

What is the BIRN?

The Biomedical Informatics Research Network

Growing Collaborative Biomedical Research Through Technological Advances

The Biomedical Informatics Research Network (BIRN), a National Institutes of Health (NIH), National Centers for Research Resources (NCRR), and U.S. Department of Health and Human Services (DHHS) supported initiative, is establishing a distributed information technology infrastructure to enable fundamentally new capabilities in large-scale studies of human disorders, such as Parkinson's, Alzheimer's, and mental retardation.

The BIRN involves a national consortium of 19 universities and 26 research groups, comprising three

neuroimaging test bed projects that are conducting structural and functional studies of neurological disease.

The BIRN Coordinating Center was established in 2001 to create, support, and distribute essential cyberinfrastructure and to pioneer the model for a persistent, scalable architecture with application beyond neuroimaging.

This integrated cyberinfrastructure is being created upon technologies supported by the next generation Internet and the National Science Foundation (NSF) Middleware Ini-



tiative, including high bandwidth, inter-institutional connectivity via Internet2, grid-based file management and computational services, software and techniques to federate databases, and shared processing, visualization, and analysis environments.

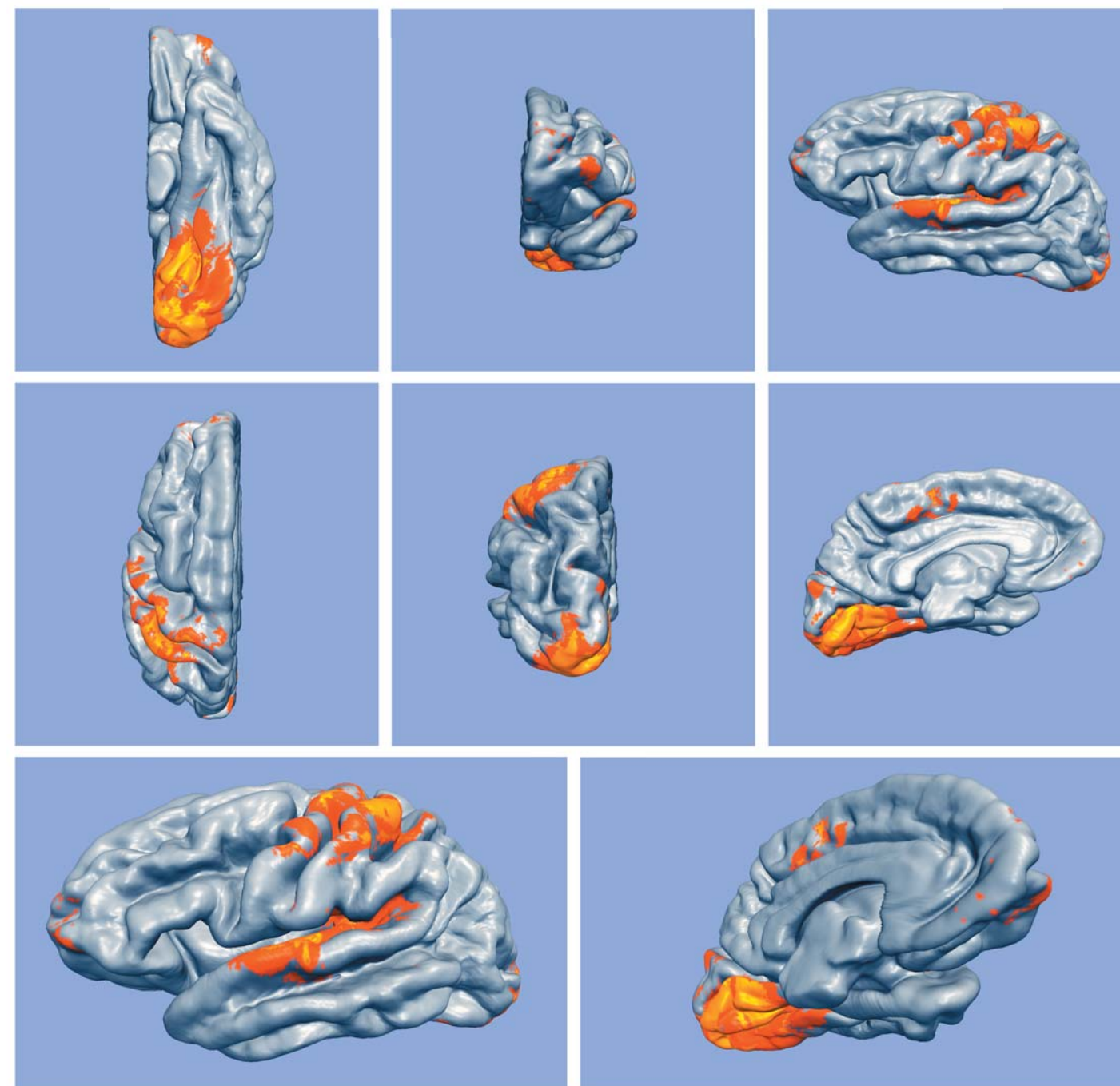
BIRN Sites



The BIRN map has been revised to show the growing BIRN consortium of 19 universities and 26 research groups, including the test beds in which they participate, that make up the BIRN initiative. Print and web versions of the up-to-date map, as well as other images available, can be found at <http://nbirn.net/Publications/Articles/press-temp.htm>.

BIRNing issues

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BIRN, GCRCs Collaborate to Support Biomedical Research

by Christine Reilley, UCSD, Vicky Rowley, UCSD, and Bob DiLaura, Chair BIRN-GCRC Working Group

In its continuing commitment to helping biomedical researchers and clinicians find more effective ways of diagnosing and treating human disease, BIRN is offering its collaborative tools to a new group of general clinical research centers (GCRCs) to promote an exchange of data and analysis tools.

The GCRCs, sponsored by the National Institutes of Health (NIH), comprise a national network of more than 80 centers and provide settings for medical investigators to conduct safe, controlled inpatient and outpatient studies of children and adults. In the initial partnership, BIRN plans to collaborate with two types of GCRCs: centers co-located at existing BIRN-participating institutions and centers with imaging facilities.

