QRR001

Quantitative DCE-MRI Image Processing Made Easy

Quantitative Imaging Reading Room Showcase

Location: QIRR, Learning Center

Participants

Qing Yang PhD (Presenter): Employee, Apollo Medical Imaging Technology Pty Ltd

BACKGROUND

Dynamic Contrast Enhanced Magnetic Resonance Imaging (DCE-MRI) is a promising method with potential to provide pharmacodynamic biomarkers to aid diagnosis and therapy monitoring of cancer. The DCE-MRI Profile recently developed by the RSNA QIBA DCE-MRI Technical Committee has provided basic standards and guideline for DCE-MRI measurements and quality control including image acquisition, post-processing and analysis. MIStar is a commercial software package providing a broad spectrum of quantitative image processing functions. The DCE-MRI quantitative functions have been used in research setting and clinical trials. The goal of MIStar is to provide an easy-to-use software tool with streamlined workflow for comprehensive DCE-MRI image processing and analysis including all features and functions described in the DCE-MRI Profile and beyond.

METHODOLOGY/APPLICATION

The MIStar software can be easily installed to run on standard desktop PCs and laptops. It provides an intuitive interface with clinical database, and can receive DICOM images directly from scanner workstation or PACS via DICOM network transfer. It can also import data from common storage media. MIStar can automatically detect all dynamic protocol parameters of DCE-MRI data acquired from different vendor scanners. Processing of the DCE-MRI data follows a streamlined workflow with the following steps: Load T_1 mapping data if available, and process tissue T_1 map; Load DCE-MRI dynamic data, and apply motion correction if required; Convert DCE-MRI signal intensity into contrast concentration using either pulse sequence signal equation method with T_1 map, or phantom calibration method if available; Select pre-contrast baseline and arterial input function using automatic, semi-automatic or manual methods at ROI or pixel level; Signal conversion of AIF profile uses blood T_1 value; (Optional) For data acquired from high field system (e.g. 3T), B_1 inhomogeneity correction may be required. If B_1 map is available, load B_1 map and apply B_1 map correction for T_1 map processing, and subsequently to DCE-MRI processing; Calculate kinetic parameter maps including Ktrans, k_{ep}, ve, v_p, etc. as well as blood normalized IAUGC$_{BN}$ for selected update period. Model fitted curve can be dynamically overlaid on measured curve for assessment of processing quality. Additional maps of goodness-of-fit and correlation coefficient are also available for quality assessment. MIStar also provides image registration to allow lesion segmentation ROIs from different data to be mirrored onto parameter maps. The intelligent ROI analysis tool provides automatic ROI grow with manual adjustment coupled with histogram analysis for easy statistical comparison and analysis. A batch processing option allows automatic prosessing of large amount of data over night with a detailed event log, which is particularly useful for clinical trials. All data including processing parameters and maps, AIF, ROI can be saved and restored later for archiving and quality control purposes. Results can also be saved in DICOM format and send to PACS for easy access and review enterprise wide.

DEMONSTRATION STRATEGY

We will provide information poster and Meet-the-Expert presentations. A MIStar demo workstation will provide hands-on demonstration of the workflow with all functions for quantitative applications in various organs of the whole body. Through hands-on experience using various demo cases, attendees will be able to learn about all aspects associated with the quantitative applications including optimization of Image acquisition parameters, processing methods with kinetic models, results interpretation with quality assessment and reporting tools.

REFERENCES AND PUBLICATIONS

Early detection of lewis lung carcinoma tumor control by irradiation using diffusion-weighted and dynamic contrast-enhanced MRI. Cheng JC, et al. PLoS One. 2013 May 2;8(5):e62762. Dynamic contrast-enhanced MRI in advanced non small-cell lung cancer patients treated with first-line bevacizumab, gemcitabine, and cisplatin. Chang YC, et al. J Magn Reson Imaging. 2012 Aug;36(2):387-965. Value of DCE-MRI and FDG-PET/CT in the prediction of response to preoperative chemotherapy with bevacizumab for colorectal liver metastases. De Bruyne S, et al. Br J Cancer. 2012 Jun 5;106(12):1926-33. Dynamic contrast-enhanced magnetic resonance imaging biomarkers predict survival and response in hepatocellular carcinoma patients treated with sorafenib and metronomic tegafur/uracil. Hsu CY, et al. J Hepatol. 2011 Oct; 55(4):858-65. Assessment of neovascular permeability in a pancreatic tumor model using dynamic contrast-enhanced (DCE) MRI with contrast agents of different molecular weights. Delrue LJ, et al. MAGMA. 2011 Aug; 24(4):225-32. Correlation between Pancreatic Microcirculation and Type 2 Diabetes in Patients with Coronary Artery Disease: Dynamic Contrast-enhanced MR Imaging. Yu CW, et al. Radiology. 2009 Sep; 252(3):704-711.

Sunday 12:30 - 1:30pm Monday 12:15pm - 1:15pm Tuesday 12:15pm - 1:15pm Wednesday 12:15pm - 1:15pm

QRR002

3D Slicer: An Open-source Platform for Segmentation, Registration, Quantitative Imaging and 3D Visualization of Multi-modal Image Data

Quantitative Imaging Reading Room Showcase

Location: QIRR, Learning Center

Participants

Sonia Marie-Aurore Pujol PhD (Presenter): Nothing to Disclose
Steve D. Pieper PhD : CEO, Isomics, Inc Employee, Isomics, Inc Owner, Isomics, Inc Research collaboration, Siemens AG. Research collaboration, Novartis AG Consultant, Wright Medical Technology, Inc
Andriy Fedorov PhD : Nothing to Disclose
Ron Kikinis MD : Nothing to Disclose

BACKGROUND

3D Slicer is an open-source software platform for medical image analysis and 3D visualization used in biomedical and clinical research worldwide. The software is supported by a multi-institution effort of several large-scale NIH-funded consortia, which include the National Alliance for Medical Image Computing (NA-MIC), the Neuroimage Analysis Center (NAC), the Quantitative Image Informatics for Cancer Research (QIICR) and the National Center for Image-Guided Therapy (NCIGT). In addition, funding from several other countries contributes to some aspects of the software. 3D Slicer is freely available under a BSD-type license with no restriction on use.

METHODOLOGY/APPLICATION

3D Slicer is developed as modular open-source software platform for delivering cutting-edge medical image analysis technology to the clinical and scientific community. The platform enables applied science oriented toward specific-subject analysis in the presence of pathology. 3D Slicer includes radiological viewing capabilities for MR, CT, PET and Ultrasound data in multiple image file formats including DICOM, standard functionalities reformatting and lightbox viewing of anatomical slices, as well as advanced 3D visualization functionalities such as surface rendering and GPU-based volume rendering. The software integrates over 100 modules with state-of-the-art tools for filtering, segmentation, registration, and quantitative analysis of multi-modal imaging data, as well diffusion tensor imaging analysis, tool tracking and real-time data fusion for image-guided intervention. In addition, the 3D Slicer Extension framework allows members of the research community to add new functionalities to the platform, and provides a mechanism for delivering complex domain-specific software to end users.

DEMONSTRATION STRATEGY

The 3D Slicer exhibit will consist in a series of thematic demonstrations using multi-modal image datasets, which include MRI, DTI, CT, PET and DCE-MRI. The exhibit will build upon the 22 hands-on demonstrations of 3D Slicer that were showcased at the RSNA 2010,2011,2012 and 2013 QIRR, as well as the two Informatics refresher courses that will be presented at RSNA 2014 (ICIA11 "Quantitative Medical Imaging for Clinical Research and Practice" S. Pujol, K. Macura, R. Kikinis; ICIA32 "3D Interactive Visualization of DICOM Images for Radiological Applications" S.Pujol, K.Shaffer, R.Kikinis) A team of 3D Slicer experts will be running the demonstrations with sample datasets or, where appropriate, data provided by attendees, and will deliver a series of daily 60-minute Meet-the-Experts sessions. The hands-on sessions will demonstrate 3D visualization functionalities (e.g. volume rendered head, thoracic and abdominal CT scans, surface rendered atlases of brain, knee, and abdomen, 3D surface reconstruction of the bronchopulmonary segments from chest CT images), segmentation tools (e.g. semi-automated segmentation of a glioma case, MRI-based automated parcellation of the human brain), quantitative imaging features (e.g. longitudinal PET/CT quantitative assessment of tumor response in a squamous cell carcinoma) as well as image-guided therapy applications (e.g. exploration of peritumoral white matter for neurosurgical planning, image registration for MR-guided prostate biopsies.). The exhibit will also include demonstrations of Slicer extensions which include the multimodal data extension for 4D Cardiac CT exploration, the pharmacokinetic modeling extension for Quantitative Imaging, the SlicerRT extension for radiotherapy research and the DataStore extension for uploading and downloading dataset files into the platform. New workflows for interactive tractography seeding, and multivolume exploration of DCE-MRI datasets of the breast will be presented.

REFERENCES AND PUBLICATIONS

The 369 3DSlicer-related publications are accessible through the Surgical Planning Lab publication database at: http://www.slicer.org/publications/pages/display/?collection=11&entriesPerPage=999999999 A sample of four publications is provided below: 1. 3DSlicer as a Tool for Interactive Brain Tumor Segmentation. Kikinis, R, Pieper S. Conf. Proc. IEEE Eng Med Biol Soc 2011; 6982-4 2. Interactive Diffusion Tensor Tractography Visualization for Neurosurgical Planning. Golby AJ, Kindlmann G, Norton I, Yarmarkovich A, Pieper S, Kikinis R. Neurosurgery. 2011 Feb; 68(2):496-505. 3. Fedorov A, Beichel R, Kalpathy-Cramer J, Finet J, Fillion-Robin J-C, Pujol S, Bauer C, Jennings D, Fennessy F, Sonka M, et al. 3D Slicer as an image computing platform for the Quantitative Imaging Network. Magnetic resonance imaging. 2012 July 6;30(9):1323-1341. 4. Oyama R., Jakab M., Terata M., Isurugi C., Kaido Y., Knasugi T., Kikuchi A., Sugiyama T., Kikinis R., Pujol S. Towards Improved Ultrasound-based Analysis and 3D Visualization of the Fetal Brain using 3D Slicer. Ultrasound Obstet Gynecol. 2013 Nov;42(5):609-10. 3DSlicer documentation, tutorials and download pages are available at www.slicer.org.

