DATA ACQUISITION

These steps involve actually acquiring the data, which means running experiments, making sure programs that are collecting data from these experiments are running smoothly, and are communicating with one another. An entire pipeline of its own.

DATA PRE-PROCESSING

This is the first step in the data mining phase. Here we assume we have, for each mouse that’s been experimented on, a set of files that correspond to the experimental sessions we care about.

Example of Raw Data:

| BLA-Insc-8/  PR D1/  Session-20211105-094928\_BLA\_INSC\_8\_PR\_D1/  2021-11-05-10-15-39\_video\_green.gpio  2021-11-05-10-15-39\_video\_green.imu  2021-11-05-10-15-39\_video\_green.isxd  BLA-Insc-8 11052021.csv  BLA-Insc-8\_PR\_D12021-11-05T11\_37\_34.csv  BLA-Insc-8\_PR\_D12021-11-05T11\_37\_39.avi  session.json  RDT D1/  Session-20211021-093007\_BLA-INSC-8-RDT-D1/  2021-10-21-09-56-28\_video\_green.gpio  2021-10-21-09-56-28\_video\_green.imu  2021-10-21-09-56-28\_video\_green.isxd  BLA-Insc-8 10212021.csv  BLA-Insc-8\_RDT\_D12021-10-21T11\_18\_05.csv  BLA-Insc-8\_RDT\_D12021-10-21T11\_18\_16.avi  session.json  **.**  **.**  **.** | .**gpio** - A isx related file that gives us the time the abet file was told that the experiment started.  .**isxd** - The 1-photon video file. Isx provides loads of functionality for preprocessing this file, it’s ultimately where you’ll identify cells, accept/reject them, and export tables of their individual fluorescence activity.  “**BLA-Insc-8 11052021.csv**” - Files that look like this are the raw ABET files (record behavioral events in experimental session).  .**avi** - A video file of the mouse in a cage throughout the experiment, will be used to extract velocity (via DeepLabCut) of the mice at any given time. |
| --- | --- |

1. Open up the preprocess\_all\_vids\_ppt.py
   1. Change the dir of where raw data files are stored
   2. Change some code to fit where the new paths are
   3. Change dir to where the preprocessed files will go

RESULT: For however many mice there were in the folder you indicated, all the .isxd files will be processed for all the sessions available in each mouse.

1. Now that you have preprocessed all the sessions for each mouse of your interest, we now have the most manual portion of our pipeline:

ACCEPTING/REJECTING CELLS

1. Open the Inscopix GUI in /home/rory/Inscopix Data Processing 1.6.0
   1. Create a new project where the mouse's preprocessed data is being stored. Example where to store:/media/rory/Padlock\_DT/BLA\_Analysis/PTP\_Inscopix\_#4/BLA-Insc-11/isx\_project
2. Accept and reject cells

EXPORT DFF TRACES

1. Make sure to save your acceptions/rejections → this will update automatically in cnmfe\_cellset.isxd file in the session folder.
2. Now export df traces using get\_dff\_tiff.py.

ABET PROCESSING

1. Make sure ABET files are in the processed mice folders.
2. Use BehavioralDriver.py.
   1. Processes however many mice there are in the root folder.

CALCIUM PROCESSING

1. Now process the dff traces with CalciumPreprocessing.py (will also do gpio abet processing).
   1. This file does housekeeping formatting of dff traces and gpio corrected ABET.
   2. One mouse at a time, will need to indicate processed data folder for that mouse and where its raw folder is located

DATA ALIGNMENT

Order matters:

1. Use the **Driver.py (Individual cell alignment)** file in Behavioral\_Calcium\_DLC\_Alignment folder to get all ways of grouping df traces together among each cell
   1. The script that it uses, “Session.py” will search for a file ending with “\_ABET\_GPIO\_processed.py”
   2. If you see cells being processed quickly for a session type, that means that the ABET file was not under a normal format (different type of experiment (AS OF 12/2/21))
   3. If 20 files are not present in cell (as indicated by the combos we care about), this means there was nan for that entire column (parameter we care about)
2. You can also align avg dff traces for a cell under a given combination for an entire session using **BetweenCellAlignment.py**.
3. Align avg dff traces of cells across similar sessions across different mice using **BetweenMiceAlignment.py\_1** for all mice.
   1. This script will look for if “BetweenCellAlignmentData” folders are made for each session
4. Run “**BetweenMiceAlignment\_2.py**” to preprocess all concat files (data truncation for jagged tables → or else an error will bring up when plotting)
   1. I could’ve just truncated after a certain index, but I’ll just leave this step here

DATA ANALYSIS

1. Use **BetweenCellsAnalysis.py** to the “BetweenMiceAlignmentData” plot however you want with the lowest level unit of data, which is avg dff traces for a cell under a given subcombination of a combination.