16th Annual UCAIR Research Symposium
November 5-6, 2004
Treasure Mountain Inn Park City, UT
The Sixteenth Annual Utah Center for Advanced Imaging Research Symposium

Friday November 5 – Saturday November 6
Treasure Mountain Inn, 255 Main Street, Park City UT
800-344-2460

Welcome to the sixteenth in a series of symposia hosted by the Utah Center for Advanced Imaging Research (UCAIR) in the Department of Radiology at the University of Utah School of Medicine. This meeting serves to bring together faculty, staff, students and affiliated researchers working on problems in medical imaging, promoting collaboration and the sharing of ideas. UCAIR (formerly MIRL, the Medical Imaging Research Lab) is located in the Center for Advanced Medical Technologies at 729 Arapeen Drive, Salt Lake City, UT 84108 and on the web at http://www.ucair.med.utah.edu. Full abstracts for all talks given at the symposium can be downloaded at http://www.ucair.med.edu/symposium-2004.pdf.

Chairman, Department of Radiology
Edwin A. “Steve” Stevens, M.D.

Director of Research, Department of Radiology
Greg Katzman

Director, UCAIR
Dennis L. Parker, Ph.D.

Symposium Organizer
Matthias Schabel, Ph.D.

Instructions to Speakers

There will be two types of presentation formats at the symposium: 25 minute extended talks with 5 minutes for questions and 10 minute short talks with 5 minutes for questions. Presentations must be provided to Larry Zeng by Friday morning in PowerPoint format on CD, flash drive, or by email to larry@ucair.med.utah.edu.

Student Presentation Award

As in previous years, all student papers presented at the symposium will be considered for the UCAIR Symposium Student Paper Award. Evaluation criteria will equally weigh clarity of presentation, quality and originality of research, and compliance with time constraints.

Winners will be recognized with their name engraved on a plaque inscribed with the names of previous years winners:

2003  Satya Vijayakumar
2002  Yijing Wu
2001  John Roberts
2000  Harshali Khare
1999  Girish Bal
1998  John Roberts
1997  Chuanyong Bai
1996  Brian Chapman
1995  Brian Chapman
1994  Shonn Hendee
1993  Anne Smith
1992  Anne Smith
1991  Jeff Thomas

Meals

A BBQ dinner will be provided Friday night at 6:30 pm in the Crescent Room of the Treasure Mountain Inn. Continental breakfast will be provided Saturday morning at 7:30 am and an oriental buffet lunch will be served at 12:15 pm. The Treasure Mountain Inn sits on the south end of Main Street in Park City, a vibrant ski town with a host of evening activities for symposium participants. There will be a family-friendly movie screening in the conference room after dinner on Friday evening and the Sundance Institute will also be showing the acclaimed documentary film “Riding Giants” at 8:00 pm at the Jim Santy Auditorium, 1255 Park Ave. Call 615-8291 for more information.

The organizers would like to gratefully acknowledge Dr. Kathryn Morton’s generous support.
Directions to the Symposium:

From Salt Lake City, take I-80 East toward Park City.

After 16 miles, take exit 145 (UT-224S) toward Kimball Junction/Park City.

Drive 6 miles to Park Avenue and continue straight.

After 1 mile, turn left onto 4th Street, then make the next right onto Main Street.

The Treasure Mountain Inn is at the end of Main Street, number 255 on the right side. Parking for symposium attendees who are not staying the night is available on the Park Avenue side of the hotel, while hotel guests have reserved parking (one vehicle per room).
### Program, Friday November 5

**1:00 pm**  
**Welcome and opening address**  
Matthias Schabel

**1:15 pm**  
**Overview of UCAIR fundraising**  
Roy Rowley

**1:30 pm**  
**Concepts in MRI Evolution**  
Dennis Parker

**Cardiac and Perfusion Imaging**

**2:00 pm**  
**Towards Understanding the Dark Rim Artifact in MRI Cardiac Perfusion Studies**  
Ed DiBella

**2:15 pm**  
**Accurate Assessment of the Arterial Input Function using MRI with Radial Sampling**  
Eugene Kholmovski

**2:30 pm**  
**3D Fluoro CT imaging with XRII-based mobile C-arm**  
Arvidas Cheryauka

**2:45 pm**  
**Evaluation of the UCAIR heart**  
Sung Moon

**3:00 pm**  
**Semiautomatic segmentation of first-pass cardiac perfusion MRI**  
Lucas Lorenzo

**3:15 pm**  
**Quantitation of Regional Cardiac Function using HARP MRI**  
Nate Pack

**3:30 pm**  
**Registration of Myocardial Perfusion Images using Mutual Information**  
Ganesh Adluru

**3:45 pm**  
**Break**

**Carotid and Blood Flow Imaging**

**4:15 pm**  
**Quantifying Vessel Movement and Orientation in Carotid Artery Magnetic Resonance Imaging**  
Emilee Minalga

**4:30 pm**  
**Comparison of Optimized Carotid Imaging at 1.5T and 3.0T**  
J. Rock Hadley

**4:45 pm**  
**Triple-contrast Technique for Black Blood Imaging with Double Inversion Preparation**  
Seong-Eun Kim

**5:00 pm**  
**Development of a Centerline/Bifurcation Voxel-mapping Frame of Reference**  
Ling Zhang

**5:15 pm**  
**Social hour**

**6:30 pm**  
**BBQ dinner**
Program, Saturday, November 6

7:30 am  Breakfast

PET

8:30 am  PET research at the U: Low-hanging fruit
         Kathryn Morton

9:00 am  Feasibility of Rapid Multi-Tracer PET Tumor Imaging
         Dan Kadrmas

9:15 am  Rapid Dual-Tracer PET Tumor Imaging: A Compartmental Modeling Approach
         Tom Rust

MRI Pulse Sequences and Algorithms

9:30 am  Two-dimensional volume selective excitation
         Glen Morrell

9:45 am  High-Resolution Diffusion Tensor MRI
         Eun-Kee Jeong

10:00 am Correction of Intensity Inhomogeneities in Multi-spectral MRI
        Prashanthi Vemuri

10:15 am  GRAPPA-UNFOLD: Application on the Temperature Measurement
          Jun-Yu Guo

10:30 am  Break

Small Animal and Molecular Imaging

11:00 am  Molecular Imaging: Role of MicroPET
          Jim Slater

11:30 am  Quantitative MRI: Challenges and Promise
          Matthias Schabel

11:45 am  Multimodality imaging and Cancer Progression in Mice
          Patrick Hawkes

12:00 noon  PEG-g-(GdDTPA-L-Cystine): A Biodegradable Macromolecular Contrast Agent for Blood Pool
            MR Imaging
            Aaron Mohs

12:15 pm  Lunch

Reconstruction and Image Processing Algorithms

1:30 pm  Diffraction tomography
          Dilip Ghosh Roy

2:00 pm  Can the range conditions help in noise reduction?
          Larry Zeng
2:15 pm  Simultaneous Estimation of Emission Distribution and Attenuator with Assistance of Novikov’s Range Conditions
Yan Yan

2:30 pm  On Denoising with the Range Condition for the Attenuated Radon Transform
Qiu Huang

2:45 pm  Noise Propagation Comparison for Iterative Reconstruction Using Line-Integral Data and Planar-Integral Data
Bin Zhang

3:00 pm  Group photo

3:30 pm  Dynamic Cardiac SPECT using a DyRoSH SPECT Camera
Rajendra Maddula

3:45 pm  Cone-beam reconstruction using the backprojection of locally-filtered projections
Jed Pack

4:00 pm  Image reconstruction for truncated parallel-beam projections
Fred Noo

4:15 pm  Stabilizing an iterative algorithm by using small detector pixels
DoSik Hwang

4:30 pm  Computer simulation results of 3-slit Solstice imaging
Rajesh Venkataraman

4:45 pm  Analytical Fan-Beam and Cone-Beam Reconstruction Algorithms with Uniform Attenuation Correction
Qiulin Tang

5:00 pm  Rotating Slat Geometry Time Detection Optimization in SPECT
Rodney Earl

5:15 pm  Adjourn
Towards Understanding the Dark Rim Artifact in MRI Cardiac Perfusion Studies
Edward Di Bella

In dynamic contrast enhanced MRI studies, numerous researchers have noticed an endocardial “dark rim” that appears when the gadolinium contrast bolus appears in the left ventricle. This artifact typically precedes tissue uptake and is transient in nature. When performing visual analysis of the images, this artifact is often not difficult to read through, since it does not remain after the bolus as do true perfusion deficits. For semi-quantitative or quantitative analysis, however, the artifact can cause significant differences in estimated flow parameters.

There are currently 3 hypotheses regarding this type of artifact:
1) Susceptibility effects. The change in the magnetic field at the interface of blood with high gadolinium concentration and tissue distorts the signal, causing the artifacts.
2) Resolution (Gibbs ringing) effects. The ringing from the sharp edge causes the artifacts.
3) Motion. Movement of the beating heart during the ~190msec acquisition causes the artifacts.

These 3 possibilities will be explained further and relevant simulations and experimental results will be shown as we seek a better understanding of this artifact.
Accurate Assessment of the Arterial Input Function using MRI with Radial Sampling  
Eugene G. Kholmovski, Edward V.R. DiBella

INTRODUCTION
The accuracy of quantitative analysis of myocardium perfusion derived from dynamic contrast enhanced T1-weighted MRI critically depends on the knowledge of the arterial input function (AIF). The AIF is typically estimated from the mean signal intensity of a region of interest (ROI) placed in the left ventricular cavity. In many practical cases, such an AIF can be unreliable due to saturation effects caused by high concentration of contrast agent (CA) and/or long saturation recovery time of the applied pulse sequence.

METHODS
In T1-weighted imaging with saturation recovery, effective saturation recovery time (eSRT) is defined by the time delay between the saturation RF pulse and the time when the central part of k-space is acquired. In a myocardial perfusion study, the choice of eSRT is a compromise between the accuracy in AIF estimate and the SNR of tissue enhancement curves. With shortening eSRT, the accuracy of the AIF estimate improves but myocardium signal decreases and vice versa. A T1-weighted pulse sequence with Cartesian sampling has only one eSRT. However, when radial sampling is used, each projection passes through the center of k-space making it possible to reconstruct a set of images with various eSRTs by using different subsets of k-space projections. Images reconstructed from subsets with short eSRTs can be used to accurately estimate AIF because saturation effects are significantly or completely suppressed for the images.

To test the proposed concept of AIF assessment, MRI studies were performed on a 3T scanner (Trio, Siemens Medical Solutions, Erlangen, Germany) using a T1-weighted turbo-FLASH sequence with saturation recovery magnetization preparation (TR/TE=1.58/0.86 ms, TI=24 ms, flip angle=12°, 96 projections with 128 readout points, FOV=380 mm, 8 mm slice thickness). A contrast agent bolus of 0.15 mmol/kg of Gd-DPTA was used. The data sampling scheme was implemented in such a way that each subset of 24 time-adjacent projections covers 180 degrees. A set of images with various eSRTs were reconstructed from the corresponding subsets of 24 projections. To suppress streaking artifacts, the high frequency components of all available projections were included in each image reconstruction.

RESULTS
Figure 1 shows AIF estimates found from the images reconstructed using a complete set and four subsets of available projections. Saturation effects are obvious in the AIFs corresponding to long eSRTs (the peaks of the AIFs with eSRT > 70 ms are practically the same). The true AIF is equivalent to the function describing change in CA concentration in the blood during the bolus passage. Typically, this function cannot be reliably recovered from MR images with one eSRT. In the case of radial sampling, images with different eSRT can be reconstructed making CA concentration calculation applicable. Figure 2 demonstrates the AIF converted to CA concentration using the AIFs shown in Fig. 1 and the analytical expression describing both magnetization evolution for SR-prepared turbo-FLASH sequence and effects of the image reconstruction scheme employed.

![Figure 1](image1.png)

**Figure 1.** The AIFs calculated from the images reconstructed from a complete set and four subsets of available projection data. The ROI was chosen in the left ventricular cavity. eSRT for the images: 1st subset – 43 ms, 2nd subset – 81 ms, 3rd subset – 119 ms, 4th subset – 157 ms, complete set – 100 ms.

![Figure 2](image2.png)

**Figure 2.** The CA concentration curve derived using the AIFs shown in Fig.1 and the analytical expression for signal intensity.

CONCLUSION
The AIF can be accurately assessed using T1-weighted sequences with radial sampling. Higher doses of CA may be applicable for quantitative myocardium perfusion measurements when sequences with radial sampling are used for imaging.
3D Fluoro CT imaging with XRII-based mobile C-arm

S.-L. Santee, S. Breham, W. Christensen, R. Purcell, and A. Cheryauka

GE Healthcare, 384 Wright Brothers Dr, Salt Lake City UT 84116

**Purpose.** Mobile C-arm fluoroscopy systems have become standard imaging devices in hospital operating rooms and surgical centers to facilitate a variety of diagnostic and interventional radiological procedures [1]. New generation of mobile (as well as higher end fixed-room) fluoroscopic systems utilizes cone-beam computer tomography to create 3D images of the anatomical structures. These ‘mobile fluoro CT’ systems make the interventional imaging convenient and cost effective to produce CT-like results at any time before, during, and after a surgical procedure. We present the imaging results obtained with the anthropomorphic phantoms and use of a standard image intensifier (XRII)-based mobile C-arm system.

**Methods.** The image quality of 3D reconstructions produced with use of a mobile C-arm mounted XRII depends on a precise determination of the ‘patient-to-gantry’ positioning and the image warping caused by optic-electrical chain distortions. We have designed the rotating table, which substitutes C motion around the patient. The table has two programmable degrees of freedom and can provide a controlled amount of misalignment and motion errors. A mobile X-ray fluoroscopic system, GE-OEC’s 9800, having a 9-inch image intensifier, a true 1Kx1K image chain, and a synchronized pulse sequence, is used to acquire 2D projection images. The projection images are corrected for beam non-uniformity and geometrical distortions (Fig 1a-b).

An FDK-type reconstruction algorithm is used under the short scan and the circular planar trajectory conditions [2].

**Results.** We show the cross-sectional (Fig 2) and rendered (Fig. 3) images of the tissue-equivalent knee and hand phantoms.

**Conclusions.** The perceptive image quality and 3D numeric data are well defined for clinical evaluation (interventional IQ) of bone structures and surgical navigation, respectively.

**References**
Fuzzy c-means algorithm for sensitivity correction and segmentation on cardiac MRI perfusion dynamic data.

Dmitri Y. Riabkov and Edward V. R. Di Bella
University of Utah
Departments of Radiology
729 Arapeen Dr., Salt Lake City, UT 84108

I. DESCRIPTION OF PURPOSE
Sensitivity correction has to be done on cardiac MRI perfusion dynamic data in order to correctly estimate kinetic parameters of the tissue. Also appropriate segmentation of the cardiac region image is needed to identify left ventricle and right ventricle blood pools and the myocardium. Segmentation within the myocardium also should be performed to estimate kinetics of different tissue regions with less error.

The sensitivity correction and segmentation can be done in several stages. Many algorithms exist for each stage. An approach akin to the fuzzy c-means algorithm might do all of the steps at once. This algorithm and its modifications has been shown to be successful for static brain and breast MR images. We try to adopt this algorithm for dynamic MR perfusion images. The potential advantage of this algorithm being applied to the dynamic data is that by better modeling it can give better handling of the errors introduced by not only the coil sensitivity but the noise and partial volume as well.

II. METHODS
The measured image data Y are modeled as a product of true intensity X and spatially varying gain field G:

$$Y_k = X_k G_k \quad \forall k \in \{1, 2, ..., N\}$$

where N is the number of pixels in the image. After logarithmic transformation:

$$y_k = x_k + \beta_k \quad \forall k \in \{1, 2, ..., N\}$$

where $\beta_k$ is the bias field at the k pixel. The standard objective function for partitioning $x_k$ into c clusters [1] is

$$J = \sum_{i=1}^{c} \sum_{k=1}^{N} u_{ik}^p \| x_k - v_i \|^2$$

where $v_i$ are the prototype intensities of the clusters and $[u_{ik}] = U$ is the partitioning matrix such that $U \in \mathbb{U}$

$$U \left\{ u_{ik} \in [0,1] \right\} \sum_{i=1}^{c} u_{ik} = 1 \forall k \land 0 < \sum_{k=1}^{N} u_{ik} < N \forall i$$

The parameter $p$ is the degree of fuzziness of the resulting classification.

The objective function

$$J = \sum_{i=1}^{N} \sum_{k=1}^{N} u_{ik}^p \| y_k - \beta_k - v_i \|^2$$

minimized relative to $u_{ik}$, $\beta_k$ and $v_i$ by the method of the steepest descent. However to enforce $U$ a special term with Lagrange multiplier is added to $J$.

$$J = J + \lambda \left( 1 - \sum_{i=1}^{c} u_{ik} \right)$$

Lagrange multiplier $\lambda$ is explicitly found for the steepest descent method using the constraint that $\sum_{i=1}^{c} u_{ik} = 1$

III. RESULTS
The results with 2D MR images of cardiac perfusion shows the performance of the algorithm in sensitivity correction Fig.1-2. Application to the dynamic data where $y$ and $v$ are treated as functions of time and $u$ and $\beta$ as constants have not yet produced positive results. However work on modifications is underway for further adaptation of this method to the dynamic case.

1) Original; 2) Sensitivity corrected; 3) Sensitivity map.

IV. DISCUSSION AND CONCLUSION
This method has a potential for better accounting of the errors arising from noise and coil sensitivity due to better modeling. If the method will be successful for the dynamic case sensitivity correction and segmentation then it may potentially be used for estimation of the kinetic parameters by introducing two compartmental modeling [2] in to the objective function.

V. REFERENCES
Evaluation of the UCAIR heart
Sung M. Moon, Jed D. Pack, Frédéric Noo
University of Utah, Dept. of Radiology, Medical Image Research Lab., Salt Lake City, UT

Introduction
An accurate model of the heart is needed for realistic simulation in x-ray computed tomography. Phantoms, such as the NCAT and the super-quadratics phantoms are unpractical for efficient CT simulation since they are voxelized and moreover these phantoms are designed for SPECT and therefore have too few details for accurate cardiac CT simulation. An accurate analytical phantom, which consisted only of the analytical objects, has been developed and named UCAIR heart in demand of phantom for efficient cardiac CT simulation.

The UCAIR heart, which is built from quadratics and biquadratics, is more efficient for simulation than voxelized phantoms, because the calculation efforts can be saved dramatically since line integrals of quadratics and biquadratics are easily computed from analytical formulae. In a previous work, we showed that quadratics and biquadratics can be used for accurate cardiac modeling for x-ray CT simulations. [1] In this work, we demonstrate structural accuracy of the UCAIR heart by comparing it with real cardiac CT scan data.

Results & Conclusions
3D views of the UCAIR heart are shown in Fig.1. Several slices, comparing a voxelized version of the UCAIR heart with real cardiac CT images, are shown in Fig.2. Figure 3 shows 3D views and parallel-beam projections of coronary arteries of the UCAIR heart.

The UCAIR heart can also be easily modified for incorporation of any cardiac disease. (See Fig.4.)

Fig.1. 3D view of the UCAIR heart (Left) slice left view (Center) right side view (Right) top view

Fig.2. Comparison slides (Top) coronal (Middle) sagittal (Bottom) transversal

Fig.3. Coronary artery phantom (Top) 3D views (Bottom) parallel-beam projection

Fig.4. UCAIR heart with diseases (Left) coarctation of the aorta (Right) arterial septal defect

References
Background: Coronary artery disease (CAD) is one of the leading causes of death in the western world. Therefore, identification and analysis of myocardial ischemic tissue has important consequences for health care and basic science research.

Motivation: Ideally, we would like to quantify the blood flow supply to different parts of the left ventricle (LV) using noninvasive imaging (e.g., MRI or PET). For that purpose, it is necessary to segment the images from perfusion. Usually, this segmentation process is performed manually and our goal is to develop and implement a semiautomatic method.

Methods: In this project, we have applied a combination of the level set technique together with a curvature penalty term and a spectral speed function that accounts for all selected time frames. To calculate the spectral speed function we compute the Mahalanobis distance from each point in the image to a sample mean taken from within the myocardium of the LV. This way, we go from a $2D + time$ image sequence to a single image. Due to the low signal to noise ratio found in raw images, it is almost impossible to avoid “leaks” in the evolution of the level sets into the LV cavity and the surrounding structures. Therefore, we have constructed a shape model of the LV and added it as another constraint to the level-set framework. The shape model is updated dynamically, based on image information and on the evolution of the level sets.

Results: We have successfully tested our algorithm with 42 different datasets. In Figure 1 we present the segmented area in green. On the left, the red contour depicts the shape model and the black and white image background the feature image used to fit the shape. On the right, we have selected one particular frame as a background.

