Data Set Description by Joy Matsui and EY Regina Kim
2011 Sep

Data Set Description

- Since subjects have anywhere from one to four time points, data has been organized by time point. We have provided a spreadsheet that is a catalog of scan site, subject ID, scan session ID, scan date, corresponding DWI and structural data (many structural images were acquired in a session different from the scan session that collected the DWI), and some quality control notes.
- For each scan session there's a set of raw dicom images and potentially three reconstructions:
  1. June 2011 processed structural data.
  2. September 2011 processed (updated segmentations) structural data.
  3. DTI processed data

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A Raw Images

Raw images are the dicom data from the scanners. These images are not corrected for bias field and not aligned into the common space yet. In figure A-1, tilted image is shown.

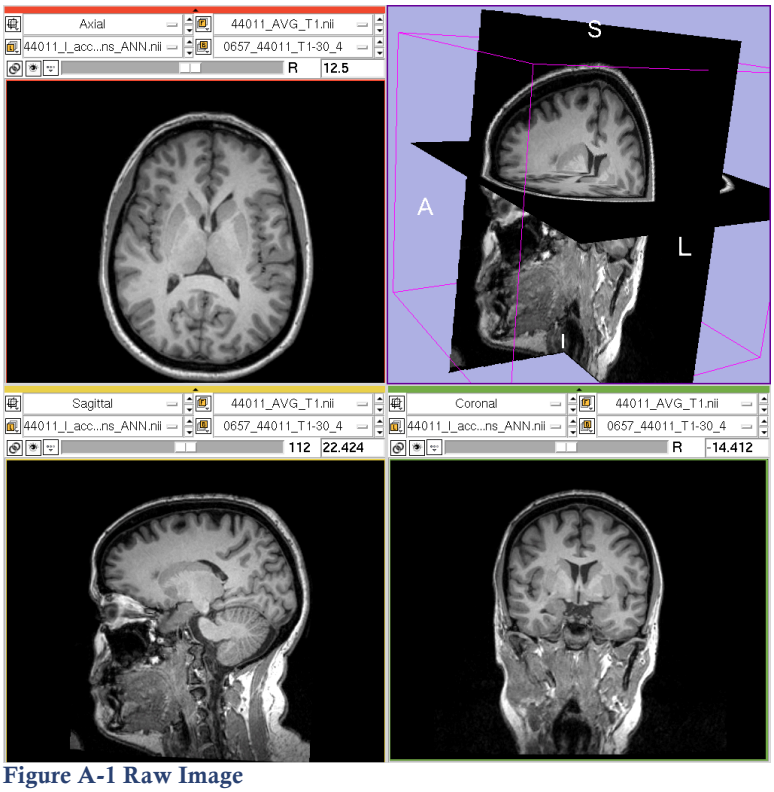

Figure A-1 Raw Image

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B DTI Data Set

- Reconstruction: ***EXPID_DWI_DTI20110901***

All diffusion weighted and diffusion tensor images are located in the *DWI_DTI* subdirectory. Most scan sessions contained three 4D DWI files with one baseline image and 78 unique diffusion gradients. Some scan sessions contained more or less DWI files and these were noted in the master spreadsheet.

B.1 Corresponding structural data

DWI and structural data were often collected in separate scan sessions, resulting in DWI and structural data having separate scan IDs. We have cataloged the DWI data with its corresponding structural data from the same time point in the master spreadsheet. All DWI/DTI data is housed in the DWI scan session subdirectory.

B.2 Processing description

B.2.a Quality control of diffusion weighted images

All DWI files in a given scan session (filename: DWI-79_##.nrrd) were first concatenated into a large file (filename: DWI_CONCAT.nrrd).

The concatenated DWI files were then put through a DWI quality control tool that removed gradients containing artifact (susceptibility artifacts, interlace artifacts, and gross-motion), averaged the multiple baseline images, and co-registered all gradients to baseline to removed eddy-current and head motion artifacts. We must note that many of the scans collected at Iowa in 2008 suffered from signal dropout in the superior parietal lobe due to table vibration. As a result, many of the gradients sampling diffusion in the z-direction were removed from those scans. The outputs of DTIPrep (filename: DWI_CONCAT_QCed.nhdr, DWI_CONCAT_QCed.raw.gz) were visually inspected to ensure artifacts were removed. The number of remaining gradients in each scan are noted in the master spreadsheet. All but one quality controlled scan contained at least 24 remaining diffusion gradients. DTIPrep was unable to remove all artifacts from a few DWI scans since they were simply too noisy. These excessively noisy DWI scans were excluded from further analysis. This is also noted in the master spreadsheet.

Another aspect of the DWI data that was noted was lobe coverage. Ratings on the coverage of frontal, parietal, temporal, and occipital lobes (poor, fair, and good) are included in the master spreadsheet.

B.2.b Alignment of DWI/DTI data into structural data space

Each gradient in the output file of DTIPrep was rigidly resampled in place to its corresponding skull-stripped T2 image (filenames: T2_skullstrip.nii.gz, Resample_DIP.nrrd). A tensor file from the resampled DWI image was generated (Resample_DIP_Tensor_Slicer_Visible.nhdr, Resample_DIP_Tensor_Slicer_Visible.raw.gz). Scalar maps were then computed from the tensor image. The types of scalars we are providing include fractional anisotropy (FA), mean diffusivity (ADC), axial diffusivity (AD), and radial

diffusivity (RD). Each scalar map was then resampled with linear interpolation via a bspline transformation into structural data space (Resample_DIP_FA_Vox_Bspline.nii.gz, Resample_DIP_ADC_Vox_Bspline.nii.gz, Resample_DIP_AD_Vox_Bspline.nii.gz, Resample_DIP_RD_Vox_Bspline.nii.gz,). The bspline transform was derived between the baseline image extracted from the DTIPrep output and its corresponding skull-stripped T2 image.

B.3 Missing DWI data

DWI data that were noted as missing cannot be found on XNAT or our file system at Iowa. We believe these data sets are missing because they were not collected.

B.4 Excluded DWI/DTI, incomplete DTI data

DWI/DTI data that were noted as excluded were deemed unusable at some point in the processing pipeline. Excluded data has not been provided to you but exists on Iowa's file system. These data sets were excluded because they could not be completely cleaned up by DTIPrep, were entirely noisy from the start, or the resampling of scalar maps into structural image space failed.

Incomplete DTI data were noted as incomplete because the corresponding structural data for that time point was missing or deemed unusable. DWI data (outputs of DTIPrep) from incomplete DTI data are provided to you but will not include tensor and scalar images because post-DTIPrep processing steps could not be completed without corresponding structural data.

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C Structural Data Set

- Reconstruction: ***EXPID_10_AUTO.NN3Tv20110901***

All the structural data set is located in the *EXPID_10_AUTO.NN3Tv20110901* directory. Every scan goes through BRAINS[1]' AutoWorkUp[2] pipeline comes to this directory. The directory includes AC-PC aligned data set, soft/hard-tissue classified image, bias-field-corrected image, posterior probability of each tissue, and segmentation of selected structures.

C.1 AC-PC Aligned Images

Spatial alignment is accomplished by finding *anterior commissure (AC)* and *posterior commissure (PC)* points. BRAINS' AutoWorkUp begins with the alignment of raw image into this common space. *The spatial alignment process results in the images being resampled into an orientation with the midsagittal plane in the center of the image space, with AC and PC pointing on a horizontal line in the midsagittal plain.*[2] Example of AC-PC aligned images is shown in figure C-1.

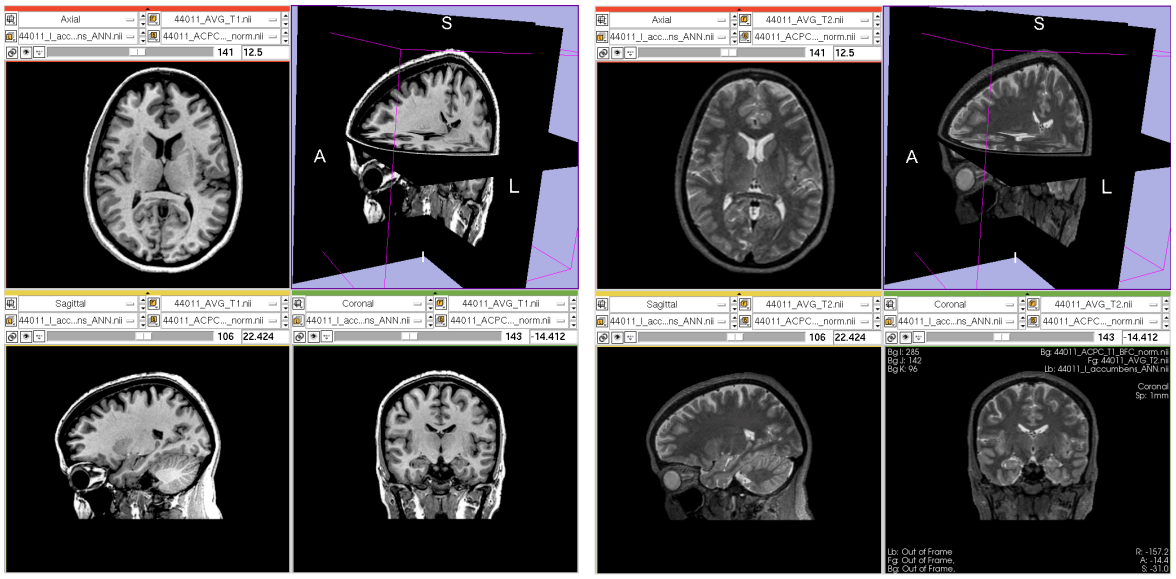

Figure C-1 AC-PC Aligned Images

C.2 Bias Field Corrected Images

- Image name conventions:
  - ACPC_T1_BFC_norm.nii.gz
  - ACPC_T2_BFC_norm.nii.gz

Bias field corrected images are given with above name scheme for both T1 and T2 weighted images. If there are more than one scans per session, there will be multiple bias field corrected images.

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[1] BRAINS: **Br**ain research: **A**nalysis of **I**mages, **N**etworks, and **S**ystems

[2] Pierson, R., Johnson, H., Harris, G., Keefe, H., Paulsen, J. S., Andreasen, N. C., & Magnotta, V. A. (2011). Fully automated analysis using BRAINS: AutoWorkup. NeuroImage, 54(1), 328–336. Elsevier Inc. doi:10.1016/j.neuroimage.2010.06.047

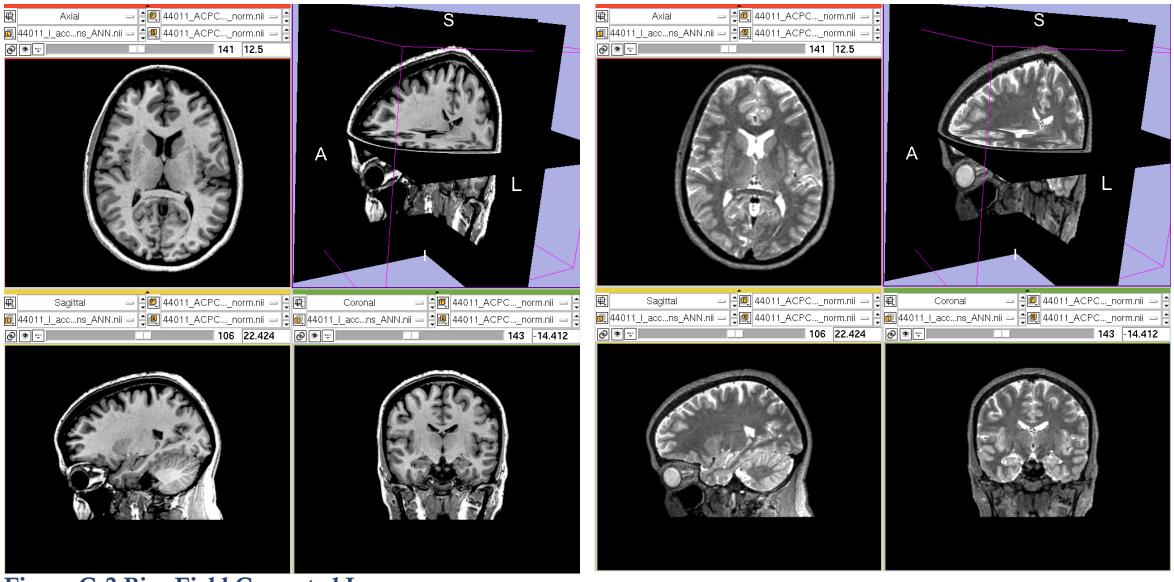

Figure C-2 Bias Field Corrected Images

C.3 Average Images

- Image name conventions:
  - AVG_T1.nii.gz
  - AVG_T2.nii.gz

If there were multiple scans per session, average of bias field corrected images are computed. This could be useful to compensate any other artifacts. Average image should be identical to the bias field corrected image when there is only one scan for the session.

