Utah Center for Advanced Imaging Research

15th Annual Symposium
2003

Prospector Square Lodge and Conference Center
September 5th and 6th
15th Annual UCAIR Symposium

Where?
The Symposium will be held in conference rooms Coalition 1 and 2 at Prospector Square Lodge and Conference Center, 2200 Sidewinder Drive, Park City UT 84060.

(435) 655 8363 (800) 239 6144 FAX (435) 655 9164

When?
Proceedings will begin at 8 a.m. on Friday September 5th and continue until 12 p.m. Saturday September 6th

Who?
The Utah Center for Advanced Imaging Research (UCAIR) is a division of the Department of Radiology at the University of Utah.

Director, Dennis L. Parker, Ph.D.
(801) 581 8654 FAX (801) 585 3592 parker@doug.med.utah.edu

Symposium Organizers are:

Anne Parker
(801) 581 8654 FAX(801) 585 3592 anne.parker@hsc.utah.edu

Roy Rowley
(801) 581 6088 FAX(801) 585 3592 rrowley@ucair.med.utah.edu
Lodging

Rooms, some shared, have been reserved for the following attendees:

Anne Haroldsen
Arvi Cheryauka
Brad Stoker
Brian Saam
Dan Kadrmas
Dennis Parker
Ed Dibella
Eun-Kee Jeong
Isaac Blatter
Jed Pack
John King
John Roberts
June Taylor
Junyu Guo
Ling Zhang
Michael Funke
Prashanthi Vemuri
Rock Hadley
Roy Rowley
Sathya Vijayakumar
Scott Miller
Seong-Eun Kim
Sung Moon

Check-in time:  4:00 p.m.
Check-out time:  10:00 a.m.

Continental breakfast  8:00 a.m.
September 5th and 6th

Two passes to the Silver Mountain Sports Club and Spa (at Prospector Square) are available per room
FRIDAY SEPTEMBER 5TH

8-9:00 CONTINENTAL BREAKFAST

8:30 UCAIR: Symposium Introduction. Greg Katzman, Vice Director of UCAIR

8:35 Welcome and State of the Department/Research Statement. Steve Stevens, Chairman of Radiology

8:45 I. MRI Measurement Techniques. Chairs: Tom Rust and Jed Pack
8:45 Temporal Sampling of MRI Myocardial Perfusion Studies: Effects with Three Analysis Methods. Ed DiBella
8:57 Investigative Study of Arterial Input Functions in Myocardial Perfusion Imaging. Sathya Vijayakumar
9:09 Flow Quantification with 3D Phase-Contrast MR Angiography. Ling Zhang
9:33 T1 Measurement of Blood. Junyu Guo
9:45 Quadruple Contrast Black Blood Imaging. Seong-Eun Kim Choi
9:57 Diffusion Tensor MRI of Brain at 1.5 T and 3.0 T. Eun Kee Jeong
10:10 BREAK

10:40 II. Post Processing and Graphics. Chairs: Rock Hadley and Sungman
10:40 A Monte Carlo Technique for Co-Registration of 3D MRA images. Craig Goodrich
10:52 Curvature-based Volume Rendering of Bone Structure from Computed Tomography. Gordon Kindleman
11:04 A Method for Tumor Volume Measurements and Classification. Isaac Blatter
11:16 Advances in Centerline Extraction. John Roberts
11:28 Accurate Modelling of the Heart Using Quadrics and Biquadrics for Efficient Cardiac CT. Sungman Moon
11:40 Statistical Based Methods for Repeatable Aneurysm Measurements. Prashanthi Vemuri
12:00 LUNCH: Catered lunch at The Grub Steak Miner Room (across the street from the Lodge)

14:00 III. Novel Image Reconstruction Techniques. Chairs: Ling Zhang and Prashanthi Vemuri
14:00 Investigation of a Saddle Trajectory for Cardiac CT Imaging in a Cone Beam Geometry. Jed Pack
14:12 Image Reconstruction via Inner Product. Larry Zeng
14:12 Iterative Reconstruction of Slit Collimator Data. Rajesh Venkataraman
14:24 Helical Cone Beam Reconstruction Using John's Equation. Frederic Noo
14:36 CT-Based Partial Volume Compensation for PET/CT Imaging. Zhiqiang Hu
14:48 SPECT with Two Second Time Resolution? Rolf Clackdoyle
15:00 BREAK
15:30 IV. PET. Chairs: Sathya Vijayakumar and John Roberts
15:30 Development of a Radiosynthesis Module for 11C-acetate. Jon King
15:42 Dual Tracer PET Imaging in Dogs with Prostate Cancer. Tom Rust
15:54 Fully-3D PET Reconstruction from Raw LOR Histograms. Dan Kadras
16:06 Estimation of Kinetic Parameters in FDG Brain Dynamic PET Without a Measured Input Function. Dmitri Riabkov

16:20 V. MRI / MEG
16:20 Patient Repositioning and Repeatability Study for Carotid Artery Imaging. Emilee Shaw
16:32 A Coil Coupling Model For Optimization Algorithms. J. Rock Hadley
16:44 Improved Gradient Performance, Increased FOV and Reduced Nerve Stimulation - A Really Good Idea. Dennis L. Parker
16:52 Magnetoencephalography Spikes Undetected by Electroencephalogram. Michael Funke

18:00 PICNIC IN THE PARK (South End Park, south of the Miners Hospital at 1354 Park Ave.)

21:00 STAR PARTY: Observations of Mars (weather permitting).

SATURDAY SEPTEMBER 6TH

7:30 CONTINENTAL BREAKFAST

8:30 VI. Biological Imaging Techniques. Chairs: Junyu Guo and Zheng-Rong Lu
8:30 Skeletal Imaging and Pharmaceutical Targeting: Initial Studies Using MRI Imaging In Rats. Scott Miller
8:42 A Novel Biodegradable Macromolecular Blood Pool MRI Contrast Agent. Zheng-Rong Lu
8:54 Grant Proposals I Have Worked On This Year. June Taylor
9:06 Microscopic Computed Tomography at the University of Utah has Utility in Both Adult and Embryonic Biological Investigation. Lance Burrell, Richard Normann, Gordon Kindlmann, James Bigler, Nick Green, Richard Coffey, Arun Badi, Norman Hu, Mario Capecchi, Charles Keller.
9:30 BREAK

10:00 VII. Functional MRI Studies. Chairs: Jim Lee and Zhiqiang Hu
10:00 The Amygdala and Fusiform Face Area in Autism. Jim Lee
10:12 Investigation into Spatial Characteristics in Pattern Separation Using fMRI. K.M. Doing-Harris
10:24 Neural Representations of Graspable Objects. Sarah Creem-Regehr
10:36 Can Imagined Motor Practice Change Cortical Representations? S. Browd

10:50 VIII. Clinical Applications. Chairs: Jim Lee and Zhiqiang Hu
11:02 MRI of the Cervical Carotid. Chun Yuan
11:14 Hyperpolarized Gas MRI: Capabilities and Potential Directions. Brian Saam

11:41 Closing remarks and awards. Dennis Parker, UCAIR Director
Abstracts

Temporal sampling of MRI Myocardial perfusion studies: Effects with three Analysis Methods
EVR DiBella, H Bal, S Vijayakumar, CJ McGann, H Buswell

Introduction: A time-series of images can be acquired to follow the time-varying distribution of an injected agent using, for example, dynamic SPECT, dynamic PET or dynamic MRI. One way of analyzing these images is to fit the time-changing distributions to a mathematical model. The model parameters then may reflect physiological quantities such as blood flow or metabolism, depending on the injected agent. While it is well established from sampling theory how rapidly time-series data must be measured in order to accurately represent temporal changes, standard sampling theory assumes no knowledge or model of the temporal data. Here we investigate the effects of different temporal samplings for model-based analysis of contrast MRI measurement of myocardial perfusion.

Methods: Dynamic acquisitions were performed with a fast gradient echo, multi-shot echo planar sequence on a GE 1.5T Signa. TR=7ms, TE effective=1.7ms, 132x96 acquisition matrix. One frame per heartbeat was acquired. Blood pool and tissue regions were manually selected and processed to obtain gadolinium concentration curves (Fig. 1). One set of curves was used to assist in obtaining realistic parameters for the XSIM model. Parameters from [1] were used along with fits to this measured dataset to create the XSIM model which was then used as the simulation gold standard. Simulated and real curves were downsampled to create four different versions: the original, sampled only every second point, every third, and every fourth. An integer “jitter” parameter was used to change the timepoint of the starting sample; results using the starting sample that produced the greatest change in the fits (the worst case) is reported. The arterial input function was not downsampled. Three means of obtaining flow-related parameters were employed. i) Upslope was calculated using a 3 point fit. ii) A two compartment model with 3 parameters ($k_{trans}$, $v_o$, $V_p$) was used to fit the curves. iii) The JW model with an axial concentration gradient in the capillaries [2] and 4 parameters ($E$, $F$, $v_o$, and $T_c$) was also used. As others have done, fitting with the JW model was repeated with different starting estimates to overcome problems with local minima.

Results: Fig. 1 shows a real data case with the fits from the two models. Fig. 2 shows an aggregate result. The results imply that:

- Upslope calculation usually most affected by slower sampling rates
- JW model not quite as robust to slower sampling rates compared to more standard 2 compartment model
- Missing beats still a major problem (and not considered here)
- MPR ratio is less sensitive to sampling rate changes but trends are consistent

Parts of this work were presented in [3].

References
Investigative Study of Arterial Input Functions in Myocardial Perfusion Imaging
Sathya Vijayakumar, EVR Di Bella

Introduction: Arterial Input Functions (AIFs) are used for the determination of the kinetic parameters when fitting the tissue contrast time curves that determine cardiac perfusion. Kinetic parameters are important to get a quantitative measure of how different the tissue uptake is for normal and diseased tissues. The input function is expressed either as a function of the concentration of contrast agent present in the left ventricle or can be obtained through arterial blood sampling. The former presents a non-invasive technique unlike the latter that requires the use of catheterization.

For perfusion MRI, we use the non-invasive method of obtaining the AIF. The use of fast sequences like EPI, multi-shot EPI (fgrst) and FLASH is required, but these have susceptibility artifacts making the accurate measurement of AIF very difficult. It is thus our motive to study the variability of the AIF with respect to the region of interest (ROI) chosen, i.e. where it is chosen (basal or apex slice) and how it is chosen (manually or clustering techniques). The effect of sampling (i.e. obtaining the cardiac images every beat or every other beat) on the variability of the kinetic parameters is also of interest. We intend to ultimately identify a way to measure the AIF that gives the least amount of bias and variance in the kinetic parameters estimated.

