Update June 1, 2021:  
Each Recording Session will have a unique fileprefix (<MonkName>\_SRT\_<StimulusSet>\_<Subset>\_<YYMMDD>\_<HHMMSS>

Files for each session:

\*\_trialTimes.csv – (Col 1-Trial**Start**Times) (Col 2 Trial**End**Times)

Times are in **seconds**

\*\_trialData.csv – nTrials x 10 file -- Contents in Column Order:

imName – Name of the file of image presented

Doesn’t have removed where audio-only, not useful except as reference

imNum – Unique numerical ID for each image

Use PicID\_3 instead

imPheeName – Identity of Money in Audio

imMatchFlag – 0-3 identifier for Stimulus Condition

0 = Image Only

1 = MATCH (Pic+Audio monkey identity same)

2 = MISMATCH (Pic+Audio, ID inconsistent)

3 = Audio Only

novel – Whether image is novel or not (each is presented twice during a session

imOff – Duration of the signal presentation (seconds)

vpltTrial – Logical, was there a stimulus presented

Only use TRUE trials for stimulus-based analyses

FALSE trials are active-foraging

A different behavioral state, could be interesting to see if they can be ID’d

Block – Session is blck-design, counts number of the block

PheeID – Identity of Monkey in Audio

PicID\_1 – Identity of Monkey in Picture

PicID\_2 – Orientation of Monkey in picture

PicID\_3 – imNum except with ActiveForage Trials removed

\*\_ChannelNums – The electrode ID number on which cell was identified (usually more than 1 per channel)

\*\_spikeTimes.csv – Spike Times vectors for each identified cell

Times are in INDEX (sample rate at 30kHz)

One row for each cell identified, variable numbers of spikes ea

Quick rundown of current/future contents:

Data Catalogs (SRT\_\* and \*\_v3)

Complete collection info on SRT and All data, respectively

Tells Monkey, Date, Stimulus Set, Electrode position, and relevant health issues

Certain data health issues are identified in some, can discuss in person, for now skip

Recordings within a given monkey+set can be compared (same units), outside are new neurons

MassivePopulationStorage

Accumulation of preprocessed unit set (currently ~3436 cells across most recordings/animals)

Contains Population\* for each of the following var sets (one cell per neuron)

D – Session Stimulus Information (behavioral has been truncated out)

Name of subject of image/call, novel/repeat, trial duration, etc

D.P is settings info, some pertains to eyepos

TrialData – Preprocessed based on image modality and stim cond

trialSpikes – 400 cells (ntrials)

One cell per trial with spiketimes during that trial (aligned to stim onset)

\*spikes (IMG/XMOD/AUD/MATCH/MISMATCH)

Same as trialSpikes, isolating only specific stimulus conditions

MATCH/MISMATCH are sub-divisions of XMOD

\*FR vars in this are not great, based on old calc method

trialSpikes – Same as above in TrialData (for ease of my access in other)

**PopulationStorageMerged** – better set for you to work with

Same data as above, but before preprocessing

Contains 1 cell for each recording session, each cell is raw outputs from sorting

SpikeTimes – Straight spiketimes of individual cell (nCells = nNeurons)

In 30kHz recording index (all Trial Timing data is in seconds)

PopulationSpikeTime – same SpikeTImes data as above, includes recording details

Name of recording tells Monkey, Stimulus set, and Recording date/time

Regarding inter-trial intervals: I need to copy over the TTL/Trial Data, will have name that can be aligned to PopulationSpikeTime