***sd\_tools* Documentation**

Set of functions for dealing with *Shusterman 2011* and *Sirotin 2015* datasets.

The datasets are first processed into two primary data structures:

**unit** – contains all the raw data (spikes, sniff-info, etc)

**md** – contains meta data for each cell-odor-concentration pair

All functions operate on **unit** and **md** structures in the following general form:

load(‘unit.mat’,’unit’);

sd = sd\_tools();

md = sd.get\_md(unit);

% call function variant 1

output = sd.func1(unit,md,…)

The output should either be a cell array of results for each entry in md or multidimensional array when conditions permit

% call function variant 2

output = sd.func2(unit,md(a),md(b),…)

Here the output is the result of a comparison operation using md(a) , md(b), and others

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% unit

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unit.mouse % numeric mouse ID, e.g. 110

unit.sess % numeric session ID, e.g. 5

unit.cell\_num % numeric cell index in spikes.mat

unit.sorted % sorted field from spikes.mat

% 0=unsorted

% 1=single unit

% 2=multi unit)

unit.odorID % string odor names for each valve

% The following are vectors for each sniff

unit.inh\_dur % inhalation durations (msec)

unit.sniff\_dur % duration of sniff (msec)

unit.valve % odor valve

unit.conc % air flow dilution of odor

unit.odorSniffNum % sniff number relative to odor onset

% 0=odor off

% 1,2,3,…,N=sniff number when odor on

% -1,-2,-3,…,N=sniffs following odor

% The following are sparse rasters binned at 1msec for

% each sniff

unit.rt % real time

unit.rw % full warped time

unit.rwt % inhalation only warped time

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% md - a structure of metadata from unit structure

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md = struct('unit\_ref', 0, ... % unit number from structure unit

'mouse', 0, ... % mouse number

'sess', 0, ... % session number

'cell\_num', 0, ... % cell number id from spikes\_mmm\_ss.mat

'valve', 0, ... % valve number for a given odor

'conc', 0, ... % concentration

'stimID', '', ... % string: '%s\_%06.2f', odor tag and concentration

'ID', ''); % meta data ID 'mmm\_ss\_ccc'

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% sniff

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sniff.mouse % numeric mouse ID, e.g. 110

sniff.sess % numeric session ID, e.g. 5

sniff.waveform % waveforms for the first 300ms for each sniff in the session