3.   FOUR INFRASTRUCTURE TOPICS

3.1   Diffusion Image Analysis

Key Investigators
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MIT: Lauren O'Donnell, Polina Golland, Tri Ngo
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GA Tech: John Melonakos, Vandana Mohan, Shawn Lankton, Allen Tannenbaum
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Summary of Progress
Significant progress was made in refining tools for diffusion-weighted imaging (DWI) and applying existing implementations to clinical studies. This progress is best documented in the 14 new papers related to diffusion tensor imaging (DTI) published since the previous year's report, with 11 appearing in high-impact journals [Neuroimage (3), IEEE TMI (2), MEDIA (2), MRM (1), Schizophr Res (3)], 2 appearing in peer-reviewed conference proceedings [(MICCAI (2)], and 1 other at a scientific workshop. These publications are excellent indicators not only that NA-MIC tools and methodologies are competitive and being recognized by highly respected medical image analysis journals, but also that the application of these tools and methodologies to clinical studies, including validation and testing, is competitive and being recognized by clinically oriented journals. The scale of these methods can be characterized as both small, such as the processing of DWI to extract fiber bundles of interest in particular patients and large, such as the population-based analysis of DWI for group comparison and hypothesis testing. Significant progress in both categories is reported.

Core 1 partners contributed to the development of methods for image preprocessing, such as filtering and artifact removal, by providing improved tractography algorithms, methods for clustering of streamlines into meaningful tracts, group-wise analysis via computational anatomy tools, and methods for quantitative analysis of tracts to provide parameters for statistical analysis. Core 2 contributed significantly not only by providing the computational environment for user-guided, interactive DTI analysis which relies on a complex user interface and sophisticated visualization, but also by developing plug-in capabilities for more automated processing modules. Core 3 made increasing use of these tools to analyze data from clinical studies, and there was significant handshaking amongst the engineers of the Core 3 partners, the methods developers of Core 1, and the engineers of Core 2. Core 5 organized several training courses, including DTI analysis, where participants could learn about the underlying imaging and image analysis concepts and the use of the Slicer software environment.

The following list summarizes the major new contributions to Diffusion Image Analysis during the present reporting period.

Major Developments in Diffusion Image Analysis

Fiber Tract Modeling, Clustering, and Quantitative Analysis (MIT): Ongoing development of population-based analysis of DTI via clustering of fiber tracts for automatic labeling has continued and resulted in a recent journal publication (O'Donnell L, *Neuroimage* 2009). As a new research direction, the group approached the challenging problem of joint registration and segmentation of DWI fiber tractography, where tract labels are assigned in an iterative framework by registration of bundles to an atlas. This results in the nonlinear joint registration of sets of DWI data into a common coordinate space, and at the same time, automatic labeling of joint tracts. Quantitative analysis in population studies is based upon correspondence obtained via clustering and labeling.

Stochastic Tractography (MIT, DBP 2): Stochastic Tractograpy was a major research effort of this group during the reporting period. Initial prototype software was integrated into Slicer 3, which brought significant challenges with regard to user interaction, visualization, and definition of data structures for subsequent statistical analysis. The advantages of Stochastic Tractography are clearly shown in areas of crossing fibers, uncertainties, considerable noise – all situations where conventional Deterministic Tractography methods would fail. Two journal papers explored the potential advantages of using the orientation distribution function from DWI rather than the simplified tensor model (Rathi, *Media* 2009; Aja-Fernandez, *TMI* 2008). This project is a joint collaboration between Core 1, Core 2, and Core 3, and nicely demonstrates the close interaction between methods development, engineering, and testing and validation in a clinical environment. Four journal publications (Kawashima, Lee, Fitzsimmons, Kubicki, *Schizophr Res*) show application of these novel analysis tools to clinical studies.

