

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 according to contra/ipsi definitions |
| tuning_table_combined.xls | simplified excel table |
| seed.mat | a saved seed to make randomizations reproducible |
| 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

...

From:
<http://dag.dokuwiki.dpz.lokal/> - **DAG wiki**

Permanent link:
http://dag.dokuwiki.dpz.lokal/doku.php?id=spike_analysis_pipeline:pipeline_overview&rev=1699894775

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