Conclusion: Our initial results suggest that combining approaches in this way achieves substantial improvements over any of the techniques used in isolation.

Figure 1 – In these images, the green area represents the final segmentation result. The background image on the left (feature image) is used to fit the shape model (red contours). The background image on the right is a selected frame with the best SNR selected for the purpose of visualization.
Quantitation of Regional Cardiac Function using HARP MRI
Nate Pack, Edward VR DiBella

Introduction: Magnetic Resonance (MR) tagging is a valuable tool for the assessment of regional left ventricular (LV) function. As magnetically embedded ‘tags’ move and deform with the motion of the heart, regions of ischemia or infarction remain stunted. In order to compensate for the impaired tissue, the surrounding myocardium bears a greater load and the adjacent tags deform more excessively. Conventional methods used to accurately quantify tag/tissue motion, require time consuming post-processing. For this reason, quantitative MR tagging has been predominantly replaced by subjective, qualitative assessments of tissue motion. Harmonic Phase (HARP) MRI is a rapid processing tool that yields potential for real-time quantitation of myocardial motion.

Methods: HARP MRI exploits the fact that tagged images have regularly distributed patches (harmonic peaks) of energy in their Fourier spectra [1]. These peaks exist due to the spatial modulation of magnetism (SPAMM) process that is used to generate tagged images. Next, a filtering process is used to isolate one of the harmonic peaks, from which complex harmonic data are extracted. From these data, the harmonic phase angle, \( \Phi \), is computed for every point in the image. The distribution of \( \Phi \) closely resembles the original tag pattern of the image, while the spatial gradient of \( \Phi \) is linearly related to the tag motion, in a direction orthogonal to the tag lines [2]. Therefore, for a spatially tagged image, a complete measure of inter-tag motion, which directly reflects tissue motion, can be computed from the HARP data. This process can be repeated in two or three dimensions (using images with transversely oriented tags) to elucidate a complete 2D or 3D distribution of tissue deformation. Once the deformation map is known, other measures of cardiac function, including tissue velocity, wall thickening, and radial or circumferential strain can be computed.

Results and Conclusions: The HARP method has been implemented to quantify the apparent 2D transmural strain in the LV of a healthy volunteer (see Figure 1). From a series of short-axis, tagged MR images, preliminary results reflect a smooth strain distribution across the LV, similar to that reported by other researchers [1]. Further processing is required to segment the myocardium (both radially and circumferentially) to quantitate the time-dependent average strain profiles for different regions of the LV throughout the cardiac cycle. Potential future applications using HARP include the correlation of 2D/3D strain maps with spatial T1 distributions and perfusion measurements in the LV.

References:
**Registration of Myocardial Perfusion Images using Mutual Information**

Ganesh Adluru and Edward V.R.Di Bella

**Introduction:** Image Registration is the process of mapping an image to a reference image so that images are aligned. Image registration is mainly of two types. Inter-modal registration, where images from different sources like MR CT PET are registered with one another and Intra-modal registration, where the images are from the same source are registered to a reference image from the same source.

Among the various methods available for registering images, the mutual information method has shown great promise when applied to rigid registration of multi-modality (inter-modal) images [1]. The same theory of mutual information is used to perform registration of dynamic MRI myocardial perfusion images (intra-modal) having motion in the left ventricle of heart.

**Method:** Mutual Information is a criterion, which can be used to measure the similarity of images. It is a quantitative measure of how well one image matches other. It is maximum when the two images are most similar to each other. The mutual information concept has its origin in information theory.

One of the simple definitions of mutual information, $I(X, Y)$ of two images ‘$X$’ and ‘$Y$’ is given by

$$I(X,Y) = H(X) + H(Y) – H(X,Y) \quad [2]$$

In the above equation the term $H(X)$ is the entropy of image $X$ computed on the probability distribution of the gray values and $H(Y)$ is the entropy for image $Y$. The term $H(X,Y)$ is the joint entropy of the two images $X$ and $Y$. Although many rigorous statistical methods are available for calculating the individual and joint entropies of the images, a simple way to calculate the entropy from ‘$p_i$’ values, probability that the image has gray value ‘$i$’, of an image $X$ is given as

$$H(X) = \sum_i p_i \log (1/p_i) = -\sum_i p_i \log p_i \quad [2]$$

The probability distribution of gray values is calculated by counting the number of times each gray value occurs in the image and dividing those numbers by the total number of occurrences. By this definition an image with low entropy consists of a single intensity, which is uniform. In the same way the entropy of image $Y$ is calculated. The joint entropy $H(X,Y)$ is calculated as

$$H(X,Y) = -\sum_{i,j} p_{(i,j)} \log p_{(i,j)} \quad [2]$$

The 'joint histogram' of two images can be used to calculate the joint probability distribution, $p_{(i,j)}$ by dividing each value in the histogram by the total number of entries in the histogram.

A joint histogram of two images $X$ and $Y$ is a combined plot of the gray values of the two images in which the value at a point $(a,b)$ corresponds to the number of points in image $X$ having gray value ‘$a$’ and number of points in image $Y$ having gray value ‘$b$’. Registration is done by applying rigid transformations to the image so as to maximize the mutual information between the image and reference image.

**Results:** The above technique of maximizing the mutual information is used for registering the dynamic MR perfusion images with a reference image by applying rigid transformations to the images. The results for one frame are shown below.

(a) – Reference Image, (b) – Image after Registration, (c) – Image before Registration, (d) – Difference Image between (b) and (a), (e) – Difference Image between (c) and (a), (f) – Difference Image between (e) and (d)

**Conclusion:** The mutual information based information is quite promising for intra-modal image registration. By improving ways to calculate the entropies of images and joint entropies better results can be achieved.

**References:**


Quantifying Vessel Movement and Orientation in Carotid Artery Magnetic Resonance Imaging.

Emilee Minalga, Rock Hadley, Dennis Parker

Introduction: Our group has been developing novel improvements for pulse sequences used for MR Imaging of the carotid arteries. We have also been working on new RF coil designs. The goal of these projects is to reduce background noise and image artifact as well as improve spatial and contrast resolution in the vessel wall and lumen images of the carotid artery. However, to accurately study the changes in morphology of the lumen and plaque over time, an improvement in patient repositioning needed to be developed. This project has focused on the development of a new patient head and neck immobilization and repositioning device, and the characterization of its effectiveness in repositioning the carotid artery so that vessel registration and image comparisons with previous scans can accurately be performed.

Methods: An approach to accurate repositioning and repeatability in carotid imaging is to immobilize the head, neck, and body and thus reducing the change in the carotid artery from previous scans. In order to immobilize the head and index it’s position for future imaging studies, we have developed a device that consistently immobilizes a patient’s head and neck on the MRI table for repeatable studies. This device includes a base plate that is anchored to an exact position in the patient table, a selection of foam head supports, and an arch that fits around the head and includes customized nose bridges and left-right stabilization posts. The foam pads for the head and lower body supports are chosen for each specific patient to match each patient’s anatomy. The arch, nose bridge, and left-right stabilization posts are all indexed and recorded for future studies.

Several studies were conducted to determine the accuracy of this head holder. MRI images were used to determine the amount of vessel displacement and orientation versus head rotation with and without the head holder. Fiducial markers are used to compute the head translation and rotation parameters for each head position using the standard imaging position as a reference. The vessel distortions were measured by computing the x, y centerline offsets in each slice with respect to the reference image centerlines. The z-translation of the vessels was determined by the change in position of the flow divider at the bifurcation.

High-resolution images of the carotid artery were taken for qualitative comparison between the use of the head holder and without the head holder. Images were taken of patients in the head holder were taken over time to display qualitatively the accuracy of repositioning.

Results and Conclusions: Assessment of the vessel distortion as a function of head position determined accuracy of the head/neck immobilization device for accurate repeatable carotid artery imaging. The study showed that the head holder more consistently repositioned the carotid arteries compared to without the head holder.
Comparison of Optimized Carotid Imaging at 1.5T and 3.0T

J. Rock Hadley, Emilee Minalga, Seong-Eun Kim, Dennis L. Parker
University of Utah, Department of Radiology – UCAIR, Salt Lake City, Utah, USA

Introduction

Magnetic resonance imaging (MRI) and angiography (MRA) of the carotid bifurcation requires high coil sensitivity to accurately detect and diagnose disease. We and others have demonstrated that substantial improvement in image detail of the anatomy and disease morphology at the carotid bifurcation can be obtained with the use of small coil arrays that are specially designed for that specific anatomy. There is also evidence that substantial improvement in the quality of carotid bifurcation images may be obtained using a higher field strength. We have recently constructed a 4-channel carotid coil for the Siemens 3T Trio scanner [1]. This design is similar to a coil design which has been optimized for imaging the carotid bifurcation at 1.5 T. The goal of this work is to compare high resolution imaging of the carotid bifurcation at 1.5T and 3T field strengths using similar coil designs optimized specifically for imaging the bifurcation. Coil designs and results of the comparisons will be presented.

Methods

Several volunteers were imaged using a standard cervical carotid imaging protocol on both a GE 1.5T SIGNA and Siemens 3T Trio scanners. The coils used for 3T imaging were similar in size to the 1.5T coils [1], but used only single sided copper substrate rather than the double sized copper substrate used for the 1.5T coils. At the 3T frequencies (123 MHz), the double sided substrate capacitance was dominating the coil tuning. Therefore, when active decoupling was attempted across the small chip capacitors, the RF current was in essence short circuited through the substrate capacitance. Using single sided copper substrate for the 3T coils has eliminated this problem. Also, cable chokes were used to eliminate cable shield currents on the 3T coils rather than the triax balun cables used for the 1.5T coils.

In addition, the cable length between coil elements and preamplifiers was significantly different between the 1.5T and 3T coils. The 1.5T coils used approximately 3 feet of cable between the coil element and preamp, where the 3T coils used only 8 inches. This translates to significant differences in cable loss [2] and preamp decoupling performance for the two sets of coils.

The standard scan sequences that were performed on the volunteers included a T1-weighted Fast Spin Echo (FSE) black blood sequence, a T2-weighted FSE black blood sequence, a Proton Density (PD) FSE black blood sequence, and a 3D time-of-flight (TOF) MOTSA sequence. Some volunteers were also imaged using a high resolution 3D TOF scan. Sequence parameters for the 3T scanner were set up to be as similar as possible to those on the 1.5T scanner. Because of Specific Absorption Rate (SAR) differences at the two field strengths, repetition times (TR) for the 3T black blood sequences were increased from 2000 to 3000 ms, and flip angles were decreased from 180° to 160°. The 3T images were acquired in sequential mode rather than interleaved mode. And, for 3T T1 images, 1 average was used compared to 2 averages for 1.5T scans. This kept the T1 image scan times for both field strengths about the same. The scan resolution, bandwidth, and echo times were kept the same at both field strengths.

