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'.
# NB: Go to Docker > Preferences, and make sure your Docker preferences allow for:
#     (1) a large amount of RAM (nrCPUs*MemoryPerCPU > 32G) (See Preferences > Advanced)
#     (2) set nr of CPU cores to 1 less than your machine has available (see Preferences > Advanced)
#     (3) increase allocated disk space in Preferences > Disk > Resize disk image (> 64G, like 100G)
#     (4) have /Applications/freesurfer/ added to Preferences > File Sharing, so that Docker can access your FreeSurfer license
./processing_scripts/s1_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/s2_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/s3_glmDenoise
```
4. Solve pRFs

```matlab
# This is a Matlab script that will run Kendrick Kay's AnalyzePRF on the two prf bar scans from the dataset.
# Note: if you have issues starting the parallel pool and are using a NYU MATLAB license,
# try to open MATLAB pointing to license '2network.lic' using the terminal command:
#                 /path/to/matlab -c /path/to/licenses/2network.lic
./processing_scripts/s4_prf
```

5. Benson atlases

```bash
# Run Noah Benson's templates on the sample data
./processing_scripts/s5_Benson_Atlases.sh
```

TODO:

- [ ] Benson atlas (anatomical)
- [ ] Benson atlas (Bayesian) (write after analyze pRF finishes)
- [ ] Make some plots of GLM Denoise results using ROIs from Benson atlases
- [ ] Make some plots of pRF maps on meshes
  - [ ] See s5 and use that to make mgz files of analyzePRF results
  - [ ] Then convert these to mesh images
- [ ] Make some times series plots of pRF
- [ ] Compute CMFs?
- [ ] Speed up analyzePRF:
  - [ ] suppress optimization output
  - [ ] we can run on HPC cluster (TODO: Jon)