Geodesic Tractography Segmentation (Georgia Tech): As an alternative to Streamline Tractography, this project develops a technique for extraction of a minimum cost curve through the tensor field, resulting in an anchor curve between source and target regions specified by the user (Niethammer, *Neuroimage* 2009). As an extension, Volumetric Fiber Segmentation based on active contours but using the anchor curves as initialization has been developed. This led to a framework for Tubular Surface Segmentations, which was presented at a conference workshop (Mohan, *MFCA* 2008).

DTI Processing and Statistical Tools (Utah 1): This research addresses the important problem of correcting artifacts of DWI. Image distortions due to eddy currents in gradient directions and susceptibility artifacts of echoplanar imaging (EPI) acquisition are corrected via a combined scheme of aligning individual gradient images and calculating a nonlinear transformation between DWIs and a geometrically correct T2-weighted image. The whole pipeline is written in ITK and is tested on a larger number of datasets. The methodology is in print and will be presented at a peer-reviewed conference (*IPMI* 2009). This group also continued further development of the volumetric white matter connectivity tool, i.e., a method dual to tractography that optimizes a shortest path through the tensor field.

Population-Based Analysis of White Matter Tracts (Utah 2): The population-based analysis system starts with DWI from a large set of subjects and yields a statistical analysis of selected fiber tracts. More information about this project is available on the NA-MIC wiki. http://www.na-mic.org/Wiki/index.php/ Projects:

DTIPopulationAnalysis The steps involved in this system include (1) calculation of image features; (2) linear and nonlinear registration into a common, unbiased coordinate system; (3) user-guided selection of tracts of interests in atlas-space; (4) mapping tract geometry back into individual images to collect subject-specific diffusion information; and (5) statistical group analysis of tract diffusion information. New activities in this reporting period include the use of a Core 1 developed methodology for group-wise registration of population of images (in collaboration with MIT). http://www.na-mic.org/Wiki/index.php/ Projects:GroupwiseRegistration Core 1 also developed a statistical framework for tract analysis based on functional data analysis (FDA). The new methods are described in a conference and a journal publication (Goodlett et al., *Neuroimage* 2009, *MICCAI* 2008). The whole system was applied to large studies of our Core 3 partner (PNL Harvard) and pediatric studies from our affiliated clinical partners at UNC. As an attempt to combine this framework with Stochastic Tractography, we have developed an efficient algorithm with a novel sampling strategy (Fan et al., *Media* 2009).

DTI Tractography Based on Navier-Stokes (UCLA): The UCLA group developed a new tractography that makes use of the Navier-Stokes method rather than conventional PDE for tracking (Hagemann, *TMI* 2009).

The sum of these activities by all partners includes the whole processing pipeline from data input via NRRD format; preprocessing and correction for artifacts and distortions; several choices for tractography tailored to different needs; and output of results for statistical analysis. A summary of the most recent progress of DTI tool development based on the point of view of the DBP 2 partner (Harvard) is available on the NA-MIC wiki, with links to all current activities. http://www.na-mic.org/Wiki/index.php/ DBP2:Harvard

Additional Information is available at the following links:

Summary of internal collaborations http://wiki.na-mic.org/Wiki/index.php/NA-MIC_Internal_Collaborations:DiffusionImageAnalysis

Detailed methods and algorithms for DWI analysis can be found in the algorithm sections of the respective Core-1 partners http://www.na-mic.org/Wiki/index.php/Algorithm:Main

DBP-2 project descriptions http://www.na-mic.org/Wiki/index.php/DBP2:Main

External and internal NAMIC collaboration pages http://www.na-mic.org/Wiki/index.php/NA-MIC_Collaborations:New

PAPERS AND PRESENTATIONS

Peer-reviewed articles in journals

Rathi Y., Michailovich O., Shenton M.E., Bouix S. Directional functions for orientation distribution estimation. *Med Image Anal.* 2009 Jun;13(3):432-44. PMID: 19269242. Kawashima T., Nakamura M., Bouix S., Kubicki M., Salisbury D., Westin C., McCarley R., Shenton M. Uncinate fasciculus abnormalities in recent onset schizophrenia and

affective psychosis: A diffusion tensor imaging study. *Schizophr Res.* 2009 May;110(1-3):119-126. PMID: 19328656.

