LHAB Longitudinal Cerebellar Volume - Collaboration Project

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Overview of Scripts

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This document contains background information about the scripts that we will be modifying to processes the LHAB data. Processing will include several steps of which the biggest ones including infratentorial cropping and longitudinal normalization.

Scripts will be uploaded to Github.

Pipeline:

1 T1 Bias Field Correction

1.1 Software needed

- Advanced Normalization Tools (ANTs) Compile from source

- 2012 MICCAI Multi-Atlas Labeling Challenge Data (training set)

- FSL

1.2 Script for one subject

`01_BiasFieldCorrection.sh`

2 Isolate the Cerebellum and Brainstem

2.1 Software needed

- Matlab

- SPM

- Spatially Unbiased Infra-tentorial Template (SUIT)
  SUIT is an SPM toolbox

2.2   Script for one subject

- Shell wrapper script. This script calls the Matlab job script.

`02_IsolateCerebellum.sh`

- Matlab job

`02_IsolateCerebellum.m`

3   Calculation of Longitudinal Normalization

3.1   Software needed

- Advanced Normalization Tools (ANTs) Compile from source

- Spatially Unbiased Infra-tentorial Template (SUIT)
  SUIT is an SPM toolbox

- FSL

3.2   Part 1: Create a Subject Template

`03_CreateSubjectTemplate.sh`

3.3   Part 2: Warp the Subject Template to SUIT space

`04_WarpSubjectToSUIT.sh`

4   Segmentation

4.1   Software needed

- Atropos, part of: Advanced Normalization Tools (ANTs) Compile from source

Note:
We don't need to use Atropos. We could use any other type of tissue segmentation.

5   Notes:

If you have already processed this dataset with FreeSurfer we could register the Freesurfer Cerebellum Label to the native subject space to refine the cerebellar outline.