

# Spike analysis pipeline overview

## Folder structure

```

^File                                     ^Info ^
| Y:\Projects\project\ephys\version main folder contains:
||
| 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 accroding to
contra/ipsi definitions      |
| tuning_table_combined.xls     | simplified excel table
|
| seed.mat                      | a saved seed to make randomizations
reproducible                  |
| Subfolders:
||
| 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
|
| ...                           |
|
* \Dropbox\DAG\phys\Monkey_phys_dpz\Sorted_neurons excel table

```

## 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**

Permanent link:

[http://dag.dokuwiki.dpz.lokal/doku.php?id=spike\\_analysis\\_pipeline:pipeline\\_overview&rev=1641839512](http://dag.dokuwiki.dpz.lokal/doku.php?id=spike_analysis_pipeline:pipeline_overview&rev=1641839512)

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

