

BIRN



A shared biomedical IT infrastructure to hasten the derivation of new understanding and treatment of disease through use of distributed knowledge



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Jeffrey Grethe: Scientific Coordinator for the BIRN-CC

by Skip Cynar, Senior Science Writer



Jeff Grethe

Dr. Jeffrey Grethe is a Principal Design Engineer with the Center for Research in Biological Systems, Department of Neurosciences at the University of California, San Diego, and the Associate Director and Scientific Coordinator of the BIRN Coordinating Center where he oversees day-to-day operations. As the team leader, he directs the creation of new software tools to support BIRN's scientists and their

collaborations at multiple centers. One of Grethe's research efforts is focused on providing the infrastructure to enable scientists to create, manage, and discover biomedical information and knowledge. In addition, Grethe is developing a computational framework to allow a researcher easy access to large scale computational resources for the analysis and visualization of medical image data through the National Alliance for Medical Imaging Computing. The focus of Grethe's efforts centers on accelerating and improving how neuroscientists conduct experimental research using virtual research communities. Grethe's passion for informatics and computer science is helping to catalyze new scientific applications throughout BIRN. I spoke with him on December 19, 2007.

Q. Where are you from?

A. I was born and raised in New Jersey to German parents and moved out to California during college when I was 20. From an early age, my interests clustered around learning how the

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Jeff Grethe at work next to Vadim Astakhov and Brian Sanders of the BIRN-CC.

brain worked, robotics, and artificial intelligence. I started at Rutgers as an undergrad in electrical engineering but decided after two years that electrical engineering was not going to provide the means to explore my interests. I followed my family to California and completed my bachelor's at UC Irvine where I studied applied mathematics. Upon receiving my bachelor's, I spent a year in an internship at BASF, the German Chemical Company, working on a neural network project, in collaboration with the University of Kaiserslautern. The project's aim was to model the biological response of the insect nervous system to various pesticides.

Around this time, several universities began creating new programs that bridged the disciplines of computer science and neuroscience, allowing me to pursue my interest in neural networks. I decided to pursue graduate work at the University of Southern California in the lab of Richard Thompson where I studied classical eyeblink conditioning, specifically how the cerebellum was involved in coordinating responses. While at USC, Thompson's lab, in collaboration with the Program in Neural Informational and Behavioral Sciences, led

by Michael Arbib, was awarded funding from the Human Brain Project, an NIH initiative to develop and support the new science of neuroinformatics. I quickly became involved with designing database informatics software for supporting a collection of electrophysiological data to be used in biologically realistic simulation models of the cerebellum. Our objective was to create a federated infrastructure that would allow the exchange of data between experimental and modeling groups. This research set the groundwork for my present and future research interests at the BIRN-CC.

After graduate school, I spent 1998-2000 at Emory University with Scott Grafton learning about imaging technologies, such as PET, sMRI, and fMRI. And when Grafton accepted a new position to set up and direct the new Dartmouth Brain Imaging Center in New Hampshire, I migrated north with him to apply my background in informatics to help establish the new Imaging Center and the recently funded fMRI Data Center, led by Michael Gazzaniga at Dartmouth University, over the next two years.

Q. What attracted you to the BIRN Coordinating Center?

A. Good timing and weather. I first met Mark Ellisman in December 2001 while presenting a talk on Dartmouth's fMRI Data Center at an NCRR-sponsored BIRN workshop. The BIRN project was just gearing up at that point, and it felt like a good fit. Besides, that year we received more than one hundred inches of snow at our house, and the prospects of moving to Southern California seemed ideal.

Q. Technology is often developed with one purpose in mind but adopted for another. How do you think the BIRN will be used?

A. I see BIRN as a cutting edge virtual laboratory for science, allowing researchers across the country to form long distance collaborations, share research data, and collaborate using Web 2.0 technologies. It is gratifying to see that other research communities are beginning to leverage BIRN technology to nurture collaborations across new domains of science by creating environments where people can build shared tools for projects spanning many institutions and disciplines.

For the research community, BIRN's main use will be associated with collaborations centered around data—providing a means for researchers to discover relevant data from other researchers and integrate those to perform subsequent analyses. BIRN has also addressed a key need for the public sharing of research data with the creation of the BIRN Data Repository (BDR). Additionally, our success with creating standardized software and hardware components for sharing data is playing an important role in two recent NIH Program Announcements designed to expand data sharing to other scientific domains.

Q. Collaborations are invaluable, but oftentimes create additional hurdles. What are some of the challenges that you have faced working with BIRN?

A. Bridging the gap between researchers and information technology folks has been a challenge at BIRN. Given our different cultures and unique vocabularies, it takes a lot of effort to cultivate productive relationships. But this effort has paid off with a new infrastructure that enables new types of research collaborations.

BIRN has proven to be a relationship builder, a catalyst for new research partnerships. The NIH's recognition of this has helped spawn new collaborative research efforts, the most recent being the two NIH program announcements. The first program announcement, SHARING DATA AND TOOLS: FEDERATION USING THE BIRN AND CaBIG INFRASTRUCTURES (PAR-07-426), is anticipated to bring tools and data to two large-scale data sharing, tool sharing frameworks (BIRN: <http://nbirn.net> and CaBIG: <https://cabig.nci.nih.gov>). Regarding BIRN, the goal is to expand data available through the BIRN Data Repository. The first submission deadline for this PA was January 2008: it will be interesting to watch.