Methods: First, the left ventricular region was manually divided into different regions to see how different the AIF obtained from each region were. Here, we assume the signal intensity is proportional to the concentration of contrast agent present and make use of the following relationship [1] to determine the input function:

\[ R_1(t) - R_1(0) = \beta C_a(t) \]  

\[ R_1(0) \text{ is the relaxation rate before the injection of contrast agent Gd-DTTPA.} \]

\[ C_a = \text{Arterial Gd concentration obtained from the image.} \]

\[ R_1(t) = \frac{1}{T_1} \text{ is calculated for every image from the signal obtained as follows:} \]

\[ R_1 = -\log\left(\frac{S_{\max} - S_{\min}}{S_{\diff}}\right) / \text{exp\_coeff} \]

\[ S_{\diff} = S_{\max} - S_{\min} \]

\[ S_{\max} \text{ and } S_{\min} = \text{Maximum and minimum signal intensity obtained from an experimental set of Gd vials.} \]

\[ S_{\text{bid}} = \text{Signal intensity of the blood curve obtained.} \]

\[ \text{exp\_coeff = value determined from a set of experimental Gd vials using the literature values of } R_1. \]

The same was done for all the slices (basal and apex) on a particular data set for rest and stress conditions.

Results and Conclusions: The AIF from the left ventricle (LV) was obtained from five different regions within the endocardium to see how different the curves look if the ROI is chosen differently Fig. 1(a). The plain black curve depicts Region 1, which was assumed to be the “truth” for this set of data. Fig 1(b) shows the curves obtained from all the slices by averaging the values obtained from the five different ROIs that were chosen. The blue curve shows the input function obtained from the apex slice (Slice 2) and the black curve shows the input function obtained from the most basal slice (Slice 7).
It is important to mention however that “truth” for the AIF right now, is assumed to be the input function with the least deviation from the mean of the signal intensities obtained from all the five regions. Also, the R1 value being used is that obtained from an experimental set of Gd vials.

Presented above are just the preliminary results obtained. Clustering [2] using the k-means algorithm is being done to help evaluate if the AIF chosen manually can be improved in conjunction with the clustering technique and if not which is better and more accurate.

References
Flow Quantification with 3D Phase Contrast MR Angiography
Ling Zhang, Dennis L. Parker

Introduction

Blood flow quantification is of great importance in assisting clinical diagnosis. The phase contrast (PC) magnetic resonance angiography (MRA) provides a noninvasive technique for measuring blood flow [1]. Lots of research has been done in flow quantification with 2D PC images [1-3]. 3D PC images seem to be dis-favored because of their need for long scan times [4]. However, the rapid developing imaging techniques have shown signs of great reduction of the scan time [5,6]. Also, 3D PC images have the advantage of providing flow information for different places in the 3D volume. Thus, flow can be traced along the interested vessel and be compared for different vessels.

In this study, the blood flow rate along part of the left and right middle cerebral arteries (MCA) were computed. In order to get more accurate flow, different methods of determining the vessel cross section area were used.

Methods

The flow rate is defined as \( F = \int \hat{n} \cdot dA \), where \( \hat{n} = \hat{v}_x \hat{x} + \hat{v}_y \hat{y} + \hat{v}_z \hat{z} \) is the velocity vector on the selected vessel cross section area. There are three ways of manipulating this integral, which leads to three ways of calculating the flow.

1. Assume the normal vector of the cross section is \( \hat{n} \), then \( dA = dA \hat{n} \), and the flow rate can be expressed as \( F = \int (\hat{n} \cdot \hat{n}) dA = \hat{n} \cdot \int dA \). Now, define a flow vector \( \hat{f} = \int \hat{n} dA = \hat{n} \int v_x dA + \hat{n} \int v_y dA + \hat{n} \int v_z dA \), then the flow rate can be calculated using the equation \( F = \hat{n} \cdot \hat{f} = n_x f_x + n_y f_y + n_z f_z \).

2. Let \( dA_x, dA_y, dA_z \) be the area increment in yz, xz and xy plane respectively, then the flow rate is \( F = \int v_x dA_x = \int v_y dA_y = \int v_z dA_z \). In order to avoid the problem of poor SNR for small velocities, we chose to compute the flow in one of the three orthogonal planes that is nearest to the actual vessel cross section.

3. If the velocity of each point on the vessel cross section is known, then \( F = \int v dA \) gives the flow through the cross section directly.

The calculation basically has four steps. First, we segment out the interested vessel and extract its centerline. Then, we choose part of the centerline and fit it into a curve described by Chebyshev polynomials. Next, we trace down the fitted curve, find the cross section for each traced point on the curve, and calculate the intensity and velocity distribution on the cross section by interpolation. Finally, different algorithms are tried to find an appropriate mask for the region of integration and then the flow is calculated using one of the three ways listed above.

Results & Conclusions

The calculated flow fluctuates greatly down the vessel as can been seen from the two figures below, which are given as an example. The mean flow rate is around 2000 (mm³/s) for the left MCA and 2100 (mm³/s) for the right MCA, if we use magnitude images to find the mask. But this may vary a lot if the mask is found on the velocity images directly. Also it turned out that method 3 is not a good way to calculate the flow since the speed on the cross section is severely distorted. The inaccurate result seems to indicate the inherent inaccuracy of the 3D PC image data, which is very susceptible to motion artifacts and other kinds of common imaging artifacts. So, accurate measurement of flow using 3D PC images calls for improvement of this imaging technique for more accurate velocity data.

References

Time efficient dual-Venc method for blood velocity measurements.

Eugene G. Kholmovski and Dennis L. Parker
UCAIR, Department of Radiology, University of Utah

I. INTRODUCTION
Magnetic resonance angiography (MRA) can be used not only to get a morphological description of the blood circulation system but also to obtain additional diagnostic information such as blood velocity distribution. To get this velocity information, a phase contrast (PC) MRA technique can be used. There are several trade-offs in the selection of parameters for PC velocity measurements. The accuracy of the velocity measurements is improved when strong velocity encoding (small Venc) is used. However, phase aliasing can corrupt the measurement because a wide range of velocities may exist in the region of imaging. Thus, the Venc must be large enough to prevent aliasing yet as small as possible to maximize measurement accuracy. In many cases it is impossible to satisfy these requirements and simultaneously get high precision velocity measurements. In such situations, it is useful to acquire sets of images with 2 Vencs (low and high) [1]. Using 2 encoding velocities for each of 3 directions, plus a reference scan yields 7 complete image sets making the scan time for high-resolution 3D velocity imaging extremely long. We have developed a novel dual-Venc PC MRA method with an improved time efficiency.

II. METHODS
The proposed dual-Venc method is described in detail for the 1D velocity measurements case. The generalization to 2D or 3D cases is quite obvious.

Data Acquisition Scheme
Two images of the same slice are acquired in an interleaved mode. The first image is a reference or baseline image:

\[ I_1(r) = I_0(r, v = 0) + I_0(r, v \neq 0) \]

where \( v \) is a blood velocity. \( I_0(r, v = 0) \) are the image areas corresponding to the stationary tissues, and \( I_0(r, v \neq 0) \) are the image areas corresponding to the flowing blood.

The second image is acquired by applying velocity encoding gradient waveforms corresponding to two different Vencs: Venc1 and Venc2. Encoding with two Vencs is realized by the changing velocity encoding gradient amplitude. Venc1 is used for odd k-space line acquisition and Venc2 is applied during even k-space line acquisition. The resulting image is given by

\[ I_2(r) = I_0(r, v = 0) + I_A(r, v \neq 0) + I_B(r, v \neq 0) \]

where \( I_A(r, v \neq 0) = I_0(r, v \neq 0) \cos \left( \frac{\phi_1 - \phi_2}{2} \right) \exp \left( i \frac{\phi_1 + \phi_2}{2} \right) \]

\[ I_B(r, v \neq 0) = i I_0(r, v \neq 0) \sin \left( \frac{\phi_1 - \phi_2}{2} \right) \exp \left( i \frac{\phi_1 + \phi_2}{2} \right) \]

where FOV is field of view in the phase-encoding direction. In the case of the flow with the constant velocity, the phases \( \phi_1 \) and \( \phi_2 \) are proportional to tissue velocity and inversely proportional to Venc1 and Venc2, respectively. The image \( I_2(r) \) consists of original (\( I_0(r, v = 0) \) and \( I_A(r, v \neq 0) \) ) and aliased (\( I_B(r, v \neq 0) \)) components.

Reconstruction Algorithm
1. Two additional images \( I_f(r) \) and \( I_d(r) \) are created from \( I_f(r) \) and \( I_d(r) \). Image 3 (4) is reconstructed from k-space data constructed in the following way: even (odd) k-space lines from the first image k-space data and odd (even) k-space lines from the second image k-space data.
2. Complex differences between \( I_f(r) \) (i=2,3,4) and \( I_f(r) \) are calculated: \( \Delta I_{I1} = I_f(r) - I_1(r) \).
3. Image \( I_2(r) \) is dealised using the known relationships between the magnitudes of the complex differences. The resulting images are the following:

\[ I_{2A}(r) = I_0(r, v = 0) + I_A(r, v \neq 0) \]

\[ I_{2B}(r) = I_0(r, v \neq 0) \]

4. Images \( I_{2A}(r) \) and \( I_{2B}(r) \) are combined to create two new images analogous to the completely sampled Venc1 and Venc2 encoded images:

\[ I_{V1}(r) = I_0(r, v = 0) + I_0(r, v \neq 0)e^{i\phi_1} \]

\[ I_{V2}(r) = I_0(r, v = 0) + I_0(r, v \neq 0)e^{i\phi_2} \]

5. Phase difference images are calculated as usual

\[ \phi_1 = PHASE \left( \frac{I_{V1}(r)}{I_1(r)} \right) \text{ where } \phi_1 \in [-\pi, \pi] \]

\[ \phi_2 = PHASE \left( \frac{I_{V2}(r)}{I_1(r)} \right) \text{ where } \phi_2 \in [-\pi, \pi] \]

III. RESULTS
Phase contrast images of phantom and healthy volunteer were acquired on a 1.5T Signa scanner (GEMS, Milwaukee, WI) using the proposed technique. Figure 1 and 2 demonstrate the results of reconstruction from dual-Venc data.

![Figure 1](image1.png)

![Figure 2](image2.png)

Figure 1. MIP of PC image volumes acquired by (a) the standard one-Venc and (b-d) the proposed dual-Venc techniques. b calculated using \( I_2(r) \) shows significant aliasing. Images c and d calculated using \( I_{2A}(r) \) and \( I_{2B}(r) \) demonstrate close to perfect dealising.

Figure 2. Phase difference images from dual-Venc data sets. Images with small Venc (a and c) show phase (velocity) aliasing for vessels with high blood velocity. Images with larger Venc (b and d) have no aliasing but small vessels are less visible than in small Venc images.

IV. DISCUSSION AND CONCLUSION
A method to improve time efficiency of double-Venc PC magnetic resonance velocity imaging has been developed. The proposed method requires four velocity encoded measurements rather than seven measurements needed for the standard dual-Venc technique to reconstruct 3D velocity map.