O'Donnell L., Westin C., Golby A.J. Tract-based morphometry for white matter group analysis. *Neuroimage.* 2009 Apr 15;45(3):832-44. PMID: 19154790.

Niethammer M., Zach C. Melonakos J., Tannenbaum A. Near-tubular fiber bundle segmentation for diffusion weighted imaging: segmentation through frame reorientation. *Neuroimage.* 2009 Mar;45(1 Suppl):S123-32. PMID: 19101640.

Lee K., Yoshida T., Kubicki M., Bouix S., Westin C., Kindlmann G., Niznikiewicz M., Cohen A., McCarley R., Shenton M. Increased diffusivity in superior temporal gyrus in patients with schizophrenia: A Diffusion Tensor Imaging study. Schizophr Res. 2009 Mar;108(1-3):33-40. PMID: 19135872.

Hageman N.S., Toga A.W., Narr K.L., Shattuck D.W. A diffusion tensor imaging tractography algorithm based on Navier-Stokes fluid mechanics. IEEE Trans Med Imaging. 2009 Mar;28(3):348-60. PMID: 19244007.

Goodlett C., Fletcher P.T., Gilmore J.H., Gerig G. Group analysis of DTI fiber tract statistics with application to neurodevelopment. Neuroimage. 2009 Mar;45(1 Suppl):S133-42. PMID: 19059345.

Zhang F., Hancock E.R., Goodlett C., Gerig G. Probabilistic white matter fiber tracking using particle filtering and von Mises-Fisher sampling. Med Image Anal. 2009 Feb;13(1):5-18. PMID: 18602332.

Fitzsimmons J., Kubicki M., Smith K., Bushell G., San José Estepar R., Westin C., Nestor P., Niznikiewicz M., Kikinis R., McCarley R., Shenton M. Diffusion tractography of the fornix in schizophrenia. Schizophr Res 2009 Jan; 107:39–46. PMID: 19046624.

Kubicki M., Styner M., Bouix S., Gerig G., Markant D., Smith K., Kikinis R., McCarley R.W., Shenton M.E. Reduced interhemispheric connectivity in schizophrenia-tractography based segmentation of the corpus callosum. Schizophr Res. 2008 Dec;106(2-3):125-31. PMID: 18829262.

Khachaturian M.H., Arsenault J., Ekstrom L.B., Tuch D.S., Vanduffel W. Focal reversible deactivation of cerebral metabolism affects water diffusion. Magn Reson Med. 2008 Nov;60(5):1178-89. PMID: 18958855.

Aja-Fernandez S., Niethammer M., Kubicki M., Shenton M.E., Westin C. Restoration of DWI data using a Rician LMMSE estimator. IEEE Trans Med Imaging. 2008 Oct;27(10):1389-403. PMID: 18815091.

Peer-reviewed full length articles in conference proceedings

Ziyan U., Westin C. Joint Segmentation of Thalamic Nuclei from a Population of Diffusion Tensor MR Images. Int Conf Med Image Comput Comput Assist Interv. 2008;11(Pt 1):279-286. PMID: 18979758.

Goodlett C., Fletcher P.T., Gilmore J.H., Gerig G. Group Statistics of DTI Fiber Bundles Using Spatial Functions of Tensor Measures. Int Conf Med Image Comput Comput Assist Interv. 2008;11(Pt1):1068-1075. PMID: 18979851.

Others (abstracts, tutorials, non peer-reviewed workshop articles)

Mohan V., Sundaramoorthi G., Melonakos J. Niethammer M., Kubicki M., Tannenbaum A. Tubular Surface Evolution for Segmentation of the Cingulum Bundle From DW-MRI. Proceedings of the Second Workshop on Mathematical Foundations of Computational Anatomy (MFCA'08), Int Conf Med Image Comput Comput Assist Interv. 2008.

