Spike analysis pipeline overview

Folder structur

Inputs	Info
\Dropbox\DAG\phys\Monkey_phys_dpz\Mon_sorted_neurons.xls	electrode locations, unit/site IDs,SNR/Stability/single ratings
\GitHub\Settings\spike_analysis\project	project and version specific settings (keys)
Y:\Data\Monkey_phys_combined_monkeypsych_TDT	raw data

Outputs in Y:\Projects\project\ephys\version:

File	Info
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
Subfolder	**Info**
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
…	

General Workflow

- ph_initiation(project,{version1,version2,…})
    1. read in general settings → project settings → version settings
    2. loop per monkey: 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
            - takes over relevant trial and state (event) information from monkeypsych_analyze output (TDT_states and saccade/reach initiation)
            - combines it with Sorted Neuron table information
            - !! Copies last 1 second of spikes to beginning of next trial
            - !! Cuts and appends last 1 second of streams to beginning of next trial
            - !! 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) and create tuning table
    - create single cell plots (ph_plot_unit_per_condition)
    - save files per session
3. format tuning table (create tuning_table_combined_CI.mat and tuning_table_combined.xls)
4. ph_get_filelist for crossreferencing with behavior
5. ph_initiate_population_analysis also runs population analysis

Synchronization

- Very important: … INDEED :)

Associated code

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