Meet-the-Experts Schedule

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QRR003

IronByMR: An ImageJ Plugin to Quantify Hepatic Fat and Iron by MR at Various Magnetic Fields

Quantitative Imaging Reading Room Showcase

Location: QIRR, Learning Center

Participants

Anita Kiani (Presenter): Nothing to Disclose
Anne Boulic : Nothing to Disclose
Jean-Louis Jagut : Nothing to Disclose
Edouard Bardou-Jacquet : Nothing to Disclose
Herve Saint-Jalmes PhD : Nothing to Disclose
Elise Bannier : Nothing to Disclose
Yves Gandon MD : Nothing to Disclose

BACKGROUND

Fat or iron liver overload is frequent and underestimated. Each of these two diseases can change the magnetic resonance (MR) liver signal intensity and influences the relative semiology of liver focal lesions such HCC or liver adenomas. In some circonstances it could also be useful to assess fat concentration within the lesion itself. Quantification methods have been proposed using MR gradient echo sequences with multiple TEs. Phase contrast has been used to assess liver steatosis (1). The progressive decrease of signal, dependent to T2*, has been demonstrated to be proportional to liver iron concentration (2). Liver to muscle ratio (LMR) was also proposed as an iron overload biomarker and has been extensively validated against biochemical liver iron concentration assessment (3). More recently, correlations between 3T MR results and liver biopsy have confirmed the iron overload increase sensitivity of high field systems (4). However, each method has their own limitations. For example, T2* calculation is not always made in taking in account the potentially associated liver steatosis or the level of the background noise. LMR results could overestimate iron concentration if surface coils have been selected instead or additionnaly to the body coil. The aim of this exhibit is to present a software which can quickly assess, simultaneously, hepatic iron and fat concentration from a single breathhold MR sequence, at 1.5 and 3T. This imageJ (NIH, Bethesda, USA) plugin is developed by a research institution and is freely downloadable on www.ironbymr.fr web site. It can be fully integrated in several PACS environnements and can be used in research purpose. A draft report can automatically be displayed but, up to now, the lack of FDA approval doesn't allow a clinical routine use. However it offers an independant standardized and well validated quantification.

METHODOLOGY/APPLICATION

IronByMR is a cross-platform plugin developed complementary to the imageJ (NIH, Bethesda, USA) software. It is designed to provide a hepatic fat and iron quantification by using simultaneously T2* and LMR calculations. It implements a comprehensive workflow able to guide the physician from image upload to the final medical report. Several PACS integrations are already

available in order to simplify the process. First, a compatible multiecho gradient MR sequence using body coil must be acquired in a single breathhold. This sequence is exported in DICOM format to the IronByMR import folder. After controlling the acquisition parameters, the software propose to select a slice level showing simultaneously liver and spleen. All echoes are detected automatically. After placing circular ROIs on liver, paraspinous muscle, spleen and background noise the plugin shows a graph plotting the signal curves used to calculate hepatic and splenic T2* parameters. This graph can be automatically integrated in the PACS. The software provides liver iron and fat concentrations taking in account all measurements and compensating calculation errors in case of combined overload. Once the analysis is completed, a word-processor window is open showing a draft report allowing the radiologist to provide the final medical report. Anonymous data can be automatically collected in an external database.

DEMONSTRATION STRATEGY

IronByMR software will be available at the exhibition to demonstrate the whole clinical workflow, and an additional poster will describe the methodological and algorithmic processes which drive the program logic and flow. An example of PACS integration will be demonstrated using a database containing 100 anonymized cases explored on different MR devices operating at 1.5 or 3T and validated by liver biopsy with biochemical quantification of iron and liver fat fraction quantification. By letting the users free to perform a real analysis we will showcase the ability of this software to quickly and accurately quantify both overloads.

REFERENCES AND PUBLICATIONS

1 - Guiu B, Petit J-M, Loffroy R, Ben Salem D, Aho S, Masson D, et al. Quantification of liver fat content: comparison of triple-echo chemical shift gradient-echo imaging and in vivo proton MR spectroscopy. Radiology. 2009;250:95-102. 2 - Wood JC, Enriquez C, Ghugre N, Tyzka JM, Carson S, Nelson MD, et al. MRI R2 and R2* mapping accurately estimates hepatic iron concentration in transfusion-dependent thalassemia and sickle cell disease patients. Blood. 2005;15;106:1460-5. 3 - Gandon Y, Olivié D, Guyader D, Aubé C, Oberti F, Sebille V, et al. Non-invasive assessment of hepatic iron stores by MRI. Lancet. 2004;363:357-62. 4 - Boulic A, Kiani A, Bardou-Jacquet E, Turlin B, Saint-Jalmes H, Gandon Y. Simultaneous liver iron overload and steatosis quantification by MRI at 3.0T. RSNA - Chicago (Il) - USA, Dec. 2013.

Meet-the-Experts Schedule

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QRR004

Combined Analysis of Dynamic Gd-EOB-DTPA-Enhanced MRI and Local Volume Computation for Quantitative Liver Function Evaluation

Quantitative Imaging Reading Room Showcase

Location: QIRR, Learning Center

Participants

Andrea Schenk PhD (Presenter): Nothing to Disclose
Longquan Chen MSc : Nothing to Disclose
Jeong Hee Yoon MD : Nothing to Disclose
Jeong Min Lee MD : Research Grant, Guerbet SA Equipment support, Siemens AG Research Grant, Bayer AG
Karsten Bergmann : Employee, Bayer AG
Hendrik Oliver Arp Laue PhD : Nothing to Disclose
Jan Strehlow MSc : Nothing to Disclose
Christian Schumann : Nothing to Disclose
Daniel Demedts MSc : Nothing to Disclose
Horst Karl Hahn PhD : Nothing to Disclose

BACKGROUND

In hepatic surgery and living donor liver transplantations, preoperative volume computation of the future remnant liver from CT or MRI data is applied to estimate the remaining liver function [1]. With respect to the disease of the organ and an inhomogeneous distribution of parenchymal function, this quantitative measurement may not reflect the real metabolic reserve sufficiently [2]. On the other hand, liver function tests applied in clinical routine (e.g. Lab values, ICG clearance) compute a global liver function value only and cannot take into account local differences. Recently, functional imaging based on dynamic Gd-EOB-DTPA-enhanced MRI was introduced [3]. This method allows computing of local uptake (input relative bloodflow, irBf) and excretion (hepatic excretion function, HEF) parameters using a parameter-free model. Quantitative liver function measurements are not only crucial in extended liver surgery, but can also be applied to assess the results of local interventions (e.g. tumor ablation), chemotherapy, and other therapies influencing the organ function.

METHODOLOGY/APPLICATION

Our software, the HEF Application, evaluates DCE-MRI data that follows a prolonged protocol [2] and guides the user step-by-step through the workflow. After import of the dynamic series a preprocessing step for motion correction is performed automatically. Results of this rigid or elastic registration process can be assessed qualitatively by different visualization methods (colored overlay, checker board, difference image, contour overlay). An input function is interactively defined by the user (one ROI or multiple ROIs), and parameter maps for HEF and irBf can be computed for individual 2D ROIs or larger volumes created with the support of a contour editor including interpolation and cutting tools. Statistical values of functional and volumetric measurements are computed for 2D and 3D ROIs and can be exported to an excel file for reporting. Alternatively to the interactive definition of ROIs, a pre-existing liver analysis can be imported to compute the functional parameters for previously defined liver regions (e.g. remnant/graft, liver segments). Additional tools for exclusion of tumor ROIs and vessel structures - defined by their irBf value - are provided. The HEF Application is currently applied in a clinical study to estimate preoperative liver function before tumor surgery. In principle, the software can be deployed for many other purposes, e.g., to quantify local differences in the liver tissue, to monitor liver function during disease or therapy, and to quantify regional liver dysfunction after local interventions.

DEMONSTRATION STRATEGY

We will present the use of the HEF Application to obtain global and local quantitative measures from functional MRI series of the liver. The visitor will learn how to estimate liver function not only from volume measurements but to gain more specific quantitative information from the combination with local analysis of contrast agent uptake and excretion. Demonstration of the software enables to study the influence of image registration and input function definition. Finally, we will discuss the influence of the MRI protocol, quality and inhomogeneities on the results of the functional and overall analysis.

REFERENCES AND PUBLICATIONS

[1] Lang H. et al.: Extended left hepatectomy with an inferior right liver vein: improved operation planning by 3-D reconstruction and computer-assisted imaging. J Am Coll Surg. 2007, 205(4):626-7. [2] Nilsson H. et al.: Dynamic gadoxetate-enhanced MRI for the assessment of total and segmental liver function and volume in primary sclerosing cholangitis. J Magn Reson Imaging. 2014, 39(4):879-86. [3] Nilsson H. et al.: Assessment of hepatic extraction fraction and input relative

blood flow using dynamic hepatocyte-specific contrast-enhanced MRI. J Magn Reson Imaging. 2009, 29(6):1323-31.