Presentations related to DTI Analysis

Goodlett, Casey, *Improved Correspondence for DTI Population Studies via Unbiased Atlas Building,* ISMRM Educational Course on Diffusion MRI Software, April 2009

Gerig, Guido, Invited panel presentation: White Matter Development in Very Early Ages: Normative Models of Healthy Growth to study Risk Populations and Disease, ACNP 2008, Scottsdale, AZ, Dec. 10, 2008

Gerig, Guido, Mapping Early Brain Development via Neuroimaging, invited presentation UCLA LONI CCB Seminar, Los Angeles, CA Nov. 7, 2008,

Gerig, Guido, Computational pipelines for clinical studies, invited talk for Tutorial on DTI, MICCAI 2008, NYU, New York Sept. 6, 2008

Gerig, Guido, Analysis of brain white matter properties via DW MRI: The role of normative atlases, invited presentation at 5th Annual World Congress of IBMISPS (Int. Brain Mapping and Intraoperative Surgical Planning Society), Los Angeles, CA August 28. 2008,

3.2   Structural Analysis

Key Investigators
MIT: Polina Golland, Kilian Pohl, Sandy Wells, Eric Grimson, Mert R. Sabuncu
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Utah: Ross Whitaker, Guido Gerig, Suyash Awate, Tolga Tasdizen, Tom Fletcher, Joshua Cates, Miriah Meyer
GaTech: Allen Tannenbaum, John Melonakos, Vandana Mohan, Tauseef ur Rehman, Shawn Lankton, Samuel Dambreville, Yi Gao, Romeil Sandhu, Xavier Le Faucheur, James Malcolm, Ivan Kolosev
Isomics: Steve Pieper
GE: Jim Miller
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Summary of Progress
Under Structural Analysis, the main topics of research for NA-MIC are structural segmentation, registration techniques, and shape analysis. These topics are interrelated and hence research in one often finds application in another. For example, shape analysis can yield useful priors for segmentation, or segmentation and registration can provide structural correspondences for use in shape analysis and so on. An overview of selected progress highlights under these broad topics follows.

Segmentation

Geodesic Tractography Segmentation: We have proposed an image segmentation technique based on augmenting the conformal (or geodesic) active contour framework with directional information. This has been applied successfully to the segmentation of neural fiber bundles such as the cingulum bundle. This framework now has been integrated into Slicer and is being tested on a population of brain datasets.

Tubular Surface Segmentation: We have proposed a new model for tubular surfaces that transforms the problem of detecting a surface in 3D space, to detecting a curve in 4D space. Besides allowing us to impose a "soft" tubular shape prior, this model also leads to computational efficiency over conventional surface segmentation approaches. We also have developed the moving end points implementation of this framework, wherein the required input is only a few points in the interior of the structure of interest. This yields the additional advantage that the framework simultaneously returns both the 3D segmentation and the 3D skeleton of the structure, thus eliminating the need for *a priori* knowledge of end points, and an expensive skeletonization step. The framework is applicable to different tubular anatomical structures in the body. We have so far applied it successfully to the cingulum bundle and blood vessels.

Local-Global Segmentation: We have proposed a novel segmentation approach that combines the advantages of local and global approaches to segmentation, by using statistics over regions that are local to each point on the evolving contour. This approach is well suited to applications with contrast differences within the structure of interest, such as in blood vessel segmentation. It is also suited to

applications such as the neural fiber bundles, where the diffusion profiles of voxels within the structure are locally similar but vary along the length of the fiber bundle itself.

