HIPPOCAMPAL SUBFIELD SEGMENTATION COMMON PROTOCOL PROJECT
SAMPLE MRI DATASET README

Last modified 3/19/2013

Overview

This dataset contains anonymized MRI images from a single healthy volunteer (male, 36 years of age). The dataset will be used by different participating research groups to provide an example of their segmentation protocol, to enable comparison, discussion and reconciliation at a joint meeting held on June 21-22 at UC Davis.

MRI Dataset Overview

The volunteer has been scanned on a 3 Tesla Siemens Trio scanner using a protocol currently in production for research studies involving hippocampal subfield imaging at the University of Pennsylvania. Included are T1 and T2 weighted MRI scans. The T1 scan is isotropic, while the T2 scan is anisotropic, with high in-plane resolution and thick slices, oriented along the main axis of the hippocampal formation (oblique coronal).

The same subject was scanned several weeks later on a 7T Siemens scanner using a T2-weighted protocol, also with anisotropic voxels and similar orientation. The 7T scan was over 30 minutes long, with signal averaging to produce a higher resolution image with good contrast.

The details of the MRI sequences are as follows:

Scan	Parameters
3 Tesla T1	Gradient echo MRI (MPRAGE) sequence. TR/TE/TI=1900/2.89/900 ms, 9 degree flip angle, 1.0 mm × 1.0 mm × 1.0 mm resolution, sagittal, acquisition time 4:26 min.
3 Tesla T2	Turbo spin echo (TSE) sequence. TR/TE: 7200/76 ms, echo train length 15, 15.2 ms echo spacing, 150 degree flip angle, 75% phase oversampling, 0.4 mm × 0.4 mm in-plane resolution, 30 interleaved slices with 2.0 mm thickness and no gap, angulated perpendicular to the long axis of the hippocampal formation, acquisition time 6:29 min
7 Tesla T2	Siemens 3D TSE work in progress sequence. TR/TE=3000/388ms, 4 averages, 6.16 ms echo spacing, variable flip angle, no phase oversampling, 0.4 mm x 0.4 mm in-plane resolution, 224 slices with 1.0 mm thickness and no gap, angulated perpendicular to the long axis of the hippocampal formation, acquisition time 29:36 min

Package Contents

FILENAME	DESCRIPTION
native/mprage_3t_bet_dr.nii native/tse_3t_dr.nii native/tse_7t_dr.nii	3 Tesla T1, 3 Tesla T2 and 7 Tesla T2 scans in NIFTI format, in its native space. The T1 image has been skull-stripped. The dynamic range of all images has been adjusted by clipping off the highest intensity values. The images are in their native space, i.e., no registration has taken place. **It is recommended that you use these images for segmentation**.
original/mprage_3t_bet.nii original/tse_3t.nii original/tse_7t.nii	Same as in “native”, but these images have not undergone the dynamic range correction. When viewing these images, the contrast in the hippocampal region needs to be adjusted.
resliced_to_7t/*.nii	This folder contains regions of interest from the 7T volume (supersampled by the factor of 2 in each dimension) and co-registered 3T T1 and T2 volumes, resliced to the same voxel space. These images are useful for comparing the 3T and 7T modalities.

FILENAME	DESCRIPTION
labels/labeltable.xlsx labels/itksnap_labelfile.txt	A spreadsheet listing a common set of segmentation labels. See notes below. A compatible label file for the program ITK-SNAP

How to Prepare Segmentations

To participate in the quantitative component of the meeting, please follow these guidelines:

- Label one of the images in the **native** directory. Please choose the modality (3 Tesla T2, 7 Tesla T2, or 3 Tesla T1) that is closest to what is used in your work.
- Label the **left hippocampal formation**. It is optional to label the right hippocampal formation.
- Use the segmentation protocol and software currently employed in your research.
- The segmentation should be an image in **NIFTI** format (assigning a single label to each voxel in the input image). We realize that this precludes partial volume segmentation, but saving segmentation as a volume simplifies sharing and analysis dramatically.
    - Use the spreadsheet in the **labels** directory to determine the numerical values that correspond to each anatomical label in your segmentation. For example, if your segmentation includes the label CA1, it should be assigned the value 1 in your segmentation (regardless of hemisphere).
        - *Note that the label file is meant to be the superset of all labels used by researchers in the field. The fact that there are labels with overlapping definitions is intentional: some researchers treat CA1+CA2 as a single label, others group CA2+CA3 together, and others label all of these subfields separately. Please use only those labels that you would normally use. If some of those labels are included in the label file, add them at the end.*
- We strongly encourage you to make sure that it is possible to load and view the segmentation in the open-source tool ITK-SNAP (free download from http://itksnap.org).
    - A label description file for ITK-SNAP is included in the **labels** directory.

If you are unable to provide a segmentation under these guidelines, please contact the organizers to determine how to include your segmentation results in the quantitative analysis.

How to Submit Segmentations

Please submit your segmentation by **June 1, 2013** to pyushkevich@gmail.com via DropBox, Google Drive or email. Your submission should include

- The segmentation in NIFTI format.
- The spreadsheet listing label ids and names, if you have made any changes to the one provided in the file **labeltable.xlsx**.