

# Spike analysis pipeline overview

## Folder structure

Y:\Projects\project\ephys\version main folder contains:

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

## General Workflow

- `ph_initiation(project, {version1, version2, ...})`
  1. loop per monkey
  2. read in general settings → project settings → version settings
  3. run `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
  1. takes over relevant trial and state (event) information
  2. combines it with Sorted Neuron table information
  3. !! Copies last 1 second of spikes to beginning of next trial
  4. !! Cuts and appends last 1 second of streams to beginning of next trial
  5. !! 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)
- create single cell plots (ph\_plot\_unit\_per\_condition)
- save files per session
- 4. format tuning table (create tuning\_table\_combined\_CI.mat and tuning\_table\_combined.xls)
- 5. ph\_get\_filelist for crossreferencing with behavior
- 6. ph\_initiate\_population\_analysis also runs population analysis

## Synchronization

- Very important: In additi

## Associated code

hmm

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

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[http://dag.dokuwiki.dpz.lokal/doku.php?id=spike\\_analysis\\_pipeline:pipeline\\_overview&rev=1641840777](http://dag.dokuwiki.dpz.lokal/doku.php?id=spike_analysis_pipeline:pipeline_overview&rev=1641840777)

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