V. REFERENCES
\textbf{T_1 Measurement of Blood}


\textbf{Introduction:} The spin-lattice relaxation coefficient $T_1$ is one of the most important parameters in MRI. $T_1$ is a noninvasive temperature indicator [1] and it is necessary for accurate perfusion measurements. Usually, $T_1$ of static tissue is relatively easy to measure. But $T_1$ of blood is harder to measure because the blood flow is pulsatile flow. In this project, we try to measure the $T_1$ of blood.

\textbf{Method:} There are two methods by which $T_1$ can be measured. One is the nulling point method, the other one is the curve fitting method. In this project, initially, the curve fitting method is used. By fitting data according to the following equation (1), we can calculate $T_1$.

$$I(\tau) = |A - Be^{-\tau/T_1}|$$

where $A$ and $B$ are constants and $\tau$ is time after the inversion pulse.

<table>
<thead>
<tr>
<th></th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>2597</td>
<td>2742</td>
<td>2656</td>
<td>2694</td>
</tr>
<tr>
<td>5</td>
<td>6</td>
<td>7</td>
<td>Mean ± std (ms)</td>
<td></td>
</tr>
<tr>
<td>2757</td>
<td>2746</td>
<td>2657</td>
<td>2693±60</td>
<td></td>
</tr>
</tbody>
</table>

Table 1: $T_1$ measurement of pulsatile flow with flow $Q = 10 ml/s$.

Single shot EPI is used to acquire image because the blood is flowing. Usually ten images at different time instants after the inversion pulse are acquired to fit equation (1) and get $T_1$. To make sure that there is enough blood inverted uniformly, a nonselective adiabatic inversion pulse is used. Since the blood flow is pulsatile, all images are acquired at the same cardiac phase by using ECG gating.

\textbf{Results:} For a static phantom, the EPI Look-Locker method was used to acquire data and after that a correction method was used to calculate the optimized $T_1$ [2]. $T_1$ of tap water ($25^\circ C$) is about 2828 ms. Table (1) show the data of pulsatile flow of tap water by the fitting method.

Later, we combined the two methods (nulling and fitting) together and got a more stable T1 (1289 ms).

\begin{figure}[h]
\centering
\includegraphics[width=0.5\textwidth]{image.jpg}
\caption{Aixal image of aorta, A for ascending aorta, B for decending aorta, C for some other part of blood}
\end{figure}

The following table shows the data for the different methods.

<table>
<thead>
<tr>
<th>T1 (ms)</th>
<th>A</th>
<th>B</th>
<th>C</th>
<th>Mean±STD</th>
</tr>
</thead>
<tbody>
<tr>
<td>Fitting</td>
<td>1379</td>
<td>1878</td>
<td>1623</td>
<td>1627±250</td>
</tr>
<tr>
<td>New</td>
<td>1281</td>
<td>1274</td>
<td>1311</td>
<td>1289±20</td>
</tr>
</tbody>
</table>

Table 2: T1 of Aorta with different methods

\textbf{References}


**Quadruple Contrast Black Blood Imaging**

Seong-Eun Kim, Jeffery Nackos*, Eugene Kholmovski, K. Craig Goodrich, Eunn-Kee Jeong, Dennis L. Parker

**INTRODUCTION:** Double Inversion technique provides a good suppression of blood signal and contrast between the vessel and wall and the lumen. But using of nonselective inversion the scan should be sequential with long scan time. Parker et al demonstrated the interleaved acquisition technique to improve the imaging efficiency of double inversion BB technique, in which the proton density (PD) and T2 weighted images were acquired from two interleaved location during 2 R-R intervals. In this work, we present a quadruple contrast technique with modifying the technique of Parker et al for more imaging efficiency. In our modification extra two T1 data acquisition were performed during TI of blood suppression. This technique results in four different contrast imaging acquisition including PD and T2 weighted along with the blood suppressed double inversion preparation and two T1 images with different echo time from same interleaved location.

**METHODS:** As shown figure 1, the nonselective rectangular hard 180° is applied at every other ECG trigger followed by the selective adiabatic 180° re-inversion for slice1. After TI selected to null the blood signal, PD and T2 data are acquired from re-inversion selected slice (slice1) followed by two T1 data acquisition with echo time of 9.0ms and 80.0ms from the next location (slice7). For better imaging efficiency T1 data are acquired between the end of PD and T2 acquisition and the next inversion preparation. Four widely separated slices (slice1, slice7, slice4, slice10) are interleaved, but the TR is kept to two cardiac cycles (2RR) by acquiring every data acquisition cycle with time delay rather than the ECG trigger. During next TR the slice order has been re-arranged to acquire all four contrast images from each four interleaved location. All studies were performed on a 1.5T GE Signa CV/NVi system. The home built phased array surface coils were placed on the neck to be centered over the bifurcation. To achieve 80ms of TE for T2 imaging ETL of 12 was used with 16 cm of FOV, 2 mm thickness and 256x256 of imaging matrix.

**RESULTS:** Quadruple contrast black blood images from a human carotid artery are shown in figure 2. For the initial trail 300ms of T1 has been selected (Fig.2-A, B). However, the optimized TI can be calculated from the steady-state solution for the magnetization from Bloch equation which is dependent on TR. T1 images with a longer echo time (80ms) shows the vessel as a dark region similar to T2 due to long echo time, but the contrast between the surrounding tissues is not same as T2. Those two echo T1 images may provide the additional information on the architecture and composition of arterial wall. For more clinical test we need to investigate the information from two T1 images and optimize the imaging parameters including TE, T1 and time delay between data acquisition.

**REFERENCES**

Diffusion Tensor MRI Of Brain at 1.5 T and 3.0 T
Eun-Kee Jeong, Ph.D.

Introduction: Diffusion tensor images (DTI) have been acquired at both 1.5 T (GE Signa) and 3.0 T (Siemens Trio). In theory, signal-to-noise ratio (SNR) at 3.0 T will be increased as in equation $M_o \propto \omega_o^{75.1}$, owing to the larger equilibrium nuclear magnetization at larger field. Higher SNR at 3.0 T will be beneficial for fMRI and high-resolution imaging.

At the same time, amount of the positional shift caused by the magnetic susceptibility difference in EPI images is doubled at 3.0 T as in $\Delta \approx \chi \frac{B_o}{\Delta k_j}$, which makes DT imaging of skull base, temporal lobe, and brain tissues near the sinus space, more difficult than at 1.5 T.

The DT image acquisition at our 1.5 T has been problematic due to the mechanical vibration of the patient table, which is induced by Lorenz force exerted on the gradient coil fixture by rapid switching of the strong diffusion gradient. It is believed that there is a strong mechanical coupling between gradient coil assembly and the patient table on our 1.5 T imaging system which has an extra long bore magnet (and table). At higher magnetic field, the force will be higher as in $\Delta F = B_o \frac{dG}{dt}$.

Methods: Diffusion tensor imaging was performed on 1.5 T (GE Signa, NV/CVi, 150 T/m/sec slew rate) and 3.0 T (Siemens Trio, 200 T/m/sec slew rate). Imaging (acquisition) parameters were 128x128 matrix, 256 mm FOV for both systems, and 3.0/0.0 mm slice thickness/gap with 6 magnitude averages for 1.5 T, and 2.0/0.0 mm slice thickness/gap with 4 complex average at 3.0 T. The coverage along slice direction was about 12 cm. TR/TEs were 12500/70 msec at 1.5 T and 8000/82 msec at 3.0 T. Data acquisition times were 16 min (1.5 T) and 8 min (3.0 T) respectively. Diffusion gradient was encoded along 12 directions. At 3.0 T, two DT imaging data set were acquired using (1) transmit/receive coil and (2) 8 channel receive-only coil set from a volunteer for comparison. RGB maps of the largest principal eigenvector and the fractional anisotropy maps were obtained using homemade program in IDL (Research System Inc., Boulder, CO).

Results and Discussions: The result of DTI at 1.5 T (GE Signa) was very sensitive to the subject’s weight and how frequently diffusion gradient was applied. Images in Fig. 1 are white-matter fiber maps in RGB; R: R/L, G: A/P, B: S/I. Red colors, representing fiber running R/L direction, in most anterior and posterior parts of brain in Fig. 1 (a, b) are artifacts, probably caused by table vibration. Artifact on the DTI fiber map was worse for lighter subject, as in (a, b) of Fig. 1 than heavier subjects (c, d). At 3.0 T, larger jerky force was exerted with physical diffusion gradient applied along R/L direction than other orthogonal or oblique directions. However, the resultant tensor maps did not show any noticeable artifact, as in Fig. 1 (a, b) for low weight subject. Images in Fig. 2 are RGB fiber maps and FA map at 1.5 T, and 3.0 T.

References
A Monte Carlo Technique for Co-Registration of 3D MRA Images
Craig Goodrich and Dennis L. Parker

Synopsis: In order to determine reproducibility of MR Angiography acquisition and segmentation, MRA images must be co-registered. MR Angiograms were interpolated, segmented and a landmark visible in all data sets was used as the center of rotation. Random angles within a user-defined range are generated and used to rotate the image. A binary (1=vessel, 0=not vessel) multiplication of the 3D volumes is summed and used as the figure of merit. The process is repeated with a diminishing range of random angles until the stop criterion is met. The algorithm obtains excellent registration of 3D segmented angiograms in a reasonable time.

Methods: Five patient volunteers have been serially scanned over a 3 year period at least four times each, in order to measure reproducibility of MR Angiography acquisition and segmentation. All MR Angiograms were acquired on a 1.5T GE NV/CVi scanner with the LX 8.4 operating system using an endcap head coil and a single volume Time of Flight spoiled gradient echo (SPGR) pulse sequence with abbreviated magnetization transfer (1). During the 3 year period many pulse sequence improvements were implemented, most notably variable TE (2), so a majority of the images were acquired with a TE on the order of 4-5msec, but with variable TE the echo time was reduced to about 2.2 ms. Images were acquired with a 22 cm FOV with an imaging matrix of 512x256x64. Raw data was saved and zero-filled interpolated offline to an image matrix of 1024x768x128.

After vessel segmentation using the ZBS algorithm (3) an anatomical landmark is chosen which is visible in all MRA sets. Typically this landmark is the tip of the basilar artery, but could be any feature in the image. This landmark is used as the center of rotation for each data set. Since user choice is not reproducible (often +- 1 or 2 pixels) the region around the anatomical feature is windowed, filtered to reduce boundary discontinuities, and cross-correlated to more precisely choose the same point of the feature in all sets.

To register two MRA image sets, the algorithm requires starting values for the three angles of rotation, the initial range of angles for the search, and parameters to control number of iterations at each range, the factor for range reduction, and the stopping criteria.

The main algorithm is essentially 2 nested loops. The outer loop simply reduces the range of the 3 random angles until the stopping range is reached. The inner loop generates 3 random angles which are used to rotate the image to be registered. A binary (1=vessel, 0=not vessel) multiplication of the 3D volumes is summed and used as the figure of merit (FOM). The FOM is tested after each rotation and if it is greater than any previous FOM it is saved along with the corresponding random angles which are then used as the range center for subsequent random angles. When reasonable good angles are found, the neighborhood near the center of rotation is tested to see if the FOM can be improved by small translations. If an improvement is found, the random angle loops are revisited.

The Code is written in IDL 5.3 (Interactive Data Language, Research Systems, Inc. Boulder Co) and C and run on a SUN ultra 80 with 2G RAM and dual 450Mhz CPU.

Results: The example registration going from Figure 1 to 2 took less than 10 minutes on the SUN ultra 80. This included 180 sets of random angles, searching the neighborhood of the center of rotation for improvement in the FOM and then repeating the random angle search with the improved center of rotation.
Conclusion: This Monte-Carlo algorithm is a robust technique capable of registering 3D segmented angiograms in a reasonable time with minimal user input.

References
Curvature-based Volume Rendering of Bone Structure from Computed Tomography
Gordon Kindlmann, Kurt Albertine

Keywords: volume rendering, transfer functions, computed tomography, anatomy

Direct volume rendering of scalar fields uses a transfer function to map locally measured data properties to opacities and colors. The domain of the transfer function is typically the one-dimensional space of scalar data values. We describe the use of curvature information in multi-dimensional transfer functions, and a direct method for computing robust curvature measurements, based on an implicit formulation of curvature and convolution-based reconstruction of the field. This development facilitates the creation of highly detailed renderings of bone anatomy and surface structure, in a visual form reminiscent of hand-drawn medical illustration. We present images and video suitable for use in anatomy education, of isolated bones and of skeletal regions.

<http://www.sci.utah.edu/~gk/head/04.png>

A Method For Tumor Volume Measurements And Classification
Isaac B. Blatter, K. Craig Goodrich

The current standard for quantification of tumors and their response to therapy is inadequate. We are working on a system to automatically measure tumor volume in order to measure response to therapy. We are also attempting to classify tumors based on the tissue types present inside a tumor. This should give a more accurate determination of the status of the tumor, it’s likely future and the patient’s health. I will present current work and future plans.
Introduction: Over the last few years, our group has developed vessel segmentation techniques for extracting vascular data from magnetic resonance angiography images. In previous MIRL symposia[1,2], we presented our work in applying existing skeletonization techniques to the extraction of centerlines from the segmented vascular data. While these algorithms performed well with select datasets, their application to a large body of angiography images revealed several weaknesses. In general, the discrete nature of the problem and computational requirements posed the greatest challenges. These problems spurred the development of faster more effective algorithms for centerline extraction.

Methods: The two main advances in our centerline extraction programs have come from vectorization of the code and the application of a center-of-mass erosion algorithm. Currently, the codes are written in the IDL(tm) programming language. Vectorization of the code involved the elimination of loops and redundant calculations for a significant time savings. The center-of-mass erosion algorithm is used to extract a set of points contained within the original volume which lie along or near the true centerline. These points are then connected using the earlier centerline algorithms.

Results: The speed improvements realized in the code were tremendous. The propagation of wavefronts, part of the centerline extraction process, now requires less than a minute where once it required an hour or more. This gain in computational efficiency was partly responsible for enabling the testing of alternative algorithms to improve centerline extraction. The center-of-mass erosion algorithm improved the smoothness of the extracted centerlines while retaining their essential topology or geometric information content.

Discussion and Conclusions: With the ability now to extract centerlines for entire vascular trees, we have begun to look at applications of centerlines. These include the measurement of SNR, CNR and flow, the registration of separate vascular image sets, and the "informational" segmentation of vessels. In the latter example, we are developing the capability to distinguish right from left and anterior from posterior vasculature. Ultimately, one would like to identify bifurcations and branches of the vessels with their anatomical designations and recognize aberrations or disease. We will discuss the improvements made to the algorithms and present some of the applications.

Introduction: An accurate model of the heart is needed for realistic simulation in x-ray computed tomography. Phantoms, such as the NCAT [1] and the super-quadrics phantoms [2] are available in the literature. However, they are all voxelized and thereby unpractical for efficient CT simulations, where the number of integrals to be computed is larger than 10 billion. Moreover, these phantoms are designed for SPECT and therefore have too few details for accurate cardiac CT simulation.

Analytical phantoms built from quadrics and biquadrics are more efficient for simulation than voxelized phantoms, because the line integrals of quadrics and bi-quadrics are easily computed from analytical formulae. In this work, we show that quadrics and biquadrics can be used for accurate cardiac modeling for x-ray CT simulations.

Methods: The analytical phantom presented here is partly based on both anatomy and CT images from the Visible Human Project (VHP) [3] The shape of each anatomical feature is approximated using overlapping ellipsoids, hyperboloids, paraboloids, toroids, and/or cylinders. The location, size, and axial directions are adjusted and clipping planes are positioned to approximate the shape of a real heart. Each mathematical object is also assigned a value that corresponds to the linear attenuation coefficient of the physical object it represents.

Once all of the above parameters have been specified, a 2D voxelized version is created and compared with real CT images. This process has been repeated several times to improve consistency with VHP information (anatomy and CT images) and also information from physiology books. [4, 5]

Results: Several representations of the analytical phantom we have designed are shown in Fig.1.

References
STATISTICAL BASED APPROACH FOR ANEURYSM VOLUME MEASUREMENTS
Prashanthi Vemuri, Eugene G. Kholmovski, Dennis L. Parker.

Introduction
Changes in the aneurysm size are both theoretically as well as empirically the basis for the clinical management of aneurysms that are to be followed non-surgically. Magnetic resonance angiography (MRA) has an advantage over X-ray angiography for follow-up of aneurysms as it is non-invasive and depicts not only the lumen but also the vascular wall and the surrounding tissues which aid in detecting and monitoring changes in aneurysm morphology.

Presently, manual measurements and segmentation based volume measurements on MRA data sets have been used to follow changes in aneurysm size. But manual measurements are time consuming, highly dependent on operator qualification and preferences and the segmentation based volume measurements are critically dependent on the quality of the segmentation technique used.

In this study, we have developed a statistical based approach for reliable detection of changes in the aneurysm size.

The statistical based approach (1)
The intensity distribution of TOF-MRA image voxels can be described as a sum of the intensity distribution (PDF) of vessel(blood) signal, $PDF_v(i)$, and the intensity distribution of the background tissues (CSF, White and gray matter, air and bones), $PDF_b(i)$:

$$PDF(i) = \alpha_v PDF_v(i) + \alpha_b PDF_b(i)$$

where $i$ is the image intensity, $\alpha_v$ and $\alpha_b$ are the fractions of the image volume occupied by the vessels and the background tissues, respectively, and $\alpha_v + \alpha_b = 1$.

The signal intensity from vessels or aneurysms in TOF-MRA is dependent on a large number of parameters, such as the flow profile, vessel size and orientation, flow velocity, flip angle, TR, etc. This makes modeling of the vessel intensity distribution $PDF_v(i)$ unreliable. However, a parametric description of the intensity distribution of stationary background tissues, $PDF_b(i)$, can be readily found from the vessel free image volume and then used to extract the vessel intensity distribution.

Steps of the Algorithm
1. Region of interest selection and intensity based segmentation.
2. Construction of the background tissue PDF for the region of interest.
3. Estimation of the background tissues parametric description.
4. Identification of vessel or aneurysm intensity distribution.

Results
Five patients with aneurysms for whom surgical intervention was not immediately chosen because of clinical considerations or patient preference were scanned repeatedly, to measure the reproducibility of the MRA technique used and to test the volume measurement method.

The acquired image volumes were co-registered using the Monte Carlo based technique (2). The statistical based approach was used to estimate the aneurysm volume for each subject. Assuming that the shape of the aneurysm can be described as a sphere, we calculate the effective radius of the aneurysm, which is used as a measure of repeatability. The estimated radii for the statistical based approach on each individual exam are well within 2% variability from the mean of the entire data set for the patient (Fig. 1(b)), showing good repeatability.

Fig 1.a. MIP of the co-registered MRA data sets of a middle cerebral aneurysm. b. Aneurysm volume measurements using the statistical based approach. Various symbols are used to identify different patient studies. The horizontal lines show the averaged value of the effective radius. c. Dependence of aneurysm volume measurements on the segmentation threshold value (solid line - statistical based approach, dashed line - segmented data)

References
Investigation of a saddle trajectory for cardiac CT imaging in cone beam geometry

J. D. Pack, F. Noo, H. Kudo

I. INTRODUCTION

Recent developments in x-ray detector technology and exact reconstruction algorithms have created the means for rapid volumetric CT imaging. As a result, the prospect of producing high resolution images of the heart without significant motion artifacts has presented itself. Such a capability would significantly improve the ability to diagnose and treat heart disease—a leading cause of death in our civilization. One difficulty is finding a data acquisition geometry that provides sufficient data for reconstruction of the cardiac volume in a short time. In this paper, a saddle trajectory for the x-ray source is presented and shown to have several properties that make it attractive for cardiac CT imaging.

II. CB CT WITH A SADDLE TRAJECTORY

The saddle trajectory is illustrated in figure 1. Taking the z-axis in the head-to-toe direction of the patient, the mathematical definition for the saddle trajectory is

\[ \mathbf{a}(\lambda) = [R \cos \lambda \sin \phi(\lambda), R \sin \lambda \sin \phi(\lambda), R \cos \phi(\lambda)] \] (1)

where \( h \) and \( R \) are two given lengths, \( \lambda \) is the (angle) parameter specifying the source position on the trajectory, and \( \phi(\lambda) = \arctan \left( \frac{R}{h \cos 2\lambda} \right) \). For any given \( \lambda \), the detector array is orthogonal to the line connecting \( \mathbf{a}(\lambda) \) to the origin \( \mathbf{z} = \mathbf{0} \) (see figure 1).

The saddle data acquisition geometry presents several properties that make it attractive for cardiac CT imaging. The first of these is that it satisfies Tuy’s condition at every point in a large volume which includes the sphere of radius \( R_m = h R / \sqrt{h^2 + R^2} \) centered on \( \mathbf{z} = \mathbf{0} \). Second, the trajectory is periodic, which is useful for cardiac imaging because data over several \( 2\pi \)-rotations can be collected then subsetted based on heart motion to achieve a high temporal-resolution reconstruction. Third, the trajectory has a low condition number [1]. Fourth, the saddle trajectory is amenable to implementation on a C-arm device or diagnostic CT scanner. Fifth, exact reconstruction is possible with projections CT scanner. Fifth, exact reconstruction is possible with projections truncated as shown in figure 1. Details of the reconstruction process are unfortunately beyond the scope of this abstract. However, they are given in [2].

