision medicine, Abdominal Aortic Aneurysm (AAA) treatment using patient-specific fenestrated endovascular grafts is an approach which enables endovascular treatment for juxtarenal AAAs. The X-ray guided procedure requires precise orientation of radiopaque markers of multiple endografts within the arteries. To avoid periprocedural complications and improve training, patient-specific 3D printed phantoms could familiarize physicians with complex procedures and new devices in a risk-free simulation environment.

Methods: CTA imaging of two patients scheduled for Fenestrated EndoVascular Aortic Repair (FEVAR) was segmented using the Vascular Modeling Toolkit (VMTK) and the Toshiba Vitrea workstation to isolate the aortic lumen, thrombus, and calcifications. A stereolithographic mesh (STL) was generated and then modified in Autodesk MeshMixer for fabrication via Stratasys Eden 260 and Objet500 Connex3 printers using multimaterial technology to simulate various mechanical properties. X-ray guided simulation of the patient-specific FEVAR procedure was performed by interventionists using demonstration grafts and accessory devices. Analysis compared treatment strategy across planned procedure to simulation procedure to patient procedure.

Results: Training with 3D printed phantoms led to informed treatment strategy including: use of iliac artery dilation; selection of different shaped selective catheters, sheaths, and guide wires to access the renal arteries; change in imaging orientation approach for renal stent deployment; and alteration in endograft stent placement. The actual patient procedures went without complications. We demonstrated how patient-specific devices and patient-specific 3D printed phantoms can help to improve clinical interventional procedures using surgical planning.

10138-24, Session 6

Soft tissue models - easy and inexpensive flexible 3D printing as a help in surgical planing of cardio-vascular disorders

Zbigniew Starosolski, Texas Children's Hospital (United States); David Ezon, Children's Hospital of Pittsburgh (United States); Rajesh Krishnamurthy, Texas Children's Hospital (United States); Nicholas Dodd, Children's Hospital of Pittsburgh (United States); Jeffrey Heinle, Children's Hospital of Pittsburgh (United States); Dean E. McKenzie, Children's Hospital of Pittsburgh (United States); Ananth Annapragada, Children's Hospital of Pittsburgh (United States)

The study was designed to asses if flexible 3D printed models with simple 3D printer could help during surgical planning phase. Simple desktop 3D printer with dual extruder for Major aortopulmonary collateral arteries (MAPCAS) was used. FDM 3D printers are inexpensive, versatile in use and easy to maintain, but complications arise when designed model is complex and has tubular structures with small diameter less than 2mm. The advantage of FDM printers is cost and simplicity of use. We use precisely selected materials to overcome the obstacles listed above. Dual extruder allows to use two different materials while printing, especially important when printing fragile structures like pulmatory vessels and supporting it structures. The latest should not be removed by hand to avoid truncation of model. We utilize water soluble PVA as a supporting structure and Porolay filament for flexible model of aortopulmonary collateral arteries. Poro-lay filament is different comparing to all other flexible ones like polymer -based. Poro-lay is rigid while printing and that allows printing small structures in diameter. It achieves flexibility after washing out printed model with water. It becomes soft in touch and jelly like. Using both PVA and Poro-lay gives a huge advantage allowing to washout supporting structures and achieve flexibility in one washing operation, saving time and avoiding human error with cleaning the model. We evaluated 6 models for MAPCAS surgical planning study. This approach is also cost-effective – average cost of materials for print is less than $15, printed in facility without any delays. Flexibility of 3D printed models have good approximation of soft tissue mimicking aortopulmonary collateral arteries. Second utilization of 3D printed models has educational value for both residents and patients' family. Simplification of 3D flexible process could help in other models of soft tissue pathologies like aneurysms, ventricular septal defects and other vascular anomalies.

Results

We created 6 different models base of patient specific anatomy. All models were printed successfully, average printing time of model took 3.23 hr, cleaning in water bath with sonicator took 4 hr. Flexible 3d printed models ware reviewed by trained personnel, showing good correlation between 2D data sets and 3D printed models. Models were printed together with airways, which relative location were useful landmarks for the surgeon during unifocalization.

New or breakthrough work to be presented

Simple and cost-effective and time effective method to produce realistic flexible models for soft tissue as example we show application to pulmonary atresia with major aortopulmonary collaterals surgery planning.

Conclusions.

Described study presents alternative approach to more sophisticated and expensive 3D printing technique like Selective Laser Sintering or Stereolithography. Allowing to obtain flexible anatomical models on lower cost and at the same time in time-saving manner.

10138-25, Session 6

Design optimization for accurate flow simulations in 3D printed vascular phantoms derived from computed tomography angiography

Kelsey N. Sommer, Toshiba Stroke and Vascular Research Ctr. (United States) and Univ. at Buffalo (United States); Rick L. Izzo, Lauren Shepard, Alexander R. Podgorzak, Stephen Rudin, Adnan H. Siddiqui, Univ. at Buffalo (United States) and Toshiba Stroke and Vascular Research Ctr. (United States); Michael Wilson, Univ. at Buffalo (United States); Erin Angel, Toshiba America Medical Systems, Inc. (United States); Zaid Said, University at Buffalo Cardiology (United States); Michael Springer, Toshiba Stroke Research Center (United States); Ciprian N. Ionita, Univ. at Buffalo (United States) and Toshiba Stroke and Vascular Research Ctr. (United States)

3D printing has been used to create complex arterial phantoms to advance device testing and physiological condition evaluation. Stereolithograhic (STL) files of patient-specific cardiovascular anatomy are acquired to build cardiological and neurological vasculature through advanced mesh-manipulation techniques. Management of distal branches in the arterial tree is important to make such phantoms practicable.

We developed a design to manage the distal arterial flow resistance and pressure thus creating physiologically and geometrically accurate phantoms. Patient specific CT data were imported into a Vital Imaging workstation, segmented, and exported as STL files. Using a mesh-manipulation program (AutoDesk Meshmixer) we created flow models of the coronary tree and the Circle of Willis. Distal arteries were connected to a compliance chamber. The phantom was then printed using a Stratasys Connex3 multi-material printer: the vessel in Tango+ and the fluid flow simulation chamber in VeroBlue. The model was connected to a programmable pump and pressure sensors measured flow characteristics through the phantoms. Physiological flow simulations for patient-specific vasculature were done for five cardiac models and one neuro-model. For the coronary phantom we obtained physiological relevant waves which oscillated between 80 and 120 mmHg and a flow rate of ~125 ml/min, within the literature reported values. The pressure wave was similar with those acquired in human patients. Thus we demonstrated that 3D printed phantoms can be used not only to reproduce the correct patient anatomy for device testing, but also for physiological simulations. This has great potential to advance treatment assessment and diagnosis.

10138-26, Session 6

Initial simulated FFR investigation using flow measurements in patient- specific 3D printed coronary phantoms

Lauren Shepard, Kelsey N. Sommer, Univ. at Buffalo (United States) and Toshiba Stroke and Vascular Research Ctr. (United States); Richard L. Izzo, Univ. at Buffalo (United States) and The Jacobs Institute (United States) and Toshiba Stroke and Vascular Research Ctr. (United States); Alexander R. Podgorsak, Univ. at Buffalo (United States) and Toshiba Stroke and Vascular Research Ctr. (United States); Michael Wilson, Said Zaid, Univ. at Buffalo (United States); Frank J. Rybicki, The Ottawa Hospital Research Institute, The Univ. of Ottawa (Canada); Dimitrios Mitsouras, Brigham and Women's Hospital (United States);

Stephen Rudin, Univ. at Buffalo (United States) and Toshiba Stroke and Vascular Research Ctr. (United States); Erin Angel, Toshiba America Medical Systems, Inc. (United States); Ciprian N. Ionita, Univ. at Buffalo (United States) and Toshiba Stroke and Vascular Research Ctr. (United States)

Purpose: Accurate patient specific phantoms for device testing or endovascular treatment planning can be 3D printed. We expand the applicability of this approach for diagnosed cardiovascular disease, in particular, for CT-geometry derived benchtop measurements of Fractional Flow Reserve, the reference standard for determination of significant individual coronary artery atherosclerotic lesions.

Materials and Methods: Images of the coronary tree during a single heartbeat were acquired with a 16cm (320x0.5mm detector row) volume CT scanner (Toshiba Acquilion ONE). These coronary CT Angiography images were used to create 4 patient specific cardiovascular models with various grades of stenosis: severe, <75% (n=1); moderate, 50-70% (n=1); and mild, <50% (n=2). DICOM volumetric images were segmented using a 3D workstation (Vital Images); the output was used to generate STL files (using AutoDesk Meshmixer), and further processed to create 3D printable geometries for flow experiments. Multimaterial printed models (Stratasys Connex3) were connected to a programmable pulsatile pump, and the pressure was measured proximal and distal to the stenosis using pressure transducers. Compliance chambers were used before and after the model to modulate the pressure wave. A flow sensor was used to ensure flow rates within physiological reported values.

Results: 3D model based FFR measurements correlated well with stenosis severity. FFR measurements for each stenosis grade were: 0.4 severe, 0.55 moderate and 0.75 mild.

Conclusions: 3D printed models of patient specific coronary arteries allows for accurate benchtop diagnosis of FFR. This approach can be used as a future diagnostic tool or for testing CT image based FFR methods.

10138-27, Session 6

3D printing for orthopedic applications: from high resolution cone Beam CT images to life size physical models

Amiee Jackson, Shusil Dangi, Yehuda K. Ben Zikri, Rochester Institute of Technology (United States); Lawrence A. Ray, Carestream Health, Inc. (United States); Cristian A. Linte, Rochester Institute of Technology (United States)

To improve safety and efficiency of orthopedic surgery and spatial conceptualization in training and education, this project focused on generating virtual models of orthopedic anatomy from clinical quality computed tomography (CT) image datasets and manufacturing life-size physical models of the anatomy using 3D printing tools. With increasing resolution in image acquisition, the project also explores capabilities of printing toward faithfully reflecting detail and features depicted in medical images. Beginning with raw CT data, several image segmentation techniques including thresholding, edge recognition, and region-growing algorithms available in packages such as ITK-SNAP or MITK were utilized to separate bone from surrounding soft tissue. After converting the resulting data to a standard 3D printing format, stereolithography (STL), using Matlab and Python scripts, the STL file was edited using Meshlab and Meshmixer. The editing process is necessary to ensure a fully connected surface (no loose elements), positive volume with manifold geometry (geometry possible in the 3D physical world), and a single, closed shell. The resulting surface is then imported into a "slicing" software to scale and orient for printing on a Flashforge Creator Pro. In printing, one must consider relationships between orientation, print bed volume, model quality, material use and cost, and print time. We generated several anatomical models of the knee and foot from both low-dose high-resolution cone-beam CT images acquired using the soon to be released scanner developed by Carestream, as well as scaled models of the skeletal anatomy of the arm and leg, together with life-size models of the hand and foot.

10138-28, Session 7

Virtual setting for training in interpreting mammography images

Jorge Luiz Pezzuol, Francisco Douglas Lima Abreu, Aline Tendolini, Simone Mendes da Silva, Márcia Aparecido Silva Bissaco, Silvia Cristina Martini Rodrigues, Univ. de Mogi das Cruzes (Brazil)

This paper presents a web system for training students or residents (users) interested in detecting breast density on mammography images. The system consists of a bank of breast images classified types of breast densities and demarcated by the skilled person (guardian) or on-line database. Planning was based on ISO / IEC 12207 or 15504. By browser (desktop or notebook), the user will see the breast images, and conduct markings density region and even classify them according to BI-RADS protocol . After marking, this will be compared to the gold standard existing in the image and base, then the system will tell you if there was the settlement of the demarcation of the area or not. The format of this marking is similar to the paint brush. The evaluation was based on the ISO / IEC 1926 and 25010: 2011 by 3 software development experts and 3 in breast radiology, assessing usability, configuration, performance and system interface through the questionnaire based on the Likert scale. Where totally agreed on usability, configuration, performance and partly on the interface. And as positives: the system can be accessed at any place and time, the hit response or error is in real time, can be used in education, the limit of the number of images depends on the computer memory size at the end the system sends the results reached by e-mail to the user, system playback on any type of screen, system complementation with other types of breast structures. Negatives is the need of internet..

10138-29, Session 7

Crowdsourcing for identification of polyp-free segments in virtual colonoscopy videos

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Virtual colonoscopy (VC) allows a physician to virtually navigate within a reconstructed 3D colon model searching for colorectal polyps. Though VC is widely recognized as a highly sensitive and specific test for identifying polyps, one limitation is the reading time, which can take over 30 minutes per patient. Large amounts of the colon are often devoid of polyps, and a way of identifying these polyp-free segments could be of valuable use in reducing the required reading time for the interrogating radiologist. To this end, we have tested the ability of the collective crowd intelligence of non-expert workers to identify polyp candidates and polyp-free regions. We presented twenty short videos flying through a segment of a virtual colon to each worker, and the crowd was asked to determine whether or not a possible polyp was observed within that video segment. We evaluated our framework on Amazon Mechanical Turk and found that the crowd was able to achieve a sensitivity of 80.0% and specificity of 86.5% in identifying video segments which contained a clinically proven polyp. Since each polyp appeared in multiple consecutive segments, all polyps were in fact identified. Using the crowd results as a first pass, 80% of the video segments could in theory be skipped by the radiologist, equating to a significant time savings and enabling more VC examinations to be performed.

10138-30, Session 7

MIIP: a web-based platform for medical image interpretation training and evaluation

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Introduction:

Medical imaging technology has revolutionized health care over the past 30 years; established imaging modalities are constantly improved and new technologies emerge. Diagnostic imaging allows doctors to find diseases earlier and improve patient outcomes, interventional / intraoperative imaging helps to remove and cure many of the detected diseases. This is especially true for ultrasound, a modality that an increasing amount of medical personal is starting to use. Needless to say the best way to acquire such skills would be to image a variety of patients and organs with different pathologies using various equipment, especially for ultrasound scanning which is a dynamic procedure. Unfortunately this is not possible for all new users of ultrasound equipment and the next best thing to do for a broader audience could be to develop a web-based platform for medical image interpretation training and evaluation that tries to incorporate all this variability.

Purpose:

The purpose of this study was to develop and evaluate a platform for improving medical image interpretation skills regardless of time and space and without the need for expensive imaging equipment or a patient to scan. The system should be general in terms of imaging modalities and application areas but as a proof of concept ultrasound for brain tumor resections and regional anesthesia needle guidance were chosen. Furthermore, it should be possible to use the system from both desktop and notebook computers as well as mobile devices like smartphones and tablets. It should also be easy to establish solutions (i.e. the ground truth) to image and video related questions.

Methods:

The MIIP (Medical Image Interpretation Platform) web application was developed using standard programming languages and tools (HTML, CSS, JavaScript, Python) and often used libraries and databases (Bootstrap, jQuery, Django, Nginx, Gunicorn, PostgreSQL) and can be accessed by the users through any Web browser on both desktop and mobile platforms. The browser creates Hypertext Transfer Protocols (HTTPs) requests for specific Uniform Resource Identifiers (URLs) that map to resources on a Web server. The server renders and returns HTML pages to the client, which the browser can display. Choosing a web application over a native app solution was mainly due to the importance of creating solutions, which is best done on a desktop computer. Furthermore, the developer can make real-time changes to the application (no compilation and no waiting for the app stores to approve the changes) and the users do not have to update the application. However, the application needs to be optimized for both desktop and mobile devices, a web application has limited access to the hardware features of a mobile device and all users of the web application must be connected to the internet all the time.

The Model (the data), View (what is shown to the user) Controller (communication between the model and the view) or MVC pattern was chosen for the MIIP web application. The benefit of using this pattern is that changes to the view will not affect how the data is handled, and vice versa (see figure 1b).

Furthermore, basic user and group administration is implemented. User accounts can be created in a number of ways (individual users can create their own accounts and a teacher can create a number of course participants for example) and the users can be organized into groups in different ways. A user of the system can have four different roles: 1) a participant / a player (a user taking a course or playing a game), 2) a data up-loader (responsible for acquiring and uploading image / video data), 3) a teacher / an expert (responsible for creating questions and establishing the ground truth) and 4) an administrator (responsible for assigning user roles and web application settings) (see figure 1c).

As for questions and question sets the following process is implemented; A data up-loader adds new image / video data to the system, tags the data with the appropriate application area, modality etc. and assigns the data to the teacher / expert that will establish the ground truth for this image – question type combination. The expert will then receive a message from the system saying that the data is available and can be annotated when he/she finds the time. When this is done the question will be part of the pool of questions that teachers can make questions sets out of and a serious game can randomly draw from, filtered by application area and image modality of course. The focus has been on two types of questions, landmark (locate the structure in an image) and outline (draw around a structure in an image) (see figure 1c). For video (sequence of frames) question an additional task is required, i.e. locate the relevant frame, for example find the optimal frame for needle insertion in ultrasound-guided nerve blocks.

A course is then created by assigning one or more groups and / or individual users to the course as well as one or more question sets. The participants can then compare their results with the ground truth and the teacher can look at the results in different ways (e.g. all questions for a given participants or all participants answers (in addition the correct) for a given question). Furthermore, a game is created by letting the player choose the type of came (e.g. application area and image modality), the level of difficulty / mode and the number of questions (e.g. 5 or 10). Global score boards are provided in compete mode.

The system has also been used in other ways, for example assessing the quality of images acquired by different scanners or reconstructed by different compounding algorithms for freehand 3D ultrasound.

Results:

A stable web application with the needed functionality for image interpretation training and evaluation has been implemented. The system has been extensively tested internally and used during an international course in ultrasound-guided neurosurgery. The web application was well received and got very good System Usability Scale (SUS) scores.

Conclusions:

It is possible to create a web platform with the necessary functionality for medical image interpretation courses and serious games. Initial testing of the system seems to be very promising. Further evaluation is needed in order to investigate if the platform have a positive effect on interpretation skills.

