

Spike analysis keys

Reading in settings(keys) has a hierarchy in spike_analysis ! Higher Priority will always override lower priority.

| Priority | Settings file | Info | Location |
|----------|-------------------------------|---|--------------------------|
| 1 | ph_general_settings.m | default, makes sure keys are present | spike_analysis folder |
| 2 | ph_project_settings.m | default settings for your project | Settings/Project |
| 3 | ph_project_version_settings.m | small deviations for one version (f.e. different dataset) | Settings/Project/version |
| 4 | additional_settings.m | probably obsolete, was used to define each run | Settings/Project/version |

Data batching (keys.batching.)

| Key | Format | Possible entries | Info |
|-----------------------|---------|--|---|
| monkeys | cellstr | {'Flaffus', 'Linus', 'Curius', 'Tesla', 'Cornelius', 'Magnus', 'TDT_brain', 'Bacchus'} | monkeys involved |
| combine_monkeys | scalar | 0/1 | combine monkeys for population analysis |
| targets | cellstr | {'dPulv_r','dPulv_l'} -> {'dPulv'} combines hemispheres | target from sorted_neurons table |
| Subregions_separately | scalar | 0/1 | Split in subregions or not |
| Subregions | cell | struct('monkey',{},{}, 'target',{},{}, 'grid_x',{NaN}, 'grid_y',{NaN}, 'z_min',{NaN}, 'z_max',{NaN}) | subregion definition by ranges |
| n_Subregions | scalar | | numel(keys.batching.Subregions) |

General settings

| Key | Format | Possible entries | Info |
|---------------------------|---------|--|--|
| keys.PSTH_binwidth | Scalar | 0.01 | resolution of PSTH's (in seconds) |
| keys.gaussian_kernel | Scalar | 0.02 | std for the convolution to derive spike density (in seconds) |
| keys.kernel_type | Char | 'gaussian' | excludes trials with non-matching effector |
| keys.condition_parameters | cellstr | {'reach_hand', 'choice', 'perturbation'} | parameters that define a unique condition |

| Key | Format | Possible entries | Info |
|---|---------|------------------|--|
| keys.position_and_plotting_arrangements | cellstr | {'hands'} | defines (somewhat hardcoded) positions in ph_arrange_positions_and_plots |
| keys.contra_ipsi_relative_to | Char | 'target' | what contra and ipsi refer to |

Trial selection keys

| Key | Format | Possible entries | Info |
|---------------------|--------|------------------------|---|
| keys.cal.datasets | Array | see dataset convention | excludes runs with non-matching dataset |
| keys.cal.completed | Scalar | 0 or 1 | excludes not completed trials (keep at 1 for now) |
| keys.cal.effectors | Array | [0,1,2,3,4,5,6] | excludes trials with non-matching effector |
| keys.cal.types | Array | [1,2,3,4,5,6] | excludes trials with non-matching type |
| keys.cal.reach_hand | Array | [0,1,2] | excludes trials with non-matching hand (no hand, left, right) |
| keys.cal.choice | Array | [0,1] | excludes trials of non-matching choice value |

Unit exclusion keys

| Key | Format | Possible entries | Info |
|---------------------|--------|------------------------|---|
| keys.cal.datasets | Array | see dataset convention | excludes runs with non-matching dataset |
| keys.cal.completed | Array | [0,1] | excludes not completed trials (keep at 1 for now) |
| keys.cal.effectors | Array | [0,1,2,3,4,5,6] | excludes trials with non-matching effector |
| keys.cal.types | Array | [1,2,3,4,5,6] | excludes trials with non-matching type |
| keys.cal.reach_hand | Array | [0,1,2] | excludes trials with non-matching hand (no hand, left, right) |
| keys.cal.choice | Array | [0,1] | excludes trials of non-matching choice value |

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

Permanent link:
http://dag.dokuwiki.dpz.lokal/doku.php?id=spike_analysis_pipeline:keys&rev=1652796261

Last update: 2022/12/29 07:15