Meet-the-Experts Schedule

Monday 12:15pm - 1:15pm Tuesday 12:15pm - 1:15pm Wednesday 12:15pm - 1:15pm

QRR005

An Application for Comparing Quantitative DCE- and DWI-MRI with Pathology Supporting Investigators Correlating Radiology, Pathology and Tumor Biology in Lung Cancer

Quantitative Imaging Reading Room Showcase

Location: QIRR, Learning Center

Participants

Hendrik Oliver Arp Laue PhD (Presenter): Nothing to Disclose
Peter Kohlmann PhD : Nothing to Disclose
Volker Dicken PhD : Contract, Soteria Medical BV
Jan Moltz : Nothing to Disclose
Oliver Sedlaczek MD : Nothing to Disclose
Janine Olesch : Nothing to Disclose
Johannes Lotz : Nothing to Disclose
Ron Kikinis MD : Nothing to Disclose
Horst Karl Hahn PhD : Nothing to Disclose

BACKGROUND

Functional imaging of tumors using DCE- and DWI-MRI measurements provide important information on staging and on the treatment options for various cancers. Nonetheless, the link between functional MRI and the underlying biology in the tissue is difficult to investigate since the localization of tissue samples in the functional MRI is challenging. Therefore, we offer a software tool allowing to evaluate quantitative DCE- and DWI-MRI using state of the art method to generate parameter maps of K^{trans},v_i,v_p and ADC in the tumor. The localization is facilitated by an interactive 3D visualization to locate a pathological specimen in the radiological data, allowing to compare the histological with the radiological parameters.

Most of the described new functionality will be available in summer of 2014 and the remaining features in early 2015.

The application is distributed to interested investigators at no costs as a binary installer for windows 7/8 64 and for Mac OS X. It is only necessary to apply with a small research proposal and to sign a license agreement ensuring the scientific use of the software.

The software has been used at the German Cancer Research Center, the University Hospital Heidelberg, both in Heidelberg, Germany and in the University Hospital Cologne.

METHODOLOGY/APPLICATION

Our application is a software for quantitative MRI of the lung providing:

- advanced DCE-MRI using motion correction, automated AIF detection, the general kinetic model (GKM), the extended GKM (eGKM), the use of B_1 and T_1 maps accounting for field and tissue properties.
- DWI-MRI, including advanced biexponential modeling.
- pulmonary perfusion (PP)-MRI indicating the perfusion status of different segments of the lung.

Now, our software also allows to align excised segments from pathology to the radiological data. The MRI sequences are aligned to a high resolution CT in order to allow a:

- two click segmentation of the tumor and some physiological structures.
- creation an interactive color 3D view of the data to manually place the segment in the tumor.
- creation of a resampled image from registered MRI data to use MRI contrast to identify soft tissue contrast features such as necrosis or adjacent physiological structures.

The localization information is then used to identify an adjacent whole slide image or a 3D reconstruction from pathology for comparison with histological information (staining, cell count, vessel properties, ...). The software is capable of reading various pathological image formats and can handle multi resolution pathological images ensuring a convenient orientation and magnification of the histological data.

DEMONSTRATION STRATEGY

The visitor will be introduced to functional MRI in oncologic radiology: the requirements of motion correction, the application of the eGKM and the benefits of DWI using either a mono or a biexponential diffusion model. Moreover, we will discuss the need for B_1 and T_1 maps with the visitor.

We will show how to generate parameter maps from the different MRI sequences and how to define the tumor volume from a high resolution CT and to align CT and MRI. The visitor will then be introduced in the navigation through the 3D representation of lung and tumor to place a segment corresponding to the pathological specimen. It will then be shown how the soft tissue contrast of MRI and the contrast agent uptake can improve the alignment of histological and pathological data.

Finally, we will show how to use the software to import, view and annotate the histological data. We will also show how simple quantification results of the pathology can be imported into the software.

REFERENCES AND PUBLICATIONS

[1] Kohlmann et al, 2011. Towards a research software platform for diagnosis and monitoring of COPD and asthma with pulmonary MRI. 5th International Workshop on Pulmonary Functional Imaging

[2] Laue et al., 2007. Softwaretools for Pharmacokinetic Modeling in the Analysis of DCE-MRI data. RSNA 2007.

[3] Ritter et al, 2011. Medical image analysis. IEEE Pulse

[4] Ng et al, 2010. Reproducibility of Perfusion Parameters in Dynamic Contrast- Enhanced MRI of Lung and Liver Tumors: Effect on Estimates of Patient Sample Size in Clinical Trials and on Individual Patient Responses. AJR

[5] Padhani et al, 2009. Diffusion-Weighted Magnetic Resonance Imaging as a Cancer Biomarker: Consensus and Recommendations. Neoplasia.

Meet-the-Experts Schedule

Sunday 12:30 - 1:30pm Monday 12:15pm - 1:15pm Tuesday 12:15pm - 1:15pm Thursday 12:15pm - 1:15pm

QRR006

Real-Time MRI for the Quantification of Inter-Heartbeat-Variation

Quantitative Imaging Reading Room Showcase

Location: QIRR, Learning Center

Participants

Anja Hennemuth PhD (Presenter): Nothing to Disclose
Teodora Chitiboi : Nothing to Disclose
Lennart Tautz : Nothing to Disclose
Markus Huellebrand : Nothing to Disclose
Stefan Braunewell PhD : Nothing to Disclose
Jens Frahm PhD : Research collaboration, Siemens AG

BACKGROUND

ECG-gated cardiac cine MRI is the gold standard method for the assessment of cardiac function. To overcome the limitations of conventional cine MRI in patients suffering from arrhythmia and shortness of breath, recent developments in acquisition technology provide real-time MRI sequences. This new technique allows for the acquisition of serial images with a temporal resolution of up to 20 ms under free breathing without ECG gating [1, 2]. Based on these data single heartbeats as well as the variation of the cardiac contraction over time can be inspected. However the application of conventional analysis tools is not possible because of the different image characteristics and the number of time frames to process. We therefore integrated new automatic processing and quantification techniques adapted to functional real-time MRI data into the OsiriX plugin CAIPI for cardiac image processing used by the CMR community [3]. The methods are available to MRI sequence developers as well as clinical researchers and can be used for the analysis of real-time MRI data for scientific purposes.

METHODOLOGY/APPLICATION

Innovative real-time MRI sequences based on undersampled radial FLASH sequences with image reconstruction by regularized nonlinear inversion capture rapid motion-induced changes. On the one hand, this enables to study patients unable to hold their breath; on the other hand, it allows for monitoring and functionally analyzing responses to physiologic challenges or arrhythmia. In more detail, the developed analysis tool deals with image series at high temporal resolution and for multiple heart cycles yielding 100-900 time frames per slice. To avoid tedious interactive analysis of the image sequences, the provided analysis is based on an automatic segmentation of the myocardium that has been validated by comparison with expert segmentations [4]. The automatic myocardium detection forms the basis for the separation of the image sequence into cardiac cycles. It is then possible to derive parameters such as the endsystolic and enddiastolic volume as well as the ejection fraction per heartbeat. The temporal (physiologic) variation of parameters can be derived and all quantitative results are presented as tables, which can be exported. Interactive exploration methods allow for the selection and inspection of single cycles as well as their comparison.

DEMONSTRATION STRATEGY

Visitors will be introduced to most recent developments for real-time MRI. We will present a solution for the quantitative analysis and inspection of functional real-time MRI data in the CAIPI OsiriX plugin. For selected cases, analysis workflows from data selection via segmentation and parameter calculation, inspection of results to report generation will be interactively performed. Cases include conventional cine MRI as well as different image sequences acquired with the new technique. Thus, visitors will learn about the differences in image characteristics and the analysis of real-time MRI data. Furthermore, the demonstration of different cases such as e.g. arrhythmia patients will show the benefit of the additional information provided by the new acquisition and quantification methods.

REFERENCES AND PUBLICATIONS

[1] Uecker, M., Zhang, S., Voit, D., Merboldt, K., Frahm, J. (2012) Real-time MRI - Recent advances using radial FLASH. Imaging Med. 4 [2] Voit, D., Zhang, S., Unterberg-Buchwald, C., Sohns, J.M., Lotz, J., Frahm, J. (2013) Real-time cardiovascular magnetic resonance at 1.5 T using balanced SSFP and 40 ms resolution. J Cardiovasc Magn Reson. [3] Huellebrand, M., Hennemuth, A., Messroghli, D., and Kuehne, T. (2014). OsiriX plugin for integrated cardiac imaging research. Proc. SPIE Medical Imaging [4] Chitiboi, T., Hennemuth, A., Tautz, L., Hüllebrand, M., Frahm, J., Linsen, L., Hahn, HK. (2014). Context-Based Segmentation and Analysis of Multi-Cycle Real-Time Cardiac MRI. IEEE International Symposium on Biomedical Imaging

Meet-the-Experts Schedule

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QRR007

Semi-automated PATLAK Plot Method for Mean Cerebral Blood Flow on Dynamic Scintigrams

Quantitative Imaging Reading Room Showcase

Location: QIRR, Learning Center

Participants

Takeshi Hara PhD (Presenter): Nothing to Disclose
Hiroshi Tago : Nothing to Disclose
Tetsuro Katafuchi : Nothing to Disclose
Daisuke Fukuoka PhD : Nothing to Disclose
Hiroshi Fujita PhD : Nothing to Disclose

BACKGROUND

Alzheimer's disease (AD) is a typical type of dementia that causes some problems with memory, thinking and behavior. The symptoms of AD usually develop and get worse without any treatment by medications. Although the medications cannot cure the AD or stop if from progressing, they will help lessen symptoms. Therefore, the early diagnosis and discrimination of AD and other type of dementia are very important to determine the drug type and the administration schedule. The dynamic scintigraphy using a radioactive medicine is used for the diagnosis of dementia disease because the examination can estimate mean cerebral blood flow (mCBF). The measurement results of CBF based on scintigrams cannot localize lobes with low blood flow, but they will be an important index to estimate the reason of the dementia before the SPECT examination to estimate regional CBF (rCBF). Minimally invasive analysis of CBF has been proposed as the PATLAK plot method. The PATLAK plot method requires many manual procedures such as determination of two ROIs of aorta and cerebrum of right and left hemisphere on the dynamic scintigram, adjusting the time activity curves (TAC), determination of slope on the plotted graph before the estimation of the mCBF. Subjective determination of those ROIs and parameters often cause of inter- or intra-variability of the measurements results. Our developed software will help operators to determine those parameters including segmentation of the ROIs, and will reduce the variability of the measuring results. The software is a non-commercially available package for users

registered by our team because of the software update and imaging device, and it is already distributed in five sites in Japan for the research purpose only with IRB approval.

METHODOLOGY/APPLICATION

The software consisted of following steps: 1) Segmentation of aorta ROI (A-ROI), 2) Segmentation of left and right brain hemispheres (B-ROIs), 3) Determination of time activity curves (TACs) from ROIs, 4) Time-shift alignments between TACs, 5) Selection of plotted points on the graph of PATLAK method, 6) Measurement results of mCBF. A-ROI was determined by comparing the TAC model from 45 cases. Mutual information (MI) between the patient TAC and every TAC in the model were obtained to determine the center location of the aorta of the patient as the highest value of MI value. B-ROIs were determined after the segmentation of body regions on MIP image and the detection results of shoulder and neck of the patient. The center of head area and inclination were obtained to fit the template for left and right brain hemispheres. The TACs were obtained after the two segmentation of ROIs. To obtain the accurate mCBF from the TACs, the time shift alignment and the selection of plotted points on the graph of PATLAK method are required. The time of the peaks of the TACs were automatically detected by using signal processing technique to align the time shift. To select the points on the graph, an experimental range from 45 cases was determined to obtain stable measurement results. Intra- and inter-observer variabilities were analyzed based on the correlation and the Bland-Altman plot method to show systematic errors between two results.

DEMONSTRATION STRATEGY

Attendees experience our new measurement software with some clinical cases. If the attendees have measured mCBFs by using conventional software, they will realize the reduction of the operation time and simple procedure for the measurements that are real-time calculation depending on the ROIs setting modified by operators. The statistical ideas for correlation and the Bland-Altman method are also demonstrated in the booth.

REFERENCES AND PUBLICATIONS

Computer assisted measurement based on automation of Patlak Plot method for mean cerebral blood flow on dynamic scintigrams, JSMBE-BMI2014-03, The 1st Conference on Biomedical Imaging, Mar. 2014. Semi-automated measurement of mean cerebral blood flow on dynamic scintigrams, Live demonstration in SPIE Medical Imaging, Feb. 2014. Automated analysis of cerebral blood flow on scintigrams, Medical Imaging in Asia, Nov. 2012.

Meet-the-Experts Schedule

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QRR008

Z-score Imaging of Torso FDG-PET SUV and Computer-aided Diagnostic System based on Anatomical Standardization

Quantitative Imaging Reading Room Showcase

Location: QIRR, Learning Center

Participants

Miho Shimizu (Presenter): Nothing to Disclose
Takeshi Hara PhD : Nothing to Disclose
Yuzuho Yamaguchi : Nothing to Disclose
Tetsuro Katafuchi : Nothing to Disclose
Daisuke Fukuoka PhD : Nothing to Disclose
Satoshi Itoh MD, PhD : Nothing to Disclose
Xiangrong Zhou PhD : Nothing to Disclose
Hiroshi Fujita PhD : Nothing to Disclose

BACKGROUND

The anatomical standardization analysis for brain FDG-PET has great contributions for the diagnosis of dementia. We have applied the approach of the standardization to torso regions for improve the diagnostic accuracy of detecting abnormal spots and temporal changes in cancer follow-up cases. To obtain Z-scores in torso regions, many normal cases have to be collected. We have archived over 200 normal cases from a complete medical checkup by using FDG-PET for cancer detection at the early stage. The software prototype will be released as standalone package in mid of 2015, but the version will not include the normal cases for Z-score calculation. The current version is in use of research setting.

METHODOLOGY/APPLICATION

Z-score mapping based on statistical image analysis was applied to the temporal subtraction technique. The subtraction images can be obtained based on the anatomical standardization results because all of the patients' scans were deformed into standard body shape. An observer study was performed without and with CAD to evaluate the usefulness of the scheme by ROC (receiver operating characteristics) analysis. Readers were asked to set their confidence levels from absolutely no change to definitely change between two scan on a continuous scale. To construct a new normal model based on SUL, each SUV in every locations of a patient was converted into SUL by using his/her body weight and height. After the SUL distribution was obtained, the deformation process was applied to construct the standardized body shape. The same procedure to construct the normal models was applied to the SUL model construction. The differences of voxel values between SUV and SUL normal models in each gender were obtained to compare the two models. The recognition performance for the 43 pairs was 96% sensitivity with 31.1 false-positive marks per scan. The average of area-under-the-ROC-curve (AUC) from four readers was increased from 0.85 without CAD to 0.90 with CAD (p=0.0389, DBM-MRMC).

DEMONSTRATION STRATEGY

Attendees will understand the fundamentals of Z-score mapping and the application to torso regions. The demonstration includes statistical fundamentals for education purpose, data specification of normal data, processing technique of image registrations and deformations and comparison of Z-score and SUV of abnormal spots. Attendees will also experience the CAD system with temporal subtraction and Z-score mapping as the environment of observer performance study.

REFERENCES AND PUBLICATIONS

Y.Shimizu, T. Hara, D. Fukuoka, X.Zhou, C.Muramatsu, T.Kobayashi, S.Ito, S.Kumita, K.Ishihara, T.Katafuchi, and H.Fujita: Diagnosis support for cancer treatment on torso FDG-PET/CT scans by using anatomical standization method, JAMIT, (2012). Y.Shimizu, T.Hara, D.Fukuoka, X.Zhou, C.Muramatsu, S.Ito, K.Hakozaki, S.Kumita, K.Ishihara, T.Katafuchi, and H.Fujita: Temporal subtraction system on torso FDG-PET scans based on statistical image analysis, Proc. of SPIE Medical Imaging, 8670, 86703F-1 - 86703F-6, (2013). Y.Shimizu, T.Hara, D.Fukuoka, X.Zhou, C.Muramatsu, S.Ito, K.Hakozaki, S.Kumita, K.Ishihara, T.Katafuchi, and H.Fujita: Analysis and construction of normal model on torso FDG-PET scans based on lean body mass, IEICE Technical Report, (2014).

Meet-the-Experts Schedule

Sunday 12:30 - 1:30pm Monday 12:15pm - 1:15pm Tuesday 12:15pm - 1:15pm

QRR009

Quantitative Imaging Biomarker Software for Neurological Disorders

Quantitative Imaging Reading Room Showcase

Location: QIRR, Learning Center

Participants

Laurent Hermoye PhD (Presenter): Shareholder, Imagilys CEO, Imagilys
Wojciech Gradkowski MENG : Employee, Imagilys Shareholder, Imagilys
Vasileios K. Katsaros MD, PhD : Nothing to Disclose
Nick Schmansky : Co-founder, CorticoMetrics LLC Manager, CorticoMetrics LLC
Bruce Fischl PhD : Investor, CorticoMetrics LLC

BACKGROUND

Many publications deal with advanced neuroimaging. However, the translation from bench to bedside remains limited. Several factors can explain this observation: Research software is powerful in algorithmic terms, but often a complex graphical user interface and workflow limit their use in clinical practice. Whereas researchers can take the time to acquire the computer skills necessary to work on multiple image formats, to adjust multiple parameters, and to maintain less common operating systems, a straightforward graphical user interface is a must-have for radiologists and clinicians. Research groups who develop software do not have dedicated distribution and support teams. Although several software packages have been widely distributed on the web, their use in clinical practice is minimal. FDA and similar international regulations regarding medical devices prevent the use of research software for clinical purposes. Research teams usually do not have quality assurance systems in place (e.g., ISO 13485), and the a-posteriori certification of research software is cumbersome. This can result in potential hazards for the patients. Conversely, MRI manufacturers are focused on the scanner's capabilities. While their proprietary workstations have limited post-processing capabilities, they lack the tools to address clinicians' needs in major neurological disorders. We address these issues, with a commercial neuroimaging software, implementing state-of-the-art algorithms in a user-friendly graphical interface, integrated in a clinical workflow. It is CE-marked for clinical use in Europe and FDA-clearance is pending. Our software is also used by pharmaceutical companies, CROs, and imaging core labs in order to quantify imaging biomarkers in the framework of clinical trials.

METHODOLOGY/APPLICATION

The software, written in JAVA, can post-process, visualize, and fuse advanced brain images acquired on all MRI, CT, or PET scanners. The Core Application can: Transfer and import DICOM images via the network, regardless of source (multi-vendor). Display images in orthogonal, mosaic, or cine view. Fuse multi-modal images in semi-transparency. Automatically register MRI, CT, and PET images. Quantify images with regions of interest (ROI). Export post-processed images and quantitative results. The fMRI Module can: Define paradigms (multi-runs, multi-conditions, multi-contrasts). Automate analysis: realign, register, analyze, threshold, and visualize fMRI images in just a few clicks. Visualize BOLD signal. Fuse fMRI images with other modalities. The Diffusion Module can: Calculate ADC, FA, and color maps. Perform fiber tracking. The DSC Perfusion Module can: Calculate CBV, CBF, MTT, TTP, and TMAX maps. Visualize and compare the perfusion signals in ROIs. The DCE Perfusion Module can: Calculate Ktrans transfer coefficient and fractional volumes. Assess vascular permeability. The Stroke Module can: Threshold TMAX and ADC maps in order to segment the infarct's core and penumbra. Review results and fuse with anatomical images. The Relaxometry Module can: Measure the T1 relaxation time, based on multiple flip angles or inversion times. Measure the T2 and T2* relaxation times, based on multi-echo sequences. The Multiple Sclerosis Module can: Register and subtract follow-up MRIs. Quantify lesion load. The Structural Segmentation Module can: Quantify brain atrophy (WM/GM/CSF) in patients with Alzheimer's disease or multiple sclerosis [1]. Quantify hippocampal atrophy and cortical thinning in patients with Alzheimer's disease [1]. The software has been used both in clinical and research settings. Since September 2011, 333 patients with brain masses have been evaluated pre-surgically and post-surgically with a multimodal imaging protocol [2-3].