Results and Conclusions

Image quality and relative SNR was significantly improved for the T1, T2 and high resolution MOTSA scans on the 3T scanner, however, for the 3T Proton Density and standard resolution MOTSA studies the images were very blurry and included significant flow artifact. It was observed that although the fractional echo was used for 3T MOTSA images, the percentage of fractional echo is not controllable and different percentages were used for the high and standard resolution MOTSA scans. We are still assessing the cause of the blurry images on the 3T scanner. Image comparisons at this point are only qualitative because of the many vendor and coil differences between the 1.5T and 3T studies. Obvious future work includes repeating the 1.5T studies on the new Siemens 1.5T Avanto scanner where the vendor and coil differences would be minimized. This could possibly allow for a quantitative comparison study based only on field strength. In addition, the 3T carotid imaging sequences need further optimization.

References

Triple Contrast Technique for Black Blood Imaging with Double Inversion Preparation

Seong-Eun Kim, Eugene G. Kholmovski, Eun-Kee Jeong, Henry R. Buswell, Jay S. Tsuruda, Dennis L. Parker

Utah Center for Advanced Imaging Research, Department of Radiology, University of Utah, 729 Arapeen Dr., Salt Lake City, Utah 84108

Magnetic resonance imaging (MRI) has been shown to be useful for visualizing disease in the carotid artery and for measuring vessel wall area. Recent publications show that images of the carotid artery with multiple contrasts can help with plaque component identification. Black blood techniques in which the signal from flowing blood is suppressed and the signal from the stationary tissues is retained provide an excellent contrast between vessel wall and lumen of the carotid artery. This contrast is critical for the measurement of wall thickness and plaque classification. Black blood imaging is usually realized by a double inversion magnetization preparation which consists of a non-selective 180° inversion pulse followed by a spatially selective 180° re-inversion pulse. Because of the nonselective inversion pulse, interleaved acquisition was initially not possible and image data has been usually acquired sequentially from a single slice before proceeding to acquisition from a subsequent slice. This sequential acquisition results in a long imaging time.

The standard protocol for carotid arterial wall imaging includes acquisition of images with various image contrasts: proton density weighted (PDw), T1 weighted (T1w), T2 weighted (T2w) images. Analysis of multi-contrast images is significantly simplified when these images are spatially registered. The acquisition of all three image contrasts requires at least two separate scans to be performed. Registration between images from multiple acquisitions is not trivial due to the physiological motions in the neck, including swallowing, respiration, etc. However, decreasing the time interval between acquisitions of various contrast images may significantly reduce misregistration. A PDw image and a T2w image can be acquired by dividing the FSE echo train into early and late echoes and constructing an image from each data set. But acquisitions of T1w images typically required a separate scan.

In this work, we present a novel pulse sequence for carotid artery study which allows acquisition of four images of different contrast weightings in a single acquisition. Two sets of the double contrast are obtained using the pulse sequence. The first set consists of PDw and T2w images obtained using double inversion preparation, and the second set provides T1w images by using a 90° saturation pulse after the non-selective inversion. The first image with short echo time is a conventional T1w and the second image provides a mixed contrast of T1 and T2 weighting. The images with such a contrast will be referenced as T1T2w in this paper. Because the ratio of the T1w and T1T2w images should be the same as the ratio of the PDw and T2w images, we recognize that the set of 4 images actually only provides 3 independent image contrasts and we refer to our technique as a triple contrast.
Development of a Centerline/Bifurcation Voxel-mapping Frame of Reference
Ling Zhang, Dennis L. Parker, John A. Roberts

I. Introduction
Quantitative measurements on 3D high resolution MRA data call for a convenient frame of reference. We intend to establish a centerline/bifurcation voxel-mapping frame of reference, which are composed of centerlines and bifurcations of a 3D vascular tree. Dynamic programming is used to extract the centerlines of the vascular tree. Then the jagged centerlines are fitted to smooth curves and split to segments between bifurcations. Each vessel voxel is then mapped to a position on a smooth segment. SNR can be measured along a chosen centerline segment and comparison of SNR for the same centerline on different datasets can be made.

II. Methods
First, the 3D source image is segmented using the ZBS algorithm [1]. Then a mask is made from the segmented image. Second, for each vessel voxel, we calculate its Distance From the closest Edge (DFE), and use this as the basis for computing the cost function. Third, the cost for each vessel voxel is computed by the following cost function:

\[
\text{cost}(x) = A \sqrt{1 - \frac{\text{DFE}(x)}{\text{max}_x \text{DFE}(x)}} + 1
\]  

(1)

Here max_DFE(x) is the local maximum DFE corresponding to voxel x. Fourth, the cost image is input to a dynamic programming algorithm which uses Dijkstra’s algorithm [2] to find the minimum cost path between each vessel voxel and the root point of the vessel tree. Then back tracing is performed for all vessel voxels in the order of decreasing path length. The tracing stops when the root point is reached or when a previous traced path is hit. The length of the traced path is recorded and compared to a predefined length threshold. The traced paths with lengths longer than the threshold are defined as centerline paths. And bifurcations are defined as the points where two paths meet. In the fifth step, the centerline paths are split into centerline segments in between bifurcations and all segments are fitted to smooth curves using Chebyshev fit and cubic spline fit [3]. Finally, each vessel voxel is mapped to a particular position on a particular fitted centerline segment.

III. Results
Figure 1 shows the extracted centerlines overlapped on the DFE image. Almost all centerlines are detected except for a few very short branches. The centerlines are reasonably well centered. After the centerline smoothing and voxel mapping procedure, we are able to calculate SNR along a chosen centerline segment easily. Figures 2 to 4 show the vessel segment selected to compute SNR for three datasets of the same person obtained at different time. The SNR curves along the centerline are displayed in Figure 5.

Fig. 1 Extracted centerlines overlapped on DFE image

Fig. 2

Fig. 3

Fig. 4

Fig. 5 SNR curves along the centerline segments shown in Fig. 2 to 4. The horizontal axis is the percent distance along the chosen centerline segment.

References:
Positron emission tomography (PET) can characterize different aspects of tumor physiology using various tracers. PET is usually limited to one tracer since there is no explicit signal for distinguishing multiple tracers. The ability to image multiple PET tracers in a single, fast imaging session would provide a wealth of complementary information for improving tumor grading, selecting the most effective therapies, and monitoring their effectiveness. We tested the feasibility of rapidly imaging multiple PET tracers using dynamic imaging techniques and staggered injection times, where the signals from each tracer are separated based upon differences in tracer half-life, kinetics, and distribution.

Time-activity curve populations for FDG (glucose metabolism), acetate (aspects of tumor growth), ATSM (hypoxia), and PTSM (blood flow) were simulated using appropriate compartment models, and noisy dual-tracer curves were computed by shifting and adding the single-tracer curves. Principal component analysis (PCA) methods were then used to study the separability of the individual-tracer signals using various measures of information-space overlap. PCA was also used to recover individual-tracer time-activity curves from dual-tracer curves. Results indicate that there is information content present for separating multi-tracer time-activity curves, and that this separability depends upon tracer kinetics, injection order and timing. While near-simultaneous injections gave poor separability, injections staggered by >10 min. resulted in data with significant information present for distinguishing the signals for individual tracers. The feasibility of recovering individual-tracer signals from multi-tracer PET data has been demonstrated. Practical approaches to multi-tracer PET will be developed and optimized in future work for a number of tracer combinations targeting a variety of tumor types.

---

**Fig. 1.** %Overlap of the information spaces for dual-tracer data, as computed by the PCA analysis using 5 principal components for each tracer. The %Overlap drops rapidly with increasing delay between injections.

**Fig. 2.** Separability Index for dual-tracer data plotted as a function of injection delay for the second tracer. The separability generally rises with increasing delay and is tracer-dependent, though there is a plateau phenomenon for dual-tracer imaging with FDG.

**Fig. 3.** Average SSE over 100 noise realizations for single-tracer TACs recovered from dual-tracer TACs using the PCA-based separation approach, plotted as a function of injection delay. The average SSEs were highest when the tracers were injected simultaneously, and they dropped rapidly with increasing injection delay. The average SSEs for single-tracer TACs are also provided for comparison.
Rapid Dual-Tracer PET Tumor Imaging: A Compartmental Modeling Approach

Thomas C. Rust and Dan J. Kadrmas

Positron Emission Tomography (PET) has the capability to characterize many aspects of tumor physiology using different radiotracers, but is currently limited to a single tracer per scan session. The objective of this work is to investigate the potential of a parallel dual-tracer compartmental modeling approach for PET tumor imaging, where differences in tracer kinetics, half-lives, and staggered injection times are utilized to recover the rate parameters for each tracer. Example time-activity curves (TACs) were simulated for \(^{18}\)F-FDG (glucose metabolism), \(^{11}\)C-Acetate (amino acid synthesis), \(^{62}\)Cu-ATSM (hypoxia), and \(^{62}\)Cu-PTSM (blood flow) using representative input functions, compartmental models, rate parameters, and noise levels for a tumor region-of-interest. Dual-tracer TACs were formed by time-shifting and adding pairs of TACs for tracers with a range of injection timing delays. In each case, 100 independent noise-realizations were simulated, and a nonlinear least squares fit was performed in order to compare the mean and standard deviation of rate parameter estimates (\(F_b, k_1, k_2, \ldots\)) for single- and dual-tracer data. Rate parameters estimated from dual-tracer data were obtained with little bias and only a marginal increase in noise as compared to single tracer results for cases with injection delays of ~10min or longer. When the second tracer was injected more rapidly, there was significant bias and increased uncertainty in the estimates. These results suggest that dual-tracer compartment modeling has the potential to yield accurate single tracer rate parameter estimates, provided that an appropriate injection timing delay is chosen.

![Fig 1. Examples of using dual-tracer compartment modeling to estimate rate parameters for FDG+Acetate, FDG+ATSM, and Acetate+ATSM imaging. Injection delays from 0 to 60 min. were studied for each tracer pair. The mean and s.d. of rate parameter estimates were studied over 100 noise realizations (see Table I), permitting comparison of the bias and noise properties of parameter estimates for dual-tracer versus single-tracer imaging.]

Table I. Rate parameter estimates (mean ± s.d., min\(^{-1}\)) for each of the dual-tracer combinations shown in figure 1.

<table>
<thead>
<tr>
<th></th>
<th>Dual-Tracer</th>
<th>Single Tracer</th>
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<tbody>
<tr>
<td>FDG (0min) + Acetate (20min)</td>
<td>(k_1): .252 ± .015 (k_2): .201 ± .023 (k_3): .050 ± .003 (k_4)</td>
<td>FDG (0min)</td>
</tr>
<tr>
<td>Acetate (0min)</td>
<td>(.848 ± .057) (.269 ± .047) (.149 ± .017)</td>
<td>(truth)</td>
</tr>
<tr>
<td>FDG (0min) + ATSM (15min)</td>
<td>(.253 ± .015) (.203 ± .022) (.050 ± .003)</td>
<td>ATSM (0min)</td>
</tr>
<tr>
<td>ATSM (0min)</td>
<td>(.415 ± .063) (.271 ± .197) (.184 ± .231) (.104 ± .067)</td>
<td>(truth)</td>
</tr>
<tr>
<td>Acetate (0min) + ATSM (15 min)</td>
<td>(.846 ± .050) (.269 ± .047) (.149 ± .021)</td>
<td>Acetate (0min)</td>
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Two Dimensional Volume Selective Excitation

Glen Morrell MD PhD

Many MR imaging situations involve imaging a specific structure which occupies only a small fraction of the field of view. For example, the spinal cord and important surrounding bony structures occupy a field of view only a few centimeters in extent in the axial plane. Currently used MRI techniques require imaging over a field of view as large as the entire sensitive volume of the RF coil to avoid image aliasing. Many phase encoding steps are required to encompass this field of view, leading to long scan times and low resolution across the structure of interest.

Two-dimensional volume selective excitation is a technique which allows selective excitation of a subset of the imaging volume whose extent in two dimensions can be specified. For instance, two dimensional volume selective excitation can be used to excite only a cylinder containing the spinal cord and surrounding bony structures of interest, leaving tissue outside this volume unexcited. Since the unexcited regions contribute no signal, imaging can be performed over a small field of view corresponding to the structures of interest with no aliasing of structures outside this field of view. Additionally, any artifacts arising from regions outside the field of view of interest are eliminated, since these regions contribute no signal.

Preliminary results of two dimensional volume selective excitation of the lumbar spine are shown, which demonstrate excitation of only the spinal cord and relevant surrounding bony structures. Decreased imaging time and increased resolution across the structures of interest are demonstrated. Additionally, artifacts arising from aortic pulsation or bowel peristalsis are eliminated.

Other applications of two dimensional volume selective excitation are suggested, including MR microscopy and improved characterization of breast lesions.
High-Resolution 3D Diffusion Tensor Imaging of the Cervical Spinal Cord at 3T

E.-K. Jeong, S.E. Kim, J. Guo, D.L. Parker

INTRODUCTION: Diffusion weighted MR echo-planar imaging (EPI) has proven to be a powerful method for examining neurological diseases in the brain. Diffusion tensor imaging may also be applied to the spinal cord, a thick neuronal fiber bundle. DTI of the spinal cord requires high spatial resolution because of the small cross-sectional dimension of the cord (< 15 mm). There is a substantial distortion on the image due to the magnetic susceptibility upon using a conventional ss-DWEPI. Two 3D DTI acquisition methods using segmented 3D EPI have been developed at 3T MRI system. DTI measurement capability of the new techniques demonstrated the fine detail of the cervical spinal cord, which no one has reported. The gray matter at the center of the spinal cord was clearly visible.

MATERIALS AND METHODS: Two 3D ms-DTI acquisition techniques include (a) 3D Composite Diffusion Encoding EPI (CODE-EPI), which would overcome some of the disadvantage of the diffusion preparation (DP) using driven equilibrium, (b) multi-shot 3D diffusion-weighted EPI (3D DWEPI). Stejskal-Tanner DW waveform was applied with a refocusing 180° RF pulse. Echo-train length (ETL) was selected (<32) to reduce both the magnetic susceptibility artifact and imaging time for full 3D DTI acquisition. Peripheral gating was used to reduce the phase error caused by the CSF pulsation. For CODE-EPI, which was consist of consecutive acquisitions of DW and DP magnetizations, a pair of crusher and rewinding crusher gradients was implemented, which not only eliminated the dependences on relative transmit phase of the tipup RF pulse, also eliminates the T1 contaminated signal. An excised dog heart was imaged with 3D CODE-EPI with (1.0 mm)3 isotropic spatial resolution. Diffusion encoding was achieved with b value 0 and 400 sec/mm2 along 7 non-collinear directions (3 orthogonal and 4 tetrahedral vertices). Siemens’ 8 channel receive only head coil was used for the data acquisition. 3D DWEPI was applied to human volunteers for high-resolution DTI of the cervical cord, with spatial acquisition resolution 1.0x1.0.2.0 mm3, b values 0 and 250 sec/mm2 along 7 directions. Peripheral gating was used to synchronize the scanning to the CSF pulsation, and homemade 4 channel coil was used, which was constructed for carotid artery imaging. The echotrain length was 7 for the acquisition. The DTI acquisition time was about 10 min for human spinal cord.

RESULTS: The DTI data was diagonalized, and RGB color map was constructed for the principal eigenvector as in Fig. 1, which represent the direction of the muscle fiber for the dog heart. The resultant DTI measurements demonstrated the helical structure of the cardiac muscle, and agreed well with previously reported result.1 DTI measurement of the cervical spinal cord is displayed in Fig. 2 in sagittal and transaxial planes. The display resolution is (0.5 mm)3 isotropic. The gray matter in the cord was clearly visible in the RGB fibermap and the fractional anisotropy map, especially on transaxial display. This is the first time DT images demonstrates the fine detail of the cervical spinal cord in 3D.

REFERENCEs

DISCUSSION: There has been very few report of 3D high-resolution DTI measurement of a human spinal cord in vivo. A previous report described a high-resolution DTI of the visual cortex in (1.7 mm)3 resolution.2 The DTI results from both in vitro animal heart and in vivo human cervical cord demonstrate the detailed fiber direction.
Correction of Intensity Inhomogeneities in Multi-spectral MRI
Prashanthi Vemuri, Eugene G. Kholmovski, Dennis L. Parker

INTRODUCTION
Magnetic Resonance Imaging (MRI) datasets can be acquired by multiple receiver coil systems to get images with improved signal-to-noise ratio (SNR) and to decrease acquisition time. In the cases when coil sensitivities are unknown, sum-of-squares (SoS) reconstruction algorithm [1] is typically applied. Intensity of SoS reconstructed image is modulated by spatially variable weighting function due to the non-uniformity of coil sensitivities. Intensity inhomogeneity correction of SoS reconstructed images is mandatory when quantitative analysis and/or tissue segmentation is required.

In this study, we have proposed a simple technique to estimate and correct the coil intensity inhomogeneity in multi-spectral MR images.

METHODS
Given \(C_1, C_2, \ldots, C_M\) \(i=1,\ldots,N\) are individual coil images from multi-contrast study consisting from \(M\) scans with different contrasts and \(C_1\text{SoS}, C_2\text{SoS}, \ldots, C_M\text{SoS}\) are the corresponding SoS images arranged in the order of decreasing SNR. The proposed intensity inhomogeneity correction technique consists of the following steps:

1. **Obtain unbiased filtered SoS images**
At first, the bias in the SOS images is removed using the technique described in [2]. Then, the unbiased images are processed by anisotropic diffusion filter [3] to reduce image noise. Due to the availability of multi-contrast images, a vector form of the filter was applied.

2. **Obtain a mask \(I_u\) of uniform tissue region**
The ratio image \(r\) between images \(C_{1\text{SoS}}\) and \(C_{2\text{SoS}}\) is used to identify the image area occupied by the dominant uniform tissue type. The mask for the uniform tissue \(I_u\) is calculated as follows
\[
I_u = \frac{C_{2\text{SoS}}}{(\sigma_r + C_{1\text{SoS}})};
\]
where \(\sigma_r = h - 0.1 < \text{value of } r < h + 0.1 = 1\)

3. **Polynomial fit to the uniform tissue region**
We assume that the coil profile is smoothly varying and fit a second-order polynomial to each individual coil image (i.e. to \(C_i, I_u\)) in the regions of uniform tissue to obtain the coil sensitivity maps \(S_i\).

4. **Sensitivity compensation**
The final images are reconstructed by correcting the overall sensitivity SoS images as it does not cause the amplification of noise in regions of low values of sensitivity profiles.

\[
C_{k\text{corrected}} = \frac{C_{k\text{SoS}}}{S_{\text{SoS}}} \quad \text{where } k=1,\ldots,M.
\]

DISCUSSION AND CONCLUSION
The proposed technique works well in eliminating the intensity inhomogeneity in multi-spectral MR images. It can also be applied for correction of intensity inhomogeneity in a single contrast image in the cases where a single uniform tissue can be identified from the statistics of the image.

REFERENCES
GRAPPA-UNFOLD: Application on the Temperature Measurement

Jun-Yu Guo, Dennis L. Parker, Robert B. Roemer

Introduction:
Magnetic Resonance Imaging Thermometry (MRIT) has been successfully used to map temperature change during thermal therapies in vivo by using the shift of the water proton resonance frequency (water PRF). To be used for control purposes and to accurately calculate SAR the multi-slice or 3D temperature measurements must be made with the shortest sampling time.

Speed is an important factor in many applications of MRI. For dynamic applications, speed can be increased using parallel imaging like GRAPPA [1] or locally dynamic techniques such as UNFOLD [2]. Recently, the combination of parallel imaging with UNFOLD was demonstrated [3]. The method proposed in this study is also one combination method, the GRAPPA-UNFOLD method. For the same speedup factor the combination of GRAPPA and UNFOLD yields more accurate phase difference and temperature images than GRAPPA alone. The comparison between the results with the GRAPPA-UNFOLD method and without this method will be shown and discussed.