The second NIH program announcement, DATA ONTOLOGIES FOR BIOMEDICAL RESEARCH (PAR-07-425), will encourage researchers to join new and important datasets to existing datasets using emerging standards through ontologies and data federation techniques, such as those developed within BIRN. These two program announcements provide opportunities for the larger scientific community to take advantage of BIRN's integrated hardware-software foundation.

Q. What do you see as the major challenge for BIRN on the horizon?

A. Expansion. With the new NIH programs I depicted, one challenge going into 2008 will be making the transition

from supporting a community of 43 neuroimaging research groups to the deployment of BIRN's core framework to a wider and more diverse biomedical research community. We anticipate some of the challenges of supporting new databases and analysis tools, such as learning how to adapt our current suite of imaging and informatics tools to other domains. Fortunately, we have gained some experience with applying BIRN's core structure to other domains of science. For example the National Database for Autism Research's (NDAR: <http://ndar.nih.gov>) portal and its underlying infrastructure is built on the BIRN foundation and allows autism researchers to utilize an integrated suite of software tools to collaboratively study autism spectrum disorder. NDAR represents a successful proof of concept for leveraging BIRN and applying it to a new science domain.

BIRN's data integration and ontology tools are successfully being leveraged by other projects, including the Neuroscience Information Framework (NIF: <http://nif.nih.gov>) and the CardioVascular Research Grid (CVRG: <http://cvrgrid.org>). The CVRG is using the BIRN collaborative portal environment for the analysis of heart structure, based on techniques developed by researchers in Morphometry BIRN and BIRN-CC. The NIF is a project designed to survey the state of Web resources for the neurosciences and provide a strategy for enhancing to and utilization of these resources. The NIF was designed as a federated system using the BIRN data integration environment to provide simultaneous query access across distributed resources.

Q. Any other challenges?

A. Relationships. With the new NIH programs, we face the challenge of cultivating the trust of new communities of researchers from different organizations and cultures, as well as assimilating new branches of science. It will take an

investment of time and special effort to establish the relationships required to spawn each successful collaboration. As we move out to the larger community, it will be a good test of how our various collaboration-focused tools will be used by new communities of researchers.

We tend to overlook this aspect because it is not something we regularly quantify. In a few years it'll be interesting to look back at what BIRN has achieved in helping to forge new research collaborations.

Q. Any advice for those considering a career in science?

A. Bringing new tools and technology to science can be very rewarding. There are a lot of problems that are interdisciplinary in nature and these can be very exciting, but also daunting at first. For a neuroinformatics researcher like myself, I constantly straddle dual disciplines: neuroscience and informatics. At times I've felt overwhelmed trying to grapple with two rapidly advancing fields of science, but I relish the challenge of leveraging knowledge from informatics and computer science to build new solutions and advance brain science. ■

BIRN-CC Hosts Rack Training



Daniel Wei, Mark James, and others from the BIRN Coordinating Center are pictured during a December 2007 training session for IT professionals responsible for the care and feeding of the growing network of BIRN racks distributed across North America and the UK. Contact Mark James (mjames@ncmir.ucsd.edu), Project Manager of the BIRN-CC, to learn more about future training opportunities offered through BIRN.

Morphometry BIRN: Release of MRI Studio and Update on LDDMM Processing Effort

by Karl Helmer, Morphometry BIRN Project Manager

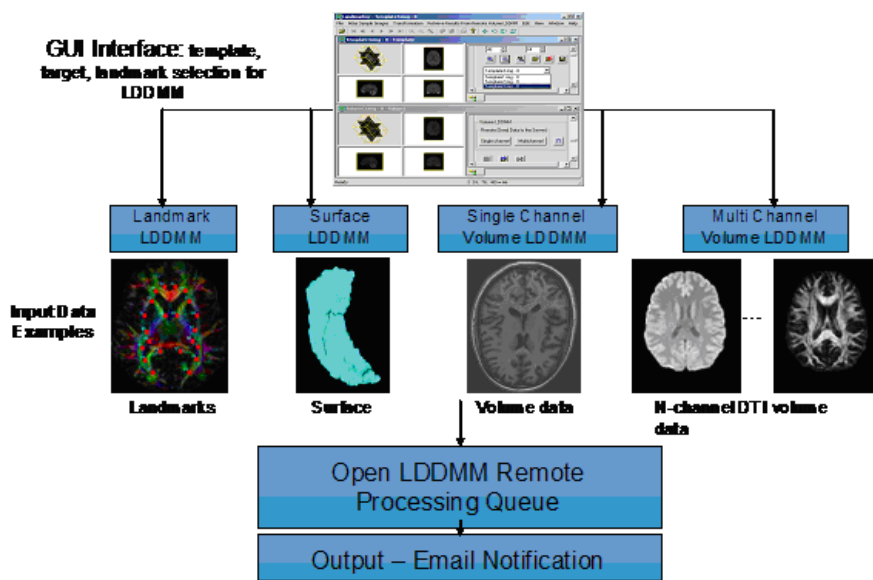


Fig. 1: Schematic of the integration of Large Deformation Diffeomorphic Metric Mapping (LDDMM) processing into MRI Studio. Possible input data include: a) a set of landmarks used for image registration, b) sets of brain structure surfaces, c) imaging volumes, d) structural- and diffusion-weighted imaging data.