Implementation

To promote the partnership, a BIRN-GCRC Implementation Session was held October 14 and 15 in Boston following the BIRN All Hands Meeting to determine how data and tool sharing can meet researchers' needs. A series of presentations introduced GCRC researchers to the BIRN, emphasizing how the grid, tools, and a data integration environment can facilitate collaborative research. (Presentations can be viewed at <http://nbirn.net/AU/Events/GCRC/index.htm>.) Members from the GCRC community also delivered presentations providing an overview of GCRC activities and core research components, which include bioinformatics imaging and biostatistics.

During the session, several GCRC investigators expressed interest in collaborating with BIRN to test the feasibility of such interactions through pilot studies as a first step. Submitted proposals for these pilot projects

are being evaluated, and work will begin in early 2005. Future implementation and availability of BIRN-GCRC collaborations will be undertaken based on the lessons learned from these initial experiments. This approach has been reviewed and was endorsed by the BIRN Executive Committee at their



The BIRN-GCRC Implementation Session promoted the use of BIRN infrastructure to facilitate research for NIH General Clinical Research Centers.

January meeting in Breckenridge, CO. A BIRN-GCRC Implementation Group, which includes representatives from BIRN, GCRCs, and the NIH, has been formed to consider how integration of pilot projects may proceed.

Mutual Benefits

These future collaborations are expected to promote an exchange of data and tools: data deposited by the GCRCs will enrich BIRN's databases, and the tools provided by BIRN will increase GCRC investigators' knowledge of and access to data available for sharing. The collaboration may also yield new imaging and bioinformatics tools to meet the unique needs of clinical researchers.

BIRN is committed to refining its infrastructure to enhance effective data-sharing and comparison of results from human and animal studies. A more refined infrastructure will guarantee that its users can efficiently pool, study, archive, and reanalyze data.

And the diversity of those users is growing rapidly. The GCRC resources bring to BIRN a variety of highly trained personnel, including nurses, nutritionists, and biostatisticians. To meet the needs of its increasingly varied audience, BIRN will tailor its tools and interfaces to ensure that users from any discipline can maintain access and find utility in its applications.

The new partnership with the GCRCs strengthens BIRN's interactions with clinical

(Continued on page 3)

XCEDE SPM XML Toolbox Released

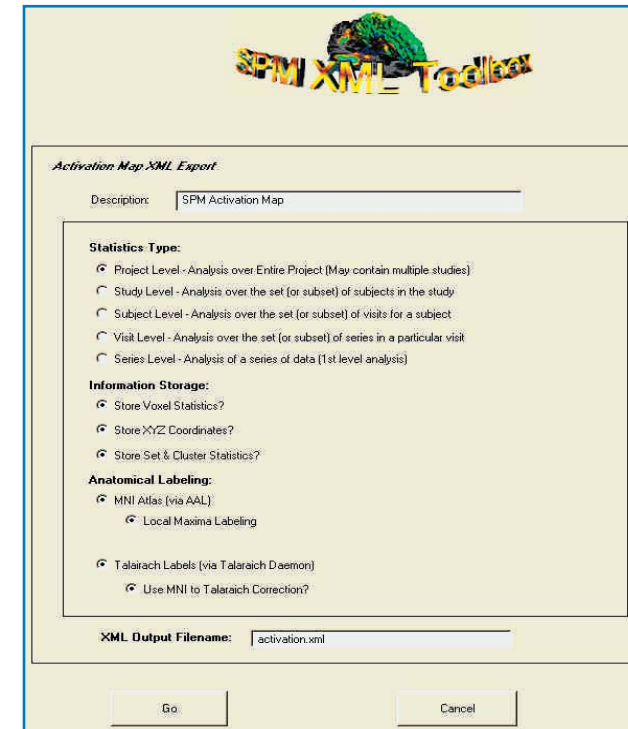
by David Keator, UCI, Syam Gadde, Duke, and Jeffrey Grethe, UCSD

The XML-based Clinical Experiment Data Exchange (XCEDE) SPM Toolbox (<http://www.nbirn.net/Resources/Users/Applications/xcede/index.htm>) has been released for statistical parametric mapping (SPM) software (<http://www.fil.ion.ucl.ac.uk/spm/>).

XCEDE was originally designed in the context of neuroimaging studies and complements the BIRN Human Imaging Database, an extensible database and intuitive web-based user interface for the management, discovery, retrieval, and analysis of clinical and brain imaging data.

This close coupling allows for an interchangeable source-sink relationship between the database and the XML files, which can be used for the import/export of data to/from the database, the standardized transport and interchange of experimental data, the local storage of experimental information within data collections, and human and machine readable description of the actual data.

To facilitate the use of the XCEDE schema, the toolbox has also been developed for the storage of neuro-imaging activation maps and anatomical labels. The toolbox supports both SPM99 and SPM2 statistical structures and has been tested on SUN, LINUX, and Microsoft



The XCEDE SPM XML Toolbox provides an extensive metadata hierarchy for describing and documenting research and clinical studies.

Windows operating systems. The toolbox has been used to capture PET and fMRI analysis results and the associated analysis model specifications. Support for anatomical labeling of results is provided via the Talairach Daemon (<http://ric.uthscsa.edu/projects/talairachdaemon.html>) and Automated Anatomical Labeling (<http://www.cyceron.fr/freeware/>) toolkits. MNI space to Talairach space corrections are supported via Matthew

Brett's mni2tal scripts (<http://www.mrc-cbu.cam.ac.uk/Imaging/Common/mnispace.shtml>).

Additional atlas support will be added as those atlases become available and can be integrated into the SPM/matlab environment.

The XCEDE schema provides an extensive metadata hierarchy for describing and documenting research and clinical studies. The schema organizes information into five general hierarchical levels:

- a complete project
- studies within a project
- subjects involved in the studies
- visits for each of the subjects
- the full description of the subject's participation during each visit

Each of these sub-schemas is composed of information relevant to that aspect of an experiment and can be stored in separate XML files or spliced into one large file

allowing for the XML data to be stored in a hierarchical directory structure along with the primary data. Each sub-schema also allows for the storage of data provenance information allowing for a traceable record of processing and/or changes to the underlying data. Additionally, the sub-schemas contain support for derived statistical data in the form of human imaging activation maps and simple statistical value lists.

BIRN Welcomes New Members

The BIRN owes its high level of functionality to the diligent work and assistance of various related institutions. These institutions contribute funding, facilities, and expert personnel who are dedicated to the success of the BIRN mission. Institutions joining BIRN include:

- Center for Medical Informatics, Yale University
- Clinical Cognitive Neuroscience Laboratory, Yale University
- Computer Science and Artificial Intelligence Laboratory, Massachusetts Institute of Technology
- Health Sciences Center, University of Tennessee, Memphis
- Center for Neuroimaging of Neurodegenerative Diseases, University of California, San Francisco
- Lineberger Comprehensive Cancer Center, University of North Carolina

Morphometry BIRN Update

by Jorge Jovicich, MGH

The National Institutes of Health (NIH) National Center for Research Resources (NCRR) has approved five years of continued support to the Morphometry BIRN. We gratefully acknowledge this support and thank NCRR personnel for their help in transitioning the project from a mix of separate grant supplements and research cores into a unified, multi-site application. (View grant award information at <http://www.ncrr.nih.gov/BIRNnews3T-MRI.asp>.)

The new funding and streamlined organization will allow Morphometry BIRN to refine and expand upon our initial developments, which consist of three main cores.

Research Cores

1) MRI Calibration Core

Optimization and validation of multi-site structural MRI acquisition and calibration methods, with extension to include more vendors, more field strengths, and additional imaging contrasts (i.e., T2 and diffusion for lesion detection white matter characterization)

2) Analysis and Visualization Core

Continued development of morphometric analysis, visualization, and interpretation tools, with the addition of Massachusetts Institute of Technology (MIT) as a new site to support machine-learning techniques (computer programs that learn to classify data, improving their ability to classify over time) to incorporate statistical modeling methods.

3) Informatics Core

Continued development of a neuroinformatics infrastructure that will deliver efficient data management, dynamic access, and application-based querying to neuroimaging data and the associated neuropsychiatry, behavioral, and neurogenetic data.

Work Plans

The work plans for the various components of these cores were discussed at the BIRN All Hands Meeting (October 12–14, Boston), with all-day workshops for each of the three cores preceding the All Hands Meeting. Progress on these new fronts has already begun.

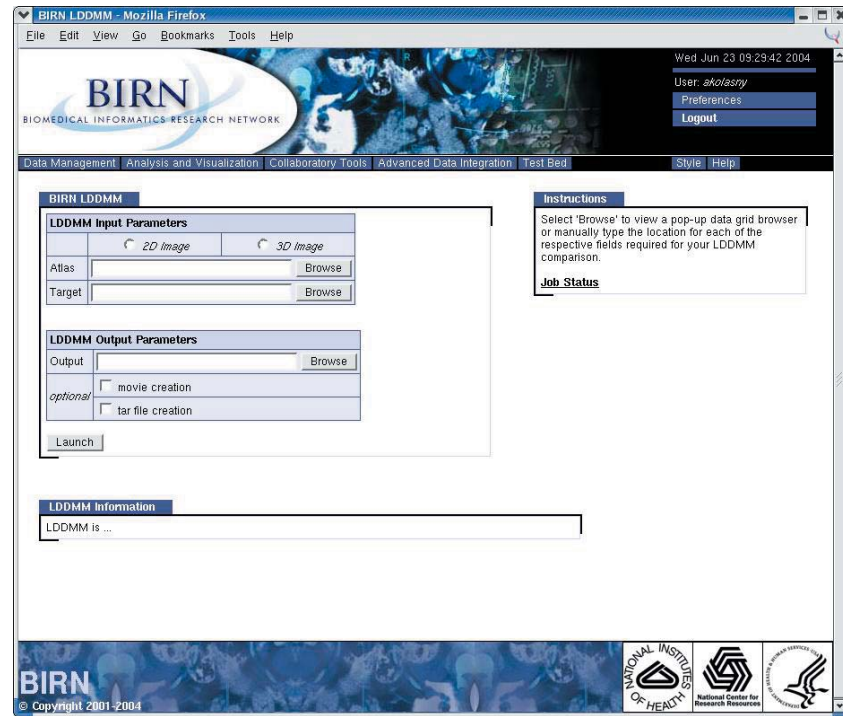
For the MRI Calibration Core, three abstracts have been submitted to the 2005 Annual Meeting of the International Society of Magnetic Resonance in Medicine. The abstracts cover test-retest reliability studies of structural images when an MRI system is upgraded with major hardware changes, which is being explored in a Massachusetts General

Hospital (MGH) study. Distortion correction mechanisms for diffusion tensor imaging are being investigated by separate Johns Hopkins University (JHU) and Duke University studies.

One example of progress in the Analysis and Visualization Core has been to demonstrate the use of the BIRN Virtual Data Grid in an application of distributed computations and distributed storage of the results. The example refers to brain structure shape analyses using the morphometry tools from JHU (Large Deformation Diffeomorphic Metric Mapping, http://cis.jhu.edu/software/lddmm/birn_portal.html) via the Teragrid (<http://www.teragrid.org>).

In this application, due to lack of local storage space at the JHU BIRN rack, the analyses uploaded the input data from the JHU BIRN rack but downloaded the results on the SRB using the UCSD fMRI BIRN rack. This represents a clear example of how multi-site computational and storage resources can be pooled and shared.

On the Informatics core, areas of progress include the refinement of a pair of public mediated databases on the Portal, which BIRN will make available to those who register at the BIRN website. Improvements in the Query Interface enabled us to demonstrate this database/query prototype at several events, including the BIRN-GCRC Implementation meeting, October 15, Boston, MA; the Society for Neuroscience NIH booth, October 23–27, San Diego, CA; and the Radiological Society of North America, November 28 through December 3, Chicago, IL.



Progress in the Analysis and Visualization Core has been to demonstrate the use of the BIRN Virtual Data Grid in an application of distributed computations and distributed storage of the results.