DEMONSTRATION STRATEGY

The software will be available on portable workstations. The software will be presented through clinically-relevant cases. The clinical cases will be summarized in educational posters, and pre-recorded demos, and the visitors will have the opportunity to acquire hands-on experience, using the software with our help. The Meet-the-Expert presentations offer the opportunity to get feedback from visitors and to discuss future development opportunities.

REFERENCES AND PUBLICATIONS

1. Fischl et al. Whole Brain Segmentation: Automated Labeling of Neuroanatomical Structures in the Human Brain. Neuron 2002, 33:341-355.
2. Katsaros et al. Multi-modality brain MRI for neurosurgical planning and neuronavigation in patients with brain tumors. ESNR Edinburgh 2012.
3. Katsaros et al. Functional MR imaging protocol for treatment decision, presurgical planning and imaging-guided surgery of brain space-occupying lesions. ASNR San Diego 2013.

Meet-the-Experts Schedule

Sunday 12:30 - 1:30pm Monday 12:15pm - 1:15pm Tuesday 12:15pm - 1:15pm Wednesday 12:15pm - 1:15pm Thursday 12:15pm - 1:15pm

QRR010

Automated Tumor Delineation Using Standardized MR Image Intensities

Quantitative Imaging Reading Room Showcase

Location: QIRR, Learning Center

Participants

Michael Schmainda (Presenter): Employee, Imaging Biometrics, LLC
Timothy Dondlinger : Officer, Imaging Biometrics, LLC

BACKGROUND

Clinical trials currently face growing demand to evaluate myriad treatment strategies for improving survival in brain cancer patients, and so the need for a timely and accurate endpoint to judge treatment efficacy has never been greater. A survey of the current NIH clinical trials database (clinicaltrials.gov) shows at least 450 active studies for glioblastoma (GBM), the most common and aggressive form of primary brain cancer. These trials rely largely on contrast-enhanced MRI (CE-MRI) as the best available method for measuring treatment response and predicting patient survival. Currently, decisions about treatment are guided by criteria (RECIST, Macdonald, RANO) that equate increasing size of CE-MRI enhancement with progressive tumor burden, treatment failure, and poor prognosis. Despite its widespread use, this approach has several limitations. First, CE-MRI

cannot distinguish tumor growth from treatment-induced parenchymal injury, so called Post-treatment Radiation Effect (PTRE), which exactly mimics tumor on CE-MRI. Secondly, tumor often coexists and variably admixes with PTRE in most patients. The histologic tumor burden therefore comprises a subcomponent of the total CE-MRI enhancement. Although the histologic tumor burden correlates with survival, CE-MRI lacks the specificity to resolve this information. Furthermore, surgical biopsy serves as the gold standard for confirming brain tumor recurrence, but currently neurosurgeons rely on CE-MRI to identify tumor-rich biopsy targets. The limitations of CE-MRI, particularly in the setting of histologic heterogeneity, commonly result in biopsy sampling errors, misdiagnosis, and insufficient tissue for analyses such as molecular profiling. These deficiencies highlight a critical need to develop a more accurate MRI method to reproducibly distinguish recurrent tumor from post-treatment radiation effect (PTRE) on a voxel-wise basis.

METHODOLOGY/APPLICATION

The key method, called delta T1 (dT1) mapping, is a simple three-step process that first requires standardization of the pre- and post-contrast images to a common intensity scale. This standardization step, which has been patented and is exclusively licensed to Imaging Biometrics LLC (IB), eliminates much of the normal variability in image contrast due to MRI system instabilities, slight differences in imaging parameters (TR, TE, etc.), and possibly even field strengths as explored in the proposed research. The 2nd and 3rd steps entail the registration of the pre- and post-contrast images followed by the creation of the difference or 'delta' T1 map, thus the dT1 map. Another method involves Perfusion MRI-Fractional Tumor Burden (pMRI-FTB), which distinguishes subregions of recurrent tumor from PTRE, and quantifies histologic tumor burden within CE-MRI enhancing lesions. The pMRI-FTB method applies a pre-established relative cerebral blood volume (relCBV) threshold, on a voxel-wise basis, to classify individual voxels as either tumor (high relCBV) or PTRE (low relCBV). This threshold has been shown to distinguish subregions of tumor and PTRE with 100% accuracy, when validated with stereotactic coregistration and histopathologic confirmation. Preliminary data using the pMRI-FTB method suggest that the volume fraction of tumor voxels strongly correlates with both histologic tumor burden and patient survival.12 Relevant and impactful clinical applications of pMRI-FTB include: 1) estimating recurrent tumor burden as a marker of treatment response and clinical outcome; and 2) identifying tumor-rich stereotactic biopsy targets for histopathologic diagnosis and molecular analysis. Thus, combining the use of pMRI-FTB with CE-MRI could markedly improve the standard of care for post-treatment surveillance imaging of recurrent disease. We would expect pMRI-FTB to help guide informed decision-making during routine clinical management, and to provide a valuable imaging endpoint for defining tumor progression and predicting survival in clinical trials.

DEMONSTRATION STRATEGY

The ability to demonstrate the delineation approach will be made available by allowing attendees the ability to 'drive' the software method via a computer workstation and anonymized test datasets. Representatives from Imaging Biometrics will be available to address any questions as well as participate in the 'Meet-the-Expert' sessions.

REFERENCES AND PUBLICATIONS

perfusion MRI quantifies recurrent glioblastoma tumor fraction, pseudoprogression, and radiation necrosis to predict survival, Hu, et. al., Neuro-Oncology doi: 10.1093/neuonc/nos112, May 2012 Standardization of relative cerebral blood volume (rCBV) image maps for ease of both inter- and intrapatient comparisons, Bedekar, et. al., Magnetic Resonance in Medicine 64:907-913 (2010) Kubben, P.L., et al., Intraobserver and interobserver agreement in volumetric assessment of glioblastoma mulitforme resection. Neurosurgery, 2010. 67(5): p. 1329-1334.

Meet-the-Experts Schedule

Sunday 12:30 - 1:30pm
Monday 12:15 - 1:15pm
Tuesday 12:15 - 1:15pm
Wednesday 12:15 - 1:15pm
Thursday 12:15 - 1:15pm

QRR011

Multiparametric MRI Approach for the Detection and Diagnosis of Prostate Cancer and Structured Reporting According to PIRADS Scoring System

Quantitative Imaging Reading Room Showcase

Location: QIRR, Learning Center

Participants

Zahia Roberge (Presenter): Nothing to Disclose

BACKGROUND

Most often the diagnosis relies on the analysis of multiple imaging techniques that generally include both morphological and functional images. While the characterization of lesions on morphological images is usually based on the visual inspection and description of the lesion aspect, functional imaging provides both qualitative and quantitative information. This multiparametric approach has proven enhanced diagnostic capabilties and is now widely used in clinical routine. A typical example of such approach is the protocol recommended by the European Society of Urogenital Radiology (ESUR) for the detection and diagnosis of prostate cancer in MRI. Initially based on the T2 anatomical sequence, the MR protocol now integrates diffustion and dynamic contraste enhanced (DCE) sequences. Both functional imaging techniques improves the sensitivity and specificity in the detection of prostate cancer. In particular, DCE MRI allows providing quantitative parameters that reflect microvascularization behavior of tumors and is thus promising to differentiate highly vascularized lesions from less vascularized ones. While this multiparametric MRI approach improves the diagnosis accuracy, its complexity may lead to variable interpreation of findings between readers. It is thus important to have a solution that faciltates the reading and permits to visualize and analyze multiparametric data in a suitable manner. We have developed a sofware solution, Myrian XP-Prostate, which automates all the necassary tasks for a structured and rigorous reading of complex prostate MRI exams. It is commercially available as a propriatary software and is interoperable with most modality workstations and PACS and fully supports DICOM standards. It is used in a number of hospitals worldwide and is relevant for clinical routine as well as for research projects.

METHODOLOGY/APPLICATION

Intrasense will demonstrate Myrian XP-Prostate, an application dedicated to the reading of prostate MR exams. The application has configuration capabilities that permit to automatically select the relevant sequences and load them into the workspace according to the user preference display layout. The module includes additional features like the capability to synchronize the scrolling in navigation to easily compare the multiple images simultaneously and contains complete measurements tools for lesion characterization. Especially, the application provides qualitative parametric maps (area under the curve, wash-in, wash-out parametric,TTP and PEI) as well as quantitative maps (ADC, permeability maps based on the Tofts-Kety model). These maps can be calculated automatically for any modality manufacturer and the quality of the processing can be controlled at any time through the interface. The PIRADS scoring system has been integrated into the application and allows communicating the findings to the referent physician in a standard manner.

DEMONSTRATION STRATEGY

The demonstrtaion strategy is based on the use of Myrian XP-Prostate. Anonymized prostate exams with different acquisition protocols and coming from different manufacturer modalities will be available. We will first present the principles and major

mechanism of the application. We will then allow the user to assess the usability, speed and the general workflow. Assistance in the usage will be provided as per user request. Especially the user will have the opportunity to go through the following features: - automatic identification of the different sequences - structured reading - anatomical center synchronization for localizing lesions in the different orientation planes - dynamic display of the time-intensity curve - automatic processing and display of subtracted series, ADC maps, DCE qualitative maps (AUC, WI/WO, TTP, PEI) - automatic processing of permeabilty maps based on the Tofts-Kety model - display of the Tofts-Kety fitting for controlling the model accuracy - generation of a structured report including relevant images, measures and scoring of lesions according to PIRADS scoring system - automatic export of the structured report to the PACS - drag and drop of of additional exams from another modality for further characterization of lesions - comparison to a prior exam in the context of active surveillance A poster will be provided with details on our general architecture and a detailed list of available functions for the multiparametric analysis of MRI prostate exams in clinical settings.