A team of programmers from Johns Hopkins University (JHU) has released a new image processing program, MRI Studio. Based on the DTI Studio program for diffusion tensor imaging, this Windows-based program enables users to perform tensor calculation, color mapping, and fiber tracking. MRI Studio builds on DTI Studio's functionality with added features for 3D visualization, region-of-interest analysis, and the ability to launch the Large Deformation Diffeomorphic Metric Mapping (LDDMM) registration tool (Fig. 1).

Specifically, MRI Studio's new LDDMM-based registration capability allows users to place landmarks on images and leverage the power of the LDDMM algorithm to register images using JHU's computing resources. The LDDMM step is a compute-intensive

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All Hands Meeting 2007

by Skip Cynar, Senior Science Writer



Above—Stuart Zola (Emory U.) talks with Barbara Alving and Greg Farber (both from NIH). Right panel, top to bottom—Gary Glover (Stanford), Kelvin Lim (U. Minn.), Randy Gollub (Harvard/MGH) and Vince Calhoun (U. New Mexico) pose for a photo in front of the NIH Natcher Conference Center; AHM attendees viewing posters; Mark Ellisman (UC San Diego) makes a point with Greg Farber and Art Toga (UCLA); Bruce Rosen (Harvard/MGH) at podium reviewing Morphometry BIRN's progress; AHM workshop participants huddle around Susumu Mori's (Johns Hopkins) laptop.



Bethesda, Maryland was the venue for the 2007 BIRN All Hands Meeting. More than 170 biomedical researchers and information technology experts convened on the National Institutes of Health's (NIH) campus for three days in mid-October 2007. Held at the NIH's Natcher Conference Center, Barbara Alving, M.D., NCRR Director, Mike Marron, Ph.D., NCRR's Director of Biomedical Technology Division, and Greg Farber, Ph.D., BIRN Project Officer, attended the meeting.

The first day of the meeting allowed researchers participating in BIRN's Mouse, Function, and Morphometry test beds and the Coordinating Center a day to meet, review progress, and set priorities. The full All Hands Meeting opened Tuesday morning with multiple training and specific working group sessions. Moderated training sessions allowed BIRN users to share in-depth and practical information about how to create, collect, and share data among neuroscientists. Among the seventeen training topics, several focused on the newest features added to the BIRN Portal, new atlasing functionality, demonstrations of semantic annotation using ontologies, discussion of updates to powerful workflow tools for integrated analysis and visualization, and an overview of the new BIRN Data Repository (BDR).

Eight moderated working groups permitted software programmers opportunities to review progress in and get feedback on a host of software tools supporting BIRN-wide functionality, such as atlas interoperability, ontology curation, and improved informatics functionality using the XML-based Clinical and Experimental Data Exchange (XCEDE) specification. ■

BIRN Well Represented at SfN 2007 Conference

by Skip Cynar, Senior Science Writer

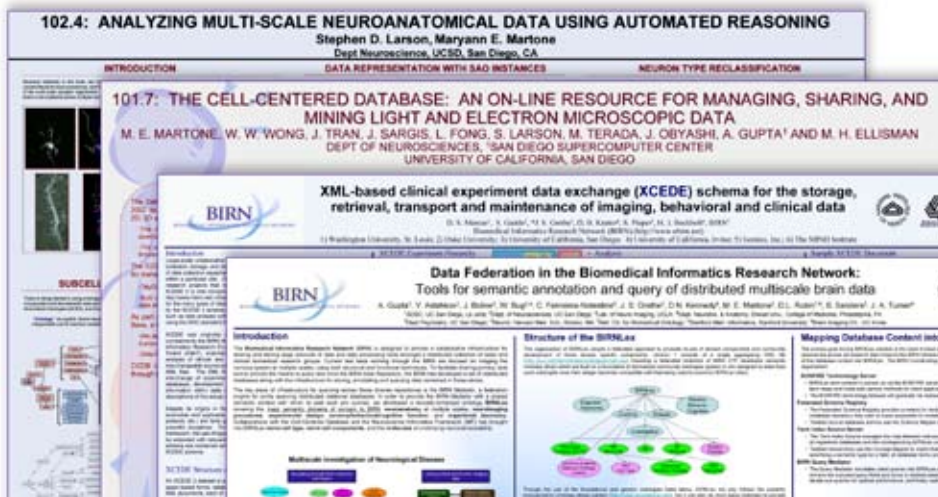
San Diego played host to the annual Society for Neuroscience Conference, November 3-7, 2007, the world's largest annual forum for presentation of emerging research on the brain and nervous system. Many BIRN researchers were among the more than 31,000 attendees and contributed more than 15 presentations.

BIRN's exhibit space enabled meeting attendees to test-drive numerous BIRN tools, including the latest version of the Mouse BIRN Atlasing Toolkit (MBAT), FBIRN's Image Processing Scripts (FIPS) and associated Human Imaging Database (HID), Morphometry BIRN's Extensible Neuroimaging Archive Toolkit (XNAT), and interactive demonstrations targeting the neuroscience community on sharing and exchanging data through the expanding BIRN Data Repository.

