Sample Data Pipeline

See Software page for installing all needed software.

MRI Sample Dataset - files
- Data live on the OSF
- Raw (Dicoms) contain the exported raw data (dicoms) from NYU's CBI
- Additional files include eye tracking data, experimental design files, and other files that did not live on the CBI acquisition computer
- Scripts contain 4 scripts to run all preprocessing and analyses

0. Download raw data (dicoms) and additional zip files, move them and unzip them:
```bash
mkdir ~/Documents/Sample_Data
mv ~/Downloads/AddThisToBIDSFolder.zip ~/Documents/Sample_Data
mv ~/Downloads/dicoms.zip ~/Documents/Sample_Data
mv ~/Downloads/processing_scripts.zip ~/Documents/Sample_Data
cd ~/Documents/Sample_Data/
unzip AddThisToBIDSFolder.zip && unzip dicoms.zip && unzip processing_scripts.zip
```

1. Preprocess MRI data (same as extracting data from CBI)
```bash
#!/usr/bin/env bash

# This script will execute many docker containers, including heudiconv, py_deface, mriqc, and fmriprep.
# Together, it will take many hours (possibly a day) to run.
# When the script is finished, you will have a BIDS compatible directory, including a derivatives folder with an fMRIprep subfolder and a freesurfer subfolder.
# Running this script is equivalent to extraction using NYU's CBI tools with the options, # 'BIDS', 'deface', 'MRIQC', and 'fmriprep'.
./processing_scripts/1_preproc-sample_code.sh
```

2. Add additional files to the preprocessed BIDS folder
```bash
#!/usr/bin/env bash

# Merge the extra files into the appropriate locations in the BIDS directory. The extra files include:
# - several stimuli files (AddThisToBIDSFolder/stimuli/*)
# - eye tracking physio files
# (AddThisToBIDSFolder/sub-wlsj042/ses-mri3t01/func/*physio*)
# - experiment specific tsv events files
# (AddThisToBIDSFolder/sub-wlsj042/ses-mri3t01/func/*events.tsv)
./processing_scripts/2_addToBIDS.sh
```

3. Run GLM Denoise
```bash
#!/usr/bin/env bash

# This is a Matlab script that will run Kendrick Kay's GLMdenoise on the two spatial frequency preferences scans from the dataset.
./processing_scripts/3_glmDenoise
```
4. Solve pRFs

# This is a Matlab script that will run Kendrick Kay's AnalyzePRF on the two prf bar scans from the dataset.
./processing_scripts/4_prf

TODO:

- Benson atlas (anatomical)
- Benson atlas (Bayesian)
- Test script 4 (analyze pRF) - try this on HPC
- Make some plots of GLM Denoise results using ROIs from Benson atlases
- Make some plots of pRF maps on meshes
- Make some times series plots of pRF
- Compute CMFs?