

# Spike analysis pipeline overview

## Folder structure

- Y:\Projects\project\ephys\version
- Y:\Data\Sortcodes\Monkey\_phys contains sorting related files
- Y:\Data\Monkey contains the behavioral data
- Y:\Data\Monkey\_phys\_mat\_from\_TDT contains recorded data, arranged in the same trial structure as the behavioral data
- Y:\Data\Monkey\_phys\_combined\_monkeypsych\_TDT contains trial structures with combined behavioral and ephys data
- Y:\Data\All\_phys\_preprocessing\_log\Monkey\_phys contains automatically created log files of all preprocessing performed
- \Dropbox\DAG\phys\Monkey\_phys\_dpz\Sorted\_neurons excel table

## General Workflow

- `ph_initiation(project,{version1,version2,...})`
- `ph_initiate_populaiton_analysis`

## Synchronization

- Very important: In additi

## Associated code

Data conversion functions are located in Github External\_modified/PLXTDT repository

- PLX2SPK
- PLX2TDT
- SEV2mat\_working
- SPK2PLX
- TDT2PLX
- TDTbin2mat\_working
- WC32SPK
- WC32SPK\_concatenated
- WC32SPK\_directly

The remaining code related to phys preprocessing (not including Waveclus and Plexon) can be found on Github Phys\_preprocessing repository

- Core functions
  1. `phys_gui_working.m`
  2. `phys_gui_execute.m`

3. TDT\_trial\_struct.m
4. ph\_combine\_MP\_and\_TDT\_data
5. DAG\_update\_sorting\_table.m
- Waveclus pipeline specific
  1. DAG\_WC3\_preprocessing.m
  2. DAG\_parse\_data\_tdt.m
  3. DAG\_SpikefilterChan.m
  4. WC32SPK\_directly.m
  5. ph\_readout\_broadband\_lag.m
- Plexon pipeline specific
  1. DAG\_create\_PLX.m
  2. DAG\_update\_plx\_file\_table.m
  3. ph\_get\_new\_plx\_extension.m
- Extra standalone functions
  1. DAG\_derive\_TDT\_streamer\_broadband\_lag.m
  2. ph\_debugging\_GUI.m
  3. DAG\_take\_over\_sortcode\_PLX2PLX.m
- Only of historical relevance
  1. DAG\_move\_sorting\_files.m Was used to transfer sortcodes to their current destination
  2. ph\_derive\_electrode\_depth.m Was used to create the first electrode\_depths file extracting from sorted\_neurons table
  3. ph\_derive\_same\_cells.m Was used to create the first same\_cells file extracting from sorted\_neurons table
  4. ph\_simulate\_history.m Was used to create the first log files

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