Shape-Based Segmentation: Standard image-based segmentation approaches perform poorly when there is little or no contrast along boundaries of different regions. In such cases, segmentation is mostly performed manually by using prior knowledge of the shape and relative location of the underlying structures combined with partially discernible boundaries. We have presented an automated approach guided by covariant shape deformations of neighboring structures, which is an additional source of prior knowledge. Captured by a shape atlas, these deformations are transformed into a statistical model by using the logistic function. The mapping between atlas and image space, structure boundaries, anatomical labels, and image inhomogeneities is estimated simultaneously within an Expectation-Maximization formulation of the Maximum A posteriori Probability (MAP) estimation problem. These results then are fed into an Active Mean Field approach, which views the results as priors to a Mean Field approximation with a curve length prior. We have applied the algorithm successfully to real MRI images, and we also have implemented it into 3D Slicer.

Re-Orientation Approach for Segmentation of DW-MRI: This work proposes a methodology to segment tubular fiber bundles from diffusion weighted magnetic resonance images (DW-MRI). Segmentation is simplified by locally reorienting diffusion information based on large-scale fiber bundle geometry. Segmentation is achieved through simple global statistical modeling of diffusion orientation, which permits convex optimization formulation of the segmentation problem, combining orientation statistics and spatial regularization. The approach compares very favorably with segmentation by full-brain streamline tractography.

Registration

Optimal Mass Transport-based Registration: We have provided a computationally efficient non-rigid/elastic image registration algorithm based on the Optimal Mass Transport theory. We use the Monge-Kantorovich formulation of the Optimal Mass Transport problem and implement the solution proposed by Haker et al. using multi-resolution and multigrid techniques to speed up the convergence. We also leverage the computation power of general-purpose graphics processing units available on standard desktop computing machines to exploit the inherent parallelism in our algorithm. We extend the work by Haker et al. who computed the optimal warp from a first order partial differential equation (PDE), an improvement over earlier proposed higher order methods and those based on linear programming. We further implement the algorithm by using a coarse-to-fine strategy, which results in phenomenal improvement in convergence. We have applied it successfully to the registration of 3D brain MRI datasets (preoperative and intra-operative), and are currently extending it to the non-rigid registration of baseline DWI to brain MRI data.

Atlas Regularization for Image Segmentation: Atlas-based approaches have demonstrated the ability to automatically identify detailed brain structures from 3-D magnetic resonance (MR) brain images. Unfortunately, the accuracy of this type of method often degrades when processing data acquired on a different scanner platform or pulse sequence in comparison with the data used for the atlas training. In this paper, we improve the performance of an atlas-based whole brain segmentation method by introducing an intensity renormalization procedure that automatically adjusts the prior

221

atlas intensity model to new input data. Validation with manually labeled test datasets has shown that the new procedure improves the segmentation accuracy (as measured by the Dice coefficient) by 10% or more for several structures including hippocampus, amygdala, caudate, and pallidum. The results verify that this new procedure reduces the sensitivity of the whole brain segmentation method to changes in scanner platforms and improves its accuracy and robustness, which thus facilitates multicenter or multisite neuroanatomical imaging studies.

Point-Set Rigid Registration: We have proposed a particle-filtering scheme for the registration of 2D and 3D point sets undergoing a rigid body transformation. Moreover, we incorporate stochastic dynamics to model the uncertainty of the registration process. We treat motion as a local variation in the pose parameters obtained from running a few iterations of the standard Iterative Closest Point (ICP) algorithm. Using this idea, we introduced stochastic motion dynamics to widen the narrow band of convergence as well as provide a dynamic model of uncertainty. In contrast with other techniques, our approach requires no annealing schedule, which reduces the computational complexity and maintains the temporal coherency of the state (i.e., no loss of information). Also, unlike most alternative approaches for point set registration, we make no geometric assumptions on the two datasets. We applied the algorithm to different alignments of point clouds and it successfully found the correct optimal transformation that aligns two given point clouds, despite the differing geometry around the local neighborhood of a point within their respective sets.

Regularization for Optimal Mass Transport: To extend the flexibility of the existing Optimal Mass Transport algorithm, we added a regularization term to the function being minimized. This term controls the tradeoff between how well two images match after registration versus how warped the transformation map can become. A weighted sum of squared differences is used to penalize having to move mass over long distances; this addition also helps to keep the transformation physically accurate by reducing the likelihood that the transformation grid will fold over itself and keeping the grid smooth.

