

Step 0: Download all relevant .dtseries.nii files to generated working directory using R script

- Run R script function to generate working directory and query downloads from HCP database
- Run R script function to trim subject list IDs to those subjects with complete data

Step 1: Download MMP and Cole brain parcellations to ROIs folder

- The CortexSubcortex parcellation has 718 ROIs, and MMP atlas has 360 ROIs.
- <https://balsa.wustl.edu/file/show/3VLx>
 - Q6_RelatedValidation210.CorticalAreas_dil_Final_Final_Areas_Group_Colors.32k_fs_LR.dlabel.nii
- <https://github.com/ColeLab/ColeAnticevicNetPartition>
 - CortexSubcortex_ColeAnticevic_NetPartition_wSubcorGSR_parcel_LR_ReorderedByNetworks.dlabel.nii
- Extract ROI labels from atlases
 - `./wb_command -cifti-label-export-table`
Pathtofile/Q1-Q6_RelatedValidation210.CorticalAreas_dil_Final_Final_Areas_Group_Colors.32k_fs_LR.dlabel.nii INDEXMAX Pathtodest/MMPLabel.txt

Step 2: Install Requisite software onto Amarel

- Installing Connectome Workbench on Amarel
 - Step 1. Open a desktop session, navigate to installing connectome workbench using firefox.
 - <https://www.humanconnectome.org/software/get-connectome-workbench>
 - Download CentOS version to your home directory.
 - Step 2. Unzip the file using `unzip filename`
 - Step 3 Optional. For autofilling wb commands, copy the `bashcomplete_wb_command` command and rename it as `.bash_completion`
 - Step 4. Type into console
 - `echo 'export`
`PATH=$PATH:/home/[netID]/filepath/workbench/bin_rh_linux64' >>`
`~/bashrc`
 - Step 5. Open new command window and type `wb_command` to validate completion
- Download gifti 1.8 package into amarel
 - Use `scp` and link path in following HCP.m MATLAB code
- Download MATLAB and bash files into amarel using `scp`
 - `scp -r path/to/directory netid@amarel.rutgers.edu:/scratch/netid/Research/name`
- Running .sh bash script files
 - Note amarel sbatch parameters at the top of the file
 - Submit jobs to the cluster using `sbatch filename.sh`

Step 3: Run preprocessStep4.sh to demean stdev and normalize .dtseries files

- Modify netid and wb_commands to fit use case
- Modify input and

Step 4: Run preprocessStep1.sh to convert dtseries.nii files into ptseries.nii files.

- Use trimmed subject ID list here
- Modify/add citfi parcellate wb_commands to fit use case
 - Change atlas path: MMP/Cole
 - Change input and output files

Step 5: Run preprocessStep3.sh to merge ptseries.nii files according to merge protocol

- <https://protocols.humanconnectome.org/HCP/3T/imaging-protocols.html>
- Exclude the first 20 columns when merging
- Resting State 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
- Task Based Data
 - For each scan type, one run was acquired with right-to-left phase encoding, and a second run with left-to-right phase encoding (in-plane FOV [field of view] rotation obtained by inverting both the RO (readout) and PE [phase encoding] gradient polarity).
 - Modify column lengths for each task
 - EMOTION 176
 - GAMBLING 253
 - LANGUAGE 316
 - MOTOR 284
 - RELATIONAL 232
 - SOCIAL 274
 - WM 405

Step 6: Run preprocessStep2.sh to convert ptseries.nii files to .gii files and convert .gii files to .txt format

Step 7: Export .txt files to output directory using R script

- Create output directory and file.rename txt files to generated output directory

Step 8: Upload .txt files to box using lftp

- Activate box authentication password under Account Settings Authentication

- Run commands in Amarel
 - `lftp ftp.box.com`
 - user netid@rutgers.edu
 - password *****
 - `mirror -R -P --only-missing /scratch/netid/Research/OutputDirectory
~/HCPfMRIExtraction/OutputDirectory`
- Files that were skipped due to error can be reuploaded by running lftp again

Step 9: Download .txt files from box to Amarel using lftp

- Run commands in Amarel
 - `lftp ftp.box.com`
 - user netid@rutgers.edu
 - password *****
 - `mirror -P --only-missing ~/HCPfMRIExtraction/OutputDirectory
/scratch/netid/Research/OutputDirectory`
- Files that were skipped due to error can be reuploaded by running lftp again