III. SIMULATION

Computer-simulated data of the FORBILD thorax phantom were generated for the saddle trajectory on a sphere \( (R = 57 \text{ cm}, \ h = 4.4 \text{ cm}) \). The heart in the phantom was modified from a solid sphere to a sphere with two small calcifications (bright spots) and two cavities. The results are displayed in figure 2. The quality of the reconstruction demonstrates that the reconstruction formula performs well in the region where Tuy’s condition is satisfied despite axial truncation.

IV. CONCLUSIONS

CB reconstruction with a saddle source trajectory is currently under investigation. At this point, it has been shown that accurate FBP reconstruction using that trajectory is possible with axially truncated data. Results from simulated data were given to demonstrate the accuracy of the reconstruction formula. The presented results are believed to be relevant for cardiac CT imaging. Several aspects of the reconstruction, including efficiency, noise propagation and sensitivity to motion are the subject of further investigation.

REFERENCES

In this abstract we propose an image reconstruction algorithm which consists of two steps:

(i) performing discrete Fourier transform of the projection data at each detector location, and

(ii) calculating an inner product of the Fourier coefficients with a pre-calculated vector.

The main advantages of this algorithm are: it works for any two-dimensional imaging geometry (e.g., parallel beam, fan beam, varying focal length fan beam), and there are no interpolations of the data involved. The pre-calculated vector depends on the detector geometry and scanning trajectory.

The following is the derivation of the algorithm.

Let $p_\theta(t)$ be the Radon transform of a 2D object $f(x, y)$ and $h(t)$ be the well-known convolution kernel of the ramp-filter. Thus we have

$$f(x, y) = \frac{1}{2\pi} \int_0^{2\pi} \int_{-\infty}^\infty p_\theta(t) h(t - t_0) dt d\theta$$

where $t_0 = \hat{x} \cdot \hat{\theta} = x \cos \theta + y \sin \theta$. (2)

Now we consider a fan-beam imaging detector that measures projection data $p_\lambda(\varphi)$, where $\lambda$ is the parameter indicating the location of the detector and $\varphi$ is detection angle as illustrated in Fig. 1. For a circular scanning trajectory with a radius $R$, $\lambda$ is the rotation angle.

By changing variables:

$$t = R \sin \varphi$$

$$\theta = \lambda + \frac{\pi}{2} - \varphi$$

$$dtd\theta = R \cos \varphi d\varphi d\lambda.$$ (5)

Equation (1) becomes

$$f(x, y) = \frac{2\pi}{R} \int_0^{\frac{\pi}{2}} \int_{-\frac{\pi}{2}}^{\frac{\pi}{2}} p_\lambda(\varphi) h(\varphi_0) \cos \varphi d\varphi d\lambda.$$ (6)

where

$\varphi_0 = \hat{\psi} \cdot \hat{\theta} - \hat{x} \cdot \hat{\theta}$

Let the Fourier expansion of $p_\lambda(\varphi)$ be

$$p_\lambda(\varphi) = \sum_m p_m^\lambda e^{im\varphi}$$

then

$$f(x, y) = \frac{2\pi}{\R} \int_0^{\frac{\pi}{2}} \int_{-\frac{\pi}{2}}^{\frac{\pi}{2}} p_m^\lambda e^{im\varphi} h(\varphi_0) \cos \varphi d\varphi d\lambda.$$ (7)

Let

$$h_m^*(x, y, \lambda) = \frac{2\pi}{\R} \int_0^{\frac{\pi}{2}} e^{im\varphi} h(\varphi_0) \cos \varphi d\varphi$$

then

$$f(x, y) = \int_0^{\frac{\pi}{2}} \sum_m p_m^\lambda h_m^*(x, y, \lambda) d\lambda.$$ (10)

Here $h^*$ is the pre-calculated vector. In practice $\lambda$ takes discrete values, and Eq. (11) can be written as an inner product of two vectors.

Similar reconstruction algorithm for imaging geometry other than fan-beam can be obtained in the same way.

Figure 1. Coordinate system for the imaging geometry.
Helical cone-beam reconstruction using John’s equation
F. Noo, M. Defrise, H. Kudo
University of Utah (USA), University of Brussels (Belgium), University of Tsukuba (Japan)

I. Abstract

This work is about image reconstruction in multi-slice x-ray computed tomography (CT) with more than 16 detector rows. With more than 4 detector rows, it is well-known that the axial divergence of the beams cannot be neglected for accurate image reconstruction. Therefore, techniques that account for this divergence are required. Among suggested techniques, there is the so-called ASSR algorithm of Kachelriess et al. [1] and Larson et al. [2], which is very attractive from a computational efficiency point-of-view. This algorithm seems to perform very well for 16-row scanners. However, for future scanners, with 32 detector rows or more, the ASSR algorithm exhibits undesirable artifacts. The purpose of this work is to develop a way to add at low computational cost a correction term to the ASSR algorithm, so that image accuracy with 32 detector rows is satisfactory. We suggest using John’s equation (see [3]) to define such a correction term. We have already worked out a chunk of the mathematics and carried on some implementation. The figure below illustrates our first implementation results using the FORBILD thorax and head phantoms.

II. References


Results using a conventional CT scanner geometry with 32 detector rows. Left: ASSR reconstruction. Right: ASSR reconstruction with added correction term.
CT-Based Partial-Volume Compensation For PET/CT Imaging
Zhiqiang Hu and Dan J. Kadrmas

Objectives: Finite resolution and discretization errors contribute to partial-volume effects in PET, causing underestimated quantitation and a loss of contrast for small objects. Current multi-modality scanners provide precisely co-registered PET/CT images, coupling high resolution morphologic information with the functional PET data. The objective of this work was to develop methodology to compensate PET lesions for partial-volume effects using co-registered CT images, for lesions having well-defined boundaries on CT.

Methods: The co-registered CT images were first segmented to identify lesion boundaries and neighboring background regions. Using these data, three approaches to performing partial-volume compensation have been studied: post-reconstruction; reconstruction-based using a multi-resolution PET image; and a hybrid method in which partial-volume compensation is achieved using continued local reconstruction over the affected volume. In all cases, the PET image is up-sampled in the region-of-interest to match the CT voxel sizes, and partial-volume recovery is achieved by modeling the PET point response function under the constraint that the lesion and neighboring volumes have locally uniform PET intensity.

Results: The proposed partial-volume compensation methods have been evaluated using a series of simulation and phantom experiments where true activity levels are known exactly. For nine lesions 0.9-5.7cc distributed within the lungs, liver, and soft tissue, activity concentrations ranged from 75-85% of the true values on uncompensated PET images. For noisefree data, the hybrid compensation method recovered 91-96% of the true activities, whereas post-reconstruction compensation recovered essentially 100%. For noisy data, the uncompensated, hybrid, and post-reconstruction images yielded 55-90%, 78-98%, and 99-150%, respectively. These results suggest that the hybrid reconstruction-based partial-volume recovery method provides accurate compensation and is fairly insensitive to statistical noise.

Conclusions: Utilization of co-registered PET/CT data permits accurate partial-volume compensation for lesions visible on both the PET and CT images. These improvements can provide more accurate SUV values, and may lead to improved monitoring of tumor response to therapy.
SPECT with Two Second Time Resolution?
Rolf Clackdoyle, John Roberts, David Donneau-Golencer

The feasibility of a stationary head SPECT scanner, called the DyRoSH (Dynamic Rotating Slant-Hole) Scanner is being investigated. The scanner would consist of three stationary detectors with slant-hole collimators rotating at 30 rpm. The collimator slant-angles and the detector orientations would be carefully chosen to ensure full tomographic capability. The hypothesis is that the imaging performance of DyRoSH SPECT at least equals that of conventional SPECT for static activity distributions. For time-varying distributions DyRoSH would have the advantages of 2 second temporal resolution, compared to at least 20 minutes for a conventional scanner to gather all projection angles.

Supported by seed funding from a Benning Award, software has been written to simulate phantom generation, photon detection, and list-mode image reconstruction for DyRoSH scanning. The temporal aspects play an important role in the simulations and eventual applications. The associated NIH project involves augmenting the software with attenuation, geometric response, and Compton Scatter to produce more realistic simulations of the DyRoSH Scanner. The three Specific Aims of the NIH proposal are 1) to compare the static imaging performance of DyRoSH against conventional SPECT, 2) to evaluate weaknesses of the DyRoSH concept: small field-of-view (FOV) and susceptibility to background contamination, and 3) to explore temporal applications: dynamic SPECT and cardiac motion. The methods for aim 1 will involve ROC studies using simulated data. For aim 2, background effects will be quantified using region-of-interest analysis, and FOV issues will be analyzed by scoring an optimized patient positioning procedure using a database of cardiac patient images. Potential benefits of dynamic SPECT will be explored by computing bias and variance of kinetic parameter estimates to those obtained using standard systems, and the potential for general patient motion correction will be studied by assigning a figure of merit to performance of simulated motions detected and corrected using center of mass techniques.

Development of Radiosynthesis Module for $^{11}$C-Acetate
Jonathan King, Dan Kadrmas PhD, Paul Christian, Jim Slater PhD, Katrina Robinson

Introduction: The development of an assortment of PET radiotracers enables investigators to understand and image various metabolic processes within the body. The radiotracer $^{11}$C acetate has been used as a cardiac PET tracer to monitor myocardial oxidative metabolism. More recently, $^{11}$C acetate has been used in cancer imaging where it has shown promise for the detection of prostate cancer. Our objective is to use established methods and techniques to develop an automated synthesis module for the production of the radiotracer $^{11}$C acetate for use in multi-tracer PET imaging.

Methods: The synthesis module consists of a series of solenoid valves, ion-exchange cartridges and five supply and reaction vessels. The module components are interconnected with TEFZEL tubing. Radioactive $[^{11}C]$ CO$_2$ gas produced at the Huntsman Cancer Institute cyclotron is released into a reaction vessel that contains methylmagnesium chloride in THF. Following this reaction the solution is hydrolyzed by the addition of acetic acid. The mixture is pulled via vacuum pressure through PS-H+ and PS-Ag+ ion-exchange cartridges where impurities are separated out. The mixture is then pulled through a PS-OH- ion exchange cartridge where $^{11}$C acetate is trapped and the remaining solution passes into a waste vessel. Pulling sterile water via vacuum pressure through the PS-OH- cartridge washes the $^{11}$C acetate product. The final step in the production of $^{11}$C acetate is the elution of the product from the PS-OH- ion exchange cartridge with a citrate buffer solution. This results in an injectable solution of $^{11}$C acetate for use in PET imaging.
**Results:** The $^{11}$C acetate product is verified through HPLC analysis using a Geiger-Muller radiation detector followed by a UV detector at 229nm.

**Conclusion:** Through the implementation of established methods we anticipate the ability to produce multiple batches of $^{11}$C acetate for use in the development of techniques for multi-tracer PET imaging.

---

**Dual Tracer PET Imaging in Dogs with Prostate Cancer**

Thomas C. Rust and Dan J. Kadrmas, Ph.D.

Multifunctional PET/CT imaging is a new research endeavor initiated by our group which is intended to take full advantage of the ability of combined PET/CT imaging to evaluate structural and functional characteristics of diseased tissue. The long-term goal of this program is to achieve the technological advances necessary to image multiple PET tracers in a single imaging session, providing information about multiple physiological processes, such as glucose metabolism, cellular proliferation, amino acid synthesis, hypoxia, and blood flow. Presently, 18F-fluorodeoxyglucose (FDG) PET is the workhorse for clinical detection and whole-body staging of many cancers. In prostate cancer, FDG PET is effective for detecting distant metastases but less effective for local disease, due to relatively slow growth and proximity to the bladder. On the other hand, 11C-acetate has demonstrated high sensitivity for local disease, but is less useful for whole-body imaging. Thus, FDG and acetate together offer complementary information that may enable more accurate grading, prognosis, and treatment selection for prostate cancer. Canines are one of a small number of species that develop prostate tumors spontaneously in nature, and the incidence of canine tumors is high enough to encourage using this model for research. The tracer kinetics, which may be essential for separating individual components from the images, are also expected to be similar in canine and human tumors. The objective of this project is to demonstrate the feasibility of simultaneous dual tracer imaging with 18F-FDG and 11C-acetate in a canine spontaneously occurring tumor model. Dogs are being recruited from local and regional animal shelters, veterinary hospitals, and clinics with assistance from the Animal Resource Center. Logistical challenges that must be overcome include scheduling camera time and personnel, synthesizing radiotracers, and designing imaging protocols. Here we present the plan for dynamic imaging of the individual and combined tracers, measuring the plasma input function by arterial blood sampling, and image analysis methods that will be used to isolate individual tracer components.
Objectives: The measured line-of-response (LOR) histograms in PET are usually rebinned into regularly-spaced projection images prior to reconstruction. Within 2D direct sinograms this involves interpolation from measured ring-based LORs to an evenly-spaced grid. In 3D mode additional interpolations arise because LORs for a given ring difference fall at different polar angles as a function of the radial offset \( s \). These interpolations degrade spatial resolution and alter the Poisson statistical nature of the data. The objectives of this work are to develop and test a rotate-and-slant projector for iterative reconstruction that maps directly to raw LOR histograms, rather than to rebinned evenly-spaced projections.

Methods: The projector first rotates the reconstructed image matrix to the azimuthal angle using the fast 3-pass method of shears. During the final pass, the regularly-spaced image voxels are resampled to the uneven LOR spacing. Projection to direct sinograms proceeds by summing the columns of the rotated image. For oblique sinograms, the rotated image is slanted by shifting each row as a function of depth and radial offset \( s \) to match the polar angle for the individual corresponding LORs. Computational efficiency is optimized utilizing several symmetries. Most significantly, after rotation, projection to many oblique sinograms can be performed at low cost.

Results: Full 3D projection to 283 bin \( \times \) 35 slice \( \times \) 336 angle \( \times \) 23 ring difference projections took 24.6s (evenly spaced), 25.8s (LOR-spacing in \( s \) but not in polar angle), and 96.0s (complete LOR-spacing; not fully optimized) on a 2GHz Pentium IV workstation. Corresponding reconstruction times for 3 iterations of OSEM were 170s, 178s, and 598s per bed. Initial analysis shows a small improvement in spatial resolution for the LOR-based method, and possible noise reductions arising from the improved Poisson statistical modeling are under investigation.

Conclusion: Iterative LOR-based reconstruction of 2D and fully-3D PET provides benefits similar to direct listmode reconstruction while maintaining a histogram-based architecture. Unnecessary interpolations are avoided, and Poisson statistics are preserved. This represents an integral step toward comprehensive system-response modeling to obtain the highest quality reconstruction.
Estimation of kinetic parameters in FDG brain dynamic PET without a measured input function.

Dmitri Y. Riabkov and Edward V. R. Di Bella
Departments of Physics and Radiology

Objective: Quantified knowledge of the glucose metabolism in the regions of the brain tissue is desirable for better diagnosis. Dynamic PET imaging with injection of FDG tracer into the vein can be used for this measurement. Kinetics of this tracer in the tissue complies to a three-compartment model, where the blood plasma is the first compartment, the tissue extracellular space is the second, and the phosphorylated state of glucose in the tissue plays the role of the third compartment for this tracer. Four kinetic parameters, $k_1, k_2, k_3, k_4$, are the transfer rates of the tracer between the compartments. Values of these parameters for the tissue region determines regional glucose metabolism.

Additional measurement of the concentration of the tracer in the arterial blood plasma (blood input) synchronously with the imaging procedure should be performed in order to measure the kinetic parameters. However since this additional measurement is difficult and risky, new algorithms of estimation of the kinetic parameters have been developed which do not require the knowledge of the blood input. Blind identification methods are one type of these methods which based on the notion of blind deconvolution [1] and do not use any assumption about the blood input. The other type are the model methods which build on the empirical models of few parameters for the blood input.

In this work the accuracy of the new methods of estimation of the four kinetic parameters $\mathbf{k} = [k_1, k_2, k_3, k_4]^T$ without knowledge of the blood input function are compared.

Methods: Two blind identification methods were considered in this study. The first one is Iterative Quadratic Maximum Likelihood (IQML) which was adapted for dynamic medical imaging [2]. Another one, Non-uniform sampling IQML (NIQML) was developed here to allow the use of a more optimal sampling schedule, since FDG brain blood input function requires a much higher rate of sampling during the first minutes of the imaging.

The accuracy of these methods were compared. Also they were compared with the Input Function Model method (IFM), which is similar to the model method proposed and investigated in [3].

Results (figures on next page): The results showed that the accuracies of the three methods are close. However the IFM method showed slightly better accuracy. In estimation of $k_1$ ratios (ratios for different ROIs) NIQML method outperformed IQML.

Discussion and Conclusion: It has been shown that Blind Identification methods work with the FDG Brain Dynamic PET conditions if three or more regions are used. Also, the usefulness of parameterized model for the input was shown for IFM method. Further work
might be useful to extend this to real data. Optimization of the time sampling schedule has been shown to be important for the accuracy of the NIQML. IQML and NIQML can be used for determining regional glucose metabolism when accurate blood input function or its empirical model are not available.

References


Patient Repositioning and Repeatability Study for Carotid Artery Imaging
Emilee Shaw, Rock Hadley, Craig Goodrich, 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 reconstruction and post-processing algorithms, as well as 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: Accurate repositioning and repeatability in carotid imaging is accomplished by correlating morphology of the carotid artery to translational and rotational orientation of the head such as extension, flexion, and rotation left and right. In order to immobilize the head and index it’s position for future imaging studies, we have developed a device that consistently immobilized a patients head and neck on the MRI table for repeated studies. This device includes a base-plate that is anchored to an exact position on 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 (see Figure 1). The foam pads for the head and lower body support are chosen for each specific patient to match each patients anatomy. The arch, nose bridge, and left / right stabilization posts are all indexed and recorded for future studies. The imaging protocol for this study includes a standard low-resolution vessel imaging sequence using a set number of prescribed slices for each patient. A large FOV is utilized which encompasses the carotid artery, and the three fiducial markers placed on the head.

The patient is scanned in a standard imaging position to acquire a reference data set. The patient is positioned systematically and imaged with varying degrees of rotation/flexion and extension keeping all imaging parameters constant. The resulting images are then processed in order to segment out the vessel structures and compute an estimate of the vessel centerlines. The 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 are measured by computing the x,y centerline offsets in each slice with respect to the reference image centerlines, and the z-translation of the vessels are determined by the change in position of the flow divider at the bifurcation.

Results and Conclusions: Assessment of the vessel distortion as a function of head position will establish the degree of accuracy needed in head position and allowable tolerance of the head / neck immobilization device for accurate repeatable carotid artery imaging.
A Coil Coupling Model for Optimization Algorithms
Rock Hadley, Dennis Parker

Introduction: We have developed a model for the signal and noise coupling between planar surface coils that accounts for the electric and magnetic coupling between coils. This model accounts for the mutual inductance coupling effects on the noise and signal voltages between coils and can incorporate the effects of a transformed preamplifier impedance. This model facilitates understanding SNR profiles for various coil combinations and is ideal for implementation in coil design optimization algorithms such as the genetic algorithm where all coupling terms need to be included in the cost function to adequately compare non-optimal chromosomes or coil configurations.

Methods: Our method is an application of the quasi-static approach to coil design using the theory of reciprocity to determine signal sensitivities of a coil in a sample from a unit current in the coil. We have used analytical equations for both the rectangular [1] and circular [2] loops and for convenience apply them on a semi-infinite slab of conducting material similar to that described by Roemer et al [3]. The Biot-Savart Law can be used for field calculations for arbitrary shaped coils and/or samples. We assume the coil signal at a point is proportional to the magnitude of the magnetic field sensitivity perpendicular to B0 at that point. We account for the mutual inductance effects in the signal using $V_{ii} = V_{ii} + \sum V_{ik}$, where $V_{ii}$ is the total signal voltage in the $i$th loop, $V_{i}$ is the signal voltage in the $i$th loop due to the sample induced signal current in the $i$th loop and $V_{ik}$ is the signal voltage in the $i$th loop due to the sample induced signal current in the $k$th loop. These expressions become:

$$|V_{ii}| = \sqrt{B_{zi}^2 + B_{xi}^2}$$ and $$|V_{ik}| = \frac{M_{ik}}{L_k} \sqrt{B_{zk}^2 + B_{zk}^2}.
$$

We use standard equations for the mutual inductance, $M_a$ [3], and self-inductances, $L_i$ and $L_k$ [4] calculations. Inclusion of this coupling accounts for any signal enhancement or degradation due to the inductive coupling from the other coils in the system. For the present simulation we combine signals from multiple coils using the square root of the variance weighted sums of the squares algorithm, as is performed in conventional imaging systems.

The various noise sources are modeled as actual or effective resistances. Assuming independence of the noise sources, noise power for each coil is proportional to the sum of ohmic coil loss ($R_e$), electric sample loss ($R_{es}$), and must also include the correlated electric noise ($R_{es}$) and mutual inductance coupling of resistance from all other coils. From Roemer we have:

$$R_{ik} = \frac{\sigma^2 A_i}{\omega a K d^3 V}.$$  The ohmic coil resistance is

$$R_c = \frac{2(a + b)}{\pi d} R_s$$ for a rectangular coil of dimensions a and b,

$$R_c = \frac{a}{d} R_s$$ for a circular coil of diameter, a, where

$$R_s = \frac{\mu_0 \omega}{2}\sigma$$ and where d and $\sigma$ are the wire diameter and conductivity, respectively [5]. The total noise for the $i^{th}$ loop becomes:

$$\text{Noise}_{ii} = R_{ii} + R_{cj} + \text{Ramp}_{j} + \sum_{k \neq i} R_{ik} + \sum_{k \neq i} \left| \frac{\omega M_{ik}}{Z_{kk}} \right|^2 \text{Re}(Z_{kk}^*)$$

where $Z_{kk}$ is the total impedance in the $k^{th}$ loop, and includes the transformed input impedance from the pre-amplifier, $\text{Ramp}$.