Registration of DW-MRI to Structural MRI: Optimal Mass Transport was applied to the problem of correcting EPI distortion in DW-MRI. A mask for white matter in DW-MRI was registered to the white matter mask extracted from the structural MRI for the same patient. Prior to registration, it is important to normalize intensities in the two masks; this was done by dividing the images into regions and uniformly normalizing over each region to assure the sum of the intensities is equal. Then, once a transformation between the white matter masks was calculated, this transformation was applied to the original DW-MRI image.

Shape Analysis

Shape Analysis Framework Using SPHARM-PDM: We have provided an analysis framework of objects with spherical topology, described by sampled spherical harmonics SPHARM-PDM. The input is a set of binary segmentations of a single brain structure, such as the hippocampus or caudate. These segmentations are first processed to fill any interior holes. The processed binary segmentations are converted to surface meshes, and a spherical parametrization is computed for the surface meshes using area preserving, distortion minimizing spherical mapping. The SPHARM description is computed from the mesh and its spherical parametrization. By using the

first order ellipsoid from the spherical harmonic coefficients, the spherical parametrizations are aligned to establish correspondence across all surfaces. The SPHARM description then is sampled into triangulated surfaces (SPHARM-PDM) via icosahedron subdivision of the spherical parametrization. These SPHARM-PDM surfaces are all spatially aligned using rigid Procrustes alignment. Group differences between groups of surfaces are computed for simple group wise comparison using the standard robust Hotelling T 2 sample metric. This tool further provides a new statistical method that allows one to test and control with subject covariates via a permutation testing of GLM-based MANCOVA metrics. Statistical p-values, both raw and corrected for multiple comparisons, result in significance maps. We provide additional visualization of the group tests via mean difference magnitude and vector maps, maps of the group covariance information, local correlation, and z-scores. We have a stable implementation, and current development focuses on integrating the current command line tools into Slicer via the Slicer execution model and XNAT integration. A first Slicer module prototype has been developed without XNAT integration.

Population Studies Using Tubular Surface Model: We have proposed a tubular shape model for the cingulum bundle which models a tubular surface as a center-line coupled with a radius function at every point along the center-line. This model shows potential for population studies on the cingulum bundle, which is believed to be involved in schizophrenia, since it provides a natural way of sampling the structure to build a feature representation of it. We are currently segmenting the cingulum bundle from a population of brain datasets, towards performing this population analysis using the Pott's Model.

Automatic Outlining of Sulci on a Brain Surface: We present a method to automatically extract certain key features on a surface. We apply this technique to outline sulci on the cortical surface of a brain, where the data is taken to be a 3D triangulated mesh formed from the segmentation of MR image slices. The problem is posed as energy minimization by penalizing the arc-length of segmenting curve using conformal factor involving the mean curvature of the underlying surface. The computation is made practical for dense meshes via the use of a sparse-field method to track the level set interfaces and regularized least-squares estimation of geometric quantities.

Additional information is available on the NAMIC wiki.
http://wiki.na-mic.org/Wiki/index.php/NA-MIC_Internal_Collaborations: StructuralImageAnalysis

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3.3   fMRI Analysis

Key Investigators
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Harvard/BWH: Sylvain Bouix, Marek Kubicki, Carl Frederick Westin, Sandy Wells

Summary of Progress

Our group provides support to NA-MIC for problems that involve the statistical variability of anatomy and function across subjects and between populations. We use computational models of such variability to improve predictions for individual subjects and to characterize populations. We work primarily with anatomical, DTI, and fMRI images. In the current reporting cycle, our efforts have been focused on two new methods in fMRI: one that characterizes functional connectivity patterns from fMRI, and a second that corrects the distortion present in EPI for registration with structural MRI.

