Detailed Description of Labeled Scans

Neuroanatomical labeling of MRI brain scans was performed at Neuromorphometrics, Inc., following the methods described in [1].

Result data are provided as two volumes in NIFTI format (see http://nifti.nimh.nih.gov/): 1) a 3D block of MRI data and 2) a 3D block of labels. The labels are integers that correspond voxel-by-voxel with the MRI data and indicate the neuroanatomical structure present at that voxel. The label numbers are an index to a list of neuroanatomical names and RGB colors. For each scan these three files are provided as a single compressed tar file (.tgz).

These groups of labeled scans are available:

Data Set Name	Min Age	Max Age	# Unique Scans	# Unique Subjects	# Repeat Scans
ADNI30	62.4	87.9	30	29	1
20Repeats	19	34	40	20	20
CANDI13	5	15	13	13	0
Colin27	27	27	1	1	0
OASIS30	18	96	30	30	0
Totals:	5	96	114	93	21

The original MRI scans were obtained from the following sources: 1) the Open Access Series of Imaging Studies (OASIS) project web site (http://www.oasis-brains.org/), 2) the Child and Adolescent NeuroDevelopment Initiative (CANDI) Neuroimaging Access Point (see http://www.nitrc.org/projects/candi_share). 3) Alzheimer's Disease Neuroimaging Initiative (ADNI) project web site (http://adni.loni.usc.edu/data-samples/access-data/). The specific scans used were from a sub-set of the "ADNI1:Screening 1.5T" and "ADNI1:Baseline 3T" (NOTE that the original ADNI MRI scans must be obtained directly from ADNI and their use falls under their license), 4) the McConnell Brain Imaging Centre (http://www.bic.mni.mcgill.ca/ServicesAtlases/Colin27Highres/), or 5) individual subjects who contributed their own scans. Details about the specific scans and the specific labels that were created for those scans is provided with the labeled scans, along with the available metadata. Note that the details, metadata, and labels created for scans obtained from any one of these sources may be slightly different from those obtained from other sources.

Preprocessing: The processing for each individual scan begins with automated bias field inhomogeneity correction [2]. Next, each scan is positionally normalized [3]. Three anatomical landmarks are located: the anterior commissure (AC), the posterior commissure (PC), and a mid-sagittal point. The scan is reoriented and resliced so that anatomical labeling can be done in coronal planes that follow the AC-PC axis. Brain extent landmarks are then chosen and scans are cropped to make efficient use of computer memory and screen area.

Outlining: The label for each voxel is determined by locating the boundaries of specific neuroanatomical regions of interest and then labeling those regions. Outlines are created and edited by highly trained Neuroanatomical Technicians (NeuroTechs) using Neuromorphometrics' software, "NVM" [4]. This tool uses histograms, isointensity contours and the manual drawing and erasing of borders where necessary. NVM has a large number of features specifically designed to let the user efficiently delineate and label anatomy in 3 dimensions. The exact specification of each region of interest is defined in 1) Neuromorphometrics' General Segmentation Protocol [5], and 2) the BrainCOLOR Cortical Parcellation Protocol [6].

To facilitate the accurate outlining of regions, the MRI data is zoomed in to twice its normal size. Outlines are made on each slice of the MRI volume and each closed outline is assigned a neuroanatomical label corresponding to that region of interest. Any questions arising from problematic neuroanatomy are to be resolved by a Consulting Neuroanatomist.

Postprocessing: MRI scans are saved in the NIFTI format at the original scan size and orientation. The 3D blocks of labels are created by assigning a label number to each voxel inside an outline. Because outlining is

performed on MRI scan data at twice the original size, the label data is shrunken before saving in the NIFTI format.

Quality Control Procedures: The main tool for quality control is the eyes of the NeuroTechs using NVM, but additional automated and visual checks are performed throughout the analysis. Each scan is inspected by a different NeuroTech or Consulting Anatomist. Labeled regions in 3D are filled in colors for each specific neuroanatomical region so that mistakes "jump out" during visual inspection. A red-green color scheme is used to check for proper left-right labeling. Labeled regions are visualized in 3D where they can be rotated and zoomed to check for errors. Volumes of regions are calculated and compared with normal value ranges, and overlap scores are calculated between individual scans and an atlas. Outliers (see [7]) in volumes or overlap scores are checked for labeling errors and the outlines are adjusted as necessary. For subjects that have been scanned twice, the volumes and overlap scores are evaluated and outlines are adjusted to increase the match.

Ongoing Improvements: Neuromorphometrics' mission is to build an ever-improving model of the structure of the living human brain. As a result, the exact protocols used to label scans are evolving over time with the goal of improving reliability and precision while capturing normal anatomic variation. Because of this and since the groups of scans that were obtained from each particular source were labeled over time, not all anatomical regions are labeled in every group.

References:

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