10138-31, Session 7

A cloud collaborative medical image platform oriented by social network

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Computer-aided diagnosis systems that use medical images and three-dimensional models as input data have greatly expanded and developed. However, building suitable image databases to assess them is still a challenge. Although there are some image databases available for this purpose, they are generally limited to certain types of exams or contain a limited number of medical cases. The objective of this work is to present the concepts and the development of a collaborative platform for sharing medical images and three-dimensional models, providing a resource to share and increase the number of images available for researchers. The collaborative cloud platform, called CATALYZER, aims to increase the availability and sharing of graphic objects, including 3D images, as well as their reports, which are essential for researches related to medical images. The platform uses concepts of social networks to allow registered users upload and download images. Their modules respect rules of integrity and restrictions for the types of users, enabling people monitoring. Besides traditional features found on social networks such as adding or search contacts, the platform offers a feed mechanism, with information about recent interactions and also allows identifying set of exams as “favorites”, enabling faster retrieval. An evaluation conducted with researchers and health professionals indicated that this proposal can be an innovative approach to create medical image databases, providing a wider variety of cases with a considerable amount of shared information among its users.

10138-32, Session 7

Principle and engineering implementation of 3D visual representation and indexing of medical diagnostic records

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Purpose:

Due to the generation of a large number of electronic imaging diagnostic records (IDR) year after year in a digital hospital, The IDR has become the main component of medical big data which brings huge values to healthcare services, professionals and administration. But a large volume of IDR presented in a hospital also brings new challenges to healthcare professionals and services as there may be too many IDRs for each patient so that it is difficult for a doctor to review all IDR of each patient in a limited appointed time slot. In this presentation, we presented an innovation method which uses an anatomical 3D structure object visually to represent and index historical medical status of each patient, which is called Visual Patient (VP) in this presentation, based on long term archived electronic IDR in a hospital, so that a doctor can quickly learn the historical medical status of the patient, quickly point and retrieve the IDR he or she interested in a limited appointed time slot.

Method:

The engineering implementation of VP was to build 3D Visual Representation and Index system called VP system (VPS) including components of natural language processing (NLP) for Chinese, Visual Index Creator (VIC), and 3D Visual Rendering Engine.There were three steps in this implementation: (1) an XML-based electronic anatomic structure of human body for each patient was created and used visually to index the all of abstract information of each IDR for each patient; (2)a number of specific designed IDR parsing processors were developed and used to extract various kinds of abstract information of IDRs retrieved from hospital information systems; (3) a 3D anatomic rendering object was introduced visually to represent and display the content of VIO for each patient.

Results:

The VPS was implemented in a simulated clinical environment including PACS/RIS to show VP instance to doctors. We setup two evaluation scenario in a hospital radiology department to evaluate whether radiologists accept the VPS and how the VP impact the radiologists’ efficiency and accuracy in reviewing historic medical records of the patients. We got a statistical results showing that more than 70% participated radiologist would like to use the VPS in their radiological imaging services. In comparison testing of using VPS and RIS/PACS in reviewing historic medical records of the patients, we got a statistical result showing that the efficiency of using VPS was higher than that of using PACS/RIS.

New Technologies and Results to be presented:

This presentation presented an innovation method to use an anatomical 3D structure object, called VP, visually to represent and index historical medical records such as IDR of each patient and a doctor can quickly learn the historical medical status of the patient through VPS. The evaluation results showed that VPS has better performance than RIS-integrated PACS in efficiency of reviewing historic medical records of the patients.

Conclusions:

In this presentation, we presented an innovation method called VP to use an anatomical 3D structure object visually to represent and index historical IDR of each patient and briefed an engineering implementation to build a VPS to implement the major features and functions of VP. We setup two evaluation scenarios in a hospital radiology department to evaluate VPS and achieved evaluation results showed that VPS has better performance than RIS-integrated PACS in efficiency of reviewing historic medical records of the patients.

10138-33, Session 8

MR efficiency using automated MRI-desktop eProtocol

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MRI protocols have instruction sheets that radiology technologists use in routine clinical practice for guidance (e.g., slice position, acquisition parameters etc.). In Mayo Clinic Arizona (MCA), there are over 900 MR protocols (ranging across neuro, body, cardiac, breast etc.) which makes maintaining and updating the protocol instructions manually, a labor intensive effort. The task is even more challenging given different vendors (Siemens, GE etc.). This is a universal problem faced by all the hospitals and/or research institutions.

To increase the efficiency of the MR practice, we designed and implemented a web-based platform (eProtocol) to automate the management of MRI protocols. It is built upon a database that automatically extracts valuable information from DICOM compliant images and provides a user-friendly interface to the technologists to create, edit and update the protocols. Advanced operations such as protocol migrations from scanner to scanner and capability to upload Multimedia content were also implemented.

To the best of our knowledge, eProtocol is the first MR protocol automated management tool being used clinically. It has been pilot tested at MCA. It is expected that this platform will improve the radiology operations efficiency with significant improvement in image quality, decreased scan time, exam consistency, practice efficiency, fewer repeat examinations and less acquisition errors for better patient outcomes, as these protocols instructions will be readily available to the technologists during scans. In addition, this web based platform can be easily extended to other modalities such as CT, Mammography, and Interventional Radiology and different vendors for protocol management.

10138-34, Session 8

System design for 3D wound imaging using low-cost mobile devices

Ekaterina Sirazitdinova, Thomas M. Deserno, Uniklinik RWTH Aachen (Germany)

The state-of-the art method of wound assessment is a manual, imprecise and time-consuming procedure. Performed by clinicians, it has limited reproducibility and accuracy, large time consumption and high costs. Novel technologies such as laser scanning microscopy, multi-photon microscopy, optical coherence tomography and hyper-spectral imaging, as well as devices relying on the structured light sensors, make accurate wound assessment possible. However, such methods have limitations due to high costs and may lack portability and availability. In this paper, we present a low-cost wound assessment system and architecture for fast and accurate cutaneous wound assessment using inexpensive consumer smartphone devices. Computer vision techniques are applied either on the device or the server to reconstruct wounds in 3D as dense models, which are generated from images taken with a built-in camera of a smartphone device. The system architecture includes imaging (smartphone), processing (smartphone or PACS) and storage (PACS) devices. It supports tracking over time by alignment of 3D models, color correction using a reference color card placed into the scene and automatic segmentation of wound regions. Using our system, we are able to detect and document quantitative characteristics of chronic wounds, including size, depth, volume, rate of healing, as well as qualitative characteristics as color, presence of necrosis and type of involved tissue.

10138-35, Session 8

Assessing the initial adaptability and impact of a mobile dictation and reporting system in the radiology department of an academic hospital

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Mobile application Mobile Radiologist 360 rolled out as part of the voice dictation system upgrade from Nuance Powerscribe 5.0 to PS360 allows an attending radiologist to edit and sign-off a report assigned by a trainee or that has been started by the radiologist on a workstation. The purpose of this study was to evaluate the adaptability and impact of this application. Report turnaround time data was extracted from the RIS (Centricity) for 60 days before- (period-1) and 60 days after- (period-2) the application implementation and then, for 60 days after end of period-2 (period-3). Adaptability of the application was evaluated using two metrics; first, the number of attending radiologists who signed-off reports using the application in periods 2 and 3, and second, the proportion of reports signed-off by the top five users of the mobile application using the application. Impact of the application was evaluated by comparing the time from initial dictation to final sign-off (time_PF) for the top five users of the mobile application to the time_PF by other five radiologists who did not use the application. 41% radiologists used the mobile application at least once during the study period; the proportion of cases signed-off using the mobile application ranged from 1% to 20%. ANOVA revealed no statistically significant effect of the mobile application system on time_PF (p=0.842). In conclusion, there was low initial adaptability and no impact of the mobile dictation application of the dictation system in reducing the time from initial dictation to final sign-off of a radiology report.

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10139-1, Session 1

Block matching and B-spline methods in deformation estimation in synthetic left ventricular model with nontransmural infarction

Jakub Zmigrodzki, Szymon Cygan, Warsaw Univ. of Technology (Poland); Konrad Werys, Institute of Cardiology (Poland) and Warsaw Univ. of Technology (Poland); Beata Lesniak-Plewinska, Warsaw Univ. of Technology (Poland); Miroslaw Kowalski, Institute of Cardiology (Poland); Krzysztof Ka?u?y?ski, Warsaw Univ. of Technology (Poland)

The cardiac elastography aims at identification of non-transmural infarctions. We compare two displacement estimation methods in application to synthetic ultrasonic data. Reference was obtained from Finite Element Modelling. Models had the form of half of an ellipsoid with 15 mm wall thickness. The homogenous model, models with transmural and nontransmural inclusion were designed. Deformation of the models were simulated using Abaqus and synthetic ultrasonic data of LAX and SAX views were generated using FieldII.

Radial (dR) and lateral (dL) displacements were estimated using a 2D correlation search with 2D stretching (2DCS) and B-spline (BS) method. Strains were estimated using least squares estimator. Mean Absolute Error (MAE) of the dR in the LAX view was approx. 6[μm] for 2DCS and 8[μm] for BS, that of the dL 30 and 24[μm] respectively. MAE of the second component of the principal strain ?2 was 0.10 and 0.14[%], respectively. These values for SAX view data were 7, 10, 42, 52[μm] and 0.47 and 1.08[%]. In the LAX view both estimation methods result in the ?2 behavior coherent with the presence of the inclusion, however the 2DCS-based results are closer to the reference. In the SAX view the BS approach results in high errors of the estimate. The ?2 profiles, LAX, show minor discrepancies with respect to the reference and show the effect of the inclusion. The strain profiles in SAX view obtained from displacements estimated using the BS method dramatically deviate from the reference. Block matching performs better in application to local strain estimation.

10139-2, Session 1

Ultrasound elastography: efficient estimation of tissue displacement using an affine transformation model

Hoda Sadat Hashemi, Concordia Univ. (Canada); Mathieu Boily, Paul A Martineau, McGill University Health Centre (MUHC) (Canada); Hassan Rivaz, Concordia Univ. (Canada) and PERFORM Ctr. (Canada)

Ultrasound elastography involves imaging mechanical properties of tissue by estimating time-delay between two frames of radio-frequency (RF) data that are obtained while the tissue is undergoing deformation. This paper presents a novel technique for time-delay estimation (TDE) of all samples of RF data simultaneously, thereby exploiting all the information in RF data for TDE. We assume tissue deformation can be approximated by an affine transformation, and hence call our method ATME (affine transformation model elastography). The affine transformation model is utilized to obtain initial estimates of axial and lateral displacement fields. The affine transformation only has six degrees of freedom (DOF), and as such, can be efficiently estimated. A nonlinear cost function that incorporates similarity of RF data intensity and prior information of displacement continuity is formulated to fine-tune the initial affine deformation field. Optimization of this function involves searching for TDE of all samples of the RF data. The optimization problem is converted to a sparse linear system of equations, which can be solved in real-time. Results on simulation and phantom data is presented for validation.

10139-3, Session 1

Dictionary learning-based spatiotemporal regularization for 3D dense speckle tracking

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Speckle tracking is a common method for non-rigid tissue motion analysis in 3D echocardiography, where unique texture patterns are tracked through the cardiac cycle. Various methods, such as optical flow, elastic registration, and block matching techniques have been proposed to track speckle motion. However, poor tracking accuracies often occur due to inherent ultrasound issues, such as image artifacts and speckle decorrelation; thus regularization is required. The aforementioned methods typically apply various spatial and temporal regularizations in a separate manner. While several methods have proposed joint spatiotemporal regularization with B-splines, parameters such as control points are chosen explicitly.

In this paper, we propose a joint spatiotemporal regularization method based on an adaptive dictionary representation of the dense 3D+time Lagrangian motion field. Dictionaries have good signal adaptive and noise-reduction properties; however, they are still prone to quantization errors. We should avoid introducing this error in cases of trajectories with accurate tracking results. Thus, we detect poorly tracked trajectories/outliers via dictionary representation error and enforce regularization only on the outliers. Our method 1.) builds data-driven 4-dimensional dictionary of Lagrangian displacements using sparse learning, 2.) automatically identifies poorly tracked trajectories or outliers based on representation errors, and 3.) performs reconstruction on the outliers only. We demonstrate the effectiveness of our approach on RF block matching speckle tracking and evaluate our performance on both tracking and strain analysis.

10139-4, Session 1

Imaging spatially varying biomechanical properties with neural networks

Cameron Hoerig, Univ. of Illinois at Urbana-Champaign (United States); Wendy Reyes, The Catholic Univ. of America (United States); Léo Fabre, Ecole Centrale de Lille (France); Jamshid Ghaboussi, Michael F. Insana, Univ. of Illinois at Urbana-Champaign (United States)

Elastography comprises a set of modalities that image the biomechanical properties of soft tissues for disease detection and diagnosis. Quasi-static ultrasound elastography, in particular, tracks sub-surface displacements resulting from an applied surface force. The local displacement information and measured surface loads may be used to compute a parametric summary of biomechanical properties; however, the inverse problem is underdetermined, limiting most techniques to estimating a single linear-elastic parameter.

We previously described a new method to develop mechanical models using a combination of computational mechanics, ultrasonic measurements and machine learning that circumvents the limitations associated with classic mathematical approaches to inverse problem. The Autoprogressive method weaves together finite element analysis and artificial neural networks (ANNs) to develop empirical models of tissue mechanical behavior using only measured force-displacement data. We are extending that work by incorporating spatial information with the material properties into a single ANN structure. Previously, the ANNs accepted only a strain vector input and computed the corresponding stress, meaning any spatial information was encoded in the finite element mesh. Now, because spatial coordinates are included as part of the input, the ANNs are able to learn the spatially varying mechanical behavior of complex media; this becomes a reconstruction algorithm. We show that a single ANN is able to describe the same mechanical behavior of an object that previously required at least two ANNs. Furthermore, we show the new ANNs can learn complex material property distributions and create images of material properties, not merely classify, filter, or otherwise process an existing image. For the first time, we present a method to image elastic moduli using artificial neural networks.

10139-5, Session 1

Feasibility of pulse wave velocity estimation from low frame rate US sequences in vivo

Maria Zontak, Matthew Bruce, Univ. of Washington (United States); Michelle Hippke, Alan Schwartz, Radiology, Alliance HealthCare Services (United States); Matthew O'Donnell, Univ. of Washington (United States)

The pulse wave velocity (PWV) is considered an important clinical parameter to evaluate CV risk, vascular adaptation, etc. There has been substantial work attempting to measure the PWV using ultrasound (US). This paper presents a fully automatic algorithm for PWV estimation from the human carotid using US sequences acquired with a Logic E9 scanner and a 9L probe. Our algorithm samples the pressure wave in time by tracking wall displacements over the sequence, and estimates the PWV by calculating the temporal shift between two sampled waves at two distinct locations. Several recent studies have utilized similar ideas along with speckle tracking tools and high frame rate (above 1 KHz) sequences to estimate the PWV. To explore PWV estimation in a more typical clinical setting, we have used focused-beam scanning, which yields relatively low frame rates and small fields of view (e.g., 200 Hz for 16.7 mm filed-of-view). For our application, even a 200 Hz frame rate is slow. In particular, the sub-frame precision required for PWV estimation reaches parts per thousand (ppt) of the frame (5 ppt for 10m/s), if the estimation is done using two nearby beams. As such, our algorithm is designed to work with low frame-rates and decreased lateral fields-of-view and includes fully automatic segmentation of the wall intima, collaborative Speckle Tracking of the 2D carotid wall motion and outlier robust PWV calculation from multiple votes using RANSAC. Finally, we evaluate our algorithm on volunteers of different ages and health conditions.

10139-6, Session 2

Ultrasound computed tomography by frequency-shift low-pass filtering and least mean square adaptive filtering

Shanshan Wang, Junjie Song, Huazhong Univ. of Science and Technology (China); Yang Peng, Huazhong Univ of Science and Technology (China) and Huazhong Univ of Science and Technology (China); Liang Zhou, Mingyue 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 detection of breast cancer. This paper investigates a signal pre-processing method based on frequency-shift low-pass filtering (FSLF) and least mean square adaptive filtering (LMSAF) for USCT image quality enhancement. FSLF is designed base on Zoom Fast Fourier Transform algorithm (ZFFT) for processing the ultrasound signal in the frequency domain, while LMSAPF is based on the least mean square (LMS) algorithm in the time domain. 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 radio-frequency (RF) data of the nylon threads and the breast phantom captured by the USCT system developed in the Medical Ultrasound Laboratory. Experimental results show that the reconstructed images of nylon threads by the proposed method had narrower main lobe width and lower side lobe level comparing to the delay-and-sum (DAS). The background noises and artifacts could also be efficiently restrained. The reconstructed image of breast phantom by the proposed method had a higher resolution and the contrast ratio (CR) could be enhanced for about 12dB to 18dB at different region of interest (ROI).

10139-7, Session 2

Multi-frequency accelerating strategy for the contrast source inversion method of ultrasound waveform tomography using pulse data

Hongxiang Lin, Takashi Azuma, Xiaolei Qu, Shu Takagi, The Univ. of Tokyo (Japan)

In this work, we construct a multi-frequency accelerating strategy for the contrast source inversion (CSI) method using pulse data in the time domain. CSI is a frequency-domain inversion method for ultrasound waveform tomography that does not require the forward solver through the reconstruction. Several prior researches show that the CSI method has a good performance of convergence and accuracy in the low-center-frequency situation. In contrast, utilizing the high-center-frequency data leads to a high-resolution reconstruction but slow convergence on large grids. Our objective is to take full advantage of all low frequency components from pulse data with the high-center-frequency data measured by the diagnostic device. First we process the raw data in the frequency domain. Then multi-frequency accelerating strategy helps recursively calculate CSI in the current frequency using the result obtained from the former frequency reconstruction. The merit of multi-frequency accelerating strategy is that computational burden at the first few iterations decreases because the number of grids is relatively less, for a fixed number of points per wavelength. In the numerical test, the pulse data were generated by the K-wave simulator and have been processed to suit the computation of the CSI method. We investigate the performance of the multi-frequency and single-frequency reconstructions and conclude that the multi-frequency accelerating strategy significantly helps keep almost the same accuracy but reduces the average computational time per iteration step.

10139-8, Session 2

3D frequency-domain ultrasound waveform tomography breast imaging

Gursharan Yash Singh Sandhu, Delphinus Medical Technologies, Inc. (United States); Cuiping Li, Olivier Roy, Delphinus Medical Technologies, Inc. (United States) and Karmanos Cancer Institute, Wayne State Univ. (United States); Erik West, Delphinus Medical Technologies, Inc. (United States); Neb Duric, Delphinus Medical Technologies, Inc. (United States) and Karmanos Cancer

Institute, Wayne State Univ. (United States)

Frequency-domain ultrasound waveform tomography is a promising method for the visualization and characterization of breast disease. It has previously been shown to accurately reconstruct the sound speed distributions of breasts of varying densities. The reconstructed images show detailed morphological and quantitative information that can help differentiate different types of breast disease including benign and malignant lesions. The attenuation properties of an ex vivo phantom have also been assessed. However, the reconstruction algorithms assumed a 2D geometry while the actual data acquisition process was not. Although clinically useful sound speed images can be reconstructed assuming this mismatched geometry, artifacts from the reconstruction process exist within the reconstructed images. This is especially true for registration across different modalities and when the 2D assumption is violated, for example, when a patient's breast is rapidly sloping. It is also true for attenuation imaging where energy lost or gained out of the plane gets transformed into artifacts within the image space. In this paper, we will briefly review ultrasound waveform tomography techniques, give motivation for pursuing the 3D method, discuss the 3D reconstruction algorithm, and show both numerical and ex vivo examples of 3D waveform tomography image reconstructions.

10139-9, Session 2

Breast imaging using waveform attenuation tomography

Cuiping Li, Delphinus Medical Technologies, Inc. (United States)

Ex vivo studies using our ultrasound waveform attenuation algorithm have shown promising results for the detection and characterization of lesions. Our preliminary study shows that the waveform attenuation image has much higher resolution and can better delineate breast lesions boundaries than the ray-based image. In this study, we preprocessed our time domain waveforms and explored the directional transducer beam pattern to better match the acquired wave fields. We have applied waveform attenuation to in vivo data and compared our waveform attenuation images with the ray-based counterparts to assess the resolution and accuracy of the waveform attenuation reconstruction.

10139-10, Session 2

Joint reconstruction of the sound speed and initial pressure distributions for ultrasound computed tomography and photoacoustic computed tomography

Thomas P. Matthews, Mark A. Anastasio, Washington Univ. in St. Louis (United States)

Accurate reconstruction of the initial pressure distribution in photoacoustic computed tomography (PACT), in general, requires knowledge of the sound speed distribution of the medium. However, the sound speed distribution is often unknown, and estimating both the sound speed and initial pressure from PACT measurements alone is unstable. An alternative is to estimate the sound speed from ultrasound computed tomography (USCT) measurements. This approach fails to exploit the acoustic information in the PACT measurements and may require many USCT measurements to accurately reconstruct the sound speed. Here, we propose a joint reconstruction method where the sound speed and initial pressure distributions are simultaneously estimated from combined PACT/USCT measurements. This approach effectively overcomes the instability of the PACT joint reconstruction problem while requiring few USCT measurements.

10139-11, Session 2

Iterative image reconstruction in elastic inhomogenous media with application to transcranial photoacoustic tomography

Joemini Poudel, Thomas P. Matthews, Kenji Mitsuhashi, Alejandro Garcia-Uribe, Lihong V. Wang, Mark A. Anastasio, Washington Univ. in St. Louis (United States)

Photoacoustic computed tomography (PACT) is an emerging computed imaging modality that exploits optical contrast and ultrasonic detection principles to form images of the photoacoustically induced initial pressure distribution within tissue. The PACT reconstruction problem corresponds to a time-domain inverse source problem, where the initial pressure distribution is recovered from the measurements recorded on an aperture outside the support of the source. A major challenge in transcranial PACT brain imaging is to compensate for aberrations in the measured data due to the propagation of the photoacoustic wavefields through the skull. To properly account for these e?ects, a wave equation-based inversion method should be employed that can model the heterogeneous elastic properties of the medium. In this study, an iterative image reconstruction method for 3D transcranial PACT is developed based on the elastic wave equation. To accomplish this, a forward model based on a finite-di?erence time-domain discretization of the elastic wave equation is established. Subsequently, gradient-based methods are employed for computing penalized least squares estimates of the initial source distribution that produced the measured photoacoustic data. Reconstructed images from both numerical phantoms as well as experimental data are employed to demonstrate the feasibility and e?ectiveness of the approach.

10139-12, Session 3

Tissue mimicking simulations for temporal enhanced ultrasound-based tissue typing

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In recent years, our group has developed, deployed and evaluated temporal enhanced ultrasound, a technology where a sequence of temporal ultrasound (TeUS) data is used for tissue typing. In in vivo and ex vivo studies, we have demonstrated that the approach is effective for detecting prostate and breast cancers. Evidence derived from our experiments suggest that both ultrasound-signal related factors - such as ultrasound-induced heat - and tissue-related factors - such as the size, density and micro-vibration of scatterers - lead to tissue typing information in temporal enhanced ultrasound. In this work, we simulate mechanical micro-vibrations of scatterers in tissue-mimicking phantoms that have various scatterer densities reflecting normal and cancerous tissue structure. Finite element modeling (FEM) is used for this purpose where the vertexes are scatterers representing cell nuclei, and their initial positions are determined by the distribution of nuclei segmented from actual digital histology scans of prostate cancer patients. Subsequently, we generate ultrasound images of the simulated tissue structure using the Field II package resulting in a temporal enhanced ultrasound time series. We demonstrate that the micro-vibrations of scatterers are captured by temporal ultrasound data and can be exploited for tissue typing

10139-13, Session 3

Improving the quantification of contrast enhanced ultrasound using a Bayesian approach

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Contrast Enhanced Ultrasound (CEUS) is a sensitive imaging technique to assess tissue vascularity, that can be useful in the quantification of different perfusion patterns. This can particularly important in the early detection and staging of arthritis. In a recent study we have shown that a Gamma-variate can accurately quantify synovial perfusion and it is flexible enough to describe many heterogeneous patterns. Moreover, we have shown that through a pixel by pixel analysis, the quantitative information gathered characterizes more effectively the perfusion. However, the SNR ratio of the data and the nonlinearity of the model makes the parameter estimation difficult. Using classical non-linear-least-squares (NLLS) approach the number of unreliable estimates (those with an asymptotic coefficient of variation greater than a user-defined threshold) is significant, thus affecting the overall description of the perfusion kinetics and of its heterogeneity.

In this work we propose to solve the parameter estimation at the pixel level within a Bayesian framework using Variational Bayes (VB), and an automatic and data-driven prior initialization.

When evaluating the pixels for which both VB and NLLS provided reliable estimates, we demonstrated that the parameter values provided by the two methods are well correlated (Pearson's correlation between 0.85 and 0.99). Moreover, the mean number of unreliable pixels drastically reduces from 54% (NLLS) to 26% (VB), without increasing the computational time (0.05 s/pixel for NLLS and 0.07 s/pixel for VB). When considering the efficiency of the algorithms as computational time per reliable estimate, VB outperforms NLLS (0.11 versus 0.25 seconds per reliable estimate respectively).

10139-14, Session 3

Speed of sound estimation for thermal monitoring during liver ablation therapy

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Thermal monitoring for ablation therapy has high demands for preserving healthy tissues while removing the malignant tissues completely. Various methods have been investigated for the thermal monitoring. However, exposure to radiation, cost-effectiveness and inconvenient hinder the use of X-ray or MRI methods. Due to the non-invasive and real-time capability of ultrasound, ultrasound is widely used in intraoperative procedures. We propose a new method for thermal monitoring using a PZT element. We insert a PZT element with an ablation device to generate the ultrasound signal in the liver tissue. The single trip time of flight is recorded from the PZT element to the ultrasound transducer. We detect the speed of sound change caused by different temperature during the ablation therapy. We performed an ex-vivo experiment with a beef liver tissue to verify the feasibility of our speed of sound estimation technique. The time of flight information is used to generate the speed of sound map by an optimization method. We successfully generated a speed of sound map for the liver tissue during the ablation and converted the speed of sound map to a temperature map. The result shows the trend of temperature change matches with a measured point. The speed of sound estimation using a single PZT element can be used for the thermal monitoring.

10139-15, Session 3

Automated breast segmentation in ultrasound computer tomography SAFT images

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Ultrasound Computer Tomography (USCT) is a promising new imaging system for breast cancer diagnosis. An essential step before further processing is to remove the water background from the reconstructed images. In this paper we present a fully-automated image segmentation method based on three-dimensional active contours. The traditional active contour method is extended by gradient vector flow and encoding the USCT aperture characteristics as additional weighting terms. A surface detection algorithm based on a ray model is developed to initialize the active contour, which is iteratively deformed to capture the breast outline in USCT reflection images. Results of the evaluation with synthetic data showed that the method is able to cope with noisy images, and is not influenced by the position of the breast and the presence of scattering objects within the breast. The proposed method was applied to 14 in-vivo images resulting in an average surface deviation from a manual segmentation of 2.9 mm. We conclude that automated segmentation of USCT reflection images is feasible and produces results comparable to a manual segmentation. By applying the proposed method, reproducible segmentation results can be obtained without manual interaction by an expert.

10139-16, Session 3

Automated timing in echocardiography

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The assessment of left ventricular function in an echocardiographic exam is essential for patient evaluation. This assessment relies on the operator being able to identify the end-diastole and end-systole in the cardiac cycle. In clinical practice, the end-diastolic and end-systolic frames are manually determined by the human operators. This process is time-consuming and intrinsically subjective and operator-dependent. In this study, we report on the development of an automated system that can identify end-diastolic and end-systolic frames in 2D echocardiography recordings. Speckle tracking echocardiography was carried out using an optimized block matching technique to obtain a dynamic velocity vector field for apical 4-chamber images. The velocity vector field, obtained from the speckle tracking, was then used to automatically define the end-diastolic and end-systolic frames. The performance of the automated system is compared with that of five accredited and experienced expert human operators. The automated system was successful in detecting end-diastolic and end-systolic frames identified by the human experts. We believe that performing as well as a human experts indicates a reasonable performance of an automated algorithm. The performance of the automated system, measured as the processing time, is superior to that of human operators. Including the speckle tracking process, an improvement of >1.8 times was achieved.

10139-17, Session 4

Ultrafast ultrasound blood flow imaging: current and future perspectives *(Keynote Presentation)*

Lasse Løvstakken, Norwegian Univ. of Science and Technology (Norway)

No Abstract Available

10139-18, Session 4

Lateral velocity estimation bias due to beamforming delay errors

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An artefact has recently been reported [1,2] in the estimation of the lateral blood velocity using speckle tracking. This artefact shows as a net velocity bias in presence of strong spatial velocity gradients such as those that occur at the edges of the filling jets in the heart. Even though this artifact has been found both in vitro and in simulated data, its causes are still undescribed.

Here we demonstrate that a potential source of this artefact can be traced to smaller errors in the beamforming setup. By inserting a small offset in the beamforming delay, one can artificially create a net lateral movement in the speckle in areas of high velocity gradient. That offset does not have a strong impact in the image quality and can easily go undetected.

10139-19, Session 4

Particle image velocimetry on simulated 3D ultrafast ultrasound from pediatric matrix TEE transducers

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Ultrafast 3D transesophageal echocardiographic (TEE) imaging, combined with 3D particle imaging velocimetry (PIV), would be ideal for tracking the complex blood flow patterns in the ventricle. We are developing a miniature matrix TEE transducer that employs micro-beamforming (µBF) and allows high framerate in 3D [1]. In this paper we compare the results of 3D PIV on simulated images using the µBF transducer and an idealized, fully sampled (FS) matrix transducer.

In FieldII [2] we have simulated the transducers and a phantom model of a 8.4mm diameter artery having a known 4D flow [3]. Forty 3D volumes, at a rate of 1000 volumes/sec, were created using parallel beamforming, where multiple receive lines in 3D were constructed using a single diverging transmission. Error in 3D velocity estimation was measured by comparing the PIV results of both transducers to the ground truth.

The results show that PIV can estimate the 4D flow on the simulated volumes generated with the arterial phantom using small transducers suitable for pediatric 3D TEE. The µBF transducer (RMSE 23.7%) achieved acceptable accuracy, comparable to that of the FS transducer (RMSE 13.8%), when using PIV. This shows the feasibility of PIV in connection with 3D TEE.

10139-20, Session 4

Estimation of left ventricular blood flow parameters: clinical application of patient-specific CFD simulations from 4D echocardiography

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Echocardiography is the most commonly used image modality in cardiology, assessing several aspects of cardiac viability. Recently, the importance of cardiac hemodynamics and 4D blood flow motion has been highlighted, however such assessment is still difficult using routine echo-imaging. For this, computational fluid dynamics (CFD)-simulations in combination with imaging has proven a valuable tool, but only a few models have been applied on clinical cases. In the following, patient-specific CFD-simulations from transthoracic dobutamin stress echocardiography have been used to analyze the left ventricular 4D blood flow in one patient. At each stress level, 4D-images were acquired using a GE Vivid E9 (4VD, 1.7MHz/3.3MHz) and velocity fields simulated using an established pathway involving endocardial segmentation, valve position identification, and solution of the incompressible Navier-Stokes equation. Flow components defined as direct flow, delayed ejection flow, retained inflow, and residual volume were calculated by particle tracing using 4th-order Runge-Kutta integration. Additionally, systolic and diastolic average velocity fields were generated. Results indicated increased direct flow, decreased delayed ejection flow, constant retained inflow, and a considerable drop in residual volume at increasing stress, without major changes in average velocity fields. To our knowledge, this feasibility study work represents one of the first clinical applications of an echo-based patient-specific CFD-model at elevated stress levels, and highlights the usefulness of using echo-based models to capture highly transient flow events. This study demonstrates the potential of patient-specific CFD-models as a tool for quantifying 4D blood flow in the heart, with future larger patient studies planned for statistical inferences.

10139-40, Session PS1

Lateral interpolation of both RF signals and cross-correlation function for higher accuracy in lateral motion estimation

Zhi Liu, Chengwu Huang, Jianwen Luo, Tsinghua Univ. (China)

In elasticity imaging, accurate lateral motion estimation is critical for some applications, e.g., cardiovascular imaging and shear strain imaging. Typically, motion estimation in the lateral direction is challenging because of low sampling frequency and lack of phase information. In previous studies, several algorithms have been proposed for better lateral estimation, such as lateral interpolation on the RF signals (Interp_RF), lateral interpolation on the cross-correlation function (Interp_CCF) and lateral interpolation on both RF signals and cross-correlation function (Interp_Both). In this work, the estimation performances of the above-mentioned three algorithms are evaluated and compared in simulations and phantom experiments. In the simulations, the root-mean-square error (RMSE) of axial/lateral displacement and strain is utilized to assess the accuracy of motion estimation. In the phantom experiments, the displacement quality metric (DQM), defined as the normalized cross-correlation between the motion-compensated reference frame and the comparison frame, and the contrast-to-noise ratio (CNR) of axial/lateral strain are used as the evaluation criteria.

The results show that the three algorithms have similar performance in axial estimation. For lateral estimation, Interp_Both performs the best as indicated by the lowest RMSEs (in simulations) or highest DQMs and CNRs (in phantom experiments) among all algorithms. Besides, a small interpolation factor (e.g., 3-5) in Interp_Both is found to obtain a good trade-off between the estimation accuracy and computational cost. Interp_Both is proved to be superior to Interp_RF or Interp_CCF and thus is suggested to be used for lateral motion estimation.

10139-41, Session PS1

An improved implementation of block matching for motion estimation in ultrasound imaging

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Ultrasound elastography has become an important procedure that provides information about the tissue dynamics and may help on the detection of tissue abnormalities. Therefore, motion estimation in a sequence of ultrasound acquisition is crucial to the quality of this information. We propose a novel algorithm to perform speckle tracking, which consists in an implementation of 2D Block Matching with two enhancements: sub-pixel linear interpolation and displacement propagation, which are able to increase resolution, reduce computation time and prevent kernel mismatching errors. This method does not require any additional hardware and provide real-time information. The proposed technique was evaluated using four different numerical phantom and its results were compared with the results from standard 2D block matching and optical flow. The proposed method outperformed the other two methods, providing an average error of 1.25 pixels, while standard 2D block matching and optical flow presented errors of 12.10 and 10.03 pixels, respectively. The proposed algorithm was also assessed with four different physical phantoms and a qualitative comparison showed that the proposed technique presented results that were compatible to the results from the built-in elastography mode of the ultrasound equipment (Ultrasonix Touch).

10139-42, Session PS1

Performance comparison of optical flow and block matching methods in shearing and rotating models

Zhi Liu, Jianwen Luo, Tsinghua Univ. (China)

Accurate myocardial motion estimation based on ultrasound imaging is of great value for evaluation of cardiac function. Typically, myocardium undergoes complex motion and deformation, including shear deformation and rotation. Thus, a compression model is insufficient for investigating the performance of different algorithms. In this study, simulated shearing and rotating models are used to study the performance of optical flow (OF) and block matching (BM) methods based on ultrasound radio-frequency (RF) data. A deforming model was simulated with applied axial shear strains of 2-6%, and a rotating model was simulated with rotation angles of 0.5-4 degrees, respectively. Axial strains of 0-2% were also applied to these two models to study the influence of applied strain on the estimation of axial shear strain and rotation. To quantify the estimation performance, the root mean square error (RMSE) is used as the evaluation criterion. The results show that OF obtains lower RMSEs in the estimated displacement, strain and rotation angle than BM, especially at large axial shear strains and rotation angles. For the shearing model, compared with BM, OF reduced the RMSEs of axial strains, lateral strains, and axial shear strains by up to 95.5%, 70.3% and 90.0%, respectively. For the rotating model, OF reduced the RMSEs of axial strains, lateral strains, and rotation angles by up to 96.9%, 93.4% and 89.7%, respectively. OF is proved to outperform BM and thus is recommended to be used for shear strain and rotation estimation. The validations of phantom and in-vivo experiments are ongoing.

10139-43, Session PS1

Left ventricular phantoms with inclusions simulating transmural and non-transmural infarctions: FEM and EchoPAC study

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The cardiac elastography evolves to enable local strain estimation and identification of non-transmural infarctions. Below we compare the strain values obtained using EchoPAC in physical left ventricular phantoms made of PVA with results of the Finite Element Modelling (FEM) studies on their counterparts. Models had the form of half of an ellipsoid with 15 mm wall thickness. The homogenous model (Healthy), transmural inclusion model (f20dX) and nontransmural inclusion (5mm thickness) model (f20d5) were designed. The inclusions were located in the mid segment.