Connectivity Analysis: One of the major goals in analysis of fMRI data is the detection of functionally homogeneous networks in the brain. We have developed a new method for characterizing functional connectivity patterns from fMRI. In contrast to the seed-based analysis typically used to identify networks of co-activation, we propose to use clustering to simultaneously estimate the networks and their representative time courses, which effectively replaces user-specified seeds. During this year, we validated this method for characterizing functional connectivity patterns from fMRI. To investigate the sensitivity of the analysis to the generative model of the signal, we implemented and compared two distinct algorithms, Mixture-Model Clustering and Spectral Clustering, in application to this problem. We validated our approach in rest state fMRI scans of 45 healthy subjects. Our results demonstrate that the detected networks are stable across subjects and across methods. At the same time, we worked with the Harvard DBP to identify relevant clinical datasets, in which our approach promises to identify the effect of a disorder. We have started a collaboration to apply the method to a group of schizophrenia patients and normal controls.

Distortion Correction for EPI-Based Functional Imaging: We developed and demonstrated a method that corrects the distortions present in echo planar images (EPI) and registers the EPI image to structural MRI scans. Our approach does not require acquisition of fieldmaps, modification of EPI acquisition parameters, or detailed knowledge of the shim system. The technique consists of two steps. First, a classifier is used to segment structural MR into an air/tissue susceptibility model. The resulting tissue map serves as input to a first order perturbation field model to compute a subject-specific fieldmap. The classifier is trained based on MR-CT image pairs, by using MR intensities as features and exploiting air segmentation in the CT images to construct labels. Second, a simultaneous shim estimation and registration algorithm is used to solve for the lower order field perturbations (shim parameters) needed to accurately unwarp and register the EPI data.

Additional information is available on the NA-MIC wiki

http://wiki.na-mic.org/Wiki/index.php/NA-MIC_Internal_Collaborations:fMRIAnalysis
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3.4   NA-MIC Kit Theme

The NA-MIC Engineering Core has, to a great extent, realized its goal of engaging the wider biomedical community. This community extends worldwide and has leveraged the efforts of many developers beyond the direct influence of NA-MIC. This has resulted in significant advances at relatively low cost. This said, and without diminishing the contributions of our many external collaborators, the senior members of the Core 2 team are:
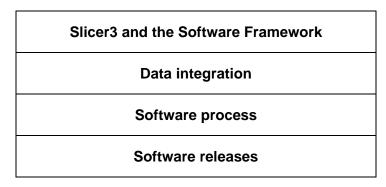
> **Key Investigators**
> **Kitware:** Will Schroeder (Core 2 PI), Sebastien Barre, Luis Ibanez, Bill Hoffman
> **GE:** Jim Miller, Xiaodong Tao
> **Isomics:** Steve Pieper, Alex Yarmarkovich, Curt Lisle, Terry Lorber
> **WUSTL:** Dan Marcus
> **UCSD:** Jeffrey Grethe

Summary of Progress
The NA-MIC-Kit consists of a framework of advanced computational resources including libraries, toolkits, and applications; as well as the support infrastructure for testing, documenting, and deploying leading-edge medical imaging algorithms and software tools. The framework has been carefully constructed to provide low-level access to libraries and modules for advanced users, plus high-level application access that non-computer professionals can use to address a variety of problems in biomedical computing.

The focus of projects in the fifth year of the NA-MIC has been on integration. Much of the foundational infrastructure has been established; however, to effectively transition advanced biomedical technology and improve software usability, the various subsystems that compose the NA-MIC-Kit have been extended to accommodate advanced algorithmic development and optimize work flow. The activities in this year's efforts can be broadly categorized as follows:

Slicer3 and the Software Framework
Data integration
Software process
Software releases

Slicer3 and the Software Framework
One of the major achievements of the past year has been the release of version 3.4 of 3D Slicer in May of 2009. http://www.slicer.org/slicerWiki/index.php/Documentation-3.4 Numerous important improvements have been made by the Engineering Core and significant new functionality has been added through other NA-MIC cores and collaborators since the release of version 3.2 in August of 2008. A few notable examples include:

