**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** contains 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
# 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
# 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-wlsubj042/ses-mri3t01/func/*physio*)
#   - experiment-specific tsv events files (AddThisToBIDSFolder/sub-wlsubj042/ses-mri3t01/func/*events.tsv)
./processing_scripts/2_addToBIDS.sh
```

### 3. Run GLM Denoise

```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
```
# 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?