BIRN Links Up With Grids Worldwide

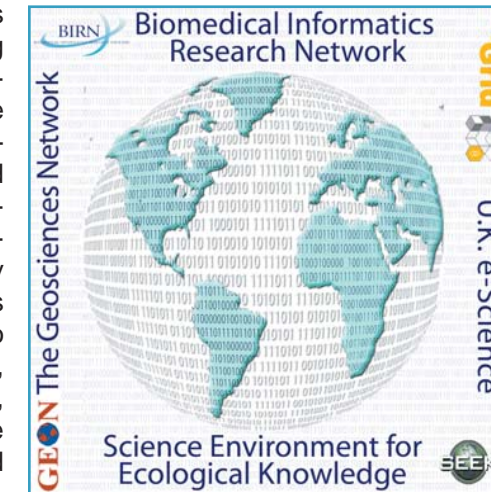
by Mark Ellisman, Director, BIRN-CC and Christine Reilley, UCSD

BIRN's core activities focus on developing and refining an end-to-end cyberinfrastructure that federates large, distributed data caches and harnesses powerful computational resources integrated with user-friendly visualization and analysis software. The goal is to help investigators share, disseminate, preserve, and analyze the massive amounts of data collected in biomedical research.

The requirements to provide such a sophisticated environment are not specific to BIRN. In fact, several grid projects from various disciplines in the United Kingdom and the United States share common technological requirements and approaches, such as knowledge-based data integration and scientific workflows.

Infrastructure Model

BIRN is serving as a leading example of an end-to-end infrastructure project for a large application community. From the portal and workflows to the core middleware (i.e., Globus and related systems), the BIRN framework is being considered as a model for other projects worldwide. Initiatives such as myGrid, a UK Research



Council's e-Science program that aims to develop infrastructural middleware to support scientists in making use of complex distributed resources, have been collaborating with BIRN in several areas. The Science Environment for Ecological Knowledge (SEEK) and the Geosciences Network (GEON), two grids based in the U.S., are also actively collaborating with BIRN.

For example, similar architectures employed by BIRN and myGrid integrate data and databases through a semantic data integration environment that bridges diverse types of data—from MRI images to microscopic data—using ontologies, a terminological description of concepts and the relationships between them.

In addition, BIRN, GEON, and SEEK are working towards interoperable standards for data integration and scientific workflows. Providing transparent access to a computing environment that enables easy orchestration

of essential applications into coordinated and flexible workflows remains a core activity of all three grid projects. These workflows are being constructed to seamlessly utilize and benefit from the cyberinfrastructure being deployed to accelerate research. myGrid is establishing similar collaborations, joining forces with related projects in the European Union, such as Comb-e-Chem, a chemistry project, and Geodise, an engineering network.

To build on these informal links already in place, a project called "Link-Up" has been funded by the e-Science program to explore common ground, share best practices, and work towards standards to provide a community-independent framework for the development of grid-based workflow applications. As part of this project, the third Link-up meeting was held October 18–22, 2004 in San

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BIRN, GCRCs Collaborate...

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cal researchers as it strives towards helping researchers and clinicians address today's increasingly complex biomedical issues.

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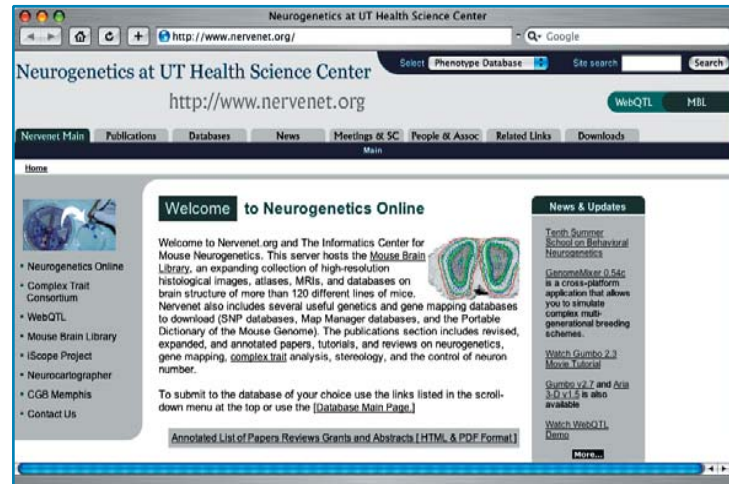
Neurogenetics Team Joins Mouse BIRN

by Jyl Boline, UCLA

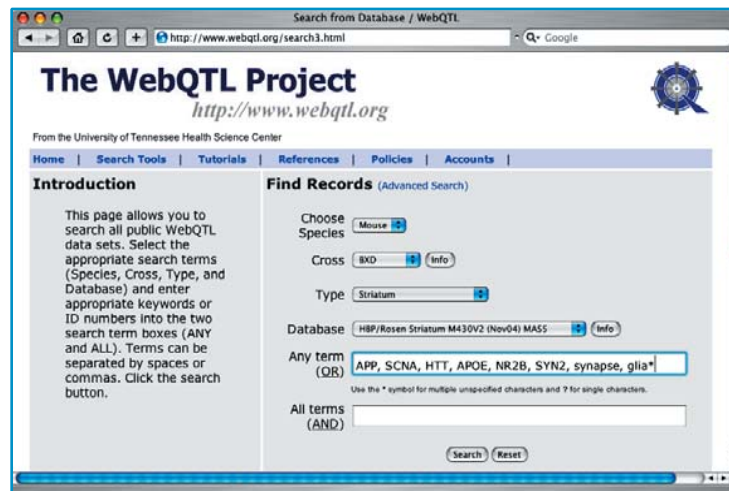
The Mouse BIRN aims to combine strengths in imaging and structural analysis of the central nervous system (CNS) with rapidly expanding genetic and genomics resources. Building powerful tools to bridge disciplines is essential for navigating and exploiting vast image and array data sets on genetically engineered mice.

To create this link, Mouse BIRN has joined with the Informatics Center for Mouse Neurogenetics team. This group of neurogeneticists from the University of Tennessee (Memphis), Drexel University (Philadelphia), and Beth Israel Deaconess Medical Center (Boston) is led by Rob Williams, director of the Complex Trait Consortium. Williams also serves as co-director of the University of Tennessee Center of Genomics and Bioinformatics and chair of the Neuroinformatics Committee of the Society for Neuroscience.

