Creating a Large Scale Morphometric Baseline from MRI Brain Scans

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Objective: create a publicly available electronic neuroanatomy resource that will advance neuroscience research and spread neuroanatomical knowledge.

Overview: Around 1000 publicly available MRI brain scans will be labeled using 60+ neuroanatomical regions of interest (ROIs). Using semiautomatic software, technicians with extensive training will apply precisely defined procedures to make outlines so that the entire brain is identified in every scan. We will then combine these results into a computerized atlas that can be used to 1) locate and identify brain regions in other scans, and 2) interactively learn brain anatomy. We will make all of our results available to the public.

Labeling Protocol: this is a collection of definitions of neuroanatomical boundaries and landmarks that can be seen using MRI. We seek to compare and harmonize existing methods as much as possible and are looking for input and feedback. Our approach is to start with the less variable and generally agreed upon ROIs and proceed to parcellate cortex in the more ambiguous regions as we accumulate experience with the variability those regions.
The cerebral cortex is divided into 45 macro-anatomically defined regions in each hemisphere that are of broad interest to the neuroimaging community. Information about 10 existing protocols has been gathered, compiled, summarized, and reviewed by our anatomical consultants. We are now seeking feedback from the general community. In addition to suggestions about the definitions of regions of interest, we are also interested in discussing the issue of labeling cortical regions using volume vs. surface based approaches.
Our collaborator, Dr. Arno Klein (Div. of Molecular Imaging and Neuropathology, Columbia University) is actively involved in this project and created a web-based survey for your input: http://www.mindboggle.info/protocols. In addition to Dr. Klein, we are working with Dr. David Shattuck and Dr. Arthur Toga (Laboratory of Neuro Imaging, UCLA) to expand the scope of our original project so that we will be able to analyze 1000 scans, instead of the originally proposed 500-600.

Here are the figures from the proposed Protocol:

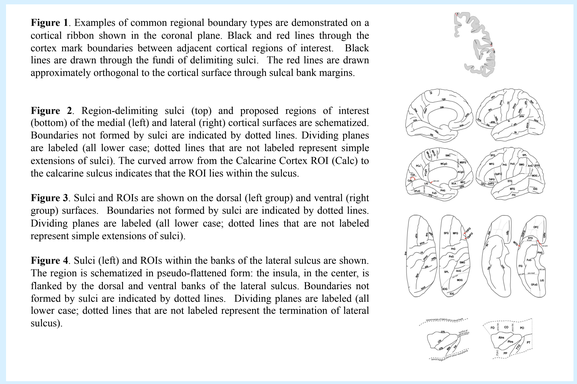


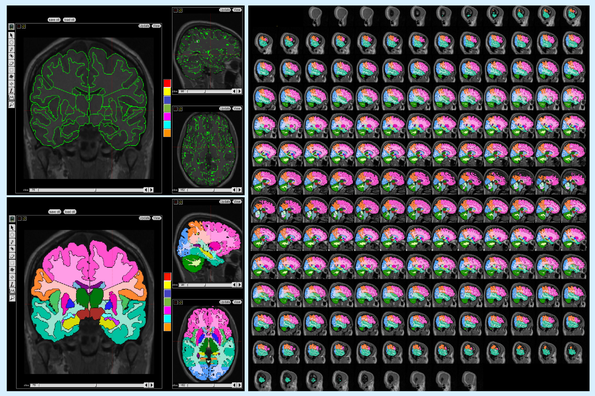
Figure 1. Examples of common regional boundary types are demonstrated on a cortical ribbon shown in the coronal plane. Black and red lines through the cortex mark boundaries between adjacent cortical regions of interest. Black lines are drawn through the fundi of delimiting sulci. The red lines are drawn approximately orthogonal to the cortical surface through sulcal bank margins.

Figure 2. Region-delimiting sulci (top) and proposed regions of interest (bottom) of the medial (left) and lateral (right) cortical surfaces are schematized. Boundaries not formed by sulci are indicated by dotted lines. Dividing planes are labeled (all lower case; dotted lines that are not labeled represent simple extensions of sulci). The curved arrow from the Calcarine Cortex ROI (Calc) to the calcarine sulcus indicates that the ROI lies within the sulcus.

Figure 3. Sulci and ROIs are shown on the dorsal (left group) and ventral (right group) surfaces. Boundaries not formed by sulci are indicated by dotted lines. Dividing planes are labeled (all lower case; dotted lines that are not labeled represent simple extensions of sulci).

Figure 4. Sulci (left) and ROIs within the banks of the lateral sulcus are shown. The region is schematized in pseudo-flattened form: the insula, in the center, is flanked by the dorsal and ventral banks of the lateral sulcus. Boundaries not formed by sulci are indicated by dotted lines. Dividing planes are labeled (all lower case; dotted lines that are not labeled represent the termination of lateral sulcus).

Labeling: The main effort of the project is to comprehensively label 1000 MRI brain scans. We have chosen the Open Access Series of Imaging Studies (OASIS) scans for the bulk of the work but will also analyze 152 normal adult brain MRI scans collected within the ICBM project (the ICBM152). We seek input on other scan sets to include. We have begun with the "validation data" set from the OASIS scans to demonstrate the technological feasibility of this project. These are repeat scans of 20 subjects (40 scans) that will allow us to calculate intra-rater variability statistics.

