

Interactions with other pipelines

because `spike_analysis` incorporates the `sorted_neurons` table (f.e. `unit_IDs` and `site_IDs`) into behavior and ephys data, it is used as a first step in all ephys analysis.

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

| File | Info |
|--|--|
| <code>population_monkey_session.mat</code> | spike data sorted by unit for each session |
| <code>sites_monkey_session.mat</code> | LFP data sorted by site for each session |
| <code>by_block_monkey_session.mat</code> | body signals sorted by block for each session |
| <code>Mon_sorted_neurons.xls</code> | copies of the used sorted neurons tables from dropbox |
| <code>keys_Monkey.mat</code> | copy of the keys used when running <code>ph_initiation</code> |
| <code>tuning_table_combined.mat</code> | Anova results stored in a table |
| <code>tuning_table_combined_CI.mat</code> | Anova results restructured according to contra/ipsi definitions |
| <code>tuning_table_combined.xls</code> | simplified excel table |
| <code>spike_shapes</code> | Spike shapes, firing rates over time, and ISI plots for re-assessing spike sorting |

The three main files come in a specific data structure, which contain the same fields except for the respective data:

- `by_block`(body signals) - only trial information and body signals
- `sites` (LFP) - additional site information and LFP, no body signals
- `population` (spikes) - additional unit information and `spike_arrival` times, no LFP, no body signals

Trial structure subfields (By_block files)

to be removed:

```

    cue_pos: NaN
    cue_shape: NaN
    all_tar_pos: [2x1 double]
    col_dim: [2x3 double]
    col_bri: [2x3 double]

```

| Condition info | Format | Info |
|-------------------------------|--------|-----------|
| <code>type</code> | scalar | from data |
| <code>effector</code> | scalar | from data |
| <code>reach_hand</code> | scalar | from data |
| <code>choice</code> | scalar | from data |
| <code>success</code> | scalar | from data |
| <code>completed</code> | scalar | from data |
| <code>correct_targets</code> | scalar | from data |
| <code>target_selected</code> | scalar | from data |
| <code>n_nondistractors</code> | scalar | from data |
| <code>n_distractors</code> | scalar | from data |

| Condition info | Format | Info |
|----------------------------|-----------|--|
| difficulty | scalar | from data |
| stimuli_in_2hemifields | scalar | from data |
| perturbation | scalar | using perturbation_groups key ?? |
| dataset | scalar | Dataset from sorted_neurons (only in spikes so far ??) |
| Timing info | Format | Info |
| date | scalar | from data |
| block | scalar | from data |
| run | scalar | from data |
| n | scalar | from data |
| trial_onset_time | scalar | from data |
| run_onset_time | scalar | from data |
| states | array | array of events marked in this trial |
| states_onset | array [s] | corresponding onset times (relative to state 2) |
| Spatial info | Format | Info |
| fix_pos | complex | x is real, y is imaginary (already preprocessed?) |
| tar_pos | complex | x is real, y is imaginary |
| stm_pos | complex | x is real, y is imaginary |
| Response info | Format | Info |
| rea_off | complex | x is real, y is imaginary |
| sac_off | complex | x is real, y is imaginary |
| sac_lat | scalar | Saccade RT (in seconds) |
| rea_lat | scalar | Reach RT (in seconds) |
| Specific data | Format | Info |
| TDT_ECG1 | array | Body signal Data (ECG1,CAP1,POX1) |
| TDT_ECG1_SR | scalar | Sampling rate |
| TDT_ECG1_t0_from_rec_start | scalar | state 2 onset relative to start of the recording (block?) |
| TDT_ECG1_tStart | scalar | (usually negative) how much of the stream is before state 2 - due to shift!! |
| LFP | array | LFP data, not called TDT_LFPx any more, but SR,t0,andtStart are... |
| arrival_times | array | in seconds, relative to this trial's state 2 |
| FR_average | scalar | average firing rate for this unit in this trial |
| accepted | scalar | trial accepted for this unit |
| FR | scalar | ?? |
| stability_rating | scalar | why is this here ?? |

Additional Site files fields

| Fieldname | Example | Info |
|-------------------|-----------------------|---|
| site_ID | 'Bac_20210706_Site_01 | as assigned in sorted_neurons, in population files this is the corresponding site for this unit |
| target | 'dPul_R' | recording target from sorted_neurons |
| perturbation_site | 'NA' | perturbation target from sorted_neurons |
| grid_x | 3 | grid location from sorted_neurons |
| grid_y | -4.5 | grid location from sorted_neurons |

| Fieldname | Example | Info |
|-----------------|----------------|---|
| electrode_depth | 45 | Aimed_electrode_depth from sorted_neurons |
| monkey | 'Bacchus_phys' | as assigned in sorted_neurons (?) |

Additional Population file fields

| Fieldname | Example | Info |
|--------------------|-------------------|---|
| unit_ID | 'Bac_20210706_01' | as assigned in sorted_neurons |
| channel | 2 | channel the unit was recorded in |
| block_unit | {3×1 cell} | which cluster in which block are combined in this unit |
| SNR_rating | 2 | SNR rating (either from sorted_neurons or automatic?) |
| Single_rating | 1 | Single rating (either from sorted_neurons or automatic?) |
| stability_rating | 2 | stability rating (either from sorted_neurons or automatic?) |
| quantSNR | 11.5 | KK automatic SNR |
| n_waveforms | 0 | apparently bugged |
| waveform_average | [1×30 single] | average waveform of this unit |
| waveform_std | [1×30 single] | std of waveform for each bin |
| waveform_width | 3.0224e-04 | width (in time?) |
| waveform_amplitude | 173.2376 | amplitude (?) |
| FR | 2.68 | average firing rate across all data |

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