Biomedical Informatics Research Network: Multi-Site Processing Pipeline for Shape Analysis of Brain Structures

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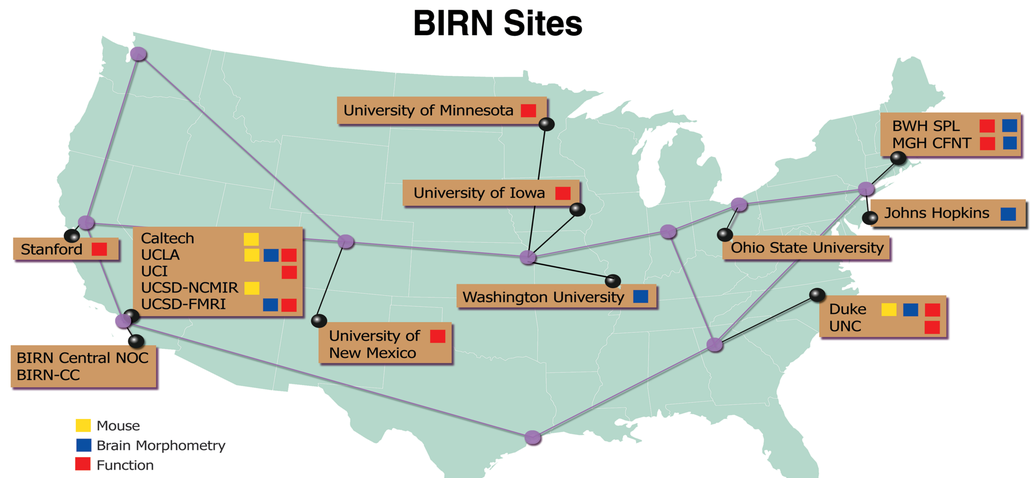
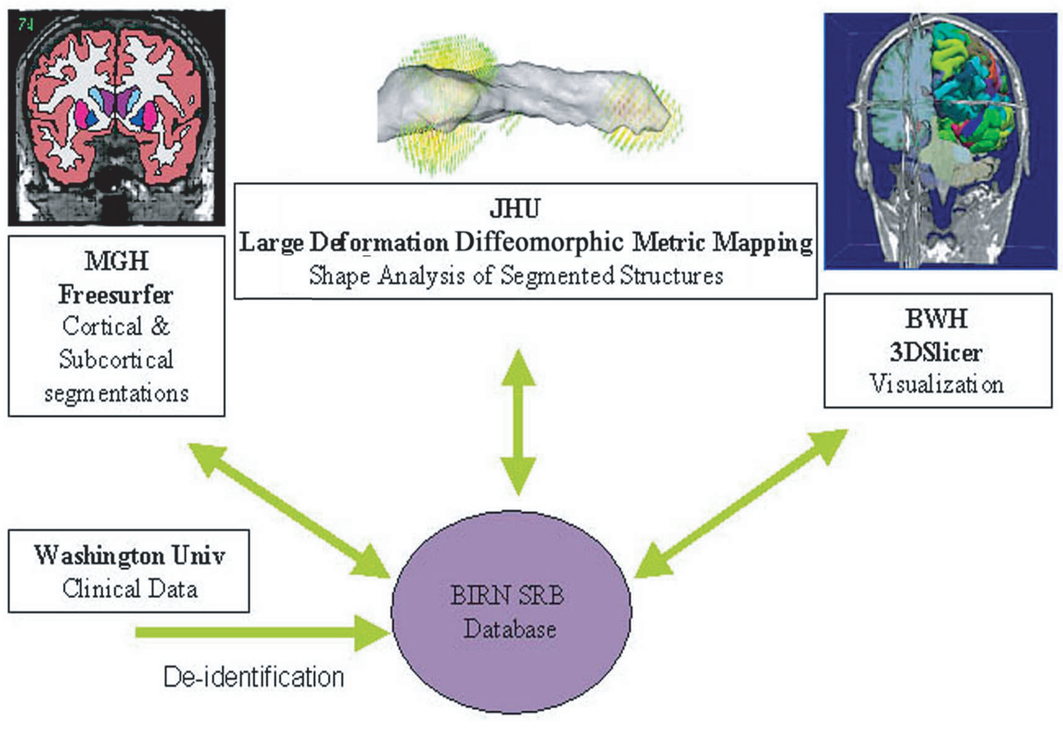
Introduction

The discipline of Computational Anatomy focuses on shape analysis of anatomical structures obtained in biomedical imaging. Under the auspices of the Brain Morphometry Biomedical Informatics Research Network (mBIRN, www.nbirn.net), a processing pipeline is being developed to enable seamless processing of brain morphometry data for sub cortical structures through the integration of multiple site applications (see right). As a testbed, the tools are being integrated to perform semi-automated shape analysis of hippocampus volumes in a study of Alzheimer's Disease (see below). Brain structural MRI data from Washington University was made available to MGH and JHU to drive the integration of the morphometric analysis tools that these sites are BIRN-enabling.