REFERENCES AND PUBLICATIONS

1. Evaluation of the PI-RADS Scoring System for classifying mpMRI findings in Men with Suspicion of Prostate Cnacer. Daniel Juncker et al. BioMed Research International. Volume 2013 (2013). 2. ESUR MR prostate guidelines 2012. Jelle O. Barentsz et al. Eur Radiol. April 2012; 22 (4): 746-757. 10.1007/S00330-011-2377-y

Meet-the-Experts Schedule

Monday 12:15pm - 1:15pm Tuesday 12:15pm - 1:15pm Wednesday 12:15pm - 1:15pm

QRR012

Auto-PERCIST: Semi-Automated PERCIST-based Analysis of PET Images

Quantitative Imaging Reading Room Showcase

Location: QIRR, Learning Center

Participants

Jeffrey P. Leal BA (Presenter): Nothing to Disclose
Richard L. Wahl MD : Patent holder, Naviscan, Inc Patent holder, GlaxoSmithKline plc Patent holder, Spectrum Pharmaceuticals, Inc Research Consultant, GlaxoSmithKline plc Research Consultant, Nihon Medi-Physics Co, Ltd Research support, General Electric Company Research support, Molecular Insight Pharmaceuticals, Inc Research support, Cell Point LLC

BACKGROUND

Auto-PERCIST is a software program which uses the PERCIST 1.0 criteria and methods to perform a semi-automated quantitative assessment of FDG-PET studies. It is available to academic partners through a beta-test program. The software automates most of the workflow required in a quantitative analysis of an FDG-PET imaging study. Image data is automatically screened for basic quality control parameters, including radiotracer dosing, tracer uptake duration, scanner and reconstruction parameters, etc. These quality control metrics are presented to the user for immediate evaluation as well as stored in an external database for automated review and report generation. Image data is then processed through an automated algorithm which identifies and measures normal reference hepatic activity. This is used to automatically calculate a PERCIST disease assessment threshold. Candidate disease objects are then automatically detected and Volume of Interest (VOI) objects generated. These VOIs are presented to the user visually along with their statistical characteristics in tabular form through an integrated display system. The user then freely scrolls between the candidate objects, classifying objects as either disease or normally FDG avid tissue. The disease classified objects can then be exported as DICOM Segmentation Objects for use in other imaging systems, such as Radiation Treatment Planning systems, and the statistical measures of each classified disease object can also be exported to an external database where they can be automatically compared to prior results and assessment reports automatically generated. Auto-PERCIST has been used extensively for the analysis of PET data in multiple clinical trials and is beginning to be used more and more in our own institution's clinical environment. The software is available to select academic partners as a beta-test after institutional MTA agreements are on file.

METHODOLOGY/APPLICATION

Auto-PERCIST is a Computer-Aided Detection (CAD) system for personalized disease detection, assessment and tracking in FDG-PET studies based on the PERCIST 1.0 criteria. The program runs on multiple platforms and was developed in the Java programming language. The application's features include the automatic identification and measurement of normal reference tissue, the automated calculation of a disease assessment threshold, automated construction of candidate disease objects, integrated graphical and tabular representations of the auto-detected candidate disease objects for quick assessment and classification by the user, and the automated transmission of all results (including disease objects as DICOM Segmentation Objects) to an external database for further analysis and report generation. In addition to the base functionality, the program also offers the user several options which allow them to customize their analysis, if so required. These options include multiple algorithms for detecting, growing and delineating the auto-detected candidate lesions, multiple VOI measurement algorithms, and the propagation of disease classified VOIs across multiple co-registered datasets, automatically generating summary and voxel-by-voxel data across multiple time-points.

DEMONSTRATION STRATEGY

We will demonstrate our software and the advantages of a program like ours for semi-automated analysis through both hands-on demonstrations and an informational poster. The hands-on demonstration will allow for both exhibitor-guided and self-driven use of the software populated with a database of representative, de-identified PET-FDG cases. This will allow the exhibit visitor to see first-hand how the application works and to explore the many processing options available to them when performing an analysis. The informational poster, which will also be made available as a handout, will present a typical analysis session in a flowchart format, highlighting the key features of the Auto-PERCIST application. Our goal for this exhibit will be to showcase how a tool such as Auto-PERCIST can increase the user's efficiency, accuracy and objectivity in their quantitative analysis of FDG-PET studies by automating many of the necessary workflow tasks while allowing the reader to focus their time and energy on those tasks most needing their expert attention.

REFERENCES AND PUBLICATIONS

Wahl RL, Jacene H, Kasamon Y, Lodge, MA. From RECIST to PERCIST: Evolving Considerations for PET Response Criteria in Solid Tumors. J Nucl Med. 2009:50(Suppl 1):122S-150S.

Meet-the-Experts Schedule

Sunday 12:30 - 1:30pm Monday 12:15pm - 1:15pm Tuesday 12:15pm - 1:15pm Wednesday 12:15pm - 1:15pm

QRR013

Automated Left Ventricle Segmentation in Late Gadolinium Enhanced MRI For Objective Myocardial Scar Assessment

Quantitative Imaging Reading Room Showcase

Location: QIRR, Learning Center

Participants

Qian Tao : Nothing to Disclose
Hildo J. Lamb MD, PhD : Nothing to Disclose
Rob J. Van Der Geest MS (Presenter): Consultant, Medis Medical Imaging Systems, Inc

BACKGROUND

Late Gadolinium Enhanced (LGE) MRI has proven clinical value for diagnosis and prognosis of post-infarct patients. A prerequisite for accurate myocardial scar assessment is the reliable segmentation of the myocardium. However, in post-infarct patients, the myocardial scar is often connected to the blood pool, with the contrast between them typically poor. The ambiguous border between myocardial scar and blood pool substantially complicates myocardium contouring, and potentially gives rise to over- or under-estimation of the scar.

METHODOLOGY/APPLICATION

We propose an automated LGE segmentation algorithm, which utilizes the myocardium morphology information from the cine sequence in the same study. In practice, the cine contours of the end-diastolic and end-systolic phases are routinely annotated for functional analysis. From the available cine contours, the potential endo- and epicardial contour sets for each LGE slice were estimated by cine-LGE registration and linear interpolation. Secondly, the match between the dual contour sets and each LGE slice was evaluated by correlating the LGE slice with the contour image constituted of edge filters adaptive to the edge direction. Finally, the global optimal contour was established by dynamic programming through the entire LGE stack. The method was validated on the LGE MR of 30 post-infarct patients with an in-plane resolution of 1.56 mm, and compared to the manual contouring results. The proposed method achieved sub-pixel accuracy in comparison to manual segmentation from experienced observers. The distances between the automated contours and manual contours were 1.0±0.8 pixels (median 0.8) for the endocardial contour, and 0.8±0.7 pixels (median 0.6) for the epicardial contour. The Dice overlap index between the segmented myocardium regions was 0.83±0.03. The Full-Width-Half-Maxima method was applied to identify the myocardial scar from the segmented myocardium region. Myocardial scar size derived from the manual contours was comparable to that from the automated contours: 23.8±16.8 ml and 22.7±15.4 ml (p=NS), with Pearson's correlation 0.87 (p<0.0001). To conclude, we have proposed an automated method to segment the myocardium in LGE for myocardial scar assessment. The method resulted in comparable performance with manual scar segmentation by experienced observers, in terms of contouring accuracy and myocardial scar size. The method does not require extra cine contour analysis than routinely performed, and reduces the observer-dependency by avoiding visual interpretation of LGE.

DEMONSTRATION STRATEGY

We will demonstrate the LGE segmentation algorithm with information poster. We will also show the software that is needed to accomplish it.

REFERENCES AND PUBLICATIONS

1. Tao Q, Milles J, Zeppenfeld K, Lamb HJ, Bax JJ, Reiber JHC, van der Geest RJ. Automated segmentation of myocardial scar in late enhancement MRI using combined intensity and spatial information. Magn. Reson. Med. 2010;64:586-594. 2. Yan AT, Shayne AJ, Brown KA, Gupta SN, Chan CW, Luu TM, Di Carli MF, Reynolds HG, Stevenson WG, Kwong RY. Characterization of the peri-infarct zone by contrast-enhanced cardiac magnetic resonance imaging is a powerful predictor of post-myocardial infarction mortality. Circulation 2006;114:32-39. 3. Roes SD, Borleffs CJW, van der Geest RJ, et al. Infarct tissue heterogeneity assessed with contrast-enhanced MRI predicts spontaneous ventricular arrhythmia in patients with ischemic cardiomyopathy and implantable cardioverter-defibrillator. Circ. Cardiovasc. Imaging 2009;2:183-190

Meet-the-Experts Schedule

Monday 12:15pm - 1:15pm Tuesday 12:15pm - 1:15pm Wednesday 12:15pm - 1:15pm

QRR014

Precision Metrics Manager V2.0: The Next Generation Workflow Management Solution for Quantitative Imaging Assessment for Clinical Trials

Quantitative Imaging Reading Room Showcase

Location: QIRR, Learning Center

Participants

Trinity Urban (Presenter): Nothing to Disclose
Robert Lewis : Software Consultant, OnePacs, LLC Software Consultant, Medken LLC
Vadim Frenkel : Nothing to Disclose
William B. Hanlon : Nothing to Disclose
Annick D. Van Den Abbeele MD : Nothing to Disclose
Gordon J. Harris PhD : Medical Advisory Board, Fovia, Inc

BACKGROUND

Objective quantitative imaging assessment of tumor response is essential in the clinical management of oncology clinical trial patients. Clinicians use this objective response information as a primary endpoint and for go/no-go decisions to determine if a patient should continue treatment. However, the current workflow for imaging tumor response assessment is inefficient and error-prone. In many instances, the clinical team transcribes lesion measurements from the radiology report or the oncologist makes the measurements themselves when they are not provided. This exhibit will focus on the utilization of a quantitative imaging tool that has been integrated with an online reporting system. The Precision Metrics Manager application was developed by the Tumor Imaging Metrics Core (TIMC) at the Dana-Farber/Harvard Cancer Center (DF/HCC) and serves as a complete workflow solution for imaging review and response assessment for oncology clinical trials. The measurement tool was built as a plug-in module upon an open-source software package (ClearCanvas, Toronto, ON), while the database and web-application was built within the asp.net/SQL server/visual basic (Microsoft, Redmond, WA) environment. The version 1.0 of the system is currently in use within the DF/HCC and Yale Cancer Center (YCC) and will be deployed at the Huntsman Cancer Institute (HCI) at the University of Utah this summer. Precision Metrics Manager V2.0 will be launched at the end of 2014 and will be available to other clinical research institutions.