Methods:
The GRAPPA-UNFOLD method is a new strategy to reconstruct the data shown in Figure 1. Suppose $G$ is a GRAPPA operator able to convert an acquired data set $K^m(k_x,k_y,k_z,t)$, where the subscript $m$ represents the coil-element number, into a k-space data set $K^u(k_x,k_y,k_z,t)$ which can be reconstructed by the UNFOLD method. Suppose $U$ is a UNFOLD operator able to reconstruct the k-space data set to the image set $I(x,y,z,t)$. So the whole process of the reconstruction is shown:

$$I(x,y,z,t) = U \{G \{K^m(k_x,k_y,k_z,t)\}\}$$

(1)

The above equation shows the reconstruction procedure for the GRAPPA–UNFOLD method. First, the k-space data of each frame with 24 reference lines can be used by GRAPPA to calculate the missing lines of k-space data required for UNFOLD method. UNFOLD is then applied to the new k-space data to reconstruct the final image. The total acceleration factor is 4. In fact, the real acceleration factor is a little bit smaller due to acquiring the extra reference lines. The temperature of hot water was monitored inside the Siemens 3T scanner for about 20 minutes using a GRE pulse sequence. The protocol is: TR = 50 ms, TE= 10 ms, resolution 256, and number of frames is 100.

Results:
The hot water cooled down inside the scanner. The temperature change is plotted in Figure 2. The black line is the temperature change from the full k-space data. The red line is the result from the k-space data in Figure 1 extracted from the full data. The blue line is the difference between these two results. Only part of the data is shown in Figure 2.

Conclusion:
The result shows that the temperature profile by using GRAPPA-UNFOLD method is good enough to monitor the temperature change even with the acceleration factor of around 4.

Reference:
Molecular Biology: Role of MicroPET
James B. Slater, Ph.D.
Cyclotron Radiochemistry Laboratory
Huntsman Cancer Institute

Molecular imaging is a multidisciplinary field that converges a wide range of basic and clinical sciences to study biological pathways. The rapid growth of molecular imaging has resulted from several factors, including recent advances in cellular and biological techniques, new imaging drug probes, and the successful development of small-animal imaging instrumentation.

Molecular imaging in living subjects offers several distinct advantages. In contrast to cell and tissue culture, in vivo animal models allow the assessment of tolerances, complementation, and redundancy in biological pathways. Such models also allow repetitive imaging and give the researcher options of multiple imaging strategies, which may decrease costs by eliminating the need to kill mice.

The various existing imaging technologies differ in five main aspects: spatial and temporal resolution, depth penetration, energy spectrum utilized, type of molecular probes, and sensitivity of detection.

To further our understanding how molecular imaging can be utilized in defining fundamental biological processes, a brief overview of the advantages and disadvantages of current animal imaging methods will be presented. In addition, emphasis on microPET and its role in understanding biological processes will be examined.
Multimodality imaging and Cancer Progression in Mice
Patrick Hawkes, Charles Keller

Understanding the genes and proteins responsible for cancer progression is essential for therapeutic intervention. Observing and serially sampling cancer progression in humans is impractical, but sophisticated mouse models can be generated. What is needed is a tool for monitoring micro-invasion and micro-metastasis. The goal of our work is to develop an in-vivo, multi-modality reporter that will allow for early detection of cancer progression in mouse cancer models, and consequent monitoring of therapeutic treatment efficacy in these models.

The focus of our work has been to create mice that can conditionally express, on cancer cells, a chimeric receptor that will facilitate imaging across multiple modalities (e.g. CT/MRI/PET/Optical). This chimeric receptor is composed of a single pass transmembrane domain, and an extracellular maltose-binding domain. This chimeric receptor has been introduced into the Rosa26 locus, a ubiquitously expressed gene locus, and has been engineered such that expression of the chimeric protein can be temporally and spatially controlled using Lox/Cre technology. The chimeric receptor’s ligand, maltose, can be labeled with a variety of different substrates such as gadolidium, iodine, radiolabeled substrates, a red fluorescent protein or cy5.5. These differently labeled maltose probes can then be intravenously injected into the genetically engineered mice. It would then be predicted that the labeled maltose would bind the tumor cell-specific chimeric receptors. Consequently, this binding activity would allow for multi-modality in vivo imaging using MRI, CT, PET, fluorescent or optical imaging (depending on the label bound to the maltose injected).

Results to date are the targeting vector for this chimeric receptor has been created and introduced into mouse embryonic stem (ES) cells. Twenty-three out of 144 Positive clones containing the desired recombinatorial event have been selected, and these ES cells will be injected into mouse blastocysts to create a genetically engineered mouse that can conditionally express this receptor. Future activation of this reporter in premalignant cells (in mouse cancer models which have already been created in our lab) will allow for early detection of proliferation, micro-invasion and micro-metastasis using multi-modal in vivo imaging. This will enable us to further understand the genetic and molecular mechanisms involved in cancer progression thus allowing for new or improved therapeutic treatment options.
Current contrast agents, while nontoxic, are poorly suited for contrast enhanced exams that require a longer enhancement window, such as cardiovascular or tumor imaging. These agents are extracellular meaning that they rapidly escape the vascular blood pool. Macromolecular contrast agents would be more optimal for use as blood pool agents because of their large size. However, the clinical application of currently researched gadolinium-based macromolecular contrast agents has been limited by two major concerns. First, the pendant chemical structures of the contrast agent may have potential toxicity. Second, they are too large to be excreted via renal filtration leading to liver accumulation and subsequent metabolic release of toxic Gd$^{3+}$ ions. In response, biodegradable PEGylated Gd-DTPA $L$-cystine copolymers, PEG-$g$-poly(GdDTPA- $co$-$L$-cystine), were synthesized and tested in mice as blood pool agents for MR imaging. These agents are biodegradable through the disulfide – thiol exchange reaction with endogenous thiols causing Gd$^{3+}$ ions to be excreted as small, safe complexes. PEG was used for it high biocompatibility and its ability to increase the hydrodynamic radius of macromolecules and decrease their clearance. The agents were synthesized from the condensation polymerization of DTPA and $L$-cystine followed by chelating with Gd(OAc)$_3$. MPEG-NH$_2$ (MW $= 2000$) was grafted to the copolymeric backbone in different ratios. In vitro testing showed that the macromolecular agent was readily degraded with the incubation of $L$-cysteine. In vivo, the agent showed superior contrast enhancement to a low molecular weight control, Gd-(DTPA-BMA), in the heart and vasculature. Significant contrast enhancement was observed by the PEGylated contrast agents 1 h after injection, while little enhancement was observed by the control agent in the blood pool. PEG-$g$-poly(GdDTPA-$co$-$L$-cystine) is a promising novel contrast agent for blood pool MR imaging.

**Figure 1.** (Left Panel) Coronal MR images of mouse heart and (right panel) descending aorta (solid arrow) and common iliac arteries (hollow arrow). The images were taken preinjection (a) and 1 (b), 5 (c), 15 (d), 30 (e) and 60 min (f) post intravenous injection of PEG$_x$-GDCP (A), PEG$_y$-GDCP (B), GDCP (C) and Gd-(DTPA-BMA) (D). Polymeric agents were given at a dose of 0.03 mmol-Gd/kg and Gd-(DTPA-BMA) was given at the standard clinical dose of 0.1 mmol/kg.
An Overview of Acoustical Diffraction Tomography

D. Roy, A. Khan and M. Schabel
Utah Center for Advanced Imaging Research
Department of Radiology
University of Utah, Salt Lake City

The most widely used methods of image reconstruction in medicine are integral equation based approaches. Computed tomography, perhaps the most popular of all medical imaging techniques, uses integral equations of the first kind in the form of Radon transforms. On the other hand, methods that use integral equations of the second kind, are primarily wave-based, and fall into the category of inverse scattering. In the latter, an unknown object is recovered from the knowledge of the scattered field that the object generates when a wave is scattered off it. Inverse scattering in medical imaging takes the form of diffraction tomography which can be acoustical and/or optical. The acoustic form of tomography is more attractive in these applications as the associated instrumentation in acoustics is relatively simple and inexpensive. In addition, the acoustic waves penetrate deeper into the body as compared to light waves. In this talk, we present an overview of acoustical diffraction tomography. The basic physical principles behind the method, its relation with computed tomography, difficulties in practical implementations, various approximations used and their limitations, are some of the topics that are discussed.
Can the range conditions help in noise reduction?

Larry Zeng

There are conflicting view points as to whether forcing projection data to satisfy the range conditions has any effects on the reconstructed images. We believe that the use of the range conditions together with the non-negativity condition does reduce noise in the reconstructed image, and that this is equivalent to using the well-known emission data ML-EM algorithm for image reconstruction.

The Radon transform range conditions (also known as the projection data consistency conditions, or the Helgason-Ludwig moment conditions) characterize the projection data obtained by the Radon transform. Researchers have attempted to use these conditions to project or force the measured (noisy) projection data into the range of the Radon transform by using the range conditions. However, this noise reduction method is not effective and no noise reduction is observed. Theoretical analysis has also been carried out. A general approach is to decompose a measured noisy projection function \( p \) into a function \( p_1 \) in the range of the Radon transform and a function \( p_2 \) that is not in the range of the Radon transform. An article published at *IEEE Transactions in Medical Imaging* [1] claims that the function \( p_2 \) has some contribution to the final reconstructed image in the form of some non-orthogonal projection. A different article in *Contemporary Mathematics* [2] concluded that \( p_2 \) is in the null-space of the Radon backprojection operator and that \( p_2 \) does not affect the reconstructed image at all so that it would be hopeless to use the range conditions to filter the projection data. In this letter, we present our opinion on this issue.

For a function \( f \) defined on a compact two-dimensional region, the Radon transform of it is given by

\[
(Rf)(s, \theta) = \int f(s \theta + t \theta^t) dt
\]

and the range conditions consist of the evenness condition

\[
(Rf)(s, \theta) = (Rf)(-s, \theta + \pi)
\]

and the moment conditions

\[
\int_0^\pi e^{i \theta} \int_0^\pi s^m (Rf)(s, \theta) ds d\theta = 0 \quad \text{for } |k| > m \geq 0.
\]

A noisy Radon projection function \( p \), which is Radon transform of some function \( f \) plus noise, can be uniquely decomposed into a summation of a function in the range of the Radon transform and a function in the null-space of the adjoint Radon transform which is the backprojector. We have

\[
\text{Range}(R) = \text{Null}(R^*)
\]

where \( \text{Range}(R) \) is the range of the Radon projection operator, and \( \text{Null}(R^*) \) is the null-space of the Radon backprojector \( R^* \). If a function \( p_1 \) is in \( \text{Range}(R) \) then there exists an image \( f \) such that \( p_1 = Rf \). If a function \( p_2 \) is in \( \text{Null}(R^*) \), then the backprojection of \( p_2 \) is a zero image. For any measured (noisy) projection function \( p \), it can always be decomposed as such \( p_1 \) and \( p_2 \).