The material of the ventricle in the FEM studies was modeled as a hyperelastic, isotropic one. The material parameters came from measurements of the PVA samples and extrapolation (inclusions). The model was deformed by applying pressure load to its inner surface. 36 kPa pressure magnitude resulted in peak systolic strain values close to those observed in healthy subjects.

A dedicated setup, the Vivid 6 scanner, probe M4S-RS and EchoPAC BT13 software were used in experiments. The strains for the corresponding layers in the FEM models were averaged over selected nodes.

The circumferential strain (CS) values from the FEM simulation and the physical experiment are qualitatively very close and correlate well with the clinical data. The experimental CS results also agree with expectations in terms of slope across the wall and effect of the inclusion. Radial strains in AntSept segment obtained from EchoPAC and FEM are close. The proposed approach (phantoms, setup) may be used for development of methods for identification of nontransmural infarctions.

10139-44, Session PS1

Novel measurement setup for evaluation of left ventricle motion and strain tracking methods

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Cardiac strain quantification using ultrasound is an active area of research. Physical left ventricle (LV) model play a significant role in the evaluation and development of myocardium strain imaging methods. Several LV models have been reported. In spite of increasing interest in LV torsion, only one commercially available model utilizes torsional deformation, but it does not allow apical views. This work presents a prototype novel physical LV model and dedicated measurement setup which do not have this limitation.

The model was made of Poly(vinyl alcohol) cryogel (PVA-c). The solution for the chamber part was doped with scattering particles to imitate the echogenicity of myocardium and to facilitate automatic segmentation of the chamber from the fixing parts. The model was mounted in a measurement setup allowing computer controlled linear motion of the basis, rotation of the apex and inflation of the ventricle and the use both ultrasound imaging planes: short (SAX) and long axis (LAX). During preliminary tests of the presented model, B-mode and M-mode images were acquired.

Experiment results confirmed the possibility to force controlled deformation of the presented LV model, including elongation/shortening in the long axis direction and twist around this axis. In consequence, the model can mimic deformations of the LV wall to a large extent. The chamber wall can be segmented in B-mode images in both projections. The model with the measurement setup may be used in a range of development and validation of echocardiographic diagnostic methods including segmentation algorithms, strain estimation methods or real time processing.

10139-45, Session PS2

Using deep learning for accurate probe position determination in sensor-less freehand ultrasound reconstruction

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Ultrasound Imaging has gained increased interest over the last decade. With a few exceptions, it is mainly used in 2D imaging. To establish a diagnostic, the experimented sonographer has to build a 3D representation inside his mind.

Numerous attempts have been made to perform a 3D reconstruction from ultrasound images acquired with a 2D probe. Positioning systems based on mechanical guidance, optical or electromagnetic sensors have been proposed.

The last decade has witnessed an increasing number of applications where artificial intelligence can be used to solve problems in medical imaging, notably related to classification and segmentation. Particularly successful have been implementations based on Deep Learning.

In our study, we show that the anatomy can be used to train a Neural Network to predict the changes in coordinates and orientation of the probe between two consecutive frames. We took several thousands frames from 14 patients along with the respective position and orientation of the probe. Those images have been divided into a training set, a cross validation set and a test set. To get the appropriate number of images, we use data augmentation techniques such as cropping, rotations and zooming.

We then used the neural network to predict the changes in coordinates between frames. Those predictions are used to compute the actual coordinates and orientations of the frames, necessary for the reconstruction. The results of the reconstruction are then compared to the volume obtained by reconstructed by using the coordinates and orientation obtained from the sensor.

10139-46, Session PS2

Limb muscle sound speed estimation by ultrasound computed tomography excluding receivers in bone shadow

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Sarcopenia is the degenerative loss of skeletal muscle ability associated with aging. One reason is the increasing of adipose ratio of muscle, which can be estimated by the speed of sound (SOS), since SOSs of muscle and adipose are different (about 7%). For SOS imaging, the conventional bent-ray method iteratively finds ray paths and corrects SOS along them by travel-times. However, the iteration is difficult to converge for soft tissue with bone inside, because of large speed variation. In this study, the bent-ray method is modified to produce SOS images for limb muscle with bone inside. The modified method includes three steps. First, travel-times are obtained by a proposed Akaike Information Criterion (AIC) with energy term (AICE) method. The energy term is employed for neglecting the transmissive wave through bone (low energy wave). It results in failed reconstruction for bone, but makes iteration convergence and gives correct SOS for skeletal muscle. Second, ray paths are traced using Fermat's principle. Finally, simultaneous algebraic reconstruction technique (SART) is employed to correct SOS along ray paths, but excluding paths with low energy wave which may pass through bone. The simulation evaluation was implemented by k-wave toolbox using a model of upper arm. As the result, SOS of muscle was 1572.0±7.3 m/s, closing to 1567.0 m/s in the model. For vivo evaluation, a ring transducer prototype was built to scan the cross sections of lower arm and leg of a healthy volunteer. And the skeletal muscle SOSs were 1564.0±14.8 and 1564.1±18.0 m/s, respectively.

10139-47, Session PS3

Non-stationary blind deconvolution of medical ultrasound scans

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The problem of limited spatial resolution that is inherent in medical ultrasound imaging can be effectively dealt with using the procedure of blind image deconvolution. The most critical limitation of this approach, however, stems from its dependence on a stationary convolution model which is incapable of properly accounting for the spatial variability of the point spread function of the ultrasound scanner in use. As a result, most of the existing algorithms can only operate on localized fragments of data images. In this work, we introduce a novel method of non-stationary blind deconvolution which is free of the aforementioned limitation.

10139-48, Session PS3

Increased clutter level in echocardiography due to specular reflection

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Many cardiovascular diseases (CVDs) can be prevented by early detection through echocardiographic examination. The image quality of state-of-the-art echocardiography allows to correctly diagnose the occurrence of CVDs in about 80% of patients. In the remaining 20% increased clutter level hinders the visualization of the heart and the assessment of its function. It is not yet well understood what are the causes for these visualization errors but they are normally connected to an impaired acoustic window.

We propose the following theory for the increased clutter level. In patients with short intercostal distance the ultrasound beam can be partially blocked by the ribs. The surface of the ribs, which behaves like a specular reflector, deflects part of the ultrasonic energy outside of the imaging plane. That energy is then scattered by off-plane tissue and travels back to the probe, either directly or via a second reflection at the rib interface. Depending on the patient morphology the deflected energy can be directed to subcutaneous fat layers, often hyperechoic. That high intensity signal is then rendered on top of the heart image as clutter noise.

We carried out the following experiment to validate the proposed theory. A PVA cryogel ventricle and a section of pig ribcage were immersed in a water bath. Ultrasound images were acquired through the ribcage with a GE E95 clinical scanner and MS5 probe (GE Vingmed, Horten, Norway). A 20G cannula was also immersed down to 1 cm in the water outside of the imaging plane at around 10 cm from the probe location. Ultrasound images were acquired with and without the cannula. When the cannula is immersed an echo is displayed in the middle of the ventricle. Manual movement of the cannula correlated perfectly with the position of the observed echo. This result confirms that specular reflection at the ribs can partially deflect the ultrasound beam so that objects outside of the imaging plane are displayed in the ultrasound image. By substituting the cannula by a hyperechoic body, an increased clutter level will be observed over the image of the ventricle. This experiment seems to indicate that the proposed theory is correct.

10139-49, Session PS3

Region growing segmentation of ultrasound images using gradients and local statistics

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Segmentation of ultrasound images is a challenging task due to the low signal to noise ratio and artifacts of the images. Current approaches for segmentation include edge-based methods using contour models, and region-based methods using region growing starting from a seed point. Model-based methods can be effective, but are application dependent and require a large set of images for training. This paper proposes an approach to segment medical ultrasound images in three stages: anisotropic diffusion filtering, region growing, and morphological closing. The filtering stage reduces speckle noise without blurring the edges. Smoothing is done iteratively inside homogeneous regions and along the edges, and is prevented across the edges. Region growing starts from a seed point and uses a homogeneity criterion for pixel merging. Adjacent pixels of the seed point are analyzed, and included in the region if their normalized gradient is lower than the noise level in the region, estimated with local statistics. This process continues until there are no more pixels that meet the merging criterion. Finally, the edges of the region are smoothed using morphological closing. The proposed methods were evaluated with ten phantom images, and converged in eight of them with accurate region delimitation. Segmentation was not possible in two images with very low contrast. Preliminary results show that the proposed method can be used for ultrasound image segmentation and does not require previous knowledge of the anatomy of the structures.

10139-50, Session PS3

Respiratory motion correction of liver contrast-enhanced ultrasound sequences by selecting reference image automatically

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Abstract Objective Respiratory motion correction is necessary to quantitative analysis of liver contrast-enhance ultrasound (CEUS) image sequences. However, traditionally manual selecting reference image would affect the accuracy of the respiratory motion correction. Methods First, the original high-dimensional ultrasound gray-level image data was mapped into a two-dimensional space by using Laplacian Eigenmaps (LE). Then, the cluster analysis was adopted using K-means, and the optimal ultrasound reference image could be gotten for respiratory motion correction. Finally, this proposed method was validated on 18 CEUS cases of VX2 tumor in rabbit liver, and the effectiveness of this method was demonstrated. Results After correction, the time-intensity curves extracted from the region of interest of CEUS image sequences became smoother. Before correction, the average of total mean structural similarity (TMSSIM) and the average of mean correlation coefficient (MCC) from image sequences were 0.45±0.11 and 0.67±0.16, respectively. After correction, the two parameters were increased obviously (P<0.001)and were 0.59±0.11 and 0.81±0.11, respectively. The average of deviation valve (DV) from image sequences before correction was 92.16±18.12. After correction, the average was reduced to one-third of the original value. Conclusions The proposed respiratory motion method could improve the accuracy of the quantitative analysis of CEUS by using the reference image based on the traditionally manual selection. This method is operated simply and has a potential in clinical application.

10139-51, Session PS3

Estimating cardiac fiber orientations in pig hearts using registered ultrasound and MR image volumes

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Heart fiber mechanics can be important predictors in current and future cardiac function. Accurate knowledge of these mechanics could enable cardiologists to provide a diagnosis before conditions progress. Magnetic resonance diffusion tensor imaging (MR-DTI) has been used to determine cardiac fiber orientations. Ultrasound is capable of providing anatomical information in real time, enabling a physician to quickly adjust parameters to optimize image scans. If known fiber orientations from a template heart measured using DTI can be accurately deformed onto a cardiac ultrasound volume, fiber orientations could be estimated for the patient without the need for a costly MR scan while still providing cardiologists valuable information about the heart mechanics. In this study, we extend our previous work and apply the method to pig hearts, which are a close representation of human heart anatomy. Experiments from pig hearts show that the registration method achieved an average Dice similarity coefficient (DSC) of 0.819 ± 0.050 between the ultrasound and deformed MR volumes and that the proposed ultrasound-based method is able to estimate the cardiac fiber orientation in pig hearts.

10139-52, Session PS3

A comparison of automated versus manual segmentation of breast UST transmission images to measure breast volume and sound speed

Mark A. Sak, Neb Duric, Peter J. Littrup, Katelyn Westerberg, Delphinus Medical Technologies, Inc. (United States); Lisa Bey-Knight, Karmanos Cancer Institute, Wayne State Univ. (United States)

Ultrasound tomography (UST) is an emerging modality that can offer quantitative measurements of breast density. These measurements can only be made after the breast tissue is segmented from the background water bath and all previous work involving UST has used masks that were created manually from the sound speed images. However, manually segmenting images is time-consuming and an automated approach would be ideal. Here, an automated masking algorithm was developed that uses attenuation images to create masks. The attenuation images can easily be thresholded from the background water bath whereas sound speed images cannot. For a pilot study involving UST scans from 16 women, the manual masking method was compared to the automated masking method. Preliminary analysis showed promise as the masks created by the two methods showed an average Dice similarity coefficient of 0.901. The manual method created masks that were systematically larger in volume than those created by the automated method by a volume of 81 cm3. Still, these results are promising and warrant further examination into the automated method of UST image segmentation which would ultimately allow for the quantitative information stored in the UST image to be easily accessed.

10139-53, Session PS4

Thermoacoustic image reconstruction based on layered tissue model

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In thermoacoustic imaging, conventional inverse source solution based on homogeneous medium assumption results in image distortions and reduced resolution. Here we present analytical inverse solution for inhomogeneous layered planar medium with the source distribution existing in all layers. This model is applicable for imaging of tissue structures such as skin, breast and abdominal imaging, where transducer aperture size is relatively smaller than the medium sizes in lateral and elevational dimensions. We performed numerical simulations for point sources. Our numerical test results show that the conventional homogeneous solution, as expected, produces incorrect locations of point sources and significantly increased side lobes, whereas our layered solution produces point sources at correct locations with narrower main lobes and lower side lobes.

10139-54, Session PS4

Linking transducer transfer function with multi-pulse excitation photoacoustic response

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Photoacoustic imaging aims to utilize the benefits of both optical and ultrasound modalities using light sources and acoustic detectors. This combination provides vast opportunities for optimization of either part of the imaging system. Furthermore, the complex interplay of optical and acoustic subsystems increases the parameter room tremendously. Addressing this interaction, we propose using semiconductor laser diodes in multi-pulse regime to study the effects of transducer transfer function on the obtained photoacoustic response.

Typically, considering thermal and stress confinement criteria of the photoacoustic signal source, preference is given to solid-state lasers for their high pulse energy and short pulse duration. However, such sources are limited in pulse width and repetition rate tunability. On the other hand, semiconductor diodes offer great flexibility, being additionally compact, robust and of a low cost.

Recent studies have shown that usage of modified excitation sequences can have several positive effects, for instance, gathering additional data on the sample or reducing the total acquisition time.

In this study, we conduct a pump-probe experiment, using multi-pulse excitation sequences with varied inter-pulse delays while registering the acoustic response. We therefore examine the link between the transducers' transfer function and the photoacoustic response of the system. We focus on low central frequency transducers as being vastly used for clinical applications.

10139-55, Session PS4

Broadband optoacoustic characterization of cMUT and PZT transducer directivity in receive mode

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Ultrasound transducer arrays which are used in optoacoustic tomography have a major impact on the overall performance of the imaging system. While it is common practice to select those transducers based on their central frequency and bandwidth, their directivity characteristic is often not taken into account. Here we introduced a calibrated optoacoustic characterization method for broadband directivity measurements of the angular transducer sensitivity. The method utilizes a simple absorbing suture in order to generate omnidirectional and broadband OA signals which are characterized with a needle hydrophone. The calibrated optoacoustic source was used to compare the frequency dependence of the angular sensitivity of a conventional piezoelectric (PZT) and a capacitive micromachined ultrasonic (cMUT) transducer with similar size and central frequency. While both technologies showed a broadband response at normal incidence, the cMUT transducer maintained reasonable sensitivity levels and broadband response at incidence angles of 40° and beyond whereas the PZT was only able to provide detectable signal-to-noise levels at incidence angles of up to 20°. We further showcase reduction in the limited-view tomographic artifacts resulting from the broader acceptance angle of the cMUT.

10139-56, Session PS4

Photoacoustic simulation study of chirp excitation response from different size absorbers

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Photoacoustic (PA) imaging is a hybrid imaging modality that integrates the strength of optical and ultrasound imaging. Nanosecond (ns) pulsed lasers used in current PA imaging systems are expensive, bulky and they often waste energy. We propose and evaluate, through simulations, the use of continuous wave (CW) laser whose amplitude is linear frequency modulated (chirp) for PA imaging. The chirp signal provides signal-to-noise ratio (SNR) improvement potential and full control over PA signal frequencies excited in the sample. The PA signal spectrum is a function of absorber size and the time frequencies present in the chirp. A mismatch between input chirp spectrum and the output PA signal spectrum can affect the compressed pulse that is recovered from cross-correlating the two. We have quantitatively characterized this effect. The k-wave Matlab tool box was used to simulate photoacoustic signals in three dimensions for absorbers ranging in size from 0.1 mm to 0.6 mm, in response to laser excitation amplitude that is linearly swept from 0.5 MHz to 4 MHz. This sweep frequency range was chosen based on the spectrum analysis of PA signal generated from ex-vivo human prostate tissue samples. In comparison, the energy wastage by ns laser pulse was also estimated. For the chirp methodology, the compressed pulse peak amplitude, pulse width, and side lobe structure parameters were extracted for different size absorbers. While the SNR increased 6 fold with absorber size, the pulse width decreased by 25%.

10139-57, Session PS5

Novel fluorescence nanobubbles for contrast-enhanced ultrasound imaging in rabbit VX2 hepatocellular carcinoma model

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Ultrasound contrast agents (UCAs) such as SonoVue or Optison have been used widely in clinic for contrast-enhanced vascular imaging. However, these microbubbles UCAs display limitations in tumor-targeted imaging due to the large sizes, nanoscaled UCAs has consequently attracted increasing attention. In this work, we synthesized nanobubbles by ultrasonic cavitation method. Then, a fluorescent marker of Alexa Fluor 680 conjugated nanobubbles (AF680-NBs) as ultrasound fluorescence tumor-selective imaging in a rabbits model. Measurement of fundamental characteristics showed that the AF680-NBs had homogeneous distribution of mean diameter of 142.4 nm and polydispersity index of 0.447. Transmission electron microscope (TEM) was performed to confirm AF680-NBs as core-shell structure containing gas. To assess in vivo tumor-selectivity of AF680-NBs, we established the rabbits liver VX2 hepatocellular carcinoma model though surgical implantation of tumor tissue in rabbit liver. The anatomical evidence showed the VX2 tumor was successfully implanted in liver of rabbit. In order to evaluate tumor targeting abilities in hepatocellular carcinoma, the rabbits were administered of AF680-NBs via ear vein, contrast-enhanced sonograms was seen in the surrounding of VX2 tumor after 10 s. The results showed that there are rich capillaries around the tumor. Computed tomography (CT) angiography and digital subtraction angiography (DSA) were performed to further confirm the location of the tumor vasculature. As expected, there are many vessels around the tumor, less vessels were found in VX2 tumor nodule. We additionally investigated the toxic of the nanobubbles towards rabbits major organs by hematoxylin-eosin (HE) staining, the results indicated the AF680-NBs is a biocompatible non-toxic lipid system. In addition, fluorescence imaging of the VX2 tumors and major organs at 0, 3, 10 and 30 min were analyzed to confirm the targeted selectivity of AF680-NBs, the experiments showed that the AF680-NBs were capable of targeting VX2 tumor. Confocal laser scanning microscopy (CLSM) was used to further determined the fluorescent microscopic localization of AF680-NBs. The results demonstrated that the nanobubbles can traverse the VX2 tumor capillaries and target to the hepatocellular carcinoma tumor cells. All these results showed that the newly prepared AF680-NBs have potential for application in molecular imaging and targeted therapy for liver tumors.

