Readