**KEY:**

**session = 9 digit session id**

**mouseid = 6 digit mouse id**

**date = 8 digit date**

**experimentid = 9 digit experiment id**

**number = a number that I don’t know what it is**

**FILES:**

**session\_mouseid\_date\_stim.pkl** Pickle file containing stimulus information. Used for stimulus alignment

**session\_mouseid\_date\_sync.h5** File containing timing information for all the relevant experiment acquisition and stimulus signals. Used for stimulus alignment.

**session\_mouseid\_date\_video\_0** Two files (h5 and avi) of the behavior camera.

**session\_mouseid\_date\_video\_1** Two files (h5 and avi) of the eye tracking camera

**session\_number\_number\_averaged\_surface\_downsample** Images taken at the surface in finding the 2P FOV

**session\_number\_number\_vasculature\_downsample** Imagestaken with epifluorescenceused to target right location for 2P FOV.

**session\_number\_number\_averaged\_depth\_downsample** Images taken at the imaging depth in finding the 2P FOV.

**session\_number\_number\_reticle** Images of reticle used for cross-platform registration

**>ophys\_experiment\_experimentid**

**experimentid\_dff.h5** contains two arrays: [‘data’] is the DF/F traces and [‘roi\_names’] is a list of unique ids for each ROI. These are the traces we want to use for analysis.

**experimentid\_input\_cell\_roi\_creation.json** JSON file used in pipeline processing. This file contains information about ROI filtering, and which ROIs would be included in the pipeline analysis and which would be excluded (valid=True/False).

**experimentid\_zstack\_local.h5**

**experimentid.h5** array of un-motion corrected (?) movie

**neuropil\_correction.h5** contains two arrays: one is the output of the neuropil subtraction and the other is the r values for each ROI used during the neuropil subtraction.

>**demix** folder: Intermediates for the demixing step.

**experimentid\_demixed\_traces.h5** traces of the output of the demixing step

>**demix\_plots** folder: plots for overlapping ROIs showing the results of the demixing.

>**neuropil\_subtraction\_plots** folder: Plots for each ROI showing the trace for the ROI, its neuropil, and the output of the neuropil subtraction

>**processed** folder:

**concat\_31Hz\_0.h5** array of motion-corrected movie

**concat\_downsample\_4Hz\_0.avi** movie file of temporally downsampled, motion-corrected movie. Very useful for seeing how stable the correction is, the activity of the cells, etc.

**log\_0.csv** dataframe of the amount of motion correction for each frame of the movie

**max\_downsample\_4Hz\_0.png** image of the max projection of the motion-corrected movie.

>**ophys\_cell\_segmentation\_run\_number**:

Intermediates used for the segmentation in generating ROI masks.

Files with QUEUE are part of the pipeline processing operations.

Json files are part of the pipeline processing operations. Some of these have some useful information (see input\_cell\_roi\_creation above).