Williams presented the team's challenges of integrating genetic, morphometric, and behavioral data sets at the 2004 BIRN All Hands Meeting. He highlighted a straightforward solution that relies on a Genetic Reference Population (GRP), a set of more than 20 genetically related strains that can be used to acquire coherent multi-scale data sets. A GRP can be exploited to computationally and biologically anneal a nearly unlimited range



The Mouse Brain Library is one of two tools being tested to decipher the genetic basis of variation in mouse brain structure.



The Informatics Center for Mouse Neurogenetics team is also testing WebQTL, which can be used to automatically annotate gene function and to explore natural variation in genes.

of traits to each other using genetic correlations.

Williams also reviewed two powerful tools that are being tested to decipher the genetic basis of variation in mouse brain structure—the Mouse Brain Library (MBL) and WebQTL.

Mouse Brain Library

The MBL contains more than 100,000 low and high-magnification images, photomosaics, and z-axis image stacks of brain sections from more than 200 genetically characterized strains. The MBL is the most diverse image database for on-line morphometry. The next key step is to register this image database into a standard atlas framework to increase its utility for semi-automated analysis and segmentation.

WebQTL

The second resource, WebQTL, is a statistical genetics application that contains a vast amount of array data on gene expression in the forebrain, cerebellum, striatum, stem cells, and liver across a large GRP called the BXD set. WebQTL can be used to automatically annotate gene function and to explore natural variation in genes that are involved in neurodegeneration and other CNS diseases such as epilepsy, schizophrenia, and autism. Although many tools allow users to assemble networks of correlated phenotypes and identify shared genetic regulators, WebQTL can rapidly identify

and map gene variants and modifiers that generate differences in brain structure, neuropharmacology, and behavior.

The Informatics Center for Mouse Neurogenetics is a welcome addition to Mouse BIRN that will enable us to expand the Mouse BIRN scope and our ability to examine the neurobiology of diseases.

BIRN Links Up With Grids Worldwide...

(Continued from page 3)

Diego to focus on recent developments in grid workflow systems and their use in specific scientific application domains. The meeting aimed to define common

approaches to workflow and service registries, workflow annotations and semantic extensions, data provenance, and workflow interoperability.

Through collaborations and knowledge-

sharing such as those at the LinK-Up conference, BIRN researchers and their colleagues have moved one step further towards the research community's vision of a global science grid.

Slicer: Visualization and More...

(Continued from page 8)

the Query Atlas project is to address this abundance of information by producing an interactive 3D and web-based knowledge-management tool for neuroscience that is coupled to the BIRN federated database.

Once a 3D MRI image with neuroanatomical labels is loaded into Slicer from the BIRN datasets, the user can identify cortical or subcortical regions. Using the Query Atlas, the user can then query multiple sources such as PubMed, Google or other databases regarding those anatomical regions and other user-specified keywords. In this way the user can get immediate feedback about other published findings pertaining to those areas of the brain (e.g., what other research has been published regarding memory function in schizophrenia and activation in the prefrontal cortex and posterior parietal lobule?). This allows the investigator to use a single software program to perform real-time literature searches while exploring a current dataset.

The figure on the previous page shows an example Query Atlas search of PubMed for publications regarding schizophrenia and five labeled points. The blue image is a view of a standard cortical surface, with activation from a sensorimotor fMRI

When used in conjunction with the Query Atlas, 3D Slicer allows the investigator to use a single software program to perform real-time literature searches while exploring a current dataset.

scan overlaid on it. The postcentral gyrus and superior temporal gyrus have been identified for the Query Atlas, as have several other regions not visible in the view shown.

New Modules in Development

The Ibrowser and the fMRIEngine are new and early-stage software modules that permit the spatial processing and analysis of fMRI time-series data within Slicer's

visualization environment. Together, the two modules form a processing pipeline for fMRI analysis and visualization within Slicer that will be interoperable with both the standard Function BIRN processing pipeline (see *BIRNING Issues* Volume 3.1) and the Federated Database. The Ibrowser and fMRIEngine modules are being developed within Slicer to organize, preview, and process multi-volume datasets, and to compute statistical activation volumes and visualize the results in the context of the subject's anatomy. From any stage in the pipeline, data may be loaded into the Ibrowser or the fMRIEngine.

AnalyzeReader, FSLReader, and BXHReader modules have been developed to promote interoperability between the Function BIRN processing pipeline and federated databases. Writers of these formats, and native input/output routines within Slicer that read and write such Function BIRN file formats as NiftI and the BIRN XML descriptors associated with them, will be developed over the next few years.

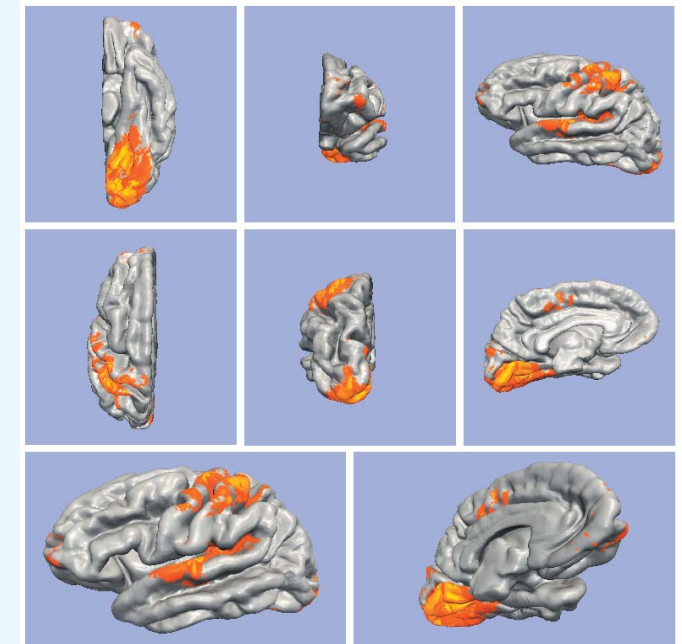
Cover Image

3D Slicer Visualizations Facilitate Function BIRN Research

The images to the left show two 3D Slicer visualization views of activation for one of the human phantoms at MGH for four runs of the sensory motor task; and the estimated ground truth for activation derived over those runs via the STAPLE algorithm.

To read more about these visualizations, see the Function BIRN article on the previous page, or look for the upcoming article in the journal *Radiology*.

Zou KH, Greve DN, Wang M, Pieper SD, Warfield SK, White NS, Manandhar S, Brown GG, Vangel MG, Kikinis R, Wells WM, III for the FIRST BIRN Research Group (in press, 2005) Factors Impacting the Reproducibility of Functional MRImaging: Preliminary Results of a Prospective Multi-Institutional Study by the Biomedical Informatics Research Network. *Radiology*.



Slicer: Visualization and More

by Jessica Turner, UCI

Visualization research in the first phase of the Function BIRN focused on improving interoperability among major software packages and their integration with parallel efforts in the Morphometry BIRN. Within both human-oriented test beds, one goal has been to display analysis results from various tools within a common software environment based on the 3D Slicer. 3D Slicer (or simply "Slicer"), an application that serves as a foundation for advanced medical image computing research, has played an integral role in Function BIRN research. Future efforts focus on extending Slicer's use with the development of modules that process and analyze fMRI time-series data within Slicer's visualization environment. Full source code and documentation are available free of charge at <http://www.slicer.org>.

What Does Slicer Do?

Slicer provides an open-source, cross-platform, and modular suite of tools for registration, segmentation, image analysis, and multi-modality visualization. Of particular use for Functional Magnetic Resonance Imaging (fMRI), Slicer allows users to view co-registered MRI images and fMRI analysis results, and to rotate the images for three dimensional reviews, including zooming toward or away from them for better inspection.

The Slicer software accesses hardware-accelerated 3D computer graphics on Windows, Linux, Solaris, and Mac OSX

platforms through the underlying open source Visualization Toolkit (VTK) processing library, which is layered atop OpenGL. This efficient and extensible system also integrates technology from the NLM-sponsored open source Insight Segmentation and Registration Toolkit (ITK), resulting in a well designed C++ class hierarchy that implements state-of-the-art medical image processing algorithms in a portable library.

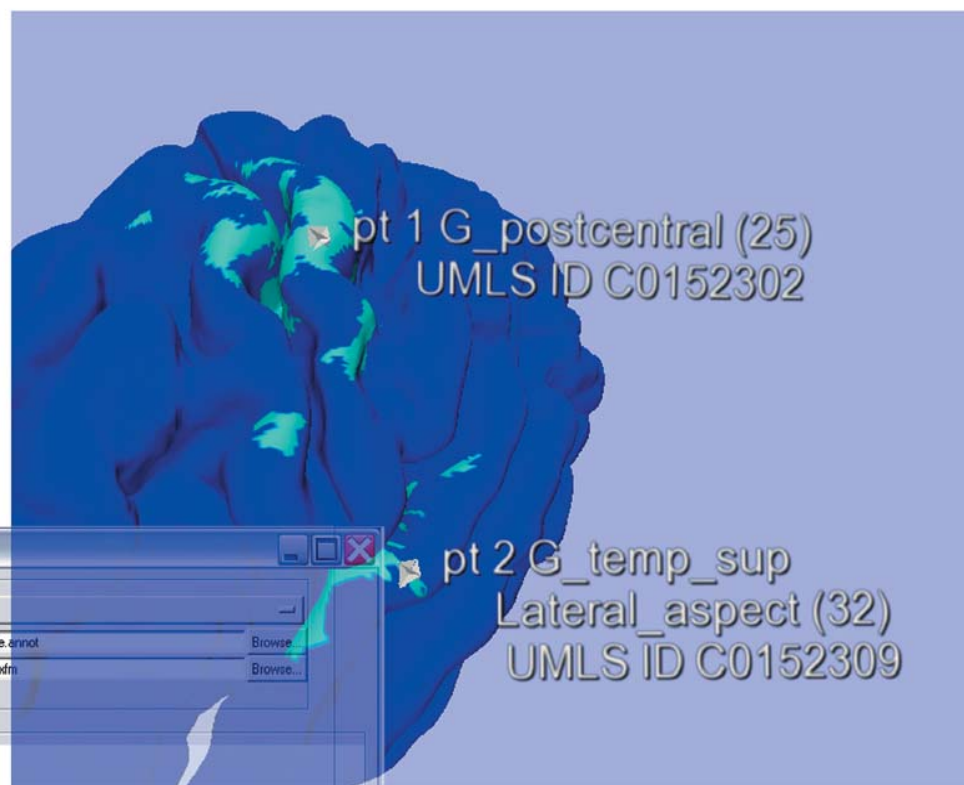
A component of other NIH-funded research, Slicer software has been tightly integrated with the National Alliance for Medical Image Computing (NAMIC) development plan to apply advanced algorithm and software engineering technologies to applications designed to leverage BIRN infrastructure.

Slicer and the Query Atlas

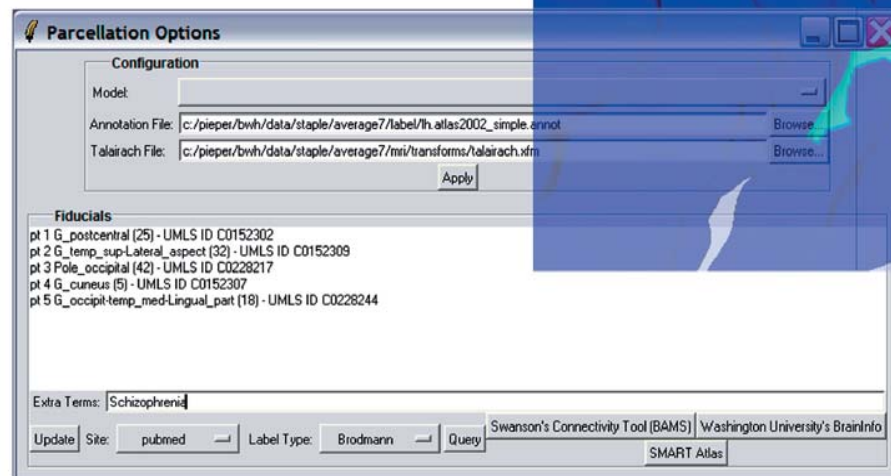
After running a statistical analysis, such

as fMRI activation differences between patient and control populations, the researcher is faced with the question of why particular areas of the cortex are affected while others are not. The relevant neuroscience literature involves thousands of publications using many different anatomical labeling schemes and providing information for many species at different scales. Segmentation and parcellation algorithms can provide specific anatomical names for individual brain structures to increasingly fine levels of detail. These regions can be given labels that have well-defined scientific meaning when they are tied to specific ontologies; for example, the UMLS (uniform medical language system, <http://www.nlm.nih.gov/research/umls/>) defines a hierarchical ontology of medically related terms. The goal of

(Continued on page 9)



3D Slicer has played an integral role in Function BIRN research. Slicer provides an open-source, cross-platform, and modular suite of tools for registration, segmentation, image analysis, and multi-modality visualization that is particularly useful with Functional Magnetic Resonance Imaging (fMRI).



NAMIC PI Kikinis Promotes "Big Science"

Ron Kikinis is a professor of radiology at Harvard Medical School and director of the Surgical Planning Laboratory (SPL) in the Department of Radiology, Brigham and Women's Hospital. He is the principal investigator for the National Alliance for Medical Image Computing (NAMIC), an NIH National Centers for Biomedical Computing (NCBC) program which is leveraging the BIRN cyberinfrastructure to facilitate multi-center image data collaborations.



Ron Kikinis

Kikinis is concentrating on developing fully automated segmentation methods and introducing computer graphics into the operating room.

Q. Where did you receive your education and what were your areas of study?

A. University of Zurich Medical School, Zurich, Switzerland: received an M.D. in medicine, 1982. My residency was in radiology, with a focus on neuroradiology. This led to an interest in image processing, and later, image guided therapy.

Q. What attracted you to the BIRN project?

A. The BIRN projects have been a unique opportunity to bring a "Big Science" perspective to our community.

Q. How do you think BIRN can be valuable/useful to the neuroscience research community?

A. I am excited by the opportunity to perform real infrastructure work for neuroscience that has not been possible in previous projects. BIRN provides a platform on which to develop a new class of algorithms and advance the fields. An excellent example is our recently awarded grant to develop a national medical image computing infrastructure. This grant, NAMIC (<http://www.na-mic.org>), is part of the NIH Roadmap's NCBC program. I serve as the overall PI for NAMIC, and many of the NCBC sites are also strongly involved in the BIRN. BIRN is providing

the critical data and cyberinfrastructure to enable the development and distribution of innovative applications software that leverages calibrated multi-center image data.

Q. How do you think the BIRN infrastructure will translate to other areas of health care research?

"Many laboratories face the same issues of large scale image data management and multi-site data sharing and collaboration. BIRN has the potential to provide off-the-shelf solutions for this growing community."

—Ron Kikinis

A. Many laboratories face the same issues of large scale image data management and multi-site data sharing and collaboration. BIRN has the potential to provide off-the-shelf solutions for this growing community. If we do our jobs right, this initiative has great potential. At the SPL, BIRN-related improvements to the 3D Slicer program have provided benefits in other research areas where the program is used such as image guided therapy. (For more information on 3D Slicer, see page 8)

Q. What are some of the challenges you have experienced working with the BIRN?

A. What the BIRN community must

understand is that we need to show measurable scientific progress in ways that are unique to BIRN. This means publishing in peer reviewed publications that demonstrate the contributions of BIRN.

Q. What major challenges do you see on the horizon?

A. BIRN is moving rapidly to provide tangible technology solutions with a broad scientific impact, as this is how the value of the project is to be determined. Spending the first years sorting out the sociology of group interaction has been a crucial step. We must now show that this step was worth the extensive time and effort we

have all put into it.

Q. Are there final thoughts you would like to add?

A. The recent NIH funded NAMIC, part of the NIH Roadmap NCBC initiatives, focuses on developing public domain, open source software for medical image computing. The initial biological projects will be driven by schizophrenia problems and will expand to a broader range of disease problems in subsequent years. NAMIC development will leverage BIRN's cyberinfrastructure development expertise for application development and use the BIRN Portal for data sharing among a distributed group of medical imaging researchers nationwide.

BIRN-CC Update

by Mark James and Patricia Maas, UCSD

The beta version of BIRN 2.0 was released by the BIRN-CC January 28 for testing. In addition to the features outlined in the October *BIRning Issues* (Vol. 3.1), another capability has been added to the release: the compute node of each rack, known as the Gcomp, will be installed with Large Diffeomorphic Deformation Metric Mapping (LDDMM) and 3D Slicer (see Function BIRN, page 8). Although these programs are already accessible through the BIRN Portal, integration into the Gcomps will enhance their interoperability with other BIRN tools.

BIRN 2.0 includes the following features:

- improved data mediation tools
- standardized security
- portal enhancements
- increased data grid capabilities
- upgraded infrastructure management tools

Sites interested in participating in the beta testing of version 2.0 should contact Vicky Rowley, BIRN-CC Infrastructure Area Lead, at (858) 822-0708 or vrowley@ucsd.edu.

All Hands Meeting (AHM) Recap

More than 150 BIRN participants attended the October 12 and 13 AHM in Boston, MA. This year's function, held to promote test bed innovation and collaboration, brought together personnel from BIRN test bed sites and included sites interested in joining the BIRN initiative.

NIH Awards BIRN-CC Five-Year Renewal

The National Center for Research Resources (NCRR) awarded five years of continued support to the BIRN-CC to develop, maintain, and improve BIRN cyberinfrastructure.

"Information technology offers tremendous potential to advance our ability to diagnose and treat disease," said NCRR Director Judith L. Vaitukaitis, M.D. "With this additional investment in the BIRN consortium, we hope to provide researchers with networked analytical tools that will greatly advance our knowledge of neurological disorders such as depression, schizophrenia, and Alzheimer's disease."

