

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
keys.position_and_plotting_arrangements	cellstr	{'hands'}	defines (somewhat hardcoded) positions in ph_arrange_positions_and_plots

Key	Format	Possible entries	Info
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

Last update: **2022/12/29 07:15**