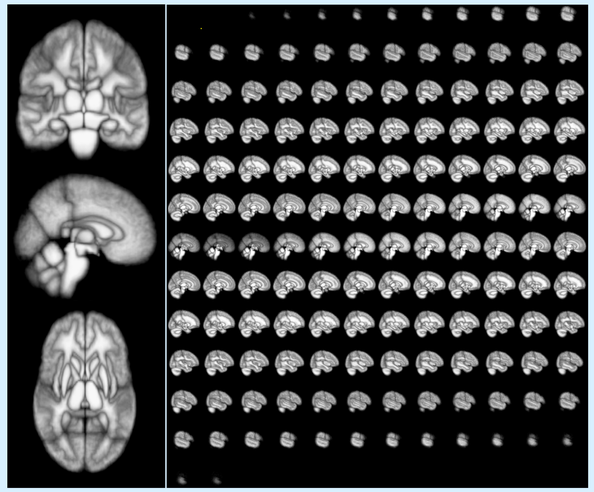


Tools: The main analysis tool (shown above) is called "NVM". It is open-source software for making precise quantitative neuroanatomical measurements in volumetric image data. Iso-intensity contours are created, edited, and then extracted into neuroanatomically labeled ROIs. "SegMentor" is a feature that provides on-line context sensitive instructions, definitions, and interactive assistance with labeling methods using a collection of HTML and XML documents. SegMentor records, plays, and allows viewing and editing of scripts. These scripts control NVM, provide short user reminders, and also provide context-sensitive information to the user via "Help" buttons which open a browser to a web page containing images and definitions that describes the specific labeling task in detail. SegMentor scripts can be created to provide an explicit and complete definition of a particular neuroanatomical measurement method. This is important because it is not possible or desirable to fit all of the details of a method into an academic publication. Developing neuroanatomical labeling methods using SegMentor facilitates the distribution of these methods and is invaluable in training. Moreover, SegMentor helps to automate the method, which decreases cost and increases reliability. By automating labeling as much as possible, user input is limited to only the steps that need to be done using the human visual system, experience and complex 3D anatomical knowledge.

Probabilistic Atlas: the atlas uses 3D thin plate spline warping with Talairach landmarks (AC, PC, midline, and all extents) to map locations in a scan to corresponding locations in the atlas.

The spatial probability of the occurrence of each neuroanatomical structure is represented and stored separately, and each individual structure is related to the atlas as a whole by storing the location of their upper left corners with respect to the Talairach landmarks in atlas space.

Dynamic Probabilistic Atlas & Brain Anatomy Instructor: The Dynamic Probabilistic Atlas (DPA) will be generated on the fly from labeled scans based on criteria such as subject age, gender, handedness, etc. The database of labeled scans will also be used to create the "MRI Brain Anatomy Instructor" (MRI BAI). This interactive neuroanatomy teaching tool based on NVM will allow "lesson" scripts to be created by professors and used by students. We are seeking a neuroanatomical expert to collaborate on creating teaching scripts for the MRI BAI.

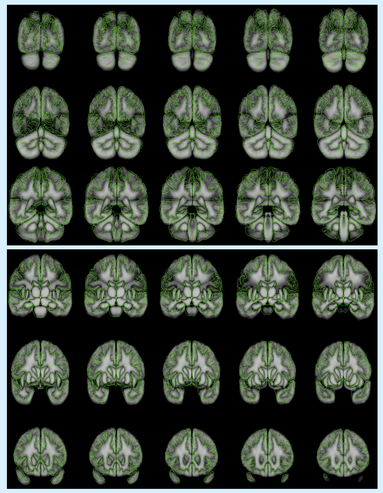


The probabilistic atlas is shown above after warping it to match an individual scan. The brightness of each voxel is the probability for the highest probability structure at that location. The brightest regions are less variable while darker areas are more variable. The dark lines that appear to separate different structures are actually just lower probabilities for the highest-probability structure. When warped onto an individual scan, only one structure can have the highest probability, but these dark regions show that where two or more atlas structures overlap in space they all have lower probabilities. Note that there appears to be a gray-white border in, for instance, the upper part of the coronal slice. This is misleading and does not match any individual's anatomy. This is merely where the atlas probabilities change from favoring gray or white on average. This is why it is important for the atlas to store each structure's probability separately.

Results & Significance: Brain Variation
This project will result in: a database of labeled scans that is two orders of magnitude larger than what is available, the dynamic probabilistic atlas of labeled brains, and a new kind of anatomy authoring tool. In each of these, the important thing is the ability to convey variation of the structure of the human brain.

Here are an individual's outlines shown on top of atlas slices:

The interactive exploration of an individual's anatomy with respect to the average shapes of ROIs as seen in the atlas will allow us to understand and develop a taxonomy of structural variation for the human brain.



As we evaluated existing protocols we focused the goals of the new protocol to i) maximize reliance upon robust anatomical landmarks, ii) minimize reliance upon arbitrary landmarks, and iii) base regional boundary definitions, to the degree possible, upon anatomical landmarks that lie immediately adjacent to that region. We have fixed the definitions of the majority of necessary boundaries and landmarks where the structural variability of the brain is low. The final protocol and large database of labeled brain scans will be significant because they will be built upon a deep understanding of the structural variability of the brain. As we go through the process of labeling 1000 scans, starting with the "obvious" (less variable) regions and proceeding towards the "difficult" (more variable) regions, the protocol will be refined and adapted based on our direct observation of case-by-case variation. The most important deliverable for this project is not just a whole lot of labeled brain scans (even if it is orders of magnitude more than previously available), the most significant deliverable is the combination of the protocol based on variation *and* the individual cases that demonstrate that variation.

Project Overview Sketch: