Spike analysis pipeline overview

Folder structure

- Y:\Projects\project\ephys\version main folder contains:
    1. population_monkey_session.mat : spike data sorted by unit for each session
    2. sites_monkey_session.mat : LFP data sorted by site for each session
    3. by_block_monkey_session.mat : body signals sorted by block for each session
    4. Mon_sorted_neurons.xls : copies of the used sorted neurons tables from dropbox
    5. keys_Monkey.mat : copy of the keys used when running ph_initiation
    6. tuning_table_combined.mat : Anova results stored in a table
    7. tuning_table_combined_CI.mat : Anova results restructured accroding to contra/ipsi definitions
    8. tuning_table_combined.xls : simplified excel table
    9. seed.mat : a saved seed to make randomizations reproducable
- Subfolders:
    1. spike_shapes : Spike shapes, firing rates over time, and ISI plots
    2. single_cell_examples : Single cell plots
    3. cell_counts : Anova results as pie plots
    4. scatter : Anova results as scatter plots (one column versus another)
    5. population_analysis : population PSTHs
    6. response timing : tuning over time plots
    7. ...
- \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