The BIRN-CC's Mark Ellisman delivered one of the four prestigious Presidential Lectures, "Integrating Neuroscience Knowledge: Brain Research in the Digital Age." His talk focused on the need for a scalable and available knowledge environment for the brain research community. It highlighted many of BIRN's accomplishments and illustrated to an audience of more than 5,000 people what tomorrow's neuroscientists might expect from neuroinformatics in an era in which scientific discoveries will hinge increasingly on the development and use of telecommunications and information technology.

The following selection of poster presentation titles indicates the range of activities arising from BIRN:

- Phenotypic differences in a set of BXD recombinant inbred mice.
- Data Federation in the Biomedical Informatics Research Network: Tools for semantic annotation and query of distributed multiscale brain data.
- Functional circuitries in healthy subjects and schizophrenic patients during a working memory task.
- A digital atlas as a framework for data management and cross-data comparison. ■



Above—Representative poster presentations from BIRN at the Society for Neuroscience 2007 conference. Right panel, top to bottom—Scenes from the SfN Conference NIF members convening at the booth, Thomas Morse (Yale), Maryann Martone, David Van Essen (SfN President, Washington U. St. Louis); Mark Ellisman; Jeremy Bockholt, David Keator, Jeffrey Grethe, and Christine Fennema-Notestine at the BIRN booth; Mark James; Mark Ellisman delivering SfN Presidential Lecture.

Function BIRN: One of these scanners is not like the other . . .

by Jessica Turner, FBIRN Project Manager

BIRN's Functional Imaging test bed (FBIRN) focuses on creating and refining user-friendly functional imaging data-sharing tools. Part of this effort requires fully testing and refining the imaging calibration and analysis methods. In 2005 we released quality assurance (QA) methods for measuring scanner stability for fMRI (the agar phantom methods and analyses). Since then, we have built on these initial efforts to develop new imaging QA measures, software, and methods for multi-site imaging quality assessments. Our goal in developing these methods is to be able to quickly and reliably determine when a scanner has fallen out of acceptable imaging parameters to avoid analyzing or sharing sub-par imaging data.

A new BIRN portal application has been developed to centralize access to agar phantom data as they become available. Named QAp, this application is available on the BIRN Portal under Biomedical Tools. The QAp is helping to make scanning analysis more robust. As agar phantom scans are uploaded to the QAp, problems with a scanner's stability as well as technologist error can be instantly recognized. Proper placement of the phantom should result in an image such as the insert shown circled in red (Fig. 2). In this scan, improper placement of the phantom led to a poor signal-to-noise ratio—usually indicating scanner instability—but was determined to be human error on visual inspection of the images.

Post-acquisition analyses of the agar phantoms include mean and standard deviation measurements, drift and percent fluctuation in signal, signal-to-noise (SNR), and signal-to-fluctuation-noise (SFNR) ratios calculated over all volumes. The large number of requests for agar phantoms from research centers around the world underscores the

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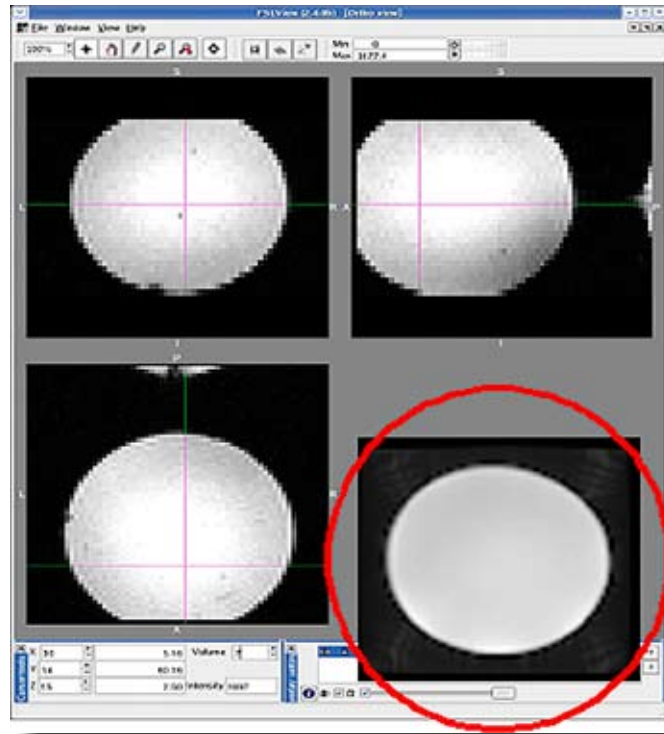


Fig. 2: fMRI images of the FBIRN stability phantom (filled with agar). This particular scan was improperly collected; the visualization of the images showed that it needed to be redone. Circled in red is an image of the phantom showing proper placement for the scan, centered in the image.

Navigation		QA report:				
Summary		000602155404/scanVisit_0006_0002/MRI_0001				
Volume means:	input					
	masked, detrended					
Mean volume difference						
Running difference						
Outlier voxels						
Smoothness (FWHM):						
X dimension						
Y dimension						
Z dimension						
Center of mass:						
X dimension	input					
	masked, detrended					
Y dimension	input					
	masked, detrended					
Z dimension	input					
	masked, detrended					
Per-slice variation:						
	AudOdd1					
	AudOdd2					
	AudOdd3					
	AudOdd4					
Mean, StdDev, SFNR:						
Mask:						
	AudOdd1					
	AudOdd2					
	AudOdd3					
	AudOdd4					

QA report:		AudOdd1 AudOdd2 AudOdd3 AudOdd4				
Summary:						
	# vols. with mean intensity abs. z-score > 2	individual	3	9	8	5
	rel. to grand mean	0	11	23	0	
	# vols. with mean intensity abs. z-score > 3	individual	0	1	2	0
	rel. to grand mean	0	5	8	0	
	# vols. with mean volume difference > 1%		0	8	17	0
	# vols. with mean volume difference > 2%		0	0	2	0
	mean FWHM	X	8.444	8.604	8.659	8.384
		Y	9.435	10.959	10.073	9.814
		Z	6.199	7.17	6.02	6.986
	# vols. with mean intensity abs. z-score > 2	individual	9	10	9	7
	rel. to grand mean	0	13	25	0	
	# vols. with mean intensity abs. z-score > 3	individual	0	1	2	0
	rel. to grand mean	0	1	10	0	
	# vols. with running difference > 1%		0	0	0	0
	# vols. with running difference > 2%		0	1	3	0
	# vols. with > 1% outlier voxels		7	45	23	7
	# vols. with > 2% outlier voxels		3	38	12	6
	mean (ROI in middle slice)		562.4	567.5	569.3	567.7
	mean SNR (ROI in middle slice)		157.8	110.4	122.5	174.0
	mean SFNR (ROI in middle slice)		178.3	128.5	94.1	167.5

Fig. 3: The sample QA report is based on a single subject's data from four sequential runs of an Auditory OddBall Task. The summary table suggests more outliers within the 2nd and 3rd runs than in the 1st and 4th runs.

Morphometry BIRN *(continued from page 5)*

process: one image requires 8 GB of memory and approximately 5 hours of processing time. To date, over 280 images have been remotely LDDMM-processed in this way. Initial limitations associated with the number of simultaneous jobs able to be run has been addressed with the installation of a new 16cpu/128GB server at JHU. A more detailed description of the step-by-step remote processing procedure, provided by Steven Pieper (Brigham and Women's Hospital in Boston), is located online at <http://wiki.na-mic.org/Wiki/index.php/Slicer3:LDDMM>. Download 32- or 64-bit versions of MRI Studio and additional information at <https://www.mristudio.org/>.

The nature of JHU's compute-intensive research is providing important feedback to Morph BIRN and the BIRN-CC on how to link the BIRN Data Grid with large-scale computational resources. To date, more than 40,000 LDDMM-volume processed jobs have logged

over 300,000 cpu/hrs of processing (~34 cpu/hrs). This workload required more than 40 Terabytes of storage. To accommodate these storage demands, the JHU group accessed storage on the TeraGrid (GPFS-WAN 220TB) along with the BIRN Data Grid and local file systems using sshfs to "glue" remote and local file systems together. This technique offers researchers a seamless experience while working with distributed data storage sites.

The BIRN-CC is working with JHU's LDDMM group to provide an enhanced version of the LDDMM portal that will utilize the NSF-funded TeraGrid for processing, allowing BIRN Data Grid users the ability to launch LDDMM jobs onto the TeraGrid for parallel processing. Current LDDMM projects include shape analysis of six brain structures using data acquired through ADNI, the Alzheimer's Disease Neuroimaging Initiative (Fig. 4). ■

Function BIRN *(continued from page 8)*

value of the BIRN phantom as a way to measure a scanner's stability.

To address the need for a quantitative, high-throughput tool to efficiently and reliably identify fMRI runs or volumes for exclusion, FBIRN developed a QA tool. The FBIRN QA tool provides a variety of measurements and summary metrics to assist researchers in evaluating the quality of fMRI datasets. It can run on native (raw) or pre-processed imaging data.

Going beyond the basic statistics offered through the agar phantom, the QA Tool provides additional outlier metrics to allow QA of detrended and/or masked data as well as new help features. In addition, we're creating a public Web presence for sharing the quantitative

review of FBIRN Phase II QA data. This effort is moving towards a set of recommended guidelines for using the QA Tool's summary results.

The browser-based QA Tool can be applied to any given fMRI task for any number of scans, and computes descriptive statistics across time for each scan. Users can view more detailed information or related images and data files, all viewable and accessible simultaneously through any Web browser. The sample QA report (Fig. 3, pg. 8) illustrates a summary table of metrics for each fMRI run based on the entire QA process. The left-most navigation bar lists available metrics that are presented in detail within the main area of the window. ■

