**Organization of datasets**

There are 3 types of experiments within this dataset:
1. Ntng - Electrophysiological recordings from opto-tagged layer II piriform cortex neurons responding to a panel of odors.
    a. There are 11 stimuli – 1 blank control stimulus and 10 odors
    b. Each stimulus was presented as 3 concentrations, only 1% (concentration #3) was used for analysis
    c. There are 15 trials for each odor at each concentration, trials 2-11 were used in the analysis
2. Ntng_Inh_Opto - Recordings from layer II piriform cortex neurons while opto-tagged semilunar cells were optogenetically suppressed during odor presentations.
    a. There are 6 stimuli – 1 blank control stimulus and 5 odors (some experiments have an additional 6th odor, but this was not used in the analysis)
    b. Each stimulus was presented at one concentration.
    c. There are 20 trials for each odor, trials 3:2:19 were used as light-off trials in the analyses and 2:2:19 were used as light-on trials in the analyses. Some experiments have 40 trials, but these extra trials were not used.
3. Ntng_Inh_Chemo - Recordings from layer II piriform cortex neurons while opto-tagged semilunar cells were chemogenetically suppressed during odor presentations.
    a. There are 7 stimuli – 1 blank control stimulus and 6 odors
    b. Each stimulus was presented at one concentration.
    c. There are 60 trials for each odor, trials 2:20 were used as baseline trials in the analyses and 41:59 were used as CNO trials in the analyses. Some experiments have additional trials, but these extra trials were not used.

Each of these has a folder containing recordings and the associated recordings are listed in a plaintext ExperimentCatalog within that folder. These can be loaded into Matlab as tables:

T = readtable('CatalogFileName', 'Delimiter', ' ');

**Processed file types and data structures**

Three types of processed data files are provided: resp [respiration], st [spike times], and efd [experiment – full data] files. These are all saved from MATLAB in the MAT format and can be loaded using the command:
load('filename', '-mat')

.resp files
These files contain information extracted from the flow sensor over the mouse's nose.
RRR – A filtered and smoothed respiration trace over the whole recording sampled at 2 kHz.
InhTimes – A list of times of minima in the respiration trace, indicating maximal inward flow.
PREX – A list of times of zero-crossings in the respiration trace that precede a minimum. These are considered the start of inhalation for spike alignment purposes.
POSTX – A list of times of zero-crossings in the respiration trace that follow a minimum.

BbyB – A structure containing simple measurements for each breath: Height (peak to peak amplitude), Width (Time from PREX to the following PREX), and Slope (Slope of negative deflection from PREX to minimum, corresponding to sharpness of inhalation).

.st files
These files contain spike times for all sorted units.

The .st file contains a structure called SpikeTimes. It has the following fields:
tsec – Each cell of tsec contains all spike times in seconds of a sorted unit.
stwarped – This field is the same as tsec, but the spike times are shifted to mimic the scenario in which they occurred at the observed respiration phase, but all breaths had the identical length to the average breath.
units – These are the unit identifiers provided by the spike-sorting program.
Wave.AverageWaveform – Each entry is a 32 channel by 48 sample matrix containing the average waveform for a unit.
Wave.Position – Each entry is an X and Y coordinate indicating the distance from the ventral tip of the electrode and leftmost channels for the amplitude-weighted average position of the average waveform.

.efd files
It is possible to do most analyses using only the .efd files because these contain spike raster structures with the spike times already aligned to the start of inhalation after odor delivery or aligned to laser stimulus onset in the case of optogenetic experiments. Loading the .efd file provides a structure called 'efd', containing the following fields and subfields:

ValveTimes
Subfields of ValveTimes are #OdorVials X #OdorConcentration cells each containing vectors with an entry for each odor delivery of the specified odor vial at each concentration.
.FVSwitchTimesOn – Time of odor onset
.FVSwitchTimesOff – Time of odor offset
.PREXIndex – Index of the breath following odor onset
.PREXTimes – Time in seconds of the inhalation following odor onset
.PREXTimesWarp – Like PREXTimes but warped for constant breath lengths, not used in our analysis
.FVTimeWarp – Like FVSwitchTimesOn but warped for constant breath lengths, not used in our analysis

ValveSpikes
The first dimension of each subfield corresponds to odor vials. The second dimension of each subfield corresponds to odor concentration and the third dimension corresponds to the entries in SpikeTimes.

For "MultiCycle" entries, there is a fourth dimension corresponding to a number of sniffs following odor delivery up to the second sniff. For Ntng recording files, the first sniff is Cycle 3. For Ntng_Inh_Opto and Ntng_Inh_Chemo recording files, the first sniff is Cycle 2.

.SpikesDuringOdor – Spike counts of each unit during the entire odor presentation. >>efd.SpikesDuringOdor{1,3,4}(2) returns the spike count of the fourth unit responding to the first odor vial at the third concentration on the second odor series.
.MultiCycleSpikeCount – Spike counts of each unit during a given respiration cycle following odor delivery. efd.MultiCycleSpikeCount{10,3,4,1}(2) returns the spike count during the first sniff after odor presentation of the fourth unit responding to the tenth odor vial at the third concentration on the second odor series.
.MultiCycleBreathPeriod – Same organization but provides the time in seconds of the sniff cycle.
.MultiCycleSpikeRate – MultiCycleSpikeCount divided by MultiCycleBreathPeriod
.RasterAlign – Each entry in .RasterAlign contains the spike times within -5 to 10 seconds of the first inhalation following odor presentation. efd.ValveSpikes.RasterAlign{10,3,4}{2} gives the spike times for the fourth isolated unit responding to the tenth odor vial at the third concentration on the second odor series. Zero is the time of inhalation.

LaserTimes
Subfields of LaserTimes are 1x1 cells containing vectors with an entry for each pulse.
.LaserOn – Time of laser onset
.LaserOff – Time of laser offset

LaserSpikes
The second dimension of each subfield of LaserTimes corresponds to the entries in SpikeTimes.
.SpikesDuringLaser – Spike counts over each laser pulse
.SpikesBeforeLaser – Spike counts over a period of equivalent length preceding each laser pulse
.SpikesDuringLaserLate – Not applicable to current datasets
.RasterAlign – Each entry in .RasterAlign contains the spike times within -5 to 10 seconds of each laser pulse. efd.LaserSpikes.RasterAlign{3}{1} gives the spike times for the third isolated unit relative to the first pulse onset.

LVTimes – Not applicable to current datasets
LVSpikes – Not applicable to current datasets

BreathStats – Mean period, mean rate, and coefficient of variation for breathing across the whole recording.

PREX – Time of negative-going zero-crossings in the respiration trace indicating the start of inhalation. Identical and redundant with the PREX described for .resp files.