Spike analysis pipeline overview

Folder structure

File	Info
Y:\Projects\project\ephys\version main folder contains:	
population_monkey_session.mat	spike data sorted by unit for each session
sites_monkey_session.mat	LFP data sorted by site for each session
by_block_monkey_session.mat	body signals sorted by block for each session
Mon_sorted_neurons.xls	copies of the used sorted neurons tables from dropbox
keys_Monkey.mat	copy of the keys used when running ph_initiation
tuning_table_combined.mat	Anova results stored in a table
tuning_table_combined_CI.mat	Anova results restructured accroding to contra/ipsi definitions
tuning_table_combined.xls	simplified excel table
seed.mat	a saved seed to make randomizations reproducable
Subfolders:	
spike_shapes	Spike shapes, firing rates over time, and ISI plots
single_cell_examples	Single cell plots
cell_counts	Anova results as pie plots
scatter	Anova results as scatter plots (one column versus another)
population_analysis	population PSTHs
response timing	tuning over time plots
…	
\Dropbox\DAG\phys\Monkey_phys_dpz\Sorted_neurons excel table	

General Workflow

- ph_initiation(project,{version1,version2,…})
    1. loop per monkey
    2. read in general settings → project settings → version settings
    3. run ph_session_processing (core function)
        - read in data from Y:\Data\Monkey_phys_combined_monkeypsych_TDT
        - run monkeypsych_analyze for saccade detection etc.
        - run ph_run_state_alignment_per_trial
            1. takes over relevant trial and state (event) information
            2. combines it with Sorted Neuron table information
            3. !! Copies last 1 second of spikes to beginning of next trial
            4. !! Cuts and appends last 1 second of streams to beginning of next trial
            5. !! excludes trials without physiology data And/or NOT matching condition
        - resort data by unit/site/block
        - plot waveforms/ISI/FR_across time per unit
        - exclude units dependent on excel entries (SNR/stability/single rating)
        - plot waveforms/ISI/FR_across time per unit again for remaining units
        - run ANOVAs (ph_ANOVAS)
        - create single cell plots (ph_plot_unit_per_condition)
        - save files per session

4. format tuning table (create tuning_table_combined_CI.mat and tuning_table_combined.xls)
5. ph_get_filelist for crossreferencing with behavior
6. ph_initiate_population_analysis also runs population analysis

Synchronization

- Very important: In additi

Associated code

hmm