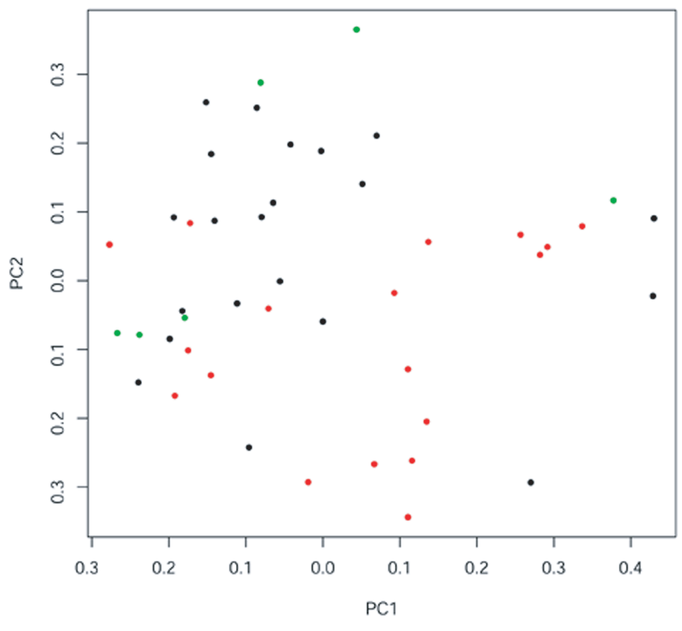


Integrating tools: Freesurfer, LDDMM and 3DSlicer via SRB

The initial data consisted of 45 subjects (21 controls, 18 Alzheimer's, 6 from a rare form of dementia, called semantic dementia) scanned using high resolution T1-weighted structural MRI at WashU. These scans were first anonymized and then automatically segmented at MGH's Martinos Center using Freesurfer [2], yielding segmented data sets. These data sets were aligned and processed at JHU's Center for Imaging Science (CIS) using the Large Deformation Diffeomorphic Metric Mapping (LDDMM) tool [1] and visualized with 3DSlicer [3] from the Surgical Planning Lab (SPL) at BWH. Briefly, LDDMM computes the velocity vectors that transform one binary image I_0 to another I_1 giving the metric distance $d(I_0,I_1)=\sqrt{\int_0^1 \|v\|_V^2\, dt}$ where the norm $\|\cdot\|_V^2$ ensures smoothness in the space of velocity vector fields that are generated by the group of infinite dimensional diffeomorphisms (which is the generalization of rotatins, translations and scale group), the necessary group for studying shape. These distances give a precise mathematical description of what shapes are similar and different. The resultant data was then uploaded into the Storage Resource Broker (SRB) [4] for sharing among institutions and for further analysis. The extensibility of Freesurfer and LDDMM to operate seamlessly on data that was acquired at neither the MGH nor the JHU BIRN sites is noteworthy. LDDMM has pushed the limits of the BIRN infrastructure and has begun to draw on the resources of the TeraGrid project. The 2025 comparisons made use of the TeraGrid computing resources. Each comparison took an estimated 8 hours to complete on a single TeraGrid node. In order to accomplish all the comparisons, an average of 70 TeraGrid nodes were used for 3 weeks in the processing. The processing created 4TB of resultant data.

Statistical Analysis of Shapes

From the 2050 LDDMM comparisons, we conducted preliminary statistical analysis of the 45x45 matrix of metric distances. The figure on the right illustrates a non-linear mapping to $\mathbb{R}^2$ of a set of high-dimensional Euclidean points which (approximately) minimize the interpoint distance distortion from the LDDMM matrix. The figure suggests there there is class-specific information in the LDDMM matrix with upper-left observations predominantly controls (black), and the other observations for dementia (red) and semantic dementia (green) elsewhere. The integrated tools are expected to enable biomedical scientists to perform shape analysis of anatomical structures arising in biology and medicine leading to better understanding of diseases and disorders with greater statistical power.



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