METHODOLOGY/APPLICATION

The Precision Metrics Manager V2.0 will further streamline quantitative assessment and resulting reports for clinical trials. The local clinical treatment team can request scan analyses, specify the time when results are needed, and view imaging results through a secure, password-protected website. On-line training and certification ensures that the imaging reviewers assess the scan according to the study protocol and specified tumor response criteria with the help of integrated response criteria conformance checks. Upon saving image measurements, quantitative metrics and annotated images are automatically uploaded

to the website. After electronic sign-off by the reviewing radiologist, the imaging time point is locked and the clinical team is automatically alerted that the assessment is ready for viewing. Results are provided on-line and on-time, before the patient is seen in the clinic for treatment decisions. The clinical team can access measurement tables, graphs, and annotated imaging in a single structured report and can print a copy of the report to serve as the source document for trial audits. Attendees will learn how this tool is being used at the DF/HCC, YCC, and HCI and how it could be utilized at other cancer centers and hospitals to improve quantitative imaging assessment.

DEMONSTRATION STRATEGY

The Precision Metrics Manager V2.0 presentation will include a demonstration of the ClearCanvas measurement plugin and integrated online workflow and data management systems developed by the TIMC. The demonstration will require the use of a Windows PC and internet access. The attendees will have hands-on experience viewing images, measuring targets, annotating non-targets, assessing the overall response, and using structured longitudinal reporting tools. We will show how the Precision Metrics Manager V2.0 can streamline image review and reporting which in turn improves data quality simplifying the auditing process. In support, we will present turnaround time and data quality metrics collected at the core facilities at DF/HCC since 2005 and at YCC since 2013.

REFERENCES AND PUBLICATIONS

Urban T, Harris GJ, Barish MA, Oliveira GR, Zondervan RL, Hanlon WB, Van den Abbeele AD. Benefits of utilizing image analysts for radiological measurements in oncology clinical trials. Applied Clinical Trials, November 2010; 19(9):32-36.

Meet-the-Experts Schedule

Sunday 12:30 - 1:30pm Monday 12:15pm - 1:15pm Tuesday 12:15pm - 1:15pm Wednesday 12:15pm - 1:15pm Thursday 12:15pm - 1:15pm

QRR015

Prostate MR Workstation: An Integrated Work-flow for Case Reading, PI-RADS Structured Reporting, Automatic Pharmacokinetic Modelling and Quantitative Analysis

Quantitative Imaging Reading Room Showcase

Location: QIRR, Learning Center

Participants

Michael A. Hicks PhD : Nothing to Disclose
Geert Litjens MSc : Nothing to Disclose
Jelle O. Barentsz MD, PhD : Nothing to Disclose
Patrik Zamecnik MD : Nothing to Disclose
Henkjan Huisman PhD (Presenter): Stockholder, QView Medical, Inc

BACKGROUND

The presented workstation is an analysis suite integrating rapid archiving, processing, reading, quantitative analysis, and structured reporting of multi-parametric prostate MR cases into a single streamlined work-flow. It features recently developed image analysis methods and is currently in active use in clinical practice, but also as a research tool, resulting in tens of peer-reviewed international publications. The software system has been certified for clinical use in Europe and Australia. The software is distributed by the Prostate MR Reference Center (PMRC) at our institution. The main goal of the PMRC is to ensure good quality prostate MR. The PMRC provides extensive training courses in prostate MR acquisition and reading including the use of this workstation to collaborating parties. PMRC also provides second readings and quality control audits.

METHODOLOGY/APPLICATION

The Prostate MR Workstation, as a system, incorporates the entire diagnostic work-flow. This includes the reception and archiving of acquired image data; subsequent automatic preprocessing; integrated reading: image visualisation, including quantitative parameter maps, measurements of anatomical structures; and structured case reporting. Cutting-edge quantitative image analysis tools in the suite include automatic pharmacokinetic (PK) modelling and bias profile correction. PK analysis includes fast, robust curve fitting and an automatic estimation/calibration of the arterial input profile - all based on the Tofts two compartment model. Structured reporting of cases includes the PI-RADS quantitative scoring of clinical observations and a Villers annotation scheme. The output of the structured reporting is passed into a document generator with an optional electronic distribution mechanism. The document generator takes structured report details and formats them into a PDF document, including the automatic workstation screen-shots, which can then optionally be sent to an EHR system, for distribution to referring physicians. The design of this system has evolved in close collaboration with many clinicians, resulting in a smooth and intuitive workflow which typically garners praise during a clinician's first interaction with the software.

DEMONSTRATION STRATEGY

The material provisions for the demonstration will include an exposition of the Prostate Workstation's quantitative analysis tools and work-flow in the form a poster. This poster will accompany the exhibit and serve to highlight the interesting facets of the demonstration. In the demonstration proper, a live, and complete, clinical work-flow will be provided, with up to fifty anonymous cases for examination, interaction, scoring and reporting. During this process, the presenter will make several full exemplar cycles through the system, while inviting attendees to interact with the system themselves. A sample of the system can be seen in the attached screen-capture. The goal of this process is to expose the novel concepts that have been implemented, while disseminating ideas to the participants, from both a clinical and research perspective. The software framework for this demonstration is technically mature, tested and certified.

REFERENCES AND PUBLICATIONS

The following articles demonstrate both the scientific and clinical achievements that have been made using the Prostate Workstation: 1. ESUR prostate MR guidelines Eur.Rad.2012, JO. Barentsz, J. Richenberg, R.Clements, P.Choyke, S.Verma, G.Villeirs, O.Rouviere and V.Logager, J.J. Fütterer 2. Prostate Cancer Localization with Dynamic Contrast-enhanced MR Imaging and Proton MR Spectroscopic Imaging1 JJ Fütterer, SW Heijmink, TWJ Scheenen, J Veltman, HJ Huisman, P Vos, CA de ... Radiology 241 (2), 449-458, 2006 3. H.J. Huisman, J.J. Fütterer, E.N.J.T. van Lin, A. Welmers, T.W.J. Scheenen, J.A. van Dalen, A.G. Visser, J.A. Witjes and J.O. Barentsz. 'Prostate cancer: precision of integrating functional MR imaging with radiation therapy treatment by using fiducial gold markers', Radiology 2005;236:311-317. 4. Accurate estimation of pharmacokinetic contrast;enhanced dynamic MRI parameters of the prostate HJ Huisman, MR Engelbrecht, JO Barentsz Journal of Magnetic Resonance Imaging 13 (4), 607-614

Meet-the-Experts Schedule

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QRR016

LI-RADS Web Application: An Online Tool for Easy LI-RADS Categorization

Quantitative Imaging Reading Room Showcase

Location: QIRR, Learning Center

Participants

Verghese George MBBS (Presenter): Nothing to Disclose
Venkateswar Rao Surabhi MD : Nothing to Disclose

BACKGROUND

The development of the Liver Imaging Reporting and Data System (LI-RADS) was supported by the American College of Radiology (ACR) to standardize the reporting and data collection of CT and MR imaging for hepatocellular carcinoma (HCC). LI-RADS attempts to classify observations in the liver as ranging from definitely benign (LR 1) to definitely HCC (LR 5), based on an algorithm employing a standard set of parameters including size, threshold growth, arterial phase enhancement, washout and capsule appearance. LI-RADS also lists multiple ancillary features along with associated rules (including tie-breaking ones) that can be used to adjust the category, at the discretion of the radiologist .The algorithm can appear daunting and complex to the average radiologist; additionally calculations involved in the evaluation of threshold growth can add to the time taken to perform the categorization. This application aims to ease the process of categorization by guiding the user through the input of the relevant clinical and imaging parameters of the hepatic observation. It then calculates the threshold growth (if applicable) and generates the LI-RADS category; if required it will also help the user adjust category by using the incorporated adjustment and tie-breaking rules. Finally, the application can generate a standardized report that may be copied and pasted for clinical use.

METHODOLOGY/APPLICATION

The application is available on the internet at the URL www.lirads.net. Based on the current version (v2013) of LI-RADS, it has been adapted to categorize only observations that demonstrate arterial-phase enhancement (LR3 and above): definite or probable benign observations are thus excluded from the categorization. On the landing page, the user is presented with a choice of two versions of the application. The 'Quick App' enables rapid categorization of an arterial-phase enhancing observation, without taking into account ancillary features or tie-breaking rules.The 'Detailed App' requires additional information about the observation, and incorporates ancillary features and tie-breaking rules to adjust category. It also generates a structured report that can be used for clinical purposes.Color coding of ancillary features facilitates easier adjustment of category.

DEMONSTRATION STRATEGY

The authors will present an informational poster highlighting the capabilities and use of the software; users will be able to interact with the application on computers connected to the internet. During the Meet-the-Expert presentations, a comprehensive demonstration of the application will be arranged; multiple anonymized liver cases will be presented with demonstration of the application performing LI-RADS categorization and automated generation of structured reports. The presentations will be interactive, with attendees encouraged to try out the application during the demonstration.

REFERENCES AND PUBLICATIONS

George V, Surabhi V R. LI-RADS Web Application: A free online tool for easy LI-RADS categorization. Available at www.lirads.net. Accessed 04/08/2014. American College of Radiology. Liver Imaging Reporting and Data System version 2013.1. Accessed 04/08/2014, from http://www.acr.org/Quality-Safety/Resources/LIRADS/. Purysko AS, Remer EM, Coppa CP, Leão Filho HM, Thupili CR, Veniero JC. LI-RADS: a case-based review of the new categorization of liver findings in patients with end-stage liver disease. *RadioGraphics* 2012;32(7):1977-1995.