10139-21, Session 5

Optimal experimental design to position transducers in ultrasound breast imaging

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We present methods to optimize the experimental setup for breast cancer detection with ultrasound tomography. This approach provides a systematic and quantitative tool to evaluate different designs and to optimize the configuration with respect to predefined design parameters.

We consider both, a time-of-flight inversion using straight rays and time-domain waveform inversion governed by the acoustic wave equation for imaging the sound speed.

The quality of different designs is measured by extracting properties from the Hessian operator of the time-of-flight or waveform differences defined in the inverse problem, i.e., the second derivatives with respect to the sound speed. Spatial uncertainties and resolution can be related to the eigenvalues of the Hessian, which provide a good indication of the quality of a given design. However, the complete spectrum is often prohibitively expensive to compute, thus suitable approximations have to be developed and analyzed. We use the trace of the Hessian operator to measure the quality of different designs, which is equivalent to the sum of all eigenvalues and requires less computational effort. In addition, we suggest to take advantage of the spatial symmetry to extrapolate the 3D experimental design from a set of 2D configurations. In order to maximize the quality criterion, we use a genetic algorithm to explore the space of possible design configurations. Numerical results show that the proposed strategies are capable of improving an initial configuration with uniformly distributed transducers, clustering them around regions with poor illumination and improving the ray coverage of the domain of interest.

10139-22, Session 5

Limited angle breast ultrasound tomography with a priori information and artifact removal

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Recently, it has been shown that by delineating suspected, relatively homogeneous structures in B-mode images from dual-sided ultrasound, one can enhance limited angle tomography to produce speed of sound images in the same view as X-ray mammographic tomography (DBT). This could allow better breast cancer detection and discrimination, as well as improved registration of the ultrasound and X-ray images because of the similarity of SOS and X-ray contrast in the breast. However, this speed of sound reconstruction method relies strongly on the B-mode or other reflection mode segmentation. If that information is limited or incorrect, artifacts will appear in the reconstructed images. Therefore, the iterative speed of sound reconstruction algorithm has been modified in the manner of simultaneously utilizing the image segmentations and removing most artifacts. The first step of incorporating a priori information is solved by any nonlinear-nonconvex optimization method while artifact removal is accomplished by employing the fast split Bregman method to perform total-variation (TV) regularization for image denoising. The proposed method was demonstrated in simplified simulations of our dual-sided ultrasound scanner. To speed these computations two opposed 20-element ultrasound linear arrays with 0.5 MHz center frequency were simulated for imaging two cylinders in a uniform background. The proposed speed of sound reconstruction method worked well with both bent-ray and full-wave inversion methods. This is the first demonstration of successful full-wave, limited angle, medical ultrasound tomography. The presented results lend credibility to possible translation of this method to clinical breast imaging application.

10139-23, Session 5

Improved misfit function for attenuation and speed reconstruction in ultrasound computed tomography

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The reconstruction of acoustic attenuation maps for transmission USCT based on the standard full-wave inversion method requires the accurate knowledge of the sound speed map in the region under study. Any deviation in the reconstructed speed maps creates a very significant bias in the

attenuation map. This is because the standard least-squared misfit function is more sensitive to time-shifts than on amplitude misalignment of the signals. In this work, we propose an improved misfit function which includes an additional term that accounts for the amplitude differences between the measured and the estimated signals. The functional gradients used to minimize the proposed misfit function were obtained using the adjoint field formulation and the fractional Laplacian wave equation. The forward and backward wave propagation were obtained with the parallelized GPU version of the software k-Wave and the optimization was performed with a line search method. A numerical phantom simulating breast tissue and noisy simulated data were used to test the performance of the proposed misfit function. The attenuation was reconstructed based on a converged speed map. To quantify the quality of the results, the mean values and its standard deviations in several regions of interest were analyzed and compared to the reference values. The proposed generalized misfit function decreases the bias in the attenuation map caused by the deviations in the speed map in 37 % for all the analyzed regions of interest.

10139-24, Session 5

Image reconstruction for ultrasound computed tomography by use of the regularized dual averaging method

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Waveform inversion methods can produce high-resolution reconstructed sound speed images for ultrasound computed tomography; however, they are very computational expensive. Source encoding methods can reduce this computational cost by formulating the image reconstruction problem as a stochastic optimization problem. Here, we solve this optimization problem by the regularized dual averaging method instead of the more commonly used stochastic gradient descent. This new optimization method allows use of non-smooth regularization functions and treats the stochastic data fidelity term in the objective function separately from the deterministic regularization function. This allows noise to be mitigated more effectively. The method further exhibits lower variance in the estimated sound speed distributions across iterations when line search methods are employed.

10139-25, Session 5

Time of flight interpolated synthetic aperture focusing technique

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Synthetic Aperture Focusing Technique (SAFT) allows fast data acquisition and optimally focused images. Yet the computational burden for 3D imaging is large as for each voxel the delay for each acquired A-scan has to be calculated, e.g. O(N^5) for N^3 voxels and N^2 A-scans. For 3D reconstruction of objects which are large in terms of the wavelength, e.g. ≥(100 wavelengths)^3, the computation of one volume might take several days on a current multicore PC. If the 3D distribution of the speed of sound is applied to correct the delays, the computation time increases further. In this work a time of flight interpolation based GPU implementation (TOFI-SAFT) is presented which accelerates our previous GPU implementation of speed of sound corrected SAFT by a factor of 7 with only minor reduction of image quality.

10139-26, Session 6

Backscattering analysis of high frequency ultrasonic imaging for ultrasound-guided breast biopsy

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A new ultrasound-guided breast biopsy technique is proposed. The technique utilizes conventional ultrasound guidance coupled with the use of a high frequency embedded ultrasound array located within the biopsy needle to improve accuracy in breast cancer diagnosis. The array within the needle is intended to be used to detect microcalcifications which are indicative of early breast cancers such as ductal carcinoma in situ (DCIS). Backscattering analysis has the potential to characterize tissues to improve localization of lesions. We conducted backscattering analysis of breast biopsy tissue specimens to show the usefulness of high frequency ultrasound for breast cancer biopsy and diagnosis.

We captured images of ex-vivo breast biopsy tissue specimens by using a single-element transducer with a bandwidth from 41 MHz to 88 MHz utilizing an Ultrasound Bio-Microscope (UBM) methodology. The echoes were processed to obtain backscattering coefficients. The slope and the 0 Hz intercept of the spectral backscattering features were calculated with linear approximation as well as the integrated backscattering coefficient (IB). All of these values were mapped in 2D and matched with each histological image for the identification of tissue type.

Ultrasound images of B-mode and IB data were compared to the histological image corresponding to each plane. Microcalcifications were identified within normal tissue. In another case, adenocarcinoma was successfully differentiated from adipose tissue. These results indicate that backscattering analysis is able to quantitatively distinguish tissues into normal and abnormal, which should help radiologists locate abnormal areas during the proposed ultrasound-guided breast biopsy with high frequency ultrasound.

10139-27, Session 6

Development of a high frequency single-element ultrasound needle transducer for anesthesia delivery

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Epidural anesthesia is one of the most commonly used and yet challenging techniques employed for pain management and anesthesia delivery. The major complications of this procedure are due to accidental dural puncture, with an incidence of 1-3%, which could lead to both temporary and irreversible permanent neurological complications. While needle placement under ultrasound (US) guidance has received increasing interest for improving accuracy, efforts to provide US guidance for epidural injections have been challenging. Poor needle visibility in US, difficulties in displaying relevant anatomical structure such as dura due to attenuation and bone shadowing, and image interpretation variability among users pose significant hurdles for any US guidance system. The difficulties in localizing the ligamentum flavum and dura with respect to the needle tip can be addressed by

integrating A-mode US, provided by a single element transducer at the needle tip, into the B-mode US guidance

system. We have taken the first steps towards providing such a guidance system. Our goal is to improve the safety of this procedure with minimum changes to the clinical workflow. This work presents the design and development of a 20 MHz single-element transducer housed at the tip of a 19 G needle. In addition, results from the initial transducer characterization tests and pulse-echo measurements from the interspinous ligament of a pig specimen are provided.

10139-28, Session 6

360-degree 3D transvaginal ultrasound system for high-dose-rate interstitial gynaecological brachytherapy needle guidance

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Treatment for gynaecological cancers often includes brachytherapy; in particular, in high-dose-rate (HDR) interstitial brachytherapy, hollow needles are inserted into the tumour and surrounding area through a template in order to deliver the radiation dose. Currently, there is no standard modality for visualising needles intra-operatively, despite the need for precise needle placement in order to deliver the optimal dose and avoid nearby organs, including the bladder and rectum. While three-dimensional (3D) transrectal ultrasound (TRUS) imaging has been proposed for 3D intra-operative needle guidance, anterior needles tend to be obscured by shadowing created by the template's vaginal cylinder. We have developed a 360-degree 3D transvaginal ultrasound (TVUS) system that uses a conventional two-dimensional side-fire TRUS probe rotated inside a hollow vaginal cylinder made from an acoustically translucent plastic (TPX). The system was validated using grid and sphere phantoms in order to test the distance and volumetric measurements. To test the potential for visualising needles, an agar phantom mimicking the geometry of the female pelvis was used. Needles were inserted into the phantom and then imaged using the 3D TVUS system. The needle trajectories and tip positions in the 3D TVUS scan were compared to their expected values and the needle tracks visualised in magnetic resonance images. Based on this initial study, 360-degree 3D TVUS imaging through an acoustically translucent vaginal cylinder is a feasible technique for intra-operatively visualising needles during HDR interstitial gynaecological brachytherapy.

10139-29, Session 7

Wave intensity analysis in mice: an ultrasound-based study in the abdominal aorta and common carotid artery

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Vascular parameters obtained by Wave Intensity Analysis (WIA) can provide information about the interaction between the vascular network and the heart. Studies in humans have already shown that WIA-derived biomarkes have a quantitative physiological meaning. We developed an image process algorithm to perform non-invasive WIA in mice and correlated WIA-derived indexes with cardiac function parameters.

High-resolution ultrasound (Vevo 2100) was used to image 16 wild-type male mice (8 weeks-old). Abdominal aorta and common carotid pulse wave velocities (PWVabd, PWVcar) were obtained processing B-Mode and PW-Doppler images and employed to assess WIA. Amplitudes of the first (W1abd, W1car) and the second (W2abd, W2car) local maxima and minimum (Wbabd,Wbcar) were evaluated; areas under the negative part of the curve were also calculated (NAabd, NAcar). Cardiac output (CO), ejection fraction (EF) fractional shortening (FS) and stroke volume (SV) were estimated; strain analysis provided strain and strain rate values for longitudinal, radial and circumferential directions (LS, LSR, RS, RSR, CS, CSR). Isovolumetric relaxation time (IVRT) was calculated from mitral inflow PW-Doppler images; IVRT values were normalized for cardiac cycle length.

W1abd was correlated with LS (R=0.65) and LSR (R=0.59), while W1car was correlated with CO (R=0.58), EF (R=0.72), MPI (R=0.54), LS (R=0.65), LSR (R=0.89), CS (R=0.71), CSR (R=0.70). Both W2abd and W2car were not correlated with IVRT.

Carotid artery WIA-derived parameters are more representative of cardiac function than those obtained from the abdominal aorta. The described US-based method can provide information about cardiac function and cardio-vascular interaction simply studying a single vascular site.

10139-30, Session 7

A step towards measuring the fetal head circumference with the use of obstetric ultrasound in a low resource setting

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Worldwide, 99% of all maternal deaths occur in low-resource countries. Ultrasound imaging can be used to detect maternal risk factors, but requires a well-trained sonographer to obtain the biometric parameters of the fetus. One of the most important biometric parameters is the fetal Head Circumference (HC). The HC can be used to estimate the Gestational Age (GA) and assess the growth of the fetus. In this paper we propose a method to estimate the fetal HC with the use of the Obstetric Sweep Protocol (OSP). With the OSP the abdomen of pregnant women is imaged with the use of sweeps. These sweeps can be taught to somebody without any prior knowledge of ultrasound within a day.

Both the OSP and the standard two-dimensional ultrasound image for HC assessment were acquired by an experienced gynecologist from fifty pregnant women in St. Luke's Hospital in Wolisso, Ethiopia. The reference HC from the standard two-dimensional ultrasound image was compared to both the manually measured HC and the automatically measured HC from the OSP data.

The median difference between the estimated GA from the manual measured HC using the OSP and the reference standard was -1.1 days (Median Absolute Deviation (MAD) 7.7 days). The median difference between the estimated GA from the automatically measured HC using the OSP and the reference standard was -6.2 days (MAD 8.6 days).

Therefore, it can be concluded that it is possible to estimate the fetal GA with simple obstetric sweeps with a deviation of only one week.

10139-31, Session 7

Examining breast parenchymal changes in women undergoing Tamoxifen treatment using UST waveform imaging

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Ultrasound tomography (UST) is an emerging modality that can offer quantitative measurements of breast density. Recent breakthroughs in UST image reconstruction involve the use of a waveform reconstruction as opposed to a ray-based reconstruction. The sound speed images that are created using the waveform reconstruction are of a much higher image quality. These waveform images offer much clearer resolution of regions of dense and fatty tissues. As part of a trial that was designed to detect breast density changes using UST sound speed imaging among women undergoing Tamoxifen, UST waveform sound speed images have been reconstructed for a limited number of participants. These initial results show that changes to the parenchymal tissue can more clearly be visualized when using the waveform sound speed images. Additional quantitative testing of the waveform images was also started and hopes to show that waveform sound speed images can be a more robust measure of breast density than ray-based reconstructions. Further analysis is still needed to understand how Tamoxifen affects breast tissue.

10139-32, Session 7

Adaptive kernel regression for freehand 3D ultrasound reconstruction

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Freehand three-dimensional (3D) ultrasound imaging enables low-cost and flexible 3D scanning of arbitrary-shaped organs, where the operator can freely move the ultrasound probe to acquire various views of the anatomy. However, the ultrasound data acquired during freehand ultrasound imaging are usually irregular, sparse, and operator dependent. Several 3D reconstruction algorithms have been proposed to synthesize 3D ultrasound volumes based on the 2D ultrasound images acquired during freehand imaging. A challenging task in these algorithms is to preserve the texture patterns in the reconstructed ultrasound volume and ensure that all gaps in the volume are correctly filled by interpolating the ultrasound data samples. This paper presents an adaptive kernel regression algorithm that can effectively reconstruct high-quality freehand 3D ultrasound volumes. The algorithm employs a kernel regression model that enables nonparametric interpolation of the voxel gray-level values. The kernel size of the regression model is adaptively adjusted based on the characteristics of the voxel that is being interpolated. In particular, when the algorithm is employed to interpolate a voxel located in a region with dense ultrasound data samples, the size of the kernel is reduced to preserve the texture patterns. On the other hand, the size of the kernel is increased in areas that include large gaps to enable effective gaps filling. The proposed adaptive kernel regression algorithm along with seven other interpolation approaches have been used to reconstruct a freehand 3D ultrasound volume of a benign breast tumor. The experimental results show that the proposed algorithm outperforms all other reconstruction approaches.

10139-33, Session 7

Quantitative 3D high resolution transmission ultrasound tomography: creating clinically relevant images

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There has been a great deal of research into ultrasound tomography for breast imaging over the past 35 years. Few successful attempts have been made to reconstruct high-resolution images using transmission ultrasound. To this end, advances have been made in 2D and 3D algorithms that utilize either time of arrival or full wave data to reconstruct images with high spatial and contrast resolution suitable for clinical interpretation. The highest resolution and quantitative accuracy result from inverse scattering applied to full wave data in 3D. However, this has been prohibitively computationally expensive, meaning that full inverse scattering ultrasound tomography has not been considered clinically viable. Here we show the results of applying a nonlinear inverse scattering algorithm to 3D data in a clinically useful time frame. This method yields Quantitative Transmission (QT) ultrasound images with high spatial and contrast resolution. We reconstruct sound speeds for various 2D and 3D phantoms and verify these values with independent measurements. The data are fully 3D as is the reconstruction algorithm, with no 2D approximations. We show that 2D reconstruction algorithms can introduce artifacts into the QT breast image which are avoided by using a full 3D algorithm and data. We show high resolution gross and microscopic anatomic correlations comparing cadaveric breast QT images with MRI to establish imaging capability and accuracy. Finally, we show reconstructions of data from volunteers, as well as an objective visual grading analysis to confirm clinical imaging capability and accuracy.

10139-34, Session 8

Speed of sound estimation for dual-stage virtual source ultrasound beamforming using point scatterers

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Synthetic transmit aperture beamforming is an increasingly used method to improve resolution in biomedical ultrasound imaging. Synthetic aperture sequential beamforming (SASB) is an implementation of this concept which features a relatively low computation complexity. Moreover, it can be implemented in a dual-stage architecture, where the first stage only applies simple single receive-focused delay-and-sum (srDAS) operations, while the second, more complex stage is performed either locally or remotely using more powerful processing. However, like traditional DAS-based beamforming methods, SASB is susceptible to inaccurate speed-of-sound (SOS) information. In this paper, we show how SOS estimation can be implemented using the srDAS beamformed image, and integrated into the dual-stage implementation of SASB, in an effort to achieve high resolution images with relatively low-cost hardware. Our approach builds on an existing per-channel radio frequency data based direct estimation method, and applies an iterative refinement of the estimate. We use this estimate for SOS compensation, without the need to repeat the first stage beamforming. Proposed and previous methods are tested on both simulation and experimental studies. The SOS accuracy of our estimation method is greater than 1.2% over the range of 1450-1620 m/s compared to the assumed SOS of 1540 m/s. Using estimated SOS, the beamforming lateral resolution of SASB is improved by 31% and 72%.