This coupling model has been implemented in a Genetic Algorithm (GA) [6] to optimize two rectangular RF coils for imaging long, tortuous structures that vary in depth along their length, such as the carotid artery in the head and neck. A two coil optimization was implemented using a chromosome describing two rectangular loop coils, chromosome $= [a_1, b_1, x_1, y_1, a_2, b_2, \Delta x, \Delta y]$, where a, b and $\Delta$ are the dimensions of the loops and the x, and y variables correspond to the center positions of the loops. The loops were simulated using a semi-conductive, infinite half-space, with the vessel structure embedded in the half-space. The cost function for the GA was the optimal reconstruction method given by Roemer [3] as $\text{refSNR} = B^T R_{ik}^{-1}B^*$, where B is the signal sensitivity vector and R is the electrically coupled noise correlation matrix for the coil array.

Results and Conclusions: The coupling model was adequate for the GA simulation of two coils, including terms where the coils were not properly overlapped for $M_a = 0$. However, computation of the cost function was extremely slow. Adaptations to the GA were made to speed up the conversion process. Adaptations to the GA code included an algorithm to find the positions of $M_a = 0$ between two coils in order to determine the $\Delta x$, and $\Delta y$ position of the second coil in the chromosomes. Once a fixed $\Delta x$ and $\Delta y$ were obtained, a second or nested GA, using a two element chromosome, was used to compute the optimal $x$, and y positions for coil 1. This nested GA is very fast since the only calculations needed for the cost function are the magnetic field sensitivities in the structure of interest. The large volume integrals in the cost function do not need to be computed since the coils are fixed in space with respect to each other. The results of the adapted GA for short vessel structures are intuitively correct. Further developments to the GA code will possibly include a third nested GA to optimize the angular position of the second coil with respect to the first. Finally the code needs to be developed for coil arrays larger than 2 coils using vectors that describe the size and position parameters of the loops as the chromosome elements. This tool allows the development of coil arrays and aids in the understanding of coil and sample coupling interactions.

References
Improved Gradient Performance, Increased Field-of-View, and Reduced Nerve Stimulation – “A really good idea”
Dennis L. Parker & J. Rock Hadley

Introduction

Gradient performance: The quality of novel rapid MRI techniques depends directly on gradient performance factors, including maximum gradient strength and slew rate (inverse of rise time). In the design of gradient coils there is always a trade-off between gradient efficiency (defined as gradient strength per unit driving current), slew rate, region of coverage, and homogeneity. Within certain limits, improvements in any one performance measure can be obtained only at the expense of one or more of the others.

Nerve stimulation: Although increased performance is technically feasible, gradient amplitudes and slew-rates have already reached a point where physiological effects such as nerve stimulation can be induced by the rapidly varying magnetic field. In general nerve stimulation depends on the strength of the electric field (rate of change of the magnetic field, dB/dt) and its duration (τ). For any specific gradient system, the maximum dB/dt and the duration it can be maintained depend on the performance limits of the gradient system (maximum amplitude and slew rate) as well as on the gradient FOV. For a given gradient system, the stimulation limits follow a relationship: 2,3:

\[ \Delta G(\tau) = SR_{\text{min}} \cdot \tau + \Delta G_{\text{min}} \]

where \( \tau \) is the duration of the gradient change, \( \Delta G \), that will induce stimulation. As the FOV increases, the stimulation limits \( \Delta G_{\text{min}} \) and \( SR_{\text{mi}} \) increase.

Coverage (FOV) of the gradient system can be reduced to enable improved gradient performance over smaller volumes. The gradient limited FOV in MRI scanners (currently about 40 cm) is generally adequate for covering the transverse dimensions of most subjects but not adequate for many applications such as covering the entire spine or the lower legs (runoff studies). However, loss of gradient performance to attain increased FOV is not desirable.

Speculation and Solution

In this presentation we provide a possible gradient design that allows increased gradient performance, an increased FOV along the length of the subject, while at the same time results in decreased nerve stimulation. The solution to be presented is technically feasible, but expensive. Using this solution, it is possible in principle to design a high performance whole body MRI scanner. Unfortunately the bore of such a full body scanner would be about 6 meters long and the magnet would cost a whole bunch of dollars. However, the design proposed could greatly improve the performance of magnets with even just 50 to 80 cm FOV’s. Such extended FOV magnets may be cost effective for some applications.

Magnetoencephalography Spikes Undetected By Electroencephalogram
Ernst Rodin, Michael Funke, Patrick Berg, Fumisuke Matsuo

Introduction: Magnetoencephalography (MEG) detects mainly those spikes which have a tangential orientation while the Electroencephalogram (EEG) can detect both radial and tangential sources. There are also cases where MEG spikes are hard to detect in the EEG and vice versa.

Objective: To ascertain why clinical EEG inspection fails on occasion to detect spikes which are clearly visible on concomitant MEG registration.

Methods: The data, worn a 10-year-old boy with Landau-Kleffner syndrome, were recorded with a whole head MEG system which allowed co-registration of 122 MEG and 32 BEG channels. Offline analysis was later performed.

Results: A 70-second sample of combined data yielded on visual inspection of the EEG 7 spikes in the left central area and none on the right. The MEG revealed additional well-defined spikes in the left central area as well as a mirror focus in the right hemisphere. A comparison of EEG detected versus undetected spikes showed that a strength of at least 1000 IT was required for an EEG spike to be clearly visible. When MEG spikes, undetected by EEG, were averaged the concomitant EEG spikes had amplitudes of about 20 µV or less and were, therefore, masked by background activity.

Conclusion: This shows a case where spikes are much clearer in the MEG than the EEG. This is unlikely to be compensated for by a denser electrode array and suggests a role for MEG in the early detection of seizure disorders.

Skeletal imaging and pharmaceutical targeting: Initial studies using MRI imaging in rats.
Scott C. Miller¹, Dong Wang², Monica Sima², Pavla Kopeckova² and Henry Kopecek².
¹Division of Radiobiology, Department of Radiology; ²Department of Pharmaceutics and Pharmaceutical Chemistry.

There is a need to improve the skeletal targeting for the delivery of pharmaceuticals. Additionally, some of these same approaches may be useful for MRI and other types of imaging. We present here some initial results in the development of skeletal targeting agents using water-soluble polymers. Two bone-targeting approaches are being explored. The first exploits the bone seeking activity of a bisphosphonate (Alendronate, Fosomax™), tetracycline, or an aspartic acid peptide. Using a conjugate that contains a fluorochrome marker (FITC), we have demonstrated bone-specific uptake. Under discussion is whether this technology may be applied to MRI or other types of imaging with the attachment of moieties such as Gd. The data to date suggests that such an agent would image sites of active formation and turnover and may be useful for conditions such as stress fractures, skeletal metastases, multiple myeloma, Paget's disease of bone, bone tumors, osteoarthritis, exotoses and other conditions. Another approach is to use a modified polymer system to target sites of skeletal inflammation (and perhaps other inflammatory sites). MRI images will be presented that demonstrate favorable localization and retention in inflammatory regions in a rat model of arthritis. As with the bone-targeted agents, this technology may also be used to identify inflammatory regions or perhaps even initial cancer foci.

We seek clinical guidance and co-investigators with imaging experience help us develop the imaging and applied aspects of this technology.

*We appreciate the assistance of Rock Hadley, Craig Goodrich and Henry Buswell on the MRI aspects of the study. Thanks to UCAIR for helping facilitate these studies.
A novel biodegradable macromolecular blood pool MRI contrast agent

Zheng-Rong Lu, Xinghe Wang, Craig Goodrich, and Dennis Parker

Department of Pharmaceutics and Pharamceutical Chemistry, University of Utah, 421 Wakara Way, Suite 318, Salt Lake City, UT 84108, USA

Introduction: The clinical application of macromolecular gadolinium complexes as MRI contrast agents is limited by the slow excretion of Gd(III) complexes after MRI exams and consequent long-term tissue accumulation of toxic gadolinium ions. We intend to design and develop biodegradable macromolecular Gd(III) complexes as safe, effective MRI blood pool contrast agents. These agents can provide effective contrast enhancement in blood pool MR imaging and then gradually degrade into smaller complexes removable by the renal filtration.

Materials and Methods: We have designed and prepared [DPTA-Gd(III)]-disulfide copolymers as a biodegradable macromolecular blood pool MRI contrast agent. The degradability of the agent has been investigated in vitro and in vivo. The metabolic clearance of the agent has been investigated in rats with Gd-(DTPA-BMA) as a control. The degradation products in rat urine have been analysed with mass spectrometry. The relaxivity of the agent has been measured at a 1.5 T MR scanner. The contrast enhancement of the agent has been investigated in rats on a 1.5 Tesla Sigma GE NV/CVi MR scanner with a LX 8.4(m4) operating system, using a 3-dimensional spoiled gradient echo (SPGR) pulse sequence.

Results: The molecular weight of the macromolecular contrast agent ranges from 18,000 to 35,000 Da. The T1 and T2 relaxivities are 4.2 and 5.0 mM⁻¹s⁻¹ per complexed Gd ion for an agent of molecular weight around 18,000 Da at 1.5 T, respectively. The disulfide bonds in the polymer backbone can be gradually cleaved in the incubation with cysteine (one of the thiols in the plasma) via thiol-disulfide exchange reaction, resulting in reduction of molecular weight of the macromolecular agent. Metabolic study has shown that the Gd complexes of the macromolecular agent excretes through renal filtration at a rate similar to the Gd-(DTPA-BMA) in a ten-day period, Figure 1. Mass spectrometric analysis of rat urine sample collected 24 hour post-injection of the macromolecular agent has shown the presence of the degradation products, indicating that the agent is degraded by the endogenous thiols into smaller excretable Gd complexes. The agent produces superior contrast enhancement in the aorta and heart over Gd-(DTPA-BMA) at a dose of 0.1 mmol-Gd/kg. The signal intensities gradually decrease in the aorta and heart in two minutes post-injection and increase gradually in the urinary bladder.

Conclusion: The novel biodegradable macromolecular agent is effective for contrast enhanced blood pool MR imaging. It can be readily degraded by the endogenous thiols and rapidly excreted via renal filtration. The new blood pool agent has a great potential for further preclinical and clinical development.

Figure 1.
fMRI Success Story: We obtained $90,895 to equip MRI4 (the 3T Trio scanner) with state-of-the-art equipment for functional brain-mapping MRI (aka fMRI). The successful application was funded from the VP’s program for Research Instrumentation Funds. The equipment to be installed in the coming months will include a visual projection system (show your patients videos) and a stereo audio center (play soothing music to send your subjects to dreamtime). While these are necessary parts to present stimuli to subjects for fMRI, they will also increase patient compliance for routine scans and decrease motion problems.

Multi-modality(PET, DCE MRI) Oncologic Imaging: A revised proposal for an ambitious Bio-engineering Research Partnership to facilitate multi-modality oncologic imaging has been resubmitted to NIH. The goal is to design and validate non-invasive imaging methodologies to measure blood flow, vascular permeability, and response to treatment of solid tumors and irradiated tissues. Ed DiBella and I are seeking to update the pharmacokinetic models currently used to interpret dynamic contrast-enhanced MR imaging of tumor blood flow and permeability to include known sources of error such as variable arterial input to tumor and the effects of water proton exchange between vascular and interstitial water pools. Dan Kadrmas would like to demonstrate the benefits of multi-tracer studies for imaging tumor blood flow and hypoxia. Zheng-Rong Lu of the Pharmaceutics Dept has synthesized polymers for prospective PET or MRI indicators that require additional study in animal tumor models. The revised proposal was greatly strengthened by adding members of the Department of Radiation Medicine at Loma Linda University in California, who will contribute the use of their microPET and 4.7T animal MR scanners and their expertise in a number of animal models.

Small-animal MR scanner(s): In order to answer questions of basic physiology and mechanism, it is often necessary to resort to studying animal models. However, the cost of state-of-the-art high-field animal MR scanners actually exceeds that for 3T human systems. One of the few funding mechanisms for such expensive systems is the National Center for Research Resources (NCRR) at the NIH, whose mission is to fund centers which provide access to expensive resources to entire geographical areas of the U.S. We have been approved to submit an application for a 7T animal MR imager/spectrometer that will accommodate animals from mice to dogs. The system would be sited at CAMT.

MRS: My student and I had very limited success in our MRS studies, but we are hoping to complete comparing normal brain MRS at 1.5T (MRI3) and 3T (MRI4)...now that the Research Agreement with Siemens has been signed and we have access to the MRS sequence code and Works-In-Progress (WIPs). On a more academic note, I solicit input from all interested parties regarding a special issue of NMR in Biomedicine, entitled Clinical MRS, for which I am the Editor.
Microscopic Computed Tomography at the University of Utah has Utility in both Adult and Embryonic Biological Investigation

Lance Burrell, Richard Normann, Gordon Kindlmann, James Bigler, Nick Green, Richard Coffey, Arun Badi, Norman Hu, Mario Capecchi, Charles Keller

Department of Human Genetics, University of Utah

Introduction: The Capecchi lab and the University of Utah recently received a small animal and microscopic computed tomography (microCT) scanner for use with sacrificed or live animals. The goal of this poster is to present the versatility of this imaging modality across a wide spectrum of specimens, embryonic, juvenile, and adult -- with and without contrast.

Methods: This 80 keVp General Electric Medical Systems EVS-RS9 scanner (<http://www.gemedicalsystems.com/rad/nm_pet/products/explorers.html>) with a 3500 x 1750 element CCD detector can be used for volumetric detection to differentiate bone from tissue/water from fat from air. Scanned areas of 88 x 88 x 43 mm can be reconstructed into 2- or 3-dimensional images at resolutions of 27 – 93 micron resolution (living animals are scanned at 46+ microns). With use of enteral (oral) barium or intravenous iodine contrast agents, other structures such as the gastrointestinal tract or the vascular system can be visualized. Without contrast, only skeletal structures can be seen with detail. Limitations of the system include the inability to see texture in non-fatty soft tissue, and the unavoidable delivery of small to moderate doses of radiation to the animal.

Results: Structures as small as 10 μm can be detected with the aid of advanced image processing. With standard embryo manipulation techniques, contrast can be administered to mid-stage mouse and chicken embryos for visualization of vascular and enteral structures. In adult mice, tumors imaging reflects the degree of proliferation and invasiveness of the cancer.

Conclusions: Microscopic computed tomography at the University has a broad potential for a number of biomedical applications.

Future Directions: Future capabilities based upon the availability of funds may include a synchronized small animal ventilator for prolonged, high resolution scans of the heart and lungs.

The Amygdala and Fusiform Face Area in Autism

James N. Lee

In normal people, the amygdala flags events of particular emotional importance to indicate that they merit further attention. If you met a bear in the woods, your amygdala would send strong signals to the rest of the brain indicating that this was an emotionally important meeting.

One area that receives input from the amygdala is the fusiform face area (FFA). In normal people this area activates strongly when looking at human faces. If your boss glares at you when you come to work, your amygdalawould send signals to the fusiform face area that something is up, and encourage you to pay attention to clues about why your boss is mad.

Autistic amygdalas are not so active. As a result, autistic subjects have impaired ability to link social stimuli with social meaning. They have diminished rates of eye contact, pay little attention to faces and have reduced ability to interpret people's feelings.

Several published fMRI studies have examined the amygdala and fusiform face area in autistic subjects performing a faces/objects task. They report reduced or absent activation in both areas, but thus far have found no correlation between fMRI activation in these areas and behavioral measures of autism.

I will report the results of a pilot fMRI study of five autistic subjects scanned during a faces/objects task. Their amygdalas had zero active voxels, and the number of active voxels in the fusiform gyrus correlates with their scores on the Autism Diagnostic Observation Schedule (ADOS), a standard behavioral test of autism.
**Investigation into Spatial Characteristics in Pattern Separation using fMRI**

Doing-Harris, KM, Kesner, RP, Creem-Regehr, SM  
Department of Psychology, University of Utah, Salt Lake City, UT 84112

The hippocampus has been determined to be highly involved in learning and memory. Based on hippocampal architecture and connectivity, computational models have been developed which assume that the hippocampus supports spatial pattern separation or orthogonalization of sensory input (O’Reilly & McClelland, 1994). The present experiment was designed to replicate two experiments in which the hippocampus appeared to support spatial pattern separation. The first was done with rats (Gilbert, Kesner & DeCoteau, 1998). The second was a behavioral study done with lesion patients (Hartman, Hopkins & Kesner, in press). Here we use fMRI with normal subjects, to test whether the hippocampus or parahippocampal gyrus is preferentially active during a spatial pattern separation task. The task used is a delayed match to sample task in which the subject must report which of two dots is in the corresponding location to a previously viewed dot. The pattern separation aspect of the task operates during the choice phase in which the dots are either spatially proximal or distal to each other. The two tasks contain patterns which are more or less difficult to separate, respectively. The results were investigated in two ways using a Region of Interest [ROI] Analysis targeting the hippocampus and parahippocampal gyrus and a Random Effects Analysis [REA] of the whole brain data. The ROI analysis shows a trend toward preferential activation in left hippocampus when the distal condition is subtracted from the proximal condition. In the REA subtracting the activation in the distal condition from the proximal condition we found the most significant cluster of activation in the left parahippocampal gyrus. We are looking into the validity of analyzing the data as an Event Related design because there is evidence that the hippocampus may be preferentially activated in the acquisition and choice phases but deactivated during delay (Monk, et al., 2002).

**Neural Representations of Graspable Objects**

Sarah Creem-Regehr, James Lee

Recent cognitive and neuroimaging studies have examined the relationship between perception and action in the context of tools. These studies suggest that tools potentiate actions even when overt actions are not required in a task. Tools are unique objects because they have a visual structure that affords action and also a specific identity. The present studies asked whether a tool’s representation for action is tied to its graspability or its semantic representation. Functional magnetic resonance imaging (fMRI) was used to examine the extent of motor representations associated with different classes of graspable objects. Participants viewed and imagined grasping images of 3D tools with handles or neutral graspable shapes. During the viewing task, motor-related regions of cortex (posterior middle temporal gyrus, ventral premotor, posterior parietal) were associated with tools compared to shapes. During the imagined grasping task, a frontal-parietal-temporal network of activation was seen with both types of objects. However, differences were found in the extent of premotor and parietal activation, and additional activation in the middle temporal gyrus at the junction of the inferior parietal lobule for tools compared to shapes. A second study is in progress that uses novel objects to examine a similar question while controlling for visual complexity and similarity. We suggest that the functional identity of graspable objects influences the extent of motor representations associated with them. These results have implications for understanding the interactions between “what” and “how” visual processing systems.
Can Imagined Motor Practice Change Cortical Representations?

Dept. of Neurosurgery$^1$, University of Utah, Salt Lake City, UT 84151 and the Depts. of Neuroscience$^2$, Neurology$^3$, Radiology$^4$, Clinical and Health Psychology$^5$, and Physical Therapy$^6$. University of Florida, Gainesville, FL 32610

It is known that the cortical representations that control specific movements are adaptable and can be modulated by practice. It has been proposed that motor imagery uses the same neuronal architecture as volitional movement. We propose that practicing a task using motor imagery can induce changes in cortical representations in the same fashion as practice by volitional movement. We randomized 25 subjects between an executed and imagined motor practice group. Subjects were imaged using functional MRI both before and after a three week practice interval. Results of performance testing indicated that both imagery and executed practice significantly improved motor performance ($p=0.001$); however, executed practice fostered significantly better results than imagery alone ($p=0.016$). Both imagery and executed practice caused a significant and equivalent increase in the size of primary motor cortex presentations ($p=0.002$). We suggest that motor imagery involves the same pathways as executed movements, principally the basal ganglia/subcortical structures and the primary motor cortex. Imagery provided less improvement in function than executed practice due to its lack of robust stimulation of subcortical structures. Primary motor cortex showed evidence of reorganization to support the learned task and we suspect that reorganization of primary motor cortex requires less robust stimulation than subcortical structures.

High Resolution Magnetic Resonance Imaging of Symptomatic Cervical Nerve Roots
Moore, K.R. and Dailey, A.T.

Cervical radiculopathy is a debilitating health problem in the United States, resulting in lost work days and substantial morbidity for those afflicted. Successful pre-operative planning requires precise pre-operative localization of clinical signs and symptoms in conjunction with imaging studies to assure the best chance of a positive outcome and minimize surgical morbidity. A sensitive imaging technique to confirm the existence of an anatomical nerve abnormality at a clinically suspected symptomatic level would enable a surgeon to more appropriately select patients for surgery. MR neurography is an MR imaging technique that provides high-resolution, highly focused MR imaging of peripheral nerves, nerve roots, and plexi. We have evaluated the feasibility of MR neurography for evaluating cervical radiculopathy and assessed its diagnostic accuracy for addressing imaging abnormalities of cervical nerve roots, and have found that it can detect subtle imaging abnormalities that correspond to clinically localizable symptoms.