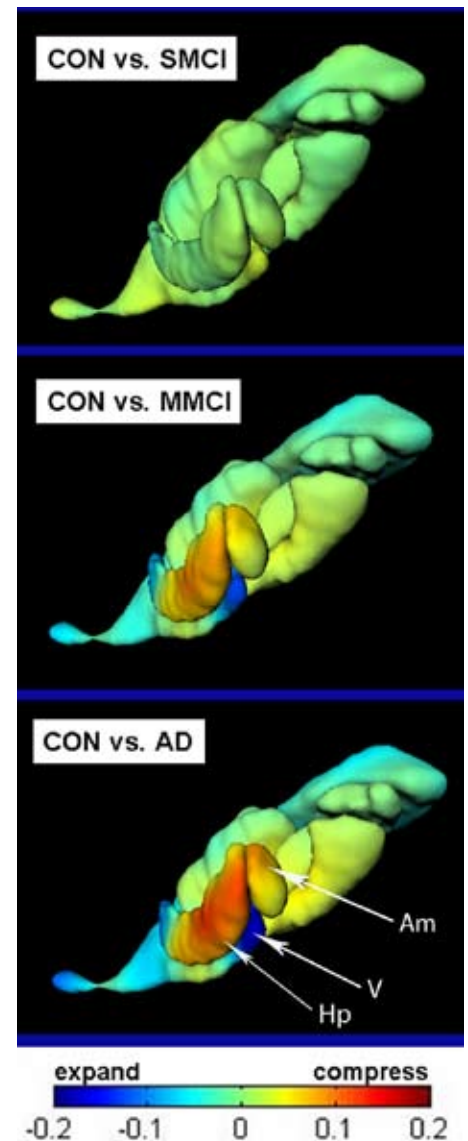


Fig. 4: Group comparison results for LDDMM processing of data from the Alzheimer's Disease Initiative study. Results from a control group (CON) are compared to those for subjects with stable mild cognitive impairment (SMCI), minimal to mild cognitive impairment (MMCI) and Alzheimer's Disease (AD). Regions with the largest changes include the hippocampus (Hp), the amygdala (Am), and ventricle (V). The color scale is in mm.

Mouse BIRN: New release of the Mouse BIRN Atlasing Toolkit

by Jyl Boline, Mouse BIRN Project Manager

A primary goal of Mouse BIRN is to create an intuitive, interoperable interface to aid in the organization, display, and query of multimodal data. MBAT is the collaborative Mouse BIRN tool designed to view, access, and query multimodal data.

We have recently released several improvements to MBAT version 2.0, which includes more powerful query tools to access multiple data and information sources and many interface improvements such as a launch page, workspaces configurable for specific tasks, a new docking framework, and ready access to Mouse BIRN data upload resources. This latest version improves and expands the query capability of MBAT. The query interface can be used for multiple data types and includes image data from multiple

sources. It also provides simple methods for comparing and analyzing these data in relation to an atlas. In addition, MBAT can also be used to access information from Web resources including the BIRN Ontology Tool (Bonfire-Fig. 6.4) and the Brain Architecture Management System (BAMS) at USC.

MBAT's underlying infrastructure is rich and diverse. Fig. 5 illustrates the scope of this project and the scientific community's desire for data sharing infrastructure. It depicts an overview of the architecture we are presently implementing. MBAT acts as a user-friendly application layer on top of multiple layers of integration, shielding the infrastructure's complexity from users. While the core infrastructure was developed by Mouse BIRN, several components originated from collaborating groups

such as the BIRN-CC, Function BIRN, NeuroCommons, the BAMS group, and others.

Download the newest version of MBAT at the BIRN Web site (http://www.nbirn.net/tools/mbat_2.0) or the new MBAT homepage (<http://cms.loni.ucla.edu/MBAT>). ■

