# BRAINS AutoWorkup Output Descriptions

# Basic Information

All data was processed using [BRAINSTools](file:////confluence/display/BRAINSPUBLIC/BRAINSTools+Software). BRAINSTools is an open-source neuroimage processing toolkit (https://github.com/BRAINSia/BRAINSTools).

We always work in physical space coordinates.  The voxel lattice means nothing to us.   Each image may have a different voxel lattice size, but the anatomical data should be located such that the AC point is at physical location (0.0,0.0,0.0), the PC point is at (0.0,0.0, ????), the voxel sizes of the generated data have been normalized to 1.0mm^3, and the direction cosigns are an identity matrix.  We follow an LPS convention and image description that is compliant with the DICOM standard.  The point source for each voxel is at the center of each voxel, and the origin represents the physical location of the point source for the first voxel stored in memory (set such that the AC point is at (0.0,0.0,0.0).

"Resampling" data into a 256^3 voxel lattice using an identity matrix will provide images in similar voxel organizations. Use an appropriate interpolator during the resampling process.

The tools used to generate these results conform to the National Alliance for Medical Imaging Computing (<https://www.na-mic.org/wiki/Main_Page)> best-practices standards. Visualization of the files is best supported by 3DSlicer <https://www.slicer.org>. Many of the BRAINSTools (https://github.com/BRAINSia/BRAINSTools) are available as modules within the 3DSlicer package.

Software packages supporting this work:

* BRAINSTools: <https://github.com/BRAINSia/BRAINSTools>
* 3DSlicer: <https://www.slicer.org>
* ANTs: <http://stnava.github.io/ANTs/>
* Nipype: <http://nipype.readthedocs.io/en/latest/>

# Organization

The data is organized according to the following directory layout:

${BASEDIR}/<SESSION>/<FILES>

Where <SESSION> is a unique identifier for one visit to the MRI scanner, and <FILES> represent the initial and derived data outputs.

### Example of Scan Session (one time in the scanner) Naming for the PREDICT\_HD project

where

* <SESSION> = "[0-9]{5}" (i.e. a 5 digit randomly generated unique number)

SESSION identifiers are globally unique. Use this value as a key to identify site, subject, and demographic information about this image set.

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**Description of Analysis Output for each scan session**

The DBGaP distribution of the imaging data contain all files in a single directory. The file names indicate more specific information of the image content and should help the user identify which file(s) are relevant for use to answer a particular question.

# Overview of BRAINSAutoWorkUp

All imaging analysis was performed at the University of Iowa Scalable Informatics, Neuroimaging, Analysis, Processing and Software Engineering (SINAPSE) laboratory. Acquired scans are processed through a fully automated procedure, BRAINS Auto Workup (BAW), improved with SyN registration from the Advanced Normalization Toolkit in the BRAINSTools package. All the scans begin with visual inspection of the raw data so that only images of sufficient quality are subjected to further processing. Each dataset, T1- and/or T2-weighted images, are processed together to improve the robustness of the procedure from complimentary information provided by multiple modalities. The best-rated T1-weighted image is spatially normalized based on prominent landmarks in MRI, including anterior and posterior commissure, and mid-sagittal plane. The remaining scans acquired of the same session are then rigidly aligned to the spatially aligned T1 image, and simultaneously processed by the automated bias-field correction (ABC) algorithm, BRAINSABC. For each given modality, BRAINSABC produces an average of independently bias-field corrected MR images resampled in 1mm x 1mm x 1mm and their respective corresponding 17 tissue probability maps, including white matter, grey matter, and CSF. At this point, all longitudinal scan sessions for given subjects are used jointly to build a subject specific atlas that best represents the average longitudinal shape with respect to minimum mean square error of displacement. This joint session template building is a normalizing step that uses the all scan sessions for a given subject to maximize consistency of subsequent measurements across scanner variation inherent in long-running longitudinal studies. The resulting data set of bias-corrected average T1 and/or T2 images are subsequently segmented for subcortical structures using an automated segmentation framework. All the development processing was blinded to clinical data, such as HD gene-expansion status, gender, and age.

# Nearly original data

Data sets with minimal changes from DICOM original data.

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| FILENAME | DESCRIPTION |
| T1-30\_2\_acpc\_deface.nii.gz  T2-30\_3\_acpc\_deface.nii.gz  T1-30\_6\_acpc\_deface.nii.gz  T1-30\_2\_acpc\_deface\_mask.nii.gz  T2-30\_3\_acpc\_deface\_mask.nii.gz  T1-30\_6\_acpc\_deface\_mask.nii.gz | T1 – A t1 weighted image  T2 – A T2 weighted image  PD – A PD weighted image  -30 – 3Tesla scan  -15 – 1.5 Tesla scan  \_# - The series number during the scan session  \_acpc indicates that physical space information was manipulated to put the data in ACPC alignment.  \_deface to indicate that he data was defaced. |
| #####\_N.json | These files contain the results of manual visual inspections of each scan series.  ###### represents the session\_ID  N represents the series number during the scan |

# ACPC Align

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| FILENAME | DESCRIPTION |
| BCD\_ACPC\_Landmarks.fcsv | output file from BRAINSConstellationDetector. A Slicer3D compatible fiducial file. |

Please reference <https://doi.org/10.1016/j.neuroimage.2017.04.012>

A. Ghayoor, J. G. Vaidya, and H. J. Johnson, “Robust Automated Constellation-Based Landmark Detection in Human Brain Imaging,” *Neuroimage*, 2017.

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| Figure 2: ACPC Anatomical Alignment, and landmark identification. |
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# AntsLabelWarpedToSubject

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| FILENAME | DESCRIPTION | |
| ../nac-hncma-atlas-2017Jan-Slicer4-7Version | | <http://www.spl.harvard.edu/publications/item/view/2037>  REFERENCE ATLAS |
| ../hncma-atlas-lut-mod2.ctbl | | The file “hncma-atlas-lut-mod2.ctbl” provides a color table needed to interpret the labels for hncma\_atlas.nii.gz |
| template\_nac\_labels | | Use the FreeSurfer color scale from Slicer3D to identify regions |
| hncma\_atlas.nii.gz | | Use the hncma-atlas-lut-mod2.ctbl  color scale from Slicer3D to identify regions |
| template\_WMPM2\_labels.nii.gz | | White matter parcellation map derived from: http://www.loni.usc.edu/ICBM/Downloads/Downloads\_Atlases.shtml |
| template\_headregion.nii.gz  template\_leftHemisphere.nii.g  template\_rightHemisphere.nii.gz  template\_ventricles.nii.gz | | Warped template head regions, left hemispheres, right hemispheres, and approximate ventrical locations. |
| rho.nii.gz  theta.nii.gz  phi.nii.gz | | Deformed polar coordinate maps from the reference atlas space. |
| r\_hippocampus\_ProbabilityMap.nii.gz  r\_globus\_ProbabilityMap.nii.gz  r\_caudate\_ProbabilityMap.nii.gz  r\_accumben\_ProbabilityMap.nii.gz  l\_thalamus\_ProbabilityMap.nii.gz  l\_putamen\_ProbabilityMap.nii.gz  l\_hippocampus\_ProbabilityMap.nii.gz  l\_globus\_ProbabilityMap.nii.gz  l\_caudate\_ProbabilityMap.nii.gz  l\_accumben\_ProbabilityMap.nii.gz  r\_thalamus\_ProbabilityMap.nii.gz  r\_putamen\_ProbabilityMap.nii.gz | | The probability maps in the atlas space were generated by warping many segmented images into the atlas space and then generating probability maps from the family of segmented images.  These files represent the atlas to subject warped versions of the probability maps for each region. |

The ANTs registration tool was used to warp the atlas labels onto each resulting subject space.

# TissueClassify

The files with the suffix "POSTERIOR\_" represent the posterior probability for the tissue type/region on a normalized scale.  These classification files are the basis of the segmentation files found in CleanedDenoisedRFSegmentations/.

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| **Image** | **FileName** | **Description** |
| /C:/3ed80c14775ca78953ab89b4ee770467 | POSTERIOR\_ACCUMBEN.nii.gz | Posterior probability for accumbens |
| /C:/794552c0544a66c28cbd9654fe92d9f5 | POSTERIOR\_AIR.nii.gz | Posterior probability for air |
| /C:/95c2b9c5ec53e25d5ff4096aef432d57 | POSTERIOR\_CAUDATE.nii.gz | Posterior probability for caudates |
| /C:/d2f8ceaff7d159f9e4f8de0966f305dd | POSTERIOR\_CRBLGM.nii.gz | Posterior probability for cerebellar gray matter |
| /C:/05b7964814b1fefff54f9eae40a4f7d7 | POSTERIOR\_CRBLWM.nii.gz | Posterior probability for cerebellar white matter |
| /C:/04a0272c275d89fa1bcbd216ea6f9233 | POSTERIOR\_CSF.nii.gz | Posterior probability for cerebral spinal fluid |
| /C:/451323ca02c640fb9b71e37eebbf1a42 | POSTERIOR\_GLOBUS.nii.gz | Posterior probability for globi |
| /C:/b8725835934ede62d7a42f5abe8573f3 | POSTERIOR\_HIPPOCAMPUS.nii.gz | Posterior probability for hippocampi |
| /C:/d39295a35507ae0c0a8b157ce71c07db | POSTERIOR\_NOTCSF.nii.gz | Posterior (not) probability for cerebral spinal fluid |
| /C:/1b066d0154012cfb8edf224c9779efb0 | POSTERIOR\_NOTGM.nii.gz | Posterior (not) probability for gray matter |
| /C:/063bf0f3ee1482b067bb604ee22c318d | POSTERIOR\_NOTVB.nii.gz | Posterior (not) probability for venous blood |
| /C:/4491f6c9c4b49c347bae61d145034c2a | POSTERIOR\_NOTWM.nii.gz | Posterior (not) probability for white matter |
| /C:/6b29949970d9527452a6853b6850fe4d | POSTERIOR\_PUTAMEN.nii.gz | Posterior probability for putamens |
| /C:/61da319402fe55b2f30505c22dafb999 | POSTERIOR\_SURFGM.nii.gz | Posterior probability for surface gray matter |
| /C:/e9e9cfa55c2920e6698138010b0a0121 | POSTERIOR\_THALAMUS.nii.gz | Posterior probability for thalami |
| /C:/c666f3e60db801b9e222720ce88983a5 | POSTERIOR\_VB.nii.gz | Posterior probability for venous blood |
| /C:/47e61f06b960c1686954b54cbb6f4462 | POSTERIOR\_WM.nii.gz | Posterior probability for white matter |
| /C:/77fb4e6274d504679dfa8801dca82df6 | fixed\_brainlabels\_seg.nii.gz | Labels for brain only |
| /C:/c1599ce4df3ec262acd47f58bb26e76b | fixed\_headlabels\_seg.nii.gz | Labels for head and brain |
| /C:/70c258f7cc128fdc031ffe093a9ef912 | t1\_average\_BRAINSABC.nii.gz | Average longitudinal T1 image |
| /C:/63849aac7d0fa0b1de416628f124dbff | t2\_average\_BRAINSABC.nii.gz | Average longitudinal T2 image |

# Brain Label (Under TissueClassify)

[1] R. E. Kim and H. J. Johnson, “Robust multi-site MR data processing: iterative optimization of bias correction, tissue classification, and registration.,” *Front. Neuroinform.*, vol. 7, no. November, pp. 1–11, 2013.

[2] A. Ghayoor, J. S. Paulsen, R. E. Kim, and H. J. Johnson, “Tissue classification of large-scale multi-site MR data using fuzzy k-nearest neighbor method,” in *Proceedings of SPIE Medical Imaging*, 2016, vol. 9784, pp. 1–7.