10139-35, Session 8

Phase-factor based beamforming to improve the visualization of hyper-echoic targets

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Clear visualization of hyper-echoic targets such as bone surfaces in ultrasound imaging is desirable for accurate registration of ultrasound to other imaging modalities or statistical models. Challenges such as strong reverberation, off-axis reflections and speed-of-sound variation reduce the contrast and resolution of the targets. In this paper, we propose a phase-factor based beamforming method which applies Hilbert transform on delay compensated channel data across the receive aperture. The accumulated phase is then calculated and utilized as the weight in the beamforming output. Using this method, the reverberation artifact of a point target is reduced about 20 dB compared with other beamforming methods such as delay and sum, Wiener, minimum variance and coherent-factor based beamforming in a point target phantom study. The resolution and contrast of hyper-echoic targets are also improved in a vertebrae phantom study.

10139-36, Session 8

Aperture domain model image reconstruction (ADMIRE) with plane wave synthesis

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In our previous studies, we demonstrated that our aperture domain model-based clutter suppression algorithm improved image quality of in vivo B-mode data obtained from focused transmit beams sequences. Our approach suppresses reverberation clutter and tackles limitations of related algorithms because it preserves RF channel signals and speckle statistics. We call the algorithm aperture domain model image reconstruction (ADMIRE). We previously focused on reverberation suppression, but ADMIRE is also effective at suppressing off-axis clutter so we are interested in how ADMIRE performs on plane wave images and also the impact of ADMIRE applied before and after synthetic beamforming of steered plane wave sequences. We employed simulated phantoms using Field II and tissue-mimicking phantoms to evaluate ADMIRE applied to plane wave sequencing. We generated images acquired from plane waves with and without synthetic aperture synthesis and measured contrast and contrast-to-noise ratio. For simulated cyst images formed from single plane wave, the contrast for DAS and ADMIRE are 15.64 dB and 28.34 dB, respectively, while the CNR values are 1.76 dB and 3.90 dB, respectively. Based on these findings, ADMIRE can improve plane wave image quality. We also assessed ADMIRE with resolution phantoms having a point target at 3 cm depth on-axis. We simulated the point spread functions from data obtained from 1 and 75 steered plane waves, along with linear scan at focus of 3 and 4 cm depth. Finally, because ADMIRE is nonlinear, we examined the outcome of applying ADMIRE before and after synthetic aperture processing on 3 steered plane waves.

10139-37, Session 8

Minimum variance beamformers for coherent plane-wave compounding

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Coherent plane-wave compounding (CPWC) is a fast ultrasound imaging technique that generates a uniform pulse-echo beam over the entire imaging region. In this study, we explore the possibility of further improving the image resolution by combining it with a minimum variance distortionless response (MVDR) beamformer. We combine these two beamformers in two different ways. First, we replace the compounding among the low-resolution images, generated in individual transmission angles, by a MVDR beamforming process. It is a combination of algorithms in the literature where the covariance matrix is calculated with the spatial smoothing. Its size is reduced for enhancing the robustness and avoiding ill-conditioning. We then propose a new method where the MVDR is performed on data extracted from each receive elements before any superposition. The new combination allows the data covariance matrix to be calculated with full size that increases the MVDR decorrelation. By demonstrating on experimental data, the images generated with the CPWC and the combination of performing the MVDR on the low-resolution images have their quality on par to each other. It indicates the degradation of MVDR performance through the spatial smoothing process. Meanwhile, the new method that allows the covariance matrix to be calculated with full size shows significant improvements on the lateral resolution.

10139-38, Session 8

Sequential CPWC: From ultrafast to ultralight

Alfonso Rodriguez-Molares, Hans Torp, Norwegian Univ. of Science and Technology (Norway); Boris Lippe, Oldelft Ultrasound B.V. (Netherlands); Lasse Løvstakken, Norwegian Univ. of Science and Technology (Norway)

Coherent plane-wave compounding (CPWC) is a beamforming method that makes it possible to reduce the number of transmit events without a major impact on the image quality. Reducing the number of transmitted pulses means higher framerate and hence enables ultrafast imaging modalities. But the same principle could be applied to reduce the number of receive events without loss of quality. A fewer number of receive events means fewer channels and hence enables ultralight systems.

This could be achieved by including a CPWC beamformer in the probe that allows to delay and sum the signals of the M elements into a set of N plane-wave signals, with N< M. This way we reduce the number of channels that must be transmitted to the scanner, cutting the costs in cables or the data transfer requirements of wireless probes.

This concept is very similar to synthetic aperture sequential beamforming (SASB). Sequential CWPC could have some advantages over SASB, such as the ability of dynamically change the system resolution and contrast by modifying the angle sequence both on transmit and on receive. In addition, the delays in CPWC change linearly across the aperture, which makes it possible to utilize delays in a cascade configuration, reducing the complexity of the built-in beamformer.

We tested the concept of Sequential CPWC on simulated (Field II) and experimental data (Verasonics Vantage 256 & L12-3v probe). In all cases a CPWC dataset of 127 plane-wave angles was recorded, covering a total angle span of 45.24°. In the simulation a single scatterer was used to study the point spread function (PSF) of the different algorithms. In the experiment a commercial phantom (CIRS Model 040GSE) was imaged containing both a hyperechoic cyst and a wire target. The acquired CPWC datasets were then post-processed to simulate the two steps of sequential CPWC by using 127, 64 and 32 plane-waves on receive.

Figure 1 shows the simulated PSF for conventional CPWC and for sequential CPWC for different number of receive plane-waves (127, 64, 32), and the corresponding lateral profiles. We observe an increased sidelobe level but only below – 60 dB, which does not have an impact on the image quality. The lateral resolution of the four methods is almost identical. Figure 2 shows experimental data for conventional CPWC and for Sequential CPWC. We do not observe any degradation in the image quality even when the number of channels used to reconstruct the image has been reduced by a factor of 4. These results confirm that Sequential CPWC could be used to reduce the number of channels in the system without loss in image quality, which may lessen the demands on the data transfer between probe and scanner.

10139-39, Session 8

Three-dimensional robotic synthetic tracked aperture ultrasound imaging: feasibility study

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Three dimensional (3D) ultrasound imaging is becoming a standard mode for medical ultrasound diagnosis applications. Conventional 3D ultrasound imaging is mostly scanned either by using a two dimensional matrix array or by motorizing a one dimensional array in the elevation direction. However, the former system is not widely assessable due to its cost, and the latter one has limited resolution and field-of-view in the elevation axis. Here, we propose a 3D ultrasound imaging system based on the synthetic tracked aperture approach, in which the robotic arm is used to provide accurate tracking and motion. While the ultrasound probe is moved by a robotic arm, each probe position is tracked and can be used to reconstruct a wider field-of-view as there are no physical barriers that restrict the elevational scanning. At the same time, synthetic aperture beamforming provides a better resolution in the elevation axis. To synthesize the elevational information, the single focal point is regarded as the virtual element, and forward and backward delay-and-sum are applied to the radio-frequency (RF) data collected through the volume. The concept is experimentally validated using a general ultrasound phantom, and the elevational resolution improvement of 2.54 and 2.13 times was measured at the target depths of 20 mm and 110 mm, respectively.

10140-1, Session 1

Determining local and contextual features describing appearance of difficult to identify mitotic figures

Ziba Gandomkar, Patrick C. Brennan, Claudia R. Mello-Thoms, The Univ. of Sydney (Australia)

Mitotic count is helpful in determining aggressiveness of breast cancer. In previous studies, it was shown that the agreement among pathologists for grading mitotic index is fairly modest as mitoses have large variety of appearances and they could be mistaken for other similar objects. In this study, different local and contextual features that differ significantly between easily identifiable mitoses and challenging ones were determined. The images were obtained from Mitosis-Atypia 2014 challenge. In total, the dataset contained 453 mitotic figures. Two pathologists annotated each mitotic figure. In case of disagreement, an opinion from a third pathologist was requested. The mitoses were grouped into three categories, those recognized as “a true mitosis” by both pathologists ,those labelled as “a true mitosis” by only one of the first two readers and also the third pathologists, and those annotated as “probably a mitosis” by all readers or majority of them. After color unmixing, the mitoses were segmented from H channel. The area of each segmented area along with intensity-based and textural features were extracted from H-channel, blue ratio channel and five different color spaces. Holistic features describing each image were also extracted. The Kruskal-Wallis H test was used to identify significantly different features. Multiple comparison was done using rank-based version of Tukey-Kramer test. The results indicated that there are local and global features which differ significantly among different groups. In addition, variations between mitoses in different groups were captured in the features from HSL and LCH color space more than other ones.

10140-2, Session 1

Fast clustering in linear 1D subspaces: segmentation of microscopic image of unstained specimens

Ivica Kopriva, Maria Brbić, Dijana Tolić, Nino Antunov-Fantulin, Institut Ruder Bošković (Croatia); Xinjian Chen, Soochow University (China)

Algorithms for subspace clustering (SC) are effective in terms of the accuracy but exhibit high computational complexity. We propose algorithm for SC of (highly) similar data points drawn from union of linear independent 1D subspaces with computational complexity that is linear in number of data points. The algorithm finds a dictionary that represents data in reproducible kernel Hilbert space (RKHS). Afterwards, data are projected into RKHS by using empirical kernel map (EKM) and that enables the proposed method to cluster linearly nonseparable data points. Segmentation is realized by applying the max operator on projected data. We prove that for noise free data proposed approach yields exact clustering into subspaces. We also prove that EKM-based projection yields less correlated data points. We demonstrate accuracy and computational efficiency of the proposed algorithm on synthetic dataset as well as on segmentation of the image of unstained specimen in histopathology.

10140-3, Session 1

Applications of QCL mid-IR imaging to the advancement of pathology

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Quantum cascade laser (QCL) infrared microscopy is a novel technique with many potential applications to histopathology. Like traditional Fourier transform infrared (FT-IR) imaging, QCL imaging derives biochemical data coupled to the spatial information of a tissue sample, and can be used to improve the diagnostic and prognostic value of assessment of a tissue biopsy. This technique also offers advantages over traditional FT-IR imaging, specifically the capacity for discrete frequency and real-time imaging. In this work we present applications of QCL imaging to tissue samples, including discrete frequency imaging, to demonstrate its compatibility with FT-IR and its potential value to pathology.

10140-4, Session 1

Data-driven sampling method for building 3D anatomical models from serial histology

Scott Doyle, Snehal Salunke, Tova Ablove, Theresa Danforth, John E. Tomaszewski, Univ. at Buffalo (United States)

In this work, we present a method for optimizing the number of serial histopathology slices required to build an accurate 3D model of tissue architecture. Our data-driven approach uses a single fully-sectioned tissue block as pilot data, builds a 3D model, and then derives a set of metrics related to the objects under biological investigation. In our work, we are interested in the 3D reconstruction of microvessel architecture in the trigone region between the vagina and the bladder as a potential avenue for drug delivery to treat bladder infection. We collect and co-register 23 serial sections of CD31-stained tissue images (6 ?m thick sections), from which five ROIs are selected for analysis. To build the model, we perform semi-automatic segmentation of the microvessesl in the ROI. Subsampled meshes are then created by removing slices from the stack, interpolating the missing data, and re-constructing the mesh. We calculate the Hausdorff distance, surface area, and mesh volume differences between the full and subsampled meshes to determine the optimal sampling rate for the modeled structures. In our application, we found that a sampling rate of 25% (corresponding to just 7 slices) was sufficient to recreate the structure of the microvessels without significant deviation from the fully-rendered mesh. This pipeline effectively minimizes the number of histopathology slides required for 3D model reconstruction, and can be utilized to either (1) reduce the overall costs of a project, or (2) enable additional analysis on the intermediate slides.

10140-5, Session 1

Automatic evaluation of skin histopathological images for melanocytic features

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Successfully detecting melanocyte cells in the skin epidermis has great significance in skin histopathology. Because of the existence of cells with similar appearance to melanocytes in hematoxylin & eosin (H&E) images of the epidermis, detecting melanocytes becomes a challenging task. This paper proposes a novel technique for the detection of melanocytes in H&E images of the epidermis, based on the melanocyte color features, in the HSI color domain. Initially, an effective soft morphological filter is applied to the H&E images in the HSI color domain to remove noise. Then a novel threshold-based technique is applied to distinguish the candidate melanocytes' nuclei. Similarly, the method is applied to find the candidate surrounding halos of the melanocytes. The candidate nuclei are associated with their surrounding halos using the suggested logical and statistical inferences. Finally, a fuzzy inference system is proposed, based on the HSI color information of a typical melanocyte in the epidermis, to calculate the similarity ratio of each candidate cell to a melanocyte. As our review on the literature shows, this is the first method evaluating epidermis cells for melanocyte similarity ratio. Experimental results on various images with different zooming factors show that the proposed method improves the results of previous works.

10140-6, Session 2

Automated wholeslide analysis of multiplex-brightfield IHC images for cancer cells and carcinoma-associated fibroblasts

Auranuch Lorsakul, Ventana Medical Systems, Inc. (United States) and Roche Tissue Diagnostics (United States); Emilia Andersson, Roche Diagnostics GmbH (Germany); Suzana Vega Harring, Hadassah Sade, Oliver Grimm, Roche Innovation Ctr. Munich (Germany); Joerg Bredno, Ventana Medical Systems, Inc. (United States)

Multiplex-brightfield IHC staining and quantitative measurement of multiple biomarkers can support therapeutic targeting to carcinoma-associated fibroblasts (CAF). This paper presents an automated digital-pathology solution to simultaneously analyze multiple biomarker expressions within a single tissue section stained with an IHC duplex assay. Our method was verified against ground truth provided by expert pathologists. In the first stage, the automated method quantified epithelial-carcinoma cells expressing cytokeratin (CK) using robust nucleus detection and supervised cell-by-cell classification algorithms with a combination of nucleus and contextual features. Using fibroblast activation protein (FAP) as biomarker for CAFs, the algorithm was trained, based on ground truth obtained from pathologists, to automatically identify tumor-associated stroma using a supervised-generation rule. The algorithm reported distance to nearest neighbor in the populations of tumor cells and activated-stromal fibroblasts as wholeslide measure of spatial relationships. A total of 45 slides from six indications (breast, pancreatic, colorectal, lung, ovarian, and head-and-neck cancers) were included for training and verification. CK-positive cells detected by the algorithm were verified by a pathologist with good agreement (R2=0.98) to ground-truth count. For the area occupied by FAP-positive cells, the inter-observer agreement between two sets of ground-truth measurements was R2=0.93 whereas the algorithm reproduced the pathologists' areas with R2=0.96. The proposed methodology enables automated image analysis to measure spatial relationships of cells stained in an IHC-multiplex assay. Our proof-of-concept results show an automated algorithm can be trained to reproduce the expert assessment and provide quantitative readouts that potentially support a cutoff determination in hypothesis testing related to CAF-targeting-therapy decisions.

10140-7, Session 2

Lumen-based detection of prostate cancer via convolutional neural networks

Jin Tae Kwak, Sejong Univ. (Korea, Republic of); Stephen M. Hewitt, National Institutes of Health (United States)

We present a deep learning approach for detecting prostate cancers. The approach consists of two steps. In the first step, we perform tissue segmentation that identifies lumens within digitized prostate tissue specimen images. Intensity- and texture-based image features are computed at five different scales, and a multiview boosting method is adopted to cooperatively combine the image features from differing scales and to identify lumens. In the second step, we utilize convolutional neural networks (CNN) to automatically extract high-level image features of lumens and to predict cancers. The segmented lumens are rescaled to reduce computational complexity and data augmentation by scaling, rotating, and flipping the rescaled image is applied to avoid overfitting. We evaluate the proposed method using tissue microarrays (TMA), including 195 tissue specimens (73 Benign and 122 Cancer). In cross-validation, the proposed method achieved an AUC of 0.95 (CI: 0.93-0.98). This demonstrates that the proposed method can potentially improve prostate cancer pathology.

10140-8, Session 2

Hierarchical patch-based co-registration of differently stained histopathology slides

Mehmet Yigitsoy, Günter Schmidt, Definiens AG (Germany)

Over the past decades, digital pathology has emerged as an alternative way of looking at the tissue at subcellular level. One of the application areas of digital pathology is the co-occurrence analysis of different cell types. Cell types can identified by staining the neighboring sections of a tissue block using different markers. However, robust fusion of structural and functional information from different stains is necessary for reproducible co-occurrence analysis of cell types. Such a fusion can be obtained via image co-registration by establishing spatial correspondences between tissue sections. Spatial correspondences can then be used to transfer various statistics about cell types between stains. However, the multi-modal nature of images and sparse distribution of interesting cell types pose several challenges for the registration of differently stained tissue sections. In this work, we propose a co-registration framework that efficiently addresses such challenges. We present a hierarchical patch-based registration of intensity normalized tissue sections. Preliminary experiments demonstrate the potential of the proposed technique for the fusion of multi-modal information from differently stained digital histopathology sections.

10140-9, Session 2

Automated high-grade prostate cancer detection and ranking on whole slide images

Chao-Hui Huang, MSD International GmbH (Singapore) and Agency for Science, Technology, and Research (Singapore); Daniel Racoceanu, Pontifical Catholic Univ. of Peru (Peru) and UPMC Sorbonne Univ. (France)

Recently, digital pathology (DP) has been largely improved due to the development of computer vision and machine learning. Automated detection of high-grade prostate carcinoma (HG-PCa) represents an impactful medical use-case showing the paradigm of collaboration between DP and computer science: given a field of view (FOV) from a whole slide image (WSI), the computer-aided system is able to determine the grade by

classifying the FOV. Various approaches have been reported based on this approach. However, Two reasons supported us to conduct this work: first, there is still a room for the improvement in terms of detection accuracy of HG-PCa; second, a clinical practice is more complex than the operation of simple image classification. Ranking is also an important step. E.g., in a clinical practice, a pathologist usually evaluates a case based on a few FOVs from the given WSI. And then, makes decision based on the most severe FOV. This important scenario of ranking is not yet being well discussed. In this work, we introduce an automated detection and ranking system for PCa based on Gleason pattern discrimination. Our experiments suggested that the proposed system is able to perform high-accuracy detection (95.57%) and excellent performance of ranking. Hence, the proposed system will be able to support the daily tasks in the medical routines of clinical pathology.

10140-10, Session 2

Automated plasmodia recognition in microscopic images for diagnosis of malaria using convolutional neural networks

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Malaria is one of the world's most common and serious tropical diseases, caused by parasites of the genus plasmodia that are transmitted by Anopheles mosquitoes. Various parts of Asia and Latin America are affected but highest malaria incidence is found in Sub-Saharan Africa. Standard diagnosis of malaria comprises microscopic detection of parasites in stained thick and thin blood films. As the process of slide reading under the microscope is an error-prone and tedious issue we are developing computer-assisted microscopy systems to support detection and diagnosis of malaria.

In this paper we focus on a deep learning (DL) approach for the detection of plasmodia and the evaluation of the proposed approach in comparison with two reference approaches. The proposed classification schemes have been evaluated with more than 180,000 automatically detected and manually classified plasmodia candidate objects from so-called thick smears. Automated solutions for the morphological analysis of malaria blood films could apply such a classifier to detect plasmodia in the highly complex image data of thick smears and thereby shortening the examination time. With such a system diagnosis of malaria infections should become a less tedious, more reliable and reproducible and thus a more objective process. Better quality assurance, improved documentation and global data availability are additional benefits.

10140-11, Session 2

A model of tumor architecture and spatial interactions with tumor microenvironment in breast carcinoma

Bassem Ben Cheikh, UPMC Sorbonne Univ. (France); Catherine Bor Angelier, UNICANCER (France); Daniel Racoceanu, UPMC Sorbonne Univ. (France)

Breast carcinomas are cancers that arise from the epithelial cells of the breast, which are the cells that line the lobules and the lactiferous ducts. Breast carcinoma is the most common type of breast cancer and can be divided into different subtypes based on the architecture of the tissue, when being examined by the pathologist under the microscope. Tumor microenvironment (TME) is the cellular environment in which a tumor develops. Being composed of varied cell types having different biological roles, TME is recognized as playing an important role in the progression of the disease. The architectural heterogeneity in breast carcinomas and the spatial interactions with TME are, to date, not well understood. Developing a spatial model of tumor architecture and spatial interactions with TME can advance our understanding of tumor heterogeneity. Furthermore, generating histological synthetic datasets can contribute in objectively validating, and comparing analytical methods that are used in digital pathology. In this work, we propose a modeling method that applies to different breast carcinoma subtypes and TME spatial distributions based on mathematical morphology. The model is based on a few morphological parameters that give access to a large spectrum of breast tumor architectures and are able to differentiate between histological subtypes such as ductal carcinoma in situ (DCIS), invasive ductal carcinomas (IDC) and invasive lobular carcinoma (ILC). In addition, a part of the parameters of the model controls the spatial distribution of TME relative to the tumor. The validation of the model has been performed by comparing morphological features between real and simulated images.

10140-12, Session 3

Identification and characterization of neutrophil extracellular trap shapes in flow cytometry

Brandon Ginley, Univ. at Buffalo (United States); Tiffany Emmons, Prabhu Sasankan, Roswell Park Cancer Institute (United States); Constantin Urban, Umeå Univ. (Sweden); Brahm H. Segal, Roswell Park Cancer Institute (United States); Pinaki Sarder, Univ. at Buffalo (United States)

Neutrophil extracellular trap (NET) formation is an alternate immunologic weapon used mainly by neutrophils. Chromatin backbones fused with proteins derived from granules are shot like projectiles onto foreign invaders. It is thought that this mechanism is highly anti-microbial, aids in preventing bacterial dissemination, is used to break down structures several sizes larger than neutrophils themselves, and may have several more uses yet unknown. NETs have been implied to have involvement in a wide array of systemic host immune defenses, including sepsis, autoimmune diseases, and cancer. Existing methods used to visually quantify NETotic versus non-NETotic shapes are extremely time-consuming and subject to user bias. These limitations are obstacles to developing NETs as prognostic biomarkers and therapeutic targets. We propose an automated pipeline for quantitatively detecting neutrophils and NET shapes captured using a flow cytometry-imaging system. Our method uses contrast limited adaptive histogram equalization to improve signal intensity in dimly illuminated NETs. From the contrast improved image, fixed value thresholding is applied to convert the image to binary. Feature extraction is performed on the resulting binary image, by calculating region properties of the resulting foreground structures. Classification of the resulting features is performed using Support Vector Machine. Our method classifies NETs from neutrophils without traps at 0.97/0.96 sensitivity/specificity on n = 387 images, and is

1500X faster than manual classification, per sample. Our automated method has potential to streamline the identification and quantification of NETs for patients with diseases associated with cancer and autoimmunity.

10140-13, Session 3

FOXP3-stained image analysis for follicular lymphoma: optimal adaptive thresholding with maximal nucleus coverage

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Immunohistochemical detection of FOXP3 antigen is a usable marker for detection of regulatory T lymphocytes (TR) in formalin fixed and paraffin embedded sections of different types of tumor tissue. TR plays a major role in homeostasis of normal immune systems where they prevent auto reactivity of the immune system towards the host. This beneficial effect of TR is frequently "hijacked" by malignant cells where tumor-infiltrating regulatory T cells are recruited by the malignant nuclei to inhibit the beneficial immune response of the host against the tumor cells. In the majority of human solid tumors, an increased number of tumor-infiltrating FOXP3 positive TR is associated with worse outcome. However, in follicular lymphoma (FL) the impact of the number and distribution of TR on the outcome still remains controversial.

In this study, we present a novel method to detect and enumerate nuclei from FOXP3 stained images of FL biopsies. The proposed method defines a new adaptive thresholding procedure, which aims to minimize under-segmented and over-segmented nuclei for coarse segmentation. Next, we integrate a parameter-less elliptical arc and line segment detector (ELSD) as additional information to refine segmentation results. Finally, we utilize a state-of-the-art super-pixel method, Simple Linear Iterative Clustering (SLIC) to split the rest of the merged nuclei. Our dataset consists of 13 region-of-interest images containing 769 negative and 88 positive nuclei. Three expert pathologists evaluated the method and reported sensitivities in detecting negative and positive nuclei ranging from 83-100% and 90-95%, and precisions of 98-100% and 99-100%, respectively. The proposed solution can be used by other researchers investigating the impact of FOXP3 positive nuclei on the outcome and prognosis in FL.

10140-14, Session 3

Context-sensitive patch histograms for detecting rare events in histopathological data

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Assessment of histopathological data is not only di?cult due to its varying appearance, e.g. caused by staining artifacts, but also due to its sheer size: Common whole slice images feature a resolution of 6000x4000 pixels. Therefore, finding rare events in such data sets is a challenging and tedious task and developing sophisticated computerized tools is not easy, especially when no or little training data is available. In this work, we propose learning-free yet e?ective approach based on context sensitive patch-histograms in order to find extramedullary hematopoiesis events in Hematoxylin-Eosin-stained images. When combined with a simple nucleus detector, one can achieve performance levels in terms of sensitivity 0.7146, specificity 0.8476 and accuracy 0.8353 which are very well comparable to a recently published approach based on random forests.

10140-15, Session 3

Automatic computational labeling of glomerular textural boundaries

Brandon Ginley, John E. Tomaszewski, Pinaki Sarder, Univ. at Buffalo (United States)

The glomerulus, a specialized bundle of capillaries, is the blood filtering unit of the kidney. Each human kidney contains about 1 million glomeruli. Structural damages in the glomerular micro-compartments give rise to several renal conditions. One of the most significant of these conditions is proteinuria, where excessive blood proteins flow freely to the urine. The sole way to confirm glomerular structural damage in renal pathology is by examining histopathological or immunofluorescence stained needle biopsies under a light microscope. This method, however, is extremely tedious and time consuming, and requires manual scoring on the number and volume of structures. Computational quantification of equivalent features promises to greatly ease this manual burden and improve the reproducibility of the analysis. The largest obstacle to computational quantification of renal tissue is the ability to recognize complex glomerular textural boundaries automatically. Here we present a computational pipeline to accurately identify glomerular boundaries with high precision and accuracy. The computational pipeline employs an integrated approach composed of Gabor filtering, Gaussian blurring, statistical F-testing, and distance transform, and performs significantly better than standard Gabor based textural segmentation method. Our integrated approach provides mean accuracy/precision of 0.89/0.97 on n = 200 Hematoxylin and Eosin (H&E) glomerulus images, and mean 0.88/0.94 accuracy/precision on n = 200 Periodic Acid Schiff (PAS) glomerulus images. Respective accuracy/precision of the Gabor filter bank based method is 0.83/0.84 for H&E and 0.78/0.8 for PAS. Our method will simplify computational partitioning of glomerular micro-compartments hidden within dense textural boundaries. Automatic quantification of glomeruli will streamline structural analysis for pathologists and nephrologists working in the clinic, and can help realize real time diagnoses and interventions.

10140-16, Session 3

Convolutional neural networks for prostate cancer recurrence prediction

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Precise prediction of treatment outcome is important for effective cancer treatment planning. We present an approach to predict the risk of prostate cancer (PCa) recurrence, for patients undergoing radical prostatectomy (RP) for whom follow up information (recurrent vs. non-recurrent) was available, through automated analysis of H&E stained tumor slides acquired at the time of treatment. Current PCa grading using Gleason score, which is based on gland shapes alone, often fail to successfully predict the recurrence. Our PCa recurrence prediction approach uses two separate convolutional neural network (CNNs). The first CNN detects nuclear centers, including separate ones for touching or overlapping nuclei, by processing small patches (51 x 51) and estimating the distance of their central pixel from the nearest nucleus boundary (distance transform). The second CNN works with larger patches (101 x 101) centered at the detected nuclear centers and estimates the probability of it belonging to a tissue sample of a patient for whom biochemical recurrence was observed after RP. The estimate of recurrence probability for a patient is based on aggregation of recurrence probabilities of nuclei detected in its tissue images. The proposed approach gave 0.81

AUC for a sample of 30 recurrent cases and 30 non-recurrent controls, after being trained on another set of 80 cases and control patients each. If validated further, such an approach might help in choosing between a combination of treatment options such as active surveillance, radical prostatectomy, radiation and hormone therapy. It can also generalize to prediction of outcomes in other cancers.

10140-17, Session 4

Leveraging unsupervised training sets for multi-scale compartmentalization in renal pathology

Brendon Lutnick, John E. Tomaszewski, Pinaki Sarder, Univ. at Buffalo (United States)

Clinical pathology relies on manual compartmentalization and quantification of biological structures, which is time consuming and often error-prone. Application of computer vision segmentation algorithms to histopathological image analysis, in contrast, can offer fast, reproducible, and accurate quantitative analysis to aid pathologists. Algorithms tunable to different biologically relevant structures can allow accurate, precise, and reproducible estimates of disease states. In this direction, we have developed a fast, unsupervised computational method for simultaneously separating all biologically relevant structures from histopathological images in multi-scale. Segmentation is achieved by solving an energy optimization problem. Representing the image as a graph, nodes (pixels) are grouped by minimizing a Potts model Hamiltonian, adopted from theoretical physics, modeling interacting electron spins. Pixel relationships (modeled as edges) are used to update the energy of the partitioned graph. By iteratively improving the clustering, the optimal number of segments is revealed. To reduce computational time, the graph is simplified using a Cantor pairing function to intelligently reduce the number of included nodes. The classified nodes are then used to train a multiclass support vector machine (SVM) to apply the segmentation over the full image. Accurate segmentations of images with as many as 10^6 pixels can be completed only in 5 sec, allowing for attainable multi-resolution visualization. To establish clinical potential, we employed our method in renal biopsies to quantitatively visualize for the first time scale variant compartments of heterogeneous intra- and extra-glomerular structures simultaneously. Implications of the utility of our method extend to fields such as oncology, genomics, and non-biological problems.

10140-18, Session 4

A computational framework to detect normal and tuberculosis infected lung from HE-stained whole slide images

Muhammad Khalid Khan Niazi, The Ohio State Univ. Medical Ctr. (United States); Gillian Beamer, Tufts Univ. (United States); Metin N. Gurcan, The Ohio State Univ. Wexner Medical Ctr. (United States)

Accurate detection and quantification of normal lung tissue in the context of Mycobacterium tuberculosis infection is of interest from a biological perspective. The automatic detection and quantification of normal lung will allow the biologists to focus more intensely on regions of interest within normal and infected tissues. We present a computational framework to extract individual tissue sections from whole slide images having multiple tissue sections. It automatically detects the background, red blood cells and handwritten digits to bring efficiency as well as accuracy in quantification of tissue sections. For efficiency, we model our framework with logical and morphological operations as they can be performed in linear time. We further divide these individual tissue sections into normal and infected areas using deep neural network. The computational framework was trained on 60 whole slide images. The proposed computational framework resulted in an overall accuracy of 99.2% when extracting individual tissue sections from 120 whole slide images in the test dataset. The framework resulted in a relatively higher accuracy (99.7%) while classifying individual lung sections into normal and infected areas. Our preliminary findings suggest that the proposed framework has good agreement on how biologists define normal and infected lung areas.

10140-19, Session 4

Evaluation of nucleus segmentation in digital pathology images through large scale image synthesis

Naiyun Zhou, Xiaxia Yu, Tianhao Zhao, Si Wen, Fusheng Wang, Wei Zhu, Tahsin Kurc, Allen Tannenbaum, Joel Saltz, Yi Gao, Stony Brook Univ. (United States)

Digital histopathology images with more than 1 Gigapixel are drawing attention in clinical, biomedical research, and computer vision fields. Among the multiple observable features spanning multiple scales in the pathology images, the nuclear morphology is one of the central criteria for diagnosis and grading. As a result, it is also the mostly studied target in image computing. Large amount of research papers have devoted to the problem of extracting nuclei from digital pathology images, which is the foundation of any further correlation study. However, the validation and evaluation of nucleus extraction have yet been formulated rigorously and systematically. Some researches report a human verified segmentation with thousands of nuclei, whereas a single whole slide image may contain up to million. The main obstacle lies in the difficulty of obtaining such a large number of validated nuclei, which is essentially an impossible task for pathologist. We propose a systematic validation and evaluation approach based on large scale image synthesis. This could facilitate a more quantitatively validated study for current and future histopathology images analysis field.

10140-20, Session 4

Image based risk score predictor: predicting disease aggressiveness using sub-visual cues from image data *(Keynote Presentation)*

Anant Madabhushi, Case Western Reserve Univ. (United States)

No Abstract Available

10140-21, Session PSMon

Automated epidermis segmentation in histopathological images of human skin stained with hematoxylin and eosin

Pawel Kleczek, AGH Univ. of Science and Technology (Poland); Grzegorz Dyduch, Jagiellonian Univ. Medical College (Poland); Joanna Jaworek-Korjakowska, Ryszard Tadeusiewicz, AGH Univ. of Science and Technology (Poland)

Background: Epidermis area is an important observation area for the diagnosis of inflammatory skin diseases and skin cancers. Therefore, in order to develop a computer-aided diagnosis system, segmentation of the epidermis area is usually an essential, initial step. This study presents an automated and robust method for epidermis segmentation in whole slide histopathological images of human skin, stained with hematoxylin and eosin.

Methods: The proposed algorithm combines the statistical analysis of color

information in normalized hematoxylin and eosin stain images, obtained by color decomposition of a general histopathological image of a skin specimen, with the shape analysis of elements in binary images obtained by thresholding the stain images.

The new technique utilizes domain-specific knowledge of morphometric and biochemical properties of skin tissue elements to segment the relevant histopathological structures in human skin.

The initial segmentation of a histopathological specimen is obtained by global thresholding of the general image. Then it is refined in a series of steps consisting in either removing or including the segmented tissue structures, depending whether or not a given structure constitutes part of the epidermis, to produce the epidermis segmentation.

Results: Experimental results on 50 skin histopathological images show that the proposed technique segments the epidermis with a mean sensitivity of 82%, a mean specificity of 99% and a mean precision of 92%. It segments effectively for different types of skin disorders and in case of lesions with inflammatory skin diseases provides a superior performance compared to the existing techniques.

10140-22, Session PSMon

Automated cancer stem cell recognition in HE stained tissue using convolutional neural networks and color deconvolution

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The analysis and interpretation of histopathological samples and images is an important discipline in the diagnosis of various diseases, especially cancer. An important factor in prognosis and treatment with the aim of a precision medicine is the determination of so-called cancer stem cells (CSC) which are known for their resistance to chemotherapeutic treatment and involvement in tumor recurrence. Using immunohistochemistry with CSC markers like CD13, CD133 and others is one way to identify CSC. In our work we aim at identifying CSC presence on ubiquitous Hematoxilyn & Eosin (H&E) staining as an inexpensive tool for routine histopathology based on their distinct morphological features.

We present initial results of a new method based on color deconvolution (CD) and convolutional neural networks (CNN). This method performs favorably (accuracy 0.936) in comparison with a state-of-the-art method based on 1D-SIFT and eigen-analysis feature sets evaluated on the same image database. We also show that accuracy of the CNN is improved by the CD pre-processing.

10140-23, Session PSMon

Convolutional neural networks for an automatic classification of prostate tissue slides with high–grade Gleason score

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Prostate cancer is the second most common cancer in men. The Gleason grading system is widely used and has been correlated to the prognostic factor, patient outcomes, local recurrence and metastasis. The grading is based on the architectural patterns shown in the histopatological samples (biopsy or radical prostatectomy) taken from the prostate.

In a Gleason grade higher than 8, cells are poorly differentiated and prognostic is adverse with a higher risk of relapse.

Therefore it is important in clinical practice to define objectively higher Gleason scores for the treatment and follow up of the patient. A fully automatic approach using patch selection and convolutional neural networks to classify whole slide prostate images is presented. The approach detects regions of interest in a WSI where relevant visual information could be sampled to generate a reliable Gleason grading score. It uses the blue ratio from an image to rank the most relevant patches that should be used for training a CNN. 235 tissue slides from the TCGA data set with their corresponding Gleason score were used. GoogleNet was selected because it generated the highest score in the validation set to classify between patches with lower Gleason (grade <7) score and higher Gleason score (grade >8).