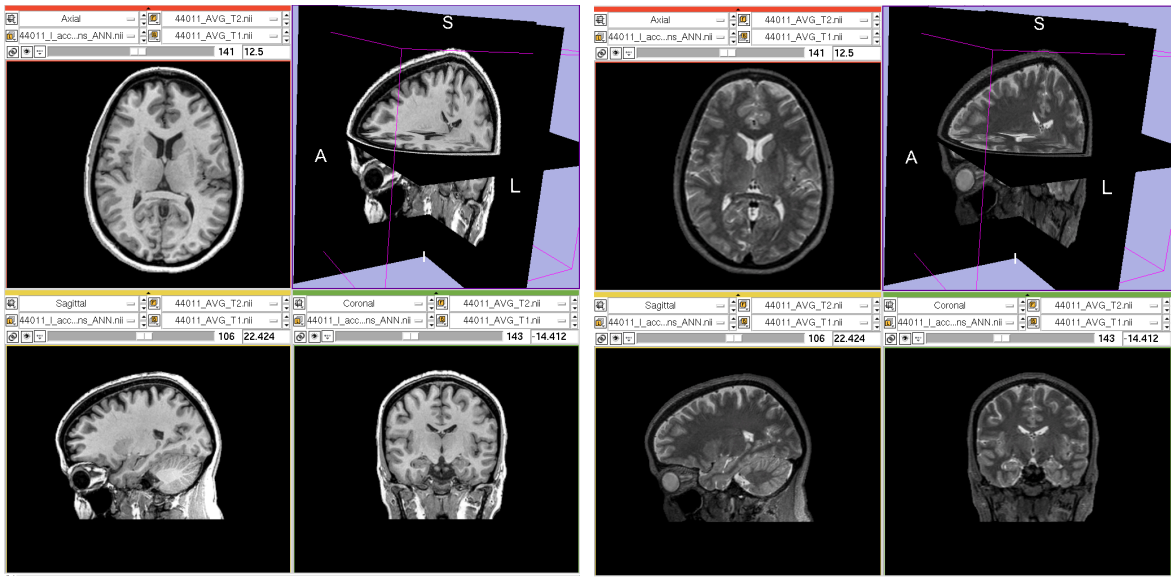

Figure C-3 Average Images

C.4 Posteriors

- Posterior images are provided only for a subset of scans.

Each image example is given below.

C.4.a White Matter Posterior:

- Image name conventions:
  - *prefix*_ACPC_POSTERIOR_WM_BRAINSABC.nii.gz

C.4.b Venous Blood Posterior:

- Image name conventions:
  - *prefix*_ACPC_POSTERIOR_VB_BRAINSABC.nii.gz

C.4.c Surface Grey Matter Posterior:

- Image name conventions:
  - *prefix*_ACPC_POSTERIOR_SURFGM_BRAINSABC.nii.gz

C.4.d CSF Posterior:

- Image name conventions:
  - *prefix*_ACPC_POSTERIOR_CSF_BRAINSABC.nii.gz

C.4.e Brain cerebellum White Matter Posterior:

- Image name conventions:
  - *prefix*_ACPC_POSTERIOR_CRBLWM_BRAINSABC.nii.gz

C.4.f Brain cerebellum Grey Matter Posterior:

- Image name conventions:
  - *prefix*_ACPC_POSTERIOR_CRBLGM_BRAINSABC.nii.gz

C.4.g Brain Basel Ganglia Grey Matter:

- Image name conventions:
  - *prefix*_ACPC_POSTERIOR_BGM_BRAINSABC.nii.gz

C.5 Segmentations

We provide *left/right caudate/globus/thalamus/putamen/hippocampus* binary images for each scan session.

- Image name conventions:
  - *location_structure*.nii.gz
  - Location has a value of *l* or *r*, indicating left or right structure respectively.
  - Structure indicating structure name as it is.
  - Ex) l_globus.nii.gz, r_putamen.nii.gz

Table 1 Structure Segmentation Notes

Region of Interests	Note
Caudate	*Inspected ALL and edited if necessary.*
Putamen	*Inspected randomly: good*
Globus	*Inspected randomly: reasonable. Structure is placed in right location but might not be so accurate.*

Thalamus	*Inspected randomly: good*
Hippocampus	*Inspected randomly: good*