- **An Integrated Data Save Dialog**
  http://www.slicer.org/slicerWiki/index.php/Modules:Saving-Documentation-3.4

- **Significant Rework of the Fiducials Interface**
  http://www.slicer.org/slicerWiki/index.php/Modules:Fiducials-Documentation-3.4

- **A Slices Module to Support Advanced Visualization Modes**
  http://www.slicer.org/slicerWiki/index.php/Modules:Slices-Documentation-3.4

- **Significant Improvements to the Interactive Label Map Editor**
  http://www.slicer.org/slicerWiki/index.php/Modules:Editor-Documentation

- **Integration of a Brain Tumor Change Tracking Module in collaboration with the Brain Science Foundation**
  http://www.slicer.org/slicerWiki/index.php/Modules:ChangeTracker-Documentation-3.4

- **Integration of a Finite Element Meshing Module as a deliverable of the NA-MIC Collaboration Grant at the University of Iowa**
  http://www.slicer.org/slicerWiki/index.php/Modules:IA_FEMesh-Documentation-3.4

- **A Medical Informatics Interface to XNAT in collaboration with BIRN**
  http://www.slicer.org/slicerWiki/index.php/Modules:FetchMI-Documentation-3.4

- **The Ability to Interactively Script Slicer in Python as well as Tcl**
  http://www.slicer.org/slicerWiki/index.php/Slicer3:Python

In addition, there have been major extensions to the diffusion imaging tools, registration tools, filters, image-guided therapy, and other core changes that enhance the utility and applicability of the software.

Data Integration
One of the keys to effective workflow is integration of computational tools with data. To this end, XNAT and BatchMake are directly accessible from Slicer3. XNAT, or the eXtensible Neuroimaging Archive Toolkit, is an open source software platform designed to facilitate management and exploration of neuroimaging and related data. XNAT database can now be directly accessed through the Slicer3 file menu with additional support for data upload and query. BatchMake is a simple, scriptable, cross-platform batch-processing tool that now interfaces to XNAT and can be launched from the Slicer3 application. This means that users can interactively configure computational experiments to process data from an XNAT data repository and then process potentially large collections of data, either locally or distributed across the grid by using Condor.

Software Process
One of the challenges facing developers has been the requirement to implement, test, and deploy software systems across multiple computing platforms. NA-MIC continues to push the state of the art with further development of the CMake, CTest/CDash, CPack, and tools for cross-platform development, testing, and packaging, respectively. In particular, this year saw significant advances in the development of the PHP-based CDash server, which now provides sophisticated query/retrieve, notification, and testing-

results navigation. The CMake system continues to grow rapidly both in the NA-MIC community as well as external to it, reaching a level of approximately 1,000 downloads per day in early 2009 (this figure does not include the CMake distributions now embedded in Linux distributions such as Debian Linux). Other important additions this year include better support for integration of execution modules into Slicer3, packaging of Slicer3 distributions for more platforms with CPack, and the introduction of GUI (Graphical User Interface) testing with the Squish tool.

Software Releases

The NA-MIC-Kit can be represented as a pyramid of capabilities, with the base consisting of toolkits and libraries, and the apex standing in for the Slicer3 user application. In between, Slicer modules are stand-alone executables that can be integrated directly into the Slicer3 application, including GUI integration, while workflows are groups of modules that are integrated together to manifest sophisticated segmentation, registration, and biomedical computing algorithms. In a coordinated NA-MIC effort, major releases of these many components were realized over the past year. These include, but are not limited to:

Slicer 3.4
VTK 5.4
ITK 3.8, 3.10, 3.12
CMake versions 2.6.1 through 2.6.4
CDash version 1.4
BatchMake 1.0.6

Additional information is available on the NA-MIC wiki

http://wiki.na-mic.org/Wiki/index.php/NA-MIC-Kit

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