In medical imaging, we only consider the non-negative image functions (or vectors), the projections are also non-negative. On the other hand, the use of the range conditions combined with the non-negativity condition on the image can significantly improve the reconstructed image in terms of noise reduction. It is interesting that this noise-reduction method is equivalent to applying the emission data ML-EM algorithm for image reconstruction, regardless of whether the noise is random or deterministic, as long as the data are non-negative. If one uses an iterative algorithm to reconstruct the image, the range conditions are automatically satisfied, because the forward pseudo-projection is performed at each iteration and any data generated by a projector satisfy the range conditions.

**References**


Simultaneous Estimation of Emission Distribution and Attenuator with Assistance of Novikov’s Range Conditions

Yan Yan, Larry Zeng

Introduction:
In general emission tomography, the main problem is to solve imaging function \( f(x) \) from the equation

\[
(Raf)(\theta,s) = \int_{x: \theta \cdot x = s} e^{-\left(Da(x, \theta)\right)} f(x) dx \quad (1)
\]

in which we put for \( x \in \mathbb{R}^2, \theta \in S^1 \). It is based on the presence of attenuation that the attenuation map \( a(x) \) is assumed to be known. The usual procedure to determine \( a(x) \) is to use separate transmission scans prior to or simultaneously with the emission scan. But in practice people hope to get the imaging from less scans and radiation. In this project, we study the case in which \( a(x) \) is unknown and try to get a simultaneous estimation of imaging map \( f(x) \) and attenuation map \( a(x) \).

Methods:
In equation (1), we have two unknowns \( f(x) \) and \( a(x) \). Some other condition is needed to solve both of them simultaneously. Novikov \([3]\) found the following condition

We explore the possibility of using this condition to get estimation of \( f(x) \) and \( a(x) \). projection data. First the verification of this condition has been done by using known attenuation map and

\[
\text{Re} \int_{S^1} e^{-Da(x, -\theta)} e^{1/2 (1+iH)Pa(\theta, x \theta^\perp)} H e^{1/2 (1-iH)Pa(\theta, x \theta^\perp)} g(\theta, x \cdot \theta^\perp) d\theta = 0
\]

Then we plan to solve this problem with an iterative ML-EM procedure and the attenuation correction from Novikov condition.

Reference:
[4] David V Finch The attenuated X-ray transform: Recent developments
On Denoising with the Range Condition for the Attenuated Radon Transform

Qiu Huang and Larry Zeng

1 Introduction

Range conditions for the Radon transform characterize the projection data obtained by the Radon transform. They are also known as consistency conditions or Helgason-Ludwig moment conditions. Researchers have attempted to utilize these conditions to reduce noise in image reconstruction. It was shown [4] that the use of range conditions together with non-negativity condition reduces noise in the reconstructed image. In practice, however, the projection data are all attenuated. Range conditions for the attenuated Radon transform are studied in this paper. We found by computer simulation that forcing the measured (noisy) projection data into the range of the attenuated Radon transform does not improve the reconstructed image. Theoretical research is still undergoing.

2 Method

The attenuated Radon transform of an activity function \( f(\vec{x}) \) is given by

\[
(R_\mu f)(\theta, s) = \int_{-\infty}^{\infty} f(s\theta + t\theta^\perp)e^{-(D_\mu)(s\theta + t\theta^\perp, \theta^\perp)}dt
\]

where

\[
\theta = \begin{pmatrix} \cos \theta \\ \sin \theta \end{pmatrix}
\]

and

\[
(D_\mu)(\vec{x}, \theta) = \int_0^\infty \mu(\vec{x} + t\theta)dt
\]

with attenuation map \( \mu \). The range condition[3] for \( R_\mu \) indicates that if \( g(\theta, s) \) satisfies

\[
Re \int_0^{2\pi} e^{-(D_\mu)(\vec{x}, \theta^\perp)}e^{\frac{1}{2}(I+iH)R_\mu}H(e^{\frac{1}{2}(I-iH)}R_\mu)(\theta, \vec{x}+\theta^\perp))d\theta = 0
\]

then, there is a function \( f(\vec{x}) \) such that \( f \) and all its derivatives are \( O(|\vec{x}|^{-2}) \) as \( |\vec{x}| \to \infty \) with \( R_\mu f = g \). \( H \) denotes Hilbert transform.

Any measured (noisy) projection data can be uniquely decomposed into two parts: one in the range of \( R_\mu \) and the other in the null space of \( R_\mu^\#[1] \). \( R_\mu^\# \) is the adjoint operator of \( R_\mu \).

Let \( g(\theta, s) \) be the noisy projection data and \( g(\theta, s) = g_R(\theta, s) + g_N(\theta, s) \). Simulation shows that

\[
\frac{1}{4\pi}Re \text{div} \int_0^{2\pi} \theta e^{(D_\mu)(\vec{x}, \theta^\perp)}(e^{-h}He^{h}g_N(\theta, \vec{x}+\theta^\perp))d\theta = 0
\]

where \( h = e^{\frac{1}{2}(I+iH)}R_\mu \). The left side of the above formula is the inversion of the attenuated Radon transform[2]. Thus, the part of projection data in the null space of \( R_\mu^\# \) has no effect to the image reconstruction.

References


Noise Propagation Comparison for Iterative Reconstruction Using Line-Integral Data and Planar-Integral Data

Bin Zhang, Gengsheng, L. Zeng

Introduction
The low efficiency of a regular parallel-hole collimator is one of the factors that limit the performance of SPECT system. One way to improve the geometric efficiency is to use planar-integral projection data which can be acquired by a rotating detector with a parallel slat collimator instead of using line-projection data. The advantage of the slat collimator is that it can measure planar-integral projection which improves the efficiency. However, it may cause higher noise amplification during the complicated reconstruction procedures.

Methods
Unlike the conventional parallel-hole collimator, the slat collimator needs to spin by itself and rotate about the object to acquire sufficient projection data for the reconstruction of a 3-D object. For simulation simplicity, a 64x64x64 cube is used for the image array, and a uniform sphere centered in the 64x64x64 cube is taken as the object. To compare with the planar projection system, the regular line-projection system is simulated using slice-by-slice approach as well. A CG-MR algorithm [1] and a ML-EM algorithm are applied to reconstruct the images for both the planar projection system and the line projection system. The signal-to-noise ratios (SNR) are calculated within the center slice of the object except the very edge of the reconstructed images. By applying the half-bin-size technique [2], the SNRs of the two systems converge after a certain number of iterations (Fig.1). The converged SNRs of the two systems are compared in terms of the object size. Noise analysis based upon the CG algorithm shows:

$$\frac{SNR_{planar}}{SNR_{line}} \propto \sqrt{\frac{N_{planar}}{N_{line}}} \cdot \frac{1}{D} \propto \sqrt{\frac{F}{D^2}} \cdot \frac{1}{D} \propto \frac{F}{D}$$

Results & Conclusions
For a given geometric efficiency parameter F, the performance of the planar-integral projection method (PPM) over the performance of the line-integral projection method (LPM) is proportional to the reciprocal of the diameter of the diameter of the object. For a small object, PPM has a better performance. For objects in large size, LPM outperforms (Fig.2).

Fig.1 Noise convergence properties of the half-bin-size technique (F represents the factor by which the geometric efficiency is increased in the case of planar projections with respect to that for line projections, \(N\) is the number of counts, and \(D\) is the diameter.)

Fig.2 Noise propagation comparison between the planar projection method and the line projection method (SNRd/SNRd) using a CG-MR algorithm (left) and a ML-EM algorithm (right).

Reference
Dynamic Cardiac SPECT using a DyRoSH SPECT Camera
Rajendra Maddula, Rolf Clackdoyle, John Roberts, Ed Di Bella

INTRODUCTION
Dynamic cardiac SPECT is typically performed on a conventional three-headed system with the detectors moving around the patient. Mechanical constraints of the moving detectors limit the maximum rotation speed to 120 degrees (full tomographic scans) in 10 seconds. In order to rotate the detectors faster the detectors of the conventional SPECT scanner are made to rotate in a circular path, which results in increase of detector distance from the patient. The 10 second sampling rate may not be sufficient to accurately track the time-varying activities in blood and tissue regions and the large detector distance may introduce bias in estimating kinetic parameters.

We are investigating a stationary SPECT camera called DyRoSH (Dynamic Rotating Slant Hole) Camera. This camera consists of three stationary detectors equipped with rotating slant hole (RSH) collimators. With this camera full tomographic images can be produced every 2 s and detectors can be placed much closer to the heart (since detectors are stationary) for better spatial resolution.

In our simulation study we examined the effects of improved temporal resolution (from conventional 10s to 2s) and spatial resolution (due to the detectors being closer to the patient) of DyRoSH camera in dynamic cardiac imaging by comparing to the dynamic imaging performance of a conventional SPECT scanner.

SIMULATIONS
A two compartmental model describing exchange of tracer between blood pool and myocardium in heart was formed [1]. Two DyRoSH SPECT scanners one with collimator rotation of 30 rpm (say DyRoSH scanner), the other with collimator rotation of 6rpm (say slow DyRoSH scanner) and two conventional 3-headed SPECT scanners, one with a 120° rotation every 10 seconds (say conventional SPECT scanner), the other with a 120° rotation every 2 seconds (say fast conventional SPECT scanner) were simulated using software written in IDL. The DyRoSH scanner and fast conventional SPECT scanners produce dynamic images every 2 s whereas conventional SPECT scanner and slow DyRoSH scanner produce dynamic images every 10 s. The fast conventional SPECT scanner is a hypothetical scanner simulated for comparison purposes which is impractical to produce. Fifty noise realization experiments were performed for each of the four scanners to estimate kinetic parameters of myocardial perfusion. The detectors of conventional SPECT scanners were made to rotate in a circular path of 34cm radius from the center of the heart. The average distance of the 3 stationary DyRoSH detectors to the heart was 21 cm.

RESULTS
The time activity curves obtained from region of interests of dynamic image reconstructions of the four scanners were passed to RFIT [2] to estimate $k_{1}$ (washin parameter) and $k_{2}$ (washout parameter) for the four scanner simulations. From 50 noise realization experiments performed for each the four scanners, a table of estimated washin and washout parameters was obtained. Bias and variance were calculated (see fig. 1) from these data.

