**Step 0: Download all relevant .dtseries.nii files to Ameral/scratch folder**

**See HCPdownload.R file.**

Log: 09/05/2020: Need to download rfMRI\_REST1\_LR\_Atlas\_MSMAll\_hp2000\_clean.dtseries.nii

from the S3 bucket. I notice that your HCPdownload.R code, you have this line: /MNINonLinear/Results/rfMRI\_REST1\_RL/rfMRI\_REST1\_RL\_Atlas\_hp2000\_clean.dtseries.nii

**Step 1: Copy a brain parcellation to working folder**

**Q1-Q6\_RelativeValidation210.CorticalAreas\_dil\_Final\_Final\_Areas\_Group\_Colors.32k\_fs\_LR.dlabel.nii**

Log: 09/05/2020 We will use two parcellations:

CortexSubcortex\_ColeAnticevic\_NetPartition\_woSubcorGSR\_parcels\_LR\_ReorderedByNetworks.dlabel.nii

And

Q1-Q6\_RelativeValidation210.CorticalAreas\_dil\_Final\_Final\_Areas\_Group\_Colors.32k\_fs\_LR.dlabel.nii

The CortexSubcortex parcellation has 718 ROIs, and Q1-Q6 atlas has 360 ROIs.

**Step 2: Run preprocessStep1updated092020.sh to demean, normalized, and generate parcellated fMRI time series data in .ptseries.nii format for each .dtseries data.**

Log: 09/05/2020 *Per Matthew Glasser’s suggestion, no need to demean, normalize at vertex level.*

preprocessStep1updated092020.sh attached and needs to be modified due to different file path names.

**Step 3: Run preprocessStep2updated092020.sh to convert all .ptseries.nii files to gifti files.** This step will generate 4 .ptseries files, one for each run. **In addition, we will try to merge all .ptseries.nii files and convert to gifti files.** This step will generate 6 merged files in the format of .ptseries.nii using wbcommend. Then we use gifti-1.8 toolbox from matlab to convert .ptseries.nii to generate GIFTI files which includes two files (.gii and .gii.data).

1. Merge Rest 1 RL + Rest 1 LR
2. Merge Rest 2 LR + Rest 2 RL
3. Rest 1 LR + Rest 2 LR
4. Rest 1 RL + Rest 2 RL
5. Rest 1 RL + Rest 1 LR + Rest 2 LR + Rest 2 RL
6. Rest 1 LR + Rest 1 RL + Rest 2 LR + Rest 2 RL

Log: 09/05/2020 preprocessStep2updated092020.sh attached and needs to be modified, especially in terms of the merge different time series component.

**Step 4: Use matlab to convert gifti files to .txt file.** The scripts are included in the preprocessStep2updated092020.sh

matlab -nodisplay -singleCompThread -r "getfn,exit"

matlab -nodisplay -singleCompThread -r "HCP,exit"

getfn.m and HCP.m are two relevant matlab files for step 4 and the matlab scripts should be stored in a folder

**Step 5: Add ROI labels to all .txt files**. First, read one gifti file to matlab and extract labels for each ROIs. Save the label files for future use.