[3] R. E. Kim, P. C. Nopoulos, J. S. Paulsen, and H. J. Johnson, “Efficient and extensible workflow: Reliable whole brain segmentation for large-scale, multi-center longitudinal human MRI analysis using high performance/throughput computing resources,” in *Lecture Notes in Computer Science (including subseries Lecture Notes in Artificial Intelligence and Lecture Notes in Bioinformatics)*, 2016, vol. 9401, pp. 54–61.

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| **Image** | **Filename** | **Description** |
| /C:/723125eb4a97f268bc12db8a82c647ca | fusion\_neuro2012\_20.nii.gz | The label fusion algorithm (ANTs MALF) applied using following images/label definition as atlases:  <http://www.cma.mgh.harvard.edu/manuals/segmentation/>  Local File: /Shared/johnsonhj/HDNI/Neuromorphometrics/2012Subscription/Data/1000/3/NIFTI/1000\_3\_glm\_LabelMap.xml |

# ACCUMULATED\_POSTERIORS

This directory contains the summed versions of the per-voxel tissue classified images (see [TissueClassify](#BRAINSAutoWorkupOutputDescriptions-Tiss)).  Unlike the "POSTERIOR\_\*" images, these images are binary, with voxel value 1 indicating inclusion in the tissue type, 0 otherwise.

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| **Image** | **FileName** | **Description** |
| /C:/93b436941b978cdd3a0494dfc3ef3fea | POSTERIOR\_BACKGROUND\_TOTAL.nii.gz | Background (air, skull, dura, etc.) |
| /C:/04a0272c275d89fa1bcbd216ea6f9233 | POSTERIOR\_CSF\_TOTALnii.gz | cerebral spinal fluid |
| /C:/ca8289dc5c2d32f5479dfc3d833aedb6 | POSTERIOR\_GLOBUS\_TOTAL.nii.gz | globus |
| /C:/6b451979c197d78c347ad0449e85831b | POSTERIOR\_GM\_TOTAL.nii.gz | gray matter |
| /C:/cc5c678d0909a6a314ac367e594377e7 | POSTERIOR\_VB\_TOTAL.nii.gz | venous blood |
| /C:/e189d04c0308bb109712939f6d46e48d | POSTERIOR\_WM\_TOTAL.nii.gz | white matter |

 These files may be useful for initializing improved segmentation algorithms. These files are of moderate quality.

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| FILENAME | DESCRIPTION |
| right\_hemisphere\_wm.nii.gz  left\_hemisphere\_wm.nii.gz | Right and left hemisphere wm maps for this subject. |

# ANTS Joint Fusion

[1] J. L. Forbes, R. E. Kim, J. S. Paulsen, and H. J. Johnson, “An Open-Source Label Atlas Correction Tool and Preliminary Results on Huntingtons Disease Whole-Brain MRI Atlases.,” *Front. Neuroinform.*, vol. 10, pp. 1–11, Aug. 2016.

[1] R. E. Kim, S. Lourens, J. D. Long, J. S. Paulsen, and H. J. Johnson, “Preliminary analysis using multi-atlas labeling algorithms for tracing longitudinal change,” *Front. Neurosci.*, vol. 9, no. JUN, pp. 1–11, Jul. 2015.

[1] H. Wang, J. W. Suh, S. R. Das, J. B. Pluta, C. Craige, and P. A. Yushkevich, “Multi-atlas segmentation with joint label fusion,” *IEEE Trans. Pattern Anal. Mach. Intell.*, vol. 35, no. 3, pp. 611–623, Jun. 2013.

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| FILENAME | DESCRIPTION |
| ../BAWHDAdultAtlas\_FreeSurferConventionColorLUT\_20160524.txt  ../BAWHD\_LobesLUT\_20160524.txt | Slicer3D compatible color lookup tables with named labels for each coded region. |
| JointFusion\_HDAtlas20\_2015\_dustCleaned\_label.nii.gz | AntsJointFusion based labeling of brain data. The labeling mostly follows the FreeSurfer labeling conventions with additions. |
| JointFusion\_HDAtlas20\_2015\_lobe\_label.nii.gz | A consolidation of the many regions into larger lobar regional measures. |
| loberVolume.json  labelVolume.json | Measurements (volume, average intensity…) for each region of the Jointfusion label maps. |