Immediately preceding and following the AHM were well-attended ancillary training sessions, which included:

- Morphometry and Function BIRN Informatics
- Morphometry Analysis and Visualization Tools
- Mouse BIRN General Working Group
- Advanced fMRI Statistical Analysis
- Clinical Queries and Data Integration

- Grid Implementations and High Performance Computing

To view photos and presentations from the AHM, see <http://nbirn.net/AU/Events/AHM2004/presentations.htm>.

BIRN-GCRC Implementation Session Follow Up

Following the AHM, the BIRN held a two-day workshop, October 14 and 15, to discuss implementing strategies that would allow additional NIH General Clinical Research Centers (GCRC) to utilize the BIRN infrastructure to facilitate their collaborative research. Session leaders included Bob DiLaura, president of the Association GCRC Information Technology Professionals, test bed project managers Jessica Turner, Jorge Jovicich, Mark James, and BIRN-CC Scientific Coordinator Jeffrey Grethe.

Twenty-three facilities from California to New York participated in the session. "From its inception, we envisioned the BIRN cyberinfrastructure as an adaptable and extensible data integration system that would be useful across the many subsets of biomedical research," stated BIRN-CC Director Mark Ellisman. "We wish to facilitate the evolution of a collaborative research community by providing a seamless interface to the researchers as end-users."

To view photos and presentations from the BIRN/GCRC Implementation Session, see <http://nbirn.net/AU/Events/GCRC/presentations.htm>.



More than 150 BIRN participants from sites across the country attended the October 12 and 13 All Hands Meeting in Boston, MA.

Participants Present Throughout the Nation

BIRN members presented posters, manned booths, and participated in panel sessions throughout the United States.

September 2004

Internet2 Member Meeting, Austin, Texas

BIRN-CC Project Manager Mark James presented the poster "Biomedical Informatics Research Network: Building a National Collaboratory for Brain Research."

October 2004

Society for Neuroscience, San Diego, California

BIRN researchers manned a booth in conjunction with NCRR to demonstrate and present its infrastructure to the neuroscience community.

November 2004

SuperComputing 04, Pittsburgh, Pennsylvania

BIRN-CC Project Manager Mark James participated in the Perspectives on Building Communities for Effective Development and Application of Cyberinfrastructure workshop. James was the NIH representative on a panel of National Science Foundation (NSF) grid implementation experts. BIRN members also participated in the NCRR Biomedical Computing Resource Centers booth.

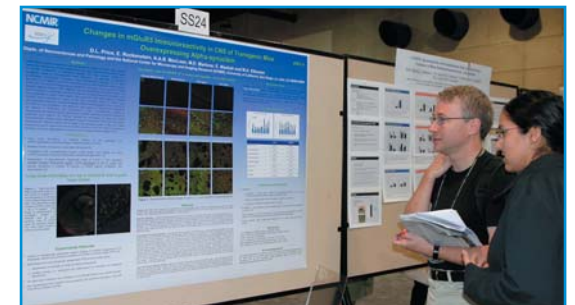
November/December 2004

Radiological Society of North America, Chicago, Illinois

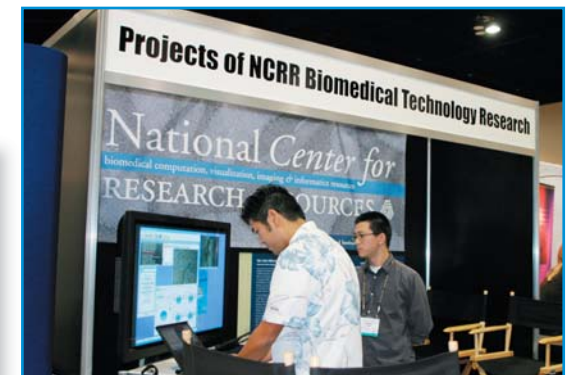
Morphometry BIRN Project Manager Jorge Jovicich, Principal Investigator Bruce Rosen, Co-PI James McFall, and BIRN-CC Scientific Coordinator Jeffrey Grethe presented eight tutorial sessions to members of the RSNA as part of the Internet2/National Library of Medicine infoRAD tutorials (<http://apps.internet2.edu/rsna2004-demos.html>).



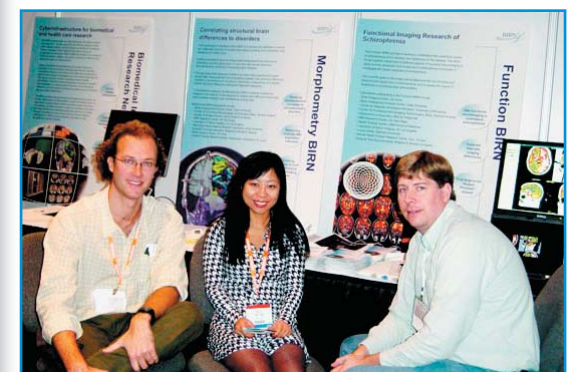
In October 2004, project managers from the BIRN-CC and Morphometry and Function BIRNs discussed BIRN research and infrastructure with attendees at the Society for Neuroscience meeting in San Diego, CA.



Mouse BIRN researcher Diana Price discusses her poster regarding the overexpression of Alpha-synuclein in transgenic mice at SFN.



BIRN participants from NCMIR held Telescience demonstrations at SFN. Telescience is closely associated with developing BIRN infrastructure.



Jorge Jovicich, Kelly Zou, and Jeffrey Grethe, among others, presented to the RSNA.

Upcoming Meetings

March 2-5, 2005

Morphometry BIRN All Hands Meeting, Miami, Florida

March 21-23, 2005

Function BIRN All Hands Meeting, UC Irvine, California

<http://www.surveymonkey.com/s.asp?u=2178800789>

April 7-9, 2005

HealthGRID 2005, Oxford, United Kingdom

<http://oxford2005.healthgrid.org/>

May 1-5, 2005

2005 Spring Internet2 Meeting, Arlington, Virginia

<http://events.internet2.edu/2005/spring-mm/gensched.html>

June 12-16, 2005

11th Annual Meeting of the Organization for Human Brain Mapping, Toronto, Canada

<http://www.meetingassistant.com/ohbm2005/>