CONCLUSIONS
Improving the temporal resolution for SPECT scanner resulted in reduction of both bias and variance in estimating the kinetic parameters. The conventional SPECT scanner showed higher bias and variance in estimating kinetic parameters compared to DyRoSH scanner presumably due to the poorer spatial resolution caused by the relatively large detector distance.

Improving the temporal resolution for SPECT scanner (from 10 s to 2 s) in dynamic imaging resulted in reduction of variance in estimating kinetic parameters but at the cost of increased bias. This 2 s temporal resolution might be too fast to get good estimates (due to lack of sufficient counts). Instead DyRoSH camera can be made to revolve at lower rpms (to get an optimum acquisition period between 2 s and 10 s) to get estimates of kinetic parameters with least bias.

REFERENCES
Cone-beam reconstruction using the backprojection of locally-filtered projections

Jed D. Pack, Frédéric Noo, Rolf Clackdoyle

Cone-beam tomography has applications in medical and industrial imaging and has taken on increased commercial appeal over the past few years due to innovations in detector technology. We introduce a flexible new solution to the cone-beam reconstruction problem. The inversion formulas employed by this methodology are based on first backprojecting a simple derivative in the projection space and then applying a Hilbert transform inversion in the image space. The local nature of the projection space filtering distinguishes this approach from conventional filtered-backprojection (FBP) methods. This characteristic together with a degree of flexibility in choosing the direction of the Hilbert transform used for inversion offers two important features for the design of data acquisition geometries and reconstruction algorithms. First, the size of the detector necessary to acquire sufficient data for accurate reconstruction of a given region is often smaller than that required by previously documented approaches. In other words, more data truncation is allowed. Second, redundant data can be incorporated for the purpose of noise reduction.

The validity of the inversion formulas along with the application of these two properties are illustrated with reconstructions from computer simulated data (see figures below). In particular, in the helical cone beam geometry, it is shown that intermittent transaxial truncation has no effect on the reconstruction in a central region which means that wider patients can be accommodated on existing scanners, and more importantly that radiation exposure can be reduced for region of interest imaging. We have also found that at maximum pitch the data outside the Tam-Danielsson window can be used to reduce image noise and thereby improve dose utilization. Furthermore, the degree of axial truncation tolerated by our approach for saddle trajectories is larger than that of previous methods.

Figures Top left: the saddle trajectory is shown along with three sample surfaces on which reconstruction can be achieved. Bottom left: reconstructions without (left) and with (right) data noise. Right: the six images shown here are 1) the original Popeye phantom; 2) a reconstruction obtained by naively applying the algorithm of Katsevich to truncated helical data; 3) a reconstruction of the same truncated data using our two-step Hilbert method; 4) a reconstruction from non-truncated data using the algorithm of Katsevich; 5) a reconstruction of noisy truncated data using our two-step Hilbert method; 6) a reconstruction from noisy non-truncated data using the algorithm of Katsevich.
Stabilizing an iterative algorithm by using small detector pixels
DoSik Hwang and Larry Zeng

Introduction: In SPECT iterative reconstruction methods, such as the ML-EM (Maximum Likelihood Expectation Maximization) algorithm, the noise propagation from the projection measurements into the reconstructed image has been a difficult problem to control as the algorithm iterates. In this paper, we show that the noise amplification can be reduced by using a detector whose bin size is smaller than the image pixel size without applying any regularization methods or changing any other factors. We compare different detector system characteristics using SVD (Singular Value Decomposition) analysis and show the noise properties in each detector system through physical phantom studies. The ML-EM algorithm when used in conjunction with a smaller detector bin size has better convergent properties, reduces noise amplification, and produces better image quality.

Method: We measure the projection data with the conventional detector and with the proposed detector which has smaller bins as shown in Fig. 1. The ML-EM was used to reconstruct images from each detector measurements. SVD analysis was performed on each detector system matrix.

Results: The singular values of each system matrix are shown in Fig.2. Fig.2 suggests that the reconstruction system of HBS is much better conditioned than that of SBS. However, there is little difference between HBS, QBS, and EBS.

Fig.3 shows the reconstructed images of the Jaszczak phantom at the 5,000th iteration and the noise properties of SBS and HBS.

SBS (a) looks much noisier than HBS (b). The third small sphere (in the right lower part of the image) is hardly recognizable in SBS, due to the amplified noise around it, while it is recognizable in HBS. (c) and (d) also show that the image reconstructed from SBS looks noisier than the image from HBS; rods in the lower part are hardly resolvable in the image from SBS, while in the image from HBS more rods can be resolved. (e) shows the noise index for SBS and HBS (solid line) over the uniform activity area. After 500 iterations, the noise in HBS doest not increase, remaining constant up to 5,000 iterations. By contrast, the noise in SBS keeps increasing throughout all iterations.

Conclusions: We have shown that an iteratively reconstructed image can be improved by using a smaller detector bin size during data acquisition. Image stability and noise reduction are significantly improved with a bin size reduction to only half of the image pixel size.
Computer simulation results of 3 – slit Solstice imaging

by
Rajesh Venkataraman
&
Larry Zeng

Abstract

A multi – slit collimator is designed for imaging of small animal Single Photon Emission Computed Tomography (SPECT). The slits increase the number of incident photons on the detector, improving the SNR. This increase in SNR is over the loss of resolution of the image. To improve the spatial resolution of the image, a semiconductor detector (like CdZnTe) is used. These detectors also provide excellent energy resolution. Cost is a major factor in limiting the size of the detector as a strip detector. This system obtains convergent planar integrals of a radioactive distribution. Projection data is collected by a step by step rotation of the collimator – detector system around the image along with the rotation of the system at each step around its central axis. The former rotation is referred to as SPECT rotation, while the latter as SPIN rotation. The preliminary phantom studies show a sub millimeter spatial resolution in the reconstructed image. The phantoms are spheres with varying density, center and radius. Data is generated by rotation of the phantom around the collimator – detector system. Rotation is done in both the SPECT and SPIN direction and at each step the collimator face sees the phantom. The data obtained from such a system are weighted planar integrals with the weights being cos(alpha)/r. The code for the data generation of this phantom is written in C programming language. Reconstruction of the image is done iteratively as these methods are able to model the noise better. Residual minimization methods like the conjugate gradient are used to reconstruct data. These algorithms work for images with local tomography property. This property is found only in planar integral data. Local tomography is obtained when the entire object is not measured and the projection data are truncated due to the limited detector size. The advantage of using the conjugate gradient method is the improvement in the speed of convergence in comparison with the standard iterative reconstruction methods like ML – EM or OS – EM. An efficient projector – backprojector pair for the imaging system is developed using the warping technique. At each projection angle the image is warped to convert the convergent planes to parallel planes so that the computational time is reduced while calculating the projections. Similarly at each backprojection angle the image is unwarped to the convergent planes to obtain the original image back. The reconstruction code for this projector – backprojector pair is written in matlab programming language.
Analytical Fan-Beam and Cone-Beam Reconstruction Algorithms with Uniform Attenuation Correction

Qiulin Tang1, Gengsheng L. Zeng2 and Grant T. Gullberg3

I. Introduction

There exist many analytical parallel-beam reconstruction algorithms that correct for uniform attenuation [1]. In this paper we consider the imaging geometry where the pinhole collimator rotates in a circle around the object. To extend analytical algorithms for the parallel-beam geometry to the cone-beam geometry, we adapt the Feldkamp’s approach [3], where at each focal point position and for every projection data point off the orbit plane, a virtual tilted image plane is used to derive the reconstruction algorithm, using a fan-beam filtered backprojection algorithm.

Some research work has been published in extending the results for uniform attenuator from the parallel-beam geometry to fan-beam geometry [4][5]. The current analytical fan-beam algorithms with attenuation correction either are inefficient or require the process of rebinning the fan-beam data into the parallel-beam data. The rebinning performed either in the spatial domain or in the frequency domain is not suitable for our cone-beam algorithm development, because the rebinned parallel-beam data are not available in the virtual tilted image plane any more. Therefore, we need to develop an efficient analytical fan-beam algorithm that compensates for uniform attenuation and does not involve any data rebinning. This fan-beam algorithm can be extended to the cone-beam imaging geometry.

II. Fan-Beam Algorithm

The well-known central-slice theorem relates the 1D Fourier transform of the parallel-beam unattenuated Radon transform to the 2D Fourier transform of the object.

First, we establish a generalized central-slice theorem that relates the 1D Fourier transform of $\rho(t)$, which is an arbitrary function of $t$ and angle $\theta$, to the 2D Fourier transform of the backprojection $b(x)$ defined as . Let the 2D Fourier transform of $b(x)$ be $B(v)$, we have

Expressing $x$ in the rotated coordinate system.

Second, we need to use the fact that the backprojected image with the parallel-beam data and the backprojected image with the fan-beam data are identical, up to a scaling factor depending on whether the fan-beam detector is flat or curved. Then we use the parallel-beam algorithm presented in [2] to reconstruct the image.

III. Cone-Beam Algorithm

Since we use a circular cone-beam vertex orbit, the projection data are not sufficient to provide an exact reconstruction. We use a method similar to Feldkamp’s [3] to develop an analytical algorithm that corrects for uniform attenuation. The essential principle is that the backprojection must be correct, meaning that the backprojection must follow the same rays the data are projected. Our cone-beam algorithm is almost the same as the fan-beam algorithm presented in Section II except that the backprojection is a cone-beam backprojection, and performed in the slice-by-slice manner.

V. References


Rotating Slat Geometry Time Detection Optimization in SPECT

Rodney Earl

This research investigates novel approaches to three dimensional image reconstruction and fidelity in Single Photon Emission Computed Tomography (SPECT), specifically using the Solstice machine developed by Phillips. SPECT imaging relies on the intravenous injection of a radionuclide or isotope in a patient resulting in nuclear decay and gamma-ray photon emission. This research explores the differences in the traditional Anger Camera detection system for gamma-ray collection and a semiconductor detection method using a Cadmium-Zinc-Tellurium crystal, and the advantages of each. This research also seeks to optimize the Signal to Noise Ratio (SNR) of the novel rotating slat geometry technique employed by the Solstice machine to generate reconstructed multi-dimensional images, and more specifically uses the Simplex minimization algorithm to find the best-fit solution to the Time array magnitude for each spin of the single head slat detection system of the Solstice machine. Phantom images are both generated and reconstructed in a computer simulation, with all possible variables tested individually as to the effect each has on the system as a whole. Also, multiple variances of the Simplex implementation were tested in this project to ensure a universal minimum was located for the Time-Array variance output result.