Meet-the-Experts Schedule

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QRR017

Aview Lung Solution: Comprehensive Workflow for Advanced Quantitative Analysis of Chronic Obstructive Pulmonary Disease at Multi-Volume Chest CT

Quantitative Imaging Reading Room Showcase

Location: QIRR, Learning Center

Participants

Namkug Kim PhD : Stockholder, Coreline Soft, Inc
Taekjin Jang : Nothing to Disclose
Minho Lee PhD : Nothing to Disclose
Jangpyo Bae MS : Nothing to Disclose
Guk-Bae Kim : Nothing to Disclose
Sang Min Lee MD : Nothing to Disclose
Joon Beom Seo MD, PhD : Nothing to Disclose
Jin Kook Kim PhD : CEO, Coreline Soft Inc
Jaeyoun Yi (Presenter): Officer, Coreline Soft Inc

BACKGROUND

Chronic obstructive pulmonary disease (COPD) is becoming more and more important, because of its persistently increasing prevalence, mortality, and disease burden. According to WHO estimates, 65 million people have moderate to severe COPD. More than 3 million people died of COPD in 2005, which corresponds to 5% of all deaths globally. MDCT imaging is a commonly-used imaging modality to assess emphysema, lung densitometry using computed tomography (CT) has proven to be an important tool for the measurement of emphysema extent and distribution. Not only it is well matched with pathology, it also correlates well with pulmonary function tests (PFT), and is sensitive in assessing progression of emphysema. The quantitative assessment of extent and distribution of size based emphysema analysis with lobe-basis and registration plays an essential role in the investigation of etiology and progress of COPD. However, there are many sources of error and obstacles in emphysema assessments including few comprehensive workflows for clinical and research usage. To address these unmet clinical needs, we have developed Aview lung solution, a computerized quantitative imaging analysis (QIA) tool for quantification of extent and distribution of size based emphysema analysis based on lobe segmentation and deformable registration with use of MDCT images; thus to provide an efficient and reliable quantification for the assessment of disease subtyping and progression for COPD patients.

METHODOLOGY/APPLICATION

A MDCT acquisition includes CT images at full inspiration and expiration and follow-up scans. Based on the length scale analysis and registration, emphysema can be classified in terms of the size, we developed a classification tool to identify size of each emphysema cluster in chest MDCT images. Our Aview lung solution includes three QIA tools: • an automated segmentation tool for segmentation of lung, airway, left/right lung, each lobe, emphysema, • a registration tool for full inspiration and expiration datasets and follow-up data set, • an automated post-processing tool for quantifying and analyzing the size distribution of emphysema clusters Aview lung solution quantifies the extent and size distribution of emphysema and provides structural report with minimum user interaction. Aview lung solution, which runs on the Aview thin client-server platform (Coreline Soft Inc.), is developed jointly by Coreline Soft Inc. and the Department of Radiology at the Asan Medical Center. The Advanced Preprocessing Server (APS) in Aview thin client-server platform provides computing facility for post-processing of MDCT images and delivers real-time interactive 2D/3D visualization to networked PCs running the Aview thin client application. The application shall be available commercially in early 2015.

DEMONSTRATION STRATEGY

The purpose of this demonstration is to showcase a comprehensive workflow of Aview lung solution for quantifying the extent and size distribution of emphysema clusters and advanced analysis on them with multi-volume chest CT including inspiration-expiration CT and follow-up CTs. The educational demonstration of Aview lung solution will use computer-based hands-on demonstration at RSNA. We will set up a thin-client platform of Aview lung solution with use of multiple computers, one for the thin client server and the other for thin-client and mobile interface. Demonstration will cover the entire workflow ranging from image acquisition protocol, automated post-processing, interactive reviewing, automated measurements, advanced analysis and structured reporting. Demonstration will select patient cases from our clinical study approved by institutional review board of Asan Medical Center, which have been anonymized in accordance with the HIPAA Privacy Rule.

REFERENCES AND PUBLICATIONS

1. Automatic Left and Right Lung Separation Using Free-Formed Surface Fitting on Volumetric CT, Youn Joo Lee, M Lee, N Kim, JB Seo, JY Park, J of Digital Imaging, April 2014 2. Thoracic cavity segmentation algorithm using multiorgan extraction and surface fitting in volumetric CT, JangPyo Bae, Namkug Kim, Sang Min Lee, Joon Beom Seo, Hee Chan Lee, Med Phys, EPub, 2014 3. Improved correlation between CT emphysema quantification and pulmonary function test by density correction of volumetric CT data based on air and aortic density, Kim SS, Seo JB, Kim N, Chae EJ, Lee YK, Oh YM, Lee SD., Eur J Radiol. 2012 May 19. 4. Quantitative Assessment of Emphysema, Air Trapping, and Airway Thickening on Computed Tomography. Young Kyung Lee, Yeon-Mok Oh, Ji-Hyun Lee, Eun Kyung Kim, Jin Hwa Lee, Namkug Kim, Joon Beom Seo, Sang Do Lee, KOLD Study Group, Beiträge zur Klinik der Tuberkulose 04/2012; 186(3):157-165. 5. Slope of emphysema index: an objective descriptor of regional heterogeneity of emphysema and an independent determinant of pulmonary function. E.J. Chae, J.B. Seo, J.W. Song, N. Kim, B.W. Park, Y.K. Lee, Y.M. Oh, S.D. Lee, and S.Y. Lim, AJR Am J Roentgenol, 2010/03. 194(3): p. W248-55.

Meet-the-Experts Schedule

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QRR018

Quantification of Cerebral Vessel Blood Flow with PCMR Imaging

Quantitative Imaging Reading Room Showcase

Location: QIRR, Learning Center

Participants

Kezhou Wang PhD (Presenter): Employee, VasSol, Inc
Lauren Ostergren : Employee, VasSol Inc
Fady T Charbel MD : Stockholder, VasSol, Inc

BACKGROUND

The 2D PCMR imaging is a non-invasive way to quantity blood flow in vessels. However, it is very time consuming and difficult to manually place the imaging plane for the intracranial vessels on the scanner due to the tortuous vascular structure and limited scanner time.
The commercially available application, NOVA (Non-invasive Optimal Vessel Analysis), was designed for the cerebral vascular applications based on the 2D PCMR and TOF principles. The application provides a unique user-friendly 3D localizer which creates 2D perpendicular imaging planes for PCMR acquisitions, thus allows efficiently and accurately quantification of blood flow for intracranial vessels. The application has been validated with in vivo and in vitro studies, and has been used clinically. It can be seamlessly fitted in the hospital workflow. Upon completion of the vessel scans, the results are automatically calculated and immediately available for review and referral physicians.

METHODOLOGY/APPLICATION

The application creates a 3D model vessels using 3D time of fly (TOF) images. Users pick vessels to be measured on the 3D model, and the application will generate the perpendicular imaging planes for the selected vessels. The blood flow volume and velocity will be automatically calculated and presented in an age matched table and a schematic vessel map for reviewing. Besides the flow numbers, a color coded velocity contours will be created for each velocity image. This will allow radiologists and MR technologists to access the measurement quantitatively and qualitatively.
The application supports DICOM. The flow report will be in DICOM format, and can be sent to PACS systems. Vessel flow results and the measurement position and orientation will be shown in the report, so that physicians will have full knowledge of the flow details.
The application has been utilized clinically in diagnosis and follow-up patients with stroke and cerebrovascular disorders, including accessing hemodynamic of vessel stenosis, assessing the collateral flow patterns in large vessel diseases, evaluating the response to angioplasty, analyzing stent and bypass intervention, diagnosing the subclavian steal syndrome, evaluating cerebral aneurysm, diagnosing the Moyamoya diseases, and etc [1,2,3].

DEMONSTRATION STRATEGY

Posters, website and a dedicated workstation will be provided for the quantitative show room. Three typical study cases will be show to attendees on posters. Each will include snapshot images and descriptions. More cases will be provided on a website for interested attendees. A dedicated workstation loaded with test cases will be provided to attendees for hands-on experience. In addition, a clinical workflow involved the application will be shown in a flow charter on a poster. Qualified engineer(s) will be available to answer attendees' questions during the meet the expert hours. Study cases: 1. Stroke Case: Using NOVA flow quantification to identify whether a stroke is embolic or hemodynamic. Identifying the origin of the symptoms will determine choice of treatment. If the stroke is embolic, the patient will receive heparin; if the stroke is hemodynamic, the EC-IC bypass may not have been sufficient to replace ICA flow. 2. Subclavian Steal Case: Pre-operative NOVA confirmed a relative right hemispheric hypoperfusion as shown by the asymmetry in right and left MCA flow. NOVA also revealed a left subclavian steal phenomenon with reversal of flow in the left vertebral artery. Post-operative NOVA documented a successful revascularization of the right hemisphere following angioplasty and stenting of a left subclavian occlusion. In the setting of a patent PCOM artery an extracranial interventional procedure allowed indirect revascularization of the intracranial anterior circulation. 3. Vertebrobasilar

Disease Case: NOVA flow quantification provides risk-stratify for patients with symptomatic vertebrobasilar disease (VBD). Base on patient's distal flow status, it is recommended medical therapy alone or intervention coupled with medical therapy. This flow based management strategy helps to defer surgery for patients with normal distal flow, whose symptoms can be attributed to embolic phenomena or small vessel disease and who are unlikely to benefit from revascularization.

REFERENCES AND PUBLICATIONS

1. Amin-Hanjani S. Diagnosis and Neurosurgical Treatment of Intracranial Vascular Occlusive Syndromes. Current Treatment Options in Cardiovascular Medicine 2009, 11:212-220

2. Prabhakaran S, Warrior L, Wells KR, Jhaveri MD, Chen M, Lopes DK. The Utility of Quantitative Magnetic Resonance Angiography in the Assessment of Intracranial In-Stent Stenosis. Stroke. 2009 Jan 22.

3. Bauer AM, Amin-Hanjani S, Alaraj A, Charbel FT. Quantitative Magnetic Resonance Angiography in the Evaluation of the Subclavian Steal Syndrome: Report of 5 Patients. J Neuroimaging. Sep 20 2008.

Meet-the-Experts Schedule

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