The architecture is 27 layers deep and the network randomly crop the RGB patches in regions of 227x227 with mean substraction. 36 out of 46 (0.782 accuracy) unseen test WSIs were correctly classified.

The best classified scores were Grade 10 (1 image) with 0.927 accuracy and Grade 8 (8 images) with 0.862 accuracy. The model can be scalable to large data sets and can generate fast results once a model has been trained.

10140-24, Session PSMon

Disease grading of heterogeneous tissue using convolutional autoencoder

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One of the main challenges of histological image analysis is the high dimensionality of the images. This can be addressed via summarizing techniques or feature engineering. However, such approaches can limit the performance of subsequent machine learning models, particularly when dealing with highly heterogeneous tissue samples. To capture the diverse features of heterogeneous tissues in large tissue images, we enhance the computational framework introduced by Zerhouni et al. in SPIE16 by addressing cellular heterogeneity, without the need of cellular annotation. We propose an autoencoder-based representation learning that simultaneously produces a dictionary of representative atoms that can be used as a base to describe the inputs. In approaches such as Bag of Visual Words, patches are hard assigned to the closest cluster. By using soft assignments that maps each patch to a set of dictionary elements, one enables a finer-grained representation of the data. Hence, one can detect both similarities and differences across patches, identify dominant patterns, i.e. frequently appearing patterns, as well as discriminant patterns, i.e. patterns that are used for very specific patches. We can then use this information both for dimensionality reduction, and to study tissue and tumor heterogeneity. We demonstrate that the number of atoms that are needed to robustly represent are staining (H&E or different IHC) dependent, thus, indicating a level of heterogeneity. By integrating this mechanism in a broader framework for disease grading, we increase AUC by as much as 0.07 from a baseline of 0.79 and reach an AUC as high as 0.97 for H&E.

10140-25, Session PSMon

A computational study on convolutional feature combination strategies for grade classification in colon cancer using fluorescence microscopy data

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The cancer diagnostic workflow is typically performed by highly specialized and trained pathologists, for which analysis is expensive both in terms of time and money. This work focuses on grade classification in colon cancer. The analysis is performed over 3 protein markers; namely E-cadherin, beta actin and colagenIV. In addition, we also use a virtual Hematoxylin & Eosin (H&E) stain. This study involves a comparison of various ways in which we can manipulate the information over the 4 different images of the tissue samples and come up with a coherent and unified response based on the data at our disposal. Pre-trained convolutional neural networks (CNNs) is the method of choice for feature extraction. The AlexNet architecture trained on the ImageNet database is used for this purpose. We extract a 4096 dimensional feature vector corresponding to the 6th layer in the network. Linear SVM is used to classify the data. The information from the 4 different images pertaining to a particular tissue sample; are combined using the following techniques: soft voting, hard voting, multiplication, addition, linear combination, concatenation and multi-channel feature extraction. We observe that we obtain better results in general than when we use a linear combination of the feature representations. We use 5-fold cross validation to perform the experiments. The best results are obtained when the various features are linearly combined together resulting in a mean accuracy of 91.27%.

10140-26, Session PSMon

Evaluating color performance of whole-slide imaging devices by multispectral-imaging of biological tissues

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Color performance is an essential factor when evaluating whole-slide imaging (WSI) devices for making purchase or regulatory decisions. Evaluating color performance of WSI devices is challenging because of the difficulty in obtaining color truth. Previously, color test targets were used by researchers and vendors to evaluate WSI devices because they can be accurately measured and reproduced. However, the spectral and structural differences between color phantoms and real tissue slides are inevitable and might confound the evaluation results. In this study, a multispectral imaging system was developed to measure the spectral transmittance of each pixel of a real tissue slide. The per-pixel spectral transmittance was then used to calculate the color truth, which would then be used to calculate the per-pixel color difference CIEDE2000 of the image generated by a WSI device. Three commercially available biological tissue slides (human colon, skin, and kidney) were used to test two WSI devices that represent legacy and modern WSI devices. The experiment results show that the mean CIEDE2000 for the modern WSI device is in [8.4, 13.08], while the legacy device in [18.02, 26.33]. The color differences with respect to histogram, image structure, and color gamut were analyzed for presenting the color characteristics of the WSI devices. The proposed methodology demonstrated a means of evaluating the color performance of WSI devices with relevant tissue slides.

10140-27, Session PSMon

Automatic Gleason grading of HE stained microscopic prostate images using deep convolutional neural networks

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In 2012 prostate cancer was the second most common cancer diagnosis for men. The diagnosis is confirmed by pathologists based on ocular inspection of prostate biopsies in order to classify them according to Gleason score. The main goal of this paper is to automate the classification using convolutional neural networks (CNNs).

The introduction of CNNs has broadened the field of pattern recognition. It replaces the classical way of designing and extracting hand-made features to use for classification with the substantially different strategy of letting the computer itself decide which features are of importance.

For automated prostate cancer classification into the classes Benign, Gleason grade 3, 4 and 5 we propose a CNN with small convolutional filters that has been trained from scratch using stochastic gradient descent with momentum. The input consists of microscopic images of haematoxylin and eosin stained tissue, the output of a coarse segmentation into regions of the four different classes. The dataset used consists of 213 images, each considered to be of one class only. Using four-fold cross-validation we obtained an error rate of 7.3%, which is significantly better than previous state of the art using the same dataset. Since good results were obtained although the dataset was rather small, the conclusion is that CNNs are a promising method for this problem. Future work includes obtaining a larger dataset, which potentially could diminish the error margin.

10140-29, Session PSMon

Integrative analysis on histopathological image for identifying cellular heterogeneity

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This study has brought together image processing, classification and spatial pattern analysis to quantitatively analyze hematoxylin and eosin-stained (H&E) tissue sections. A mixture of tumor and normal cells (intratumoral heterogeneity) and complex tissue architecture of most samples complicate the interpretation of their cytological profiles. To address these challenges, first we describe an automatic nuclei segmentation of histology section and then show de-convoluting cellular heterogeneity by clustering individual segmented nuclei based on their morphological profiles. Furthermore, we devise spatial pattern analysis for analyzing spatial arrangement and architectural organization of individual nuclei. These studies could benefit H&E section analysis by refining and complementing individual analyses.

10140-30, Session PSMon

Extraction of glomeruli in whole slide imaging of kidney biopsy specimens

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The pathological diagnosis of transplanted kidney is performed according to the Banff Classification in order to gain an accurate understanding of the condition of a kidney. The pathological diagnosis of a transplanted kidney is extremely difficult and, as such, a variety of methods for diagnosis, including diagnosis by electron microscope, are being considered currently. Quantification of the diagnostic information derived by image processing is required for such purposes. This study proposes an automatic extraction method for normal glomeruli for the purpose of quantifying EVG-stained pathology specimens, and we provide a report on the package of methods that we have created for identifying the cortical region of Whole Slide Imaging (WSI) and extraction of the glomerulus in the cortex.

10140-31, Session PSMon

Unsupervised segmentation of HE breast images

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Combining information about biomarkers with morphology from H&E staining may provide more insights into the heterogeneity of ductal carcinoma in situ (DCIS) than either alone. We are working towards a computer-based identification and description system for DCIS. As part of this software, we are developing a region of interest finder to segment glands for further processing, such as identification of DCIS and to extract H&E based information such as nuclear morphology, presence of necrosis, etc.

The unique aspect of the segmentation algorithm design is that it is tolerant of variability in staining and requires no user interaction. To achieve stain variation tolerance we use unsupervised learning and iteratively interrogate the image for information. Using simple rules, such as “haematoxylin stains nuclei”, and iteratively assessing the resultant objects (flat, small objects are stromal cells), the system builds up a knowledge base so that it is not dependent upon manual annotations. While the system starts with resolution-based assumptions, these are quickly replaced by the knowledge gained.

The algorithm pipeline is designed to find the simplest items first (segment stains), then segment interesting subclasses and objects (stroma, lymphocytes) and build information until it is possible to segment cell groups (blobs) that are normal, DCIS, and the range of benign glands. Once blobs are found, they can be quantitatively described to identify those that represent DCIS. In this work we present the early results where the Haematoxylin stain ranges from blue to red dominant in RGB space.

10140-32, Session PSMon

Optimized color decomposition of localized whole slide images and convolutional neural network for intermediate prostate cancer classification

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This paper presents a fully automatic approach to grade intermediate prostate malignancy with hematoxylin & eosin-stained whole slide images. Deep learning architectures such as convolutional neural networks have been utilized in the domain of histopathology for automated carcinoma detection and classification. However, few work show its power in discriminating intermediate Gleason patterns, due to sporadic distribution of prostate glands on stained biopsy samples. We propose optimized hematoxylin decomposition on localized images, followed by convolutional neural network to classify Gleason patterns 3+4 and 4+3 without handcrafted features or gland segmentation. Crucial glands morphology and structural relationship of nuclei are extracted twice in different color space to mimic pathologists’ visual examination. Our novel classification scheme evaluated on 169 whole slide images yielded a 70.41% accuracy and the area under the receiver operating characteristic curve of 0.7247.

10140-33, Session PSMon

Topological descriptors for quantitative prostate cancer morphology analysis

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We aim to discover new quantitative image-based prognostic biomarkers for prostate cancer, focusing on an investigation of novel concepts from computational topology applied to prostate cancer glandular architecture. The current standard for prostate cancer grading is the modified Gleason score, which is a subjective rating system based on an analysis of high-level tissue architecture and glandular shape and organization. However, Gleason scoring exhibits high intra-observer and inter-observer variability between pathologists, and may not capture all potentially prognostic information contained in glandular growth patterns. We introduce new topological descriptors that capture architectural features of prostate glands in pathology images. In this work, we demonstrate the potential effectiveness of persistent homology to recognize and quantify glandular architectural features. Specifically, we computed persistence diagrams from nuclear-segmented prostate cancer slides of Gleason grades 3 and 4, and show that information on morphological subtypes is encoded in longer cycle persistence (Gleason 3) and later cycle birth-times (Gleason 4). Our results point to the ability to quantify distributions of gland cycles and cycle inter-relatedness, with the further ability to window the diagrams and isolate features contributing to the diagrams, which is useful in interpreting quantitative shape descriptors in histological context. Ongoing work is aimed at investigating classification of an image library based on these descriptors and comparison to standard Gleason grade classifications.

10140-34, Session PSMon

Panning artifacts in digital pathology images

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In making a pathologic diagnosis, a pathologist uses cognitive processes: perception, attention, memory, and search (Pena and Andrade-Filho, 2009). Typically, this involves focus while panning from one region of a slide to another, using either a microscope in a traditional workflow or software program and display in a digital pathology workflow (DICOM Standard Committee, 2010). We theorize that during panning operation, the pathologist receives information important to diagnosis efficiency and/or correctness. As compared to an optical microscope, panning in a digital pathology image involves some visual artifacts due to the following: (i) the frame rate is finite; (ii) time varying visual signals are reconstructed using imperfect zero-order hold. Specifically, after pixel's digital drive is changed, it takes time for a pixel to emit the expected amount of light. In this study, we identify basic visual tasks related to pathology diagnosis, in which we measure the effect of panning artifacts at various levels of image color contrast, panning speed, panel response time, and frame rate in terms of performance and efficiency. Previous work suggests that 49% of navigation was conducted in low-power/overview with digital pathology (Molin et al., 2015), but the influence of display factors was not measured. Our preliminary results suggest visual tasks that involve tissue structure are more impacted by panning artifacts than those that only involve color. The results of this study can be used to develop automatic quality assessment algorithms for digital pathology as well as defining design specifications for future WSI systems.

10140-36, Session PSMon

Tissue classification of liver pathological tissue specimens image using spectral features

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In digital pathology diagnosis, accurate recognition and quantification of the tissue structure is an important factor for computer-aided diagnosis. However, the classification accuracy of cytoplasm is low in Hematoxylin and eosin (HE) stained liver pathology specimens because the RGB color values of cytoplasm are almost similar to that of fibers. In this paper, we propose a new tissue classification method for HE stained liver pathology specimens by using hyperspectral image. At first we select valid spectra from the image to make a clear distinction between fibers and cytoplasm, and then classify five types of tissue based on the bag of features (BoF). The tissue classification accuracy in overall was improved by 15% compared with RGB values only classification, and it was further improved by 1% by adding spectral features. In particular, it was improved by 3-4% in fibers and cytoplasm.

10140-37, Session PSMon

Color normalization of histology slides using graph regularized sparse NMF

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Computer based automatic medical image processing and quantification are becoming popular in digital pathology. However, preparation of histology slides can vary widely due to differences in staining equipment, procedures and reagents, which can reduce the accuracy of algorithms that analyze their color and texture information. To reduce the unwanted color variations, various supervised and unsupervised color normalization methods have been proposed. Compared with supervised color normalization methods, unsupervised color normalization methods have advantages of time and cost efficiency, and universal applicability. Most of the unsupervised color normalization methods for histology are based on stain separation. Based on the fact that stain concentration cannot be negative and different parts of the tissue absorb different stains, nonnegative matrix factorization (NMF), and particularly its sparse version (SNMF), are good candidates for stain separation. However, most of the existing unsupervised color normalization method like PCA, ICA, NMF and SNMF fail to consider important information about sparse manifolds that its pixels occupy, which could potentially result in loss of texture information during color normalization. Manifold learning methods like Graph Laplacian have proven to be very effective in interpreting high-dimensional data. In this paper, we propose a novel unsupervised stain separation method called graph regularized sparse nonnegative matrix factorization (GSNMF). By considering the sparse prior of stain concentration together with manifold information from high-dimensional image data, our method shows better performance in stain color deconvolution than existing unsupervised color deconvolution methods, especially in keeping connected texture information. To utilize the texture information, we construct a nearest neighbor graph between patches of an image based on their distances using heat kernel in L*a*b* space. The representation of a pixel in the stain density space is constrained to follow the distance of the patches centered at these pixels in the neighborhood graph. Utilizing color matrix transfer method with the stain concentrations found using our GSNMF method, the color normalization performance was also better than existing methods.

10140-38, Session PSMon

Frequency analysis of gaze points with CT colonography interpretation using eye gaze tracking system

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Purpose

It is important for understanding image interpretation process to investigate eye tracking gaze points of experts for trainees. We investigated gaze points of CT colonography (CTC) interpretation process and analyzed difference of that of experts and trainees. In this study, we attempted to understand how trainees can be improved to a level achieved by experts in viewing for CTC.

Method

We used an eye gaze point sensing system, Gazefineder (JVCKENWOOD Corporation Tokyo,Japan), which detect pupil point and corneal reflection point by the dark pupil eye tracking. This system supplies gaze points images and excel file data. The subjects are radiological technologists experienced and inexperienced reading CTC. We performed observer experiments of reading virtual pathology images and examined observer's image interpretation process using gaze data. Furthermore, we examined eye tracking frequency analysis in a method using the Fast Fourier Transform (FFT).

Results

We understand difference between expert and trainee by frequency analysis. The result of trainee has a lot of high-frequency component and low-frequency component together. In contrast, both component of expert's were relative low. Refer to the amount of eye movement every 0.02s we recongnized that the expert interpret images slowly and calmly. On the other hand, trainee was moving eyes quickly and also looking wide range.

Conclusion

We can assess difference of the gaze point on CTC between experts and trainee by the eye gaze point sensing system and frequency analysis. The better way of CTC interpretation for trainee is shown by using gaze data.

10140-39, Session PSMon

Application of machine learning for in vivo identification of at risk cervical tissue using multispectral digital colposcope images

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Background: Cervical cancer is the second most common cancer in women, worldwide, especially in developing counties it is the leading cause of cancer death among women due to limited cancer screening tools. Cervical cancer if diagnosed early (cervical intraepithelial neoplasia) can be readily treated and patients have much a greater chance of survival. This highlights the importance of designing effective cervical cancer screening/evaluation methods.

Study goals: It has been demonstrated that we can take advantage of optical technology to significantly improve cervical cancer screening. The goal of this study is to integrate reflectance and fluorescence imaging with machine learning approaches to design an effective evaluation tool for cervical cancer screening.

Study Materials/Design: In a preliminary study we obtained multispectral digital colposcope (MDC) images from 50 Loop electrosurgical excision procedure (LEEP) patients. The LEEP specimens were cut into 8-12 piece and a pathologist mapped out for each section all areas of normal, CIN1, CIN2, CIN3 and the sections realigned to make a pathology representation of the LEEP tissue. Using this pathological annotation as our gold standard we then asked 10 experts to trace onto the MDC images where they thought the abnormal pathology existed. We then calculated a probability map for each patient using the traced areas. Finally we used boosted tree classifier to separate normal (< CIN2) vs. Abnormal (>CIN1) regions.

Results and Conclusion: We obtained about 89% accuracy and % 86 precision when we used the whole dataset. Currently we are working on this dataset to improve the system accuracy and robustness.

10140-40, Session PSMon

Content-based histopathological image retrieval for whole slide image database using binary codes

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Content-based image retrieval (CBIR) has been widely researched for medical images. In application of histopathological images, there are two issues that need to be carefully considered. The one is that the digital slide is stored in a spatially continuous image with a size of more than 10k$x10K pixels. The other is that the size of query image varies in a large range according to different diagnostic conditions. It is a challenging work to retrieve the eligible regions for the query image from the database that consists of whole slide images (WSIs). In this paper, we proposed a CBIR framework for the WSI database and size-scalable query images. Each WSI in the database is encoded and stored in a matrix of binary codes. When retrieving, the query image is first encoded into a set of binary codes and analysed to pre-choose a set of proposal regions from database using hashing method. Then a multi-binary-code-based similarity measurement based on hamming distance is designed to rank proposal regions. Finally, the top relevant regions and their locations in the WSIs along with the diagnostic information are returned to assist pathologists in diagnoses. The effectiveness of the proposed framework is evaluated in a fine-annotated WSIs database of epithelial breast tumours. The experimental results show that proposed framework is both effective and efficiency for content-based whole slide image retrieval.