**Recommended level-2 analysis procedures to replicate level-1 PiB data:**

**Scripts for processing located in: /ifs/loni/faculty/mbraskie/HABLE/PET/amyloidpet/code/Centiloid\_Analysis/Scripts**

**Google Doc for keeping track:**

<https://docs.google.com/spreadsheets/d/1LNDtMlfnW9ZECc4uI2syTxuGGPEjAqvxpuQwSp782o0/edit#gid=192540646>

**Google Doc for Values:**

<https://docs.google.com/spreadsheets/d/1cBU5XjKnGz3w3DN-0y53lDT0ByBTolH9_0jwlgfOk1s/edit#gid=336818468>

**Tab: Centiloid Analysis**

**To create subject directories, run:**

**./mkdirectory (add subjects)**

**MAKE SURE FILES ARE UNZIPPED (.NII ENDING) OTHERWISE SPM WILL NOT RUN**

1. Manually reorient the subject data to match the Montreal Neurological Institute (MNI) template provided with the SPM8 software (in [your SPM8 path]/canonical/avg152T1.nii)
   * Use "**Display**" module in SPM8 (see p.143 in SPM8 manual)
   * Reorient the data so that the mm coordinate of the Anterior Commissure is within about 3cm from [0 0 0] and the orientation is within about 15o of MNI space.

**Does not need to be done for MPRAGE**

* + A few PET images need to be flipped along the y-axis for the correct orientation. Do so by putting "-1" in the "resize (y)" box. (Do not reorient these images by putting "-3.14" in the "yaw (rad)" box as it will result in a left-right flip.) [

**Needs to be done for PET**

**Tutorial for setting origin:** <https://www.youtube.com/watch?v=AwNJAUKLhqY>

**Reference for where to set the origin (doesn’t have to be exact but try to get as close as possible to image below):**

**A close up of a person

Description automatically generated**

**Script for Steps 2- 8 is Centiloid\_Analysis\_job.m**

**Open in MATLAB and change the subjects that you want to run. Everything else is already set up the way it needs to be**

**Checking registrations after MATLAB code has run:**

**./check\_registration.sh (add subjects to check)**

**Decrease opacity of PET and MPRAGE to see if they align properly with MNI template**

1. Coregister subject MRI to MNI template
   * Use “**Coregister: Estimate**” module
   * Reference Image: avg152T1.nii (in [your SPM8 path]/canonical/avg152T1.nii)
   * Source Image: subject MRI
   * Keep all default parameters
2. QC subject MRI to MNI template coregistration
   * Use "**Check Reg**" function in SPM8
   * \*The goal of this registration is to bring subject MRI in rough alignment with the MNI template. It is acceptable if the two images are not perfectly aligned\*
3. Coregister subject PET to subject MRI
   * Use “**Coregister: Estimate**” module
   * Reference Image: subject MRI
   * Source Image: subject PET
   * Keep all default parameters
4. QC subject PET to MRI coregistration
   * Use "**Check Reg**" function in SPM8
   * Ensure that subject PET image is well-aligned to subject MRI
5. Apply unified segmentation to subject MRI
   * Use "**Segment**" module in SPM8
   * Keep all default parameters
   * If you do not wish to save any output image files, under "Output Files", you can change "Grey Matter" and "White Matter" to "None", and "Bias Corrected" to "Don't Save Corrected".
6. Apply normalization parameters to transform subject PET and subject MRI into MNI-space
   * Use “**Normalise: Write**” module
   * Parameter File: \*\_seg\_sn.mat (forward transformation parameter)
   * Images to Write: subject PET and subject MRI
   * Change "Bounding box" to [NaN NaN NaN; NaN NaN NaN]
     + This tells SPM to use the same bounding box as the template.
7. QC subject PET to MNI-template transformation
   * Use "**Check Reg**" function in SPM8

**VOIS located in: /ifs/loni/faculty/mbraskie/HABLE/PET/amyloidpet/Centiloid\_Analysis/Centiloid\_Std\_VOI/nifti/2mm**

1. Download the standard VOIs from the GAAIN website

* Download the 2mm resolution VOIs if you normalized to the avg152T1.nii template as described above (to match the 2mm resolution of that template).
* We recommend downloading and using the NIFTI images provided rather than converting from DICOM.

**Code for extracting SUVRs:**

**./get\_SUVRs.sh (add subjects)**

**CSV file with values located in: /ifs/loni/faculty/mbraskie/HABLE/PET/amyloidpet/Centiloid\_Analysis/FBB\_SUVR.csv**

1. Extract PiB SUV values from normalized PET images using standard VOIs
   * One example program to use is **fslstats** from the FSL Toolbox

**To convert SUVR to CL:**

1. **FBB SUVR = Cortical SUVR / Whole Cerebellum SUVR**
2. **CL Value = 153.4 X FBB SUVR – 154.9**

**Ref: https://link.springer.com/article/10.1007/s00259-017-3749-6**

After all files have been created, run permissions script to open access to files