makeChanMap\_SKM.m make channel map file for new probe config

Call runKiloSort4Intan2.m

[ops,savePath] = mergeIntanOFPCSystem2(savePath) % folder containing intan data should be named after XXXX\_ephys. Otherwise it won’t work. Intan data files should be one file per channel

Kilosort performs badely in aligning spike waveforms. It may be because the kilosort uses the average weight of waveform for unit sorting, which does not determine the peak/valley locations precisely. If it happens, waveform realignment may be needed. To calculate spike waveform, we can get traces from template files which may make the width bigger (because of the misalignment) or extract raw traces and then realign them before averaging.

Kilosort can detect spikes (from two units) happen next to each other, because it uses template matching algorithm. The previous package I used will miss the later one, because of the refractory period.

Kilosort can assign spikes with changing amplitude (for example distance change, or bursting) to the source unit.

StandardConfig\_SKM.m (configuration file for kilosort)

saveKiloSortResultstoMat.m (convert npy files to mat files for data analysis)

extractMedianWFs.m (calculate spike waveform)

checkRefractoryPeriodViolations\_KiloSort.m (calculate refractory period violation)

One unit can have multiple spike templates (spike shape), but only one cluster (unit ID).

64 channel half hour recording generates 12GB data.

Threshold for Refractory period violation is 1ms for thalamus, 2ms for cortex.

Kilosort output files: (check the tutorial of NPY-matlab)

Amplitudes.npy (maybe amplitude of templates or clusters)

Channel-map

Channel-positions

Cluster-groups.csv (attribute of unit: noise, good unit, bad unit)

Params.py

Pc-feature-ind.npy (check tutorial)

Pc-featurs.npy

Phy.log (history)

Rez.mat (this file saves the results from kilosort. However phy does not update it when merging or splitting happens. Therefore use it only to extract parameters used in the kilosorting)

Similar\_templates.npy

Spike\_clusters.npy (id of units individual spikes belong to)

Spike\_templates.npy(id of templates individual spikes belong to)

Spike\_times.npy (time of individual spikes)

template… (template of spikes; amplitude cross channels)

1. High expression of stGtACR cause toxicity. Therefore mix full titer of flex- stGtACR with highly diluted cre virus (60-80folds to 1011). Finish experiments 2-3 weeks after injection. At 4 weeks, neurons are dying.
2. Apply agrose to the cortex to help silicone electrode penetrate through.
3. Try Cambridge neurotech probes (thinner for long probes-15micron, 7mm; sharper tip; p-dot processed; taper tip fiber); H2/H4

MEMO: coding changes to kilosort

System 2 com from SK

System 3 Andreanne added A1x16 channel probe