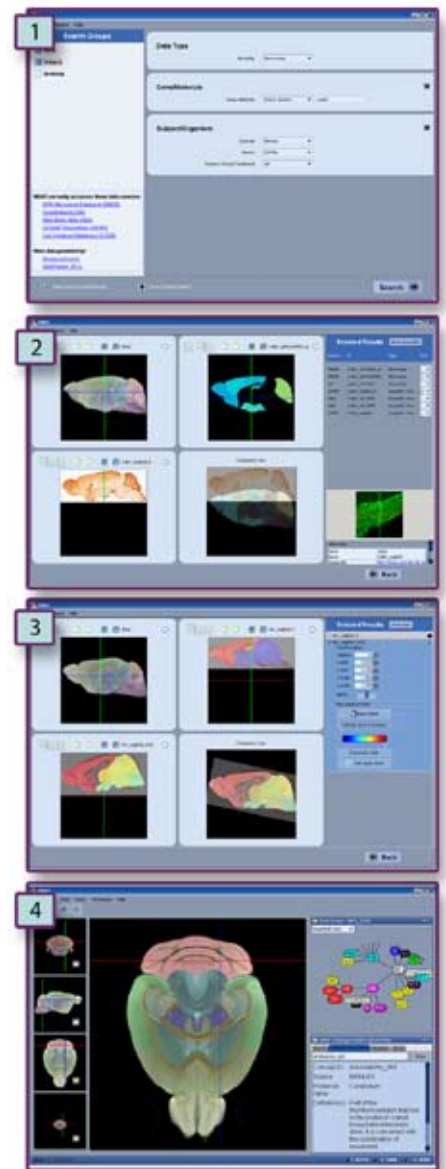
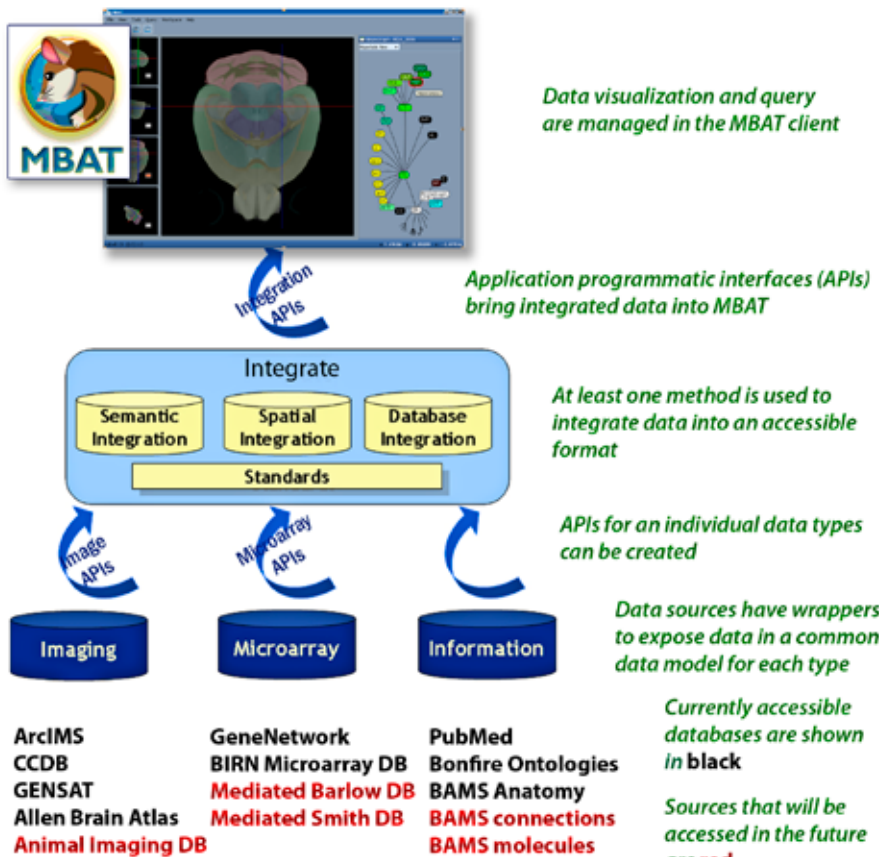


Fig. 6: MBAT Screenshots. 1) MBAT's Query interface; 2) MBAT enables users to access and display multiple types of data from distributed sources; 3) MBAT users can analyze gene expression; 4) MBAT also provides access to BON-FIRE, BIRN's ontology manager.

Fig. 5: Data integration framework of MBAT

Mouse BIRN: Neonatal Atlases of the Mouse Brain

by Erh-Fang Lee and Jyl Boline, LONI/UCLA

The Mouse BIRN group shares several 3D atlases, including several of different modalities and developmental stages of mouse—all ready to be visualized using Mouse BIRN's Atlas Toolkit (MBAT). These atlases are available to the public for download from the BIRN Data Repository, <http://www.nbirn.net/bdr/index.shtm>.

The latest addition to this group is a set of postnatal day zero (P0) C57Bl/6J mouse neonatal atlases. One atlas contains 13 delineated structures generated from an average MR of 8 mice. Another atlas contains 145 delineated structures generated from a Nissl volume reconstructed from 150 registered histological sections 50 μ m apart (Fig. 7, provided by Dr. Erh-Fang Lee, Laboratory of Neuro Imaging, UCLA).

Due to the lack of consistent fiducial points that can be used to position neonatal mouse brains, experimental data of this developmental stage are usually collected with an arbitrary brain orientation, making it difficult to manage data derived from stained slices of neonatal brains using canonical planes. Since digital atlases can be sectioned at a user defined oblique plane, this plane can be

used to house individual experimental data such as those generated using immuno-histochemical staining and *in situ* hybridization. The gene expression data from stained brain slices precisely localize the distribution of gene products in 2D. Registering these datasets in atlas space allows this information to be integrated in an anatomical framework,

thus greatly enhancing the significance of single studies. Subsequently, data from separate sources can be compared and correlated with each other, thus facilitating cross-modality, cross-community data analysis for individual studies.

Erh-Fang Lee, Jyl Boline, and Arthur Toga recently reported on using these atlases as a high-resolution anatomical framework of the neonatal mouse brain for managing gene expression data in the inaugural issue of *Frontiers in Neuroinformatics*. This paper addresses the issue of managing experimental data in a common atlas space in order to facilitate comparisons for information acquired from different studies and modalities. By normalizing *in situ* hybridization data collected from public databases, co-expression patterns can be represented by anatomical models (Fig. 8), which provides better data realization and gives added insight into the relationship between gene expression and anatomical systems. ■

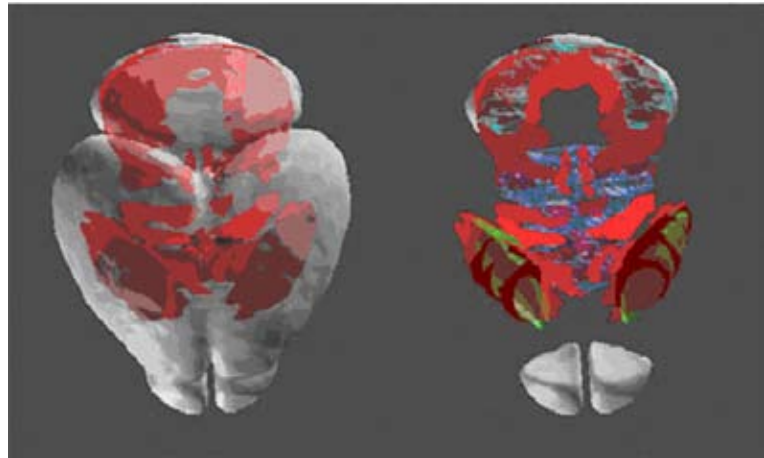


Fig. 8. (Left) Reconstruction of the expression pattern of *Six3* gene from a single batch of *in situ* hybridization assays (Gray et al., 2004) acquired from the MGI database. Co-display of ROI objects from data at different planes allows for relating the global gene expression pattern to 3D brain anatomy. (Right) The ROI objects are shown with the anatomical models of the olfactory bulb (white), basal ganglia (green), thalamus (blue), and inferior colliculus (cyan).

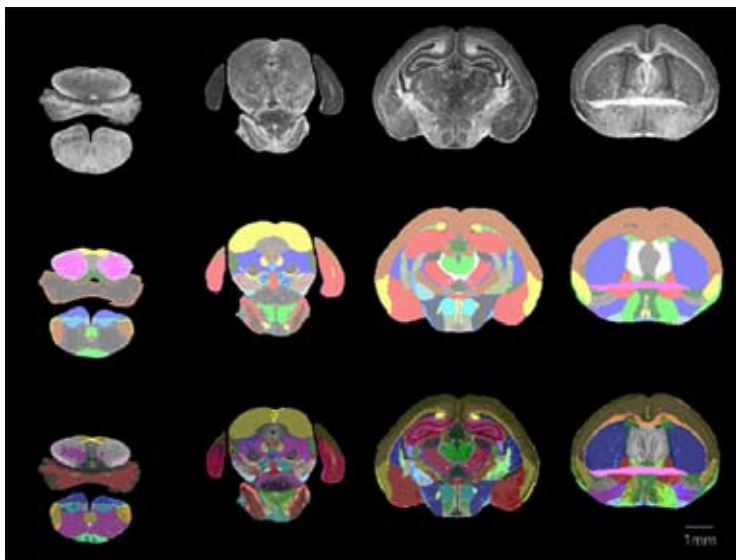


Fig. 7. Examples from the Nissl atlas. Top row: Nissl, Middle row: delineations, Bottom row: combined Nissl and delineations.

What is the BIRN?

The Biomedical Informatics Research Network

Growing Collaborative Biomedical Research Through Technological Advances

Drawing upon the expertise and technologies available at numerous institutions, Biomedical Informatics Research Network (BIRN) is building an infrastructure of networked high-performance computers, data integration standards, and other emerging technologies, to pave the way for medical researchers to transform the treatment of disease. Launched in 2001 as an initiative of the National Institutes of Health's National Center for Research Resources, BIRN has developed a collaborative environment for biomedical research and clinical information management.

A central component of BIRN is its Coordinating Center, overseeing the networking, distributed storage, and software development needs of three neuroimaging test beds. The Function BIRN Test Bed employs functional neuroimaging to explore the underlying causes of schizophrenia and to subsequently assess the impact of new treatments on functional brain abnormalities. The Brain

Morphometry Test Bed focuses on pooling acquired data across neuroimaging sites to investigate if specific anatomical differences are diagnostic of specific memory dysfunctions, such as depression, mild Alzheimer's disease, and mild cognitive impairment. Collaborators in the Mouse BIRN Test Bed utilize multi-modal and multi-scale imaging data from mouse models of neurological disorders to better understand schizophrenia, Parkinson's disease, multiple sclerosis, attention-deficit hyperactivity disorder, and brain cancer.

The NIH's National Database of Autism Research (NDAR) is an early adopter of BIRN's federated infrastructure that will foster collaboration across a diverse community of researchers and autism advocacy groups, NDAR is looking to BIRN to realize its mission of advancing the science of autism and speeding the discovery of new therapies. NDAR can be found on the World Wide Web at <http://ndar.nih.gov/>. ■

Building on the success of BIRN, NIH has released two program announcements: **Data Ontologies for Biomedical Research** (PAR-07-425), and **Sharing Data and Tools: Federation Using the BIRN and caBIG Infrastructures** (PAR-07-426). The purpose of these NIH Program Announcements is to encourage researchers to use the caBIG™ and BIRN infrastructures to share data and tools under these infrastructures or use the infrastructures to federate significant data sets. More information on the program announcements is available at the BIRN Web site: <http://www.nbirn.net/nih/index.shtm>.



The growing BIRN infrastructure is enabling fundamentally new capabilities in large-scale studies of human disorders. Currently, 30 universities and hospitals and 43 research groups participate in one or more of the four test beds and associated collaborative projects. Print and Web versions of the up-to-date map as well as other images are available for download at http://nbirn.net/about/archive/media_images.shtm