**Midnight Scan Club Pipeline:** Preprocessing Steps

**Packages set-up & versions**

ANTs, AFNI, FSL, R, Python, and Spyder installation instructions and set-up are found at their respective websites:

* ANTs: <http://stnava.github.io/ANTs/>
* AFNI: <https://afni.nimh.nih.gov/pub/dist/doc/htmldoc/background_install/install_instructs/index.html>
* FSL: <https://fsl.fmrib.ox.ac.uk/fsl/fslwiki/FslInstallation>
* R: <https://cran.r-project.org/bin/macosx/>
  + Required R packages can be installed from within R by calling the install.packages() command with the package name as an argument.
* Python: <https://docs.spyder-ide.org/current/installation.html>
* Spyder: <https://docs.spyder-ide.org/current/installation.html>
  + Either through Anaconda or without Anaconda (recommended):

For version specific links follow the instructions listed here:

Python: [version 3.7.9](https://www.python.org/downloads/release/python-379/)  
FSL: [version 6.0.4](https://fsl.fmrib.ox.ac.uk/fsldownloads_registration/download/fsl=10,o_s=19,d_type=release/)

AFNI: Precompiled binary macos\_10.12\_local version AFNI\_21.1.16: Go to [this link](https://afni.nimh.nih.gov/pub/dist/doc/htmldoc/background_install/download_links.html#to-browse-all-afni-packages-and-atlases) to learn how to download the older version: ***file 2022.04.29.1755*** [***macos\_10.12\_local.tgz***](https://afni.nimh.nih.gov/pub/dist/tgz/macos_10.12_local.tgz)

Convert3D Medical Image Processing Tool: [any version](https://sourceforge.net/projects/c3d/)

ANTs: [Release 1.9.x](https://sourceforge.net/projects/advants/files/ANTS/ANTS_1_9_x/) (instructions to download are at the bottom of the page, or [further details here](https://brianavants.wordpress.com/2012/04/13/updated-ants-compile-instructions-april-12-2012/) for the newest version)

If continuing with surface processing these additional programs are needed:

FreeSurfer [version 6.0](https://docs.spyder-ide.org/current/installation.html)

Connectome Workbench [version 1.4.2](https://github.com/Washington-University/workbench/tree/v1.4.2)

Ciftify [version 2.3.3](https://github.com/edickie/ciftify/tree/2.3.3)

**Preprocessing T1w images**

**We will be using an adult MNI template for the data**

MNI\_ICBM152 nifti must be downloaded and saved to a folder called “mni” for script to run. Download the MNI ICBM 2009c Nonlinear Asymmetric nifti files [here](https://www.bic.mni.mcgill.ca/ServicesAtlases/ICBM152NLin2009).

Steps:

* FSL FLIRT to coregister and FSL maths to average the 4 images into 1 averaged T1w and T2w image
* ANTs N4BiasFieldCorrection to correct for inhomogeneities
* ANTs BrainExtraction to remove skull and non-brain tissue using MNI 152 T1 and T2 images
* ANTs Registration to warp to MNI template
* ANTs Atropos to create tissue segmentations of CSF, GM, WM
* ANTs Apply Transformations to warp segmentations back to native space
* Fslmaths to create binary mask of CSF, GM, WM
* AFNI mask tool to erode CSF, GM, WM segments

**Preprocessing BOLD images**

Steps:

* FSL slicetimer for slice time correction
* FSL fugue for field map distortion correction
* FSL MCFLIRT for rigid body realignment
* FSL BET for skull stripping
* FSL FLIRT BBR to register the first session’s EPI image to the averaged T1 weighted image via the averaged T2w image (as modelled from Gordon et al.)
* EPI Images from sessions 2 to 10 underwent the same procedure using GSL BET and linear registration of each EPI image to the reference EPI image using the first session

**Censoring volumes**

* Calculate high motion volumes using Power FD approach (FD threshold of 0.2mm)
* Outputs csv of high motion volumes session

**Filtering**

Steps:

* Create temporal mask using Power FD csv
* Make an excel file with regression data for detrending and run detrend
* Bandpass filter via fft and ifft
* Fslmeants to find the global signal after filtering
* Fslmeants to find the signal for CSF and WM after filtering
* filterhmp to detrend, interpolate, filter data
* Make an excel file with all confound regression data and run full regression on whole brain
* FSL Maths to add the mean to the output of the last step
* Warp EPI to appropriate template MNI 152 T1 using ANTs apply transform

**Surface Processing**

**Create surface brains using terminal scripts**

Steps:

* Use Freesurfer recon\_all pipeline for cortical reconstruction
* Run ciftify\_recon\_all pipeline from Ciftify to create surface brains from freesurfer images
* Project BOLD EPI images onto the surface brains using ciftify\_subject\_fmri (smooth the output using sigma=4mm)
* Use wb command cifti-parcellate and the Schaefer2018 1000 parcel dlabel to parcellate from 91282 vertices to 1000 parcels
* Outputs preprocessed BOLD cifti surface file as shown below
  + - Use wb\_view from [Connectome workbench](https://www.humanconnectome.org/software/connectome-workbench) to open .spec file for your participant and then open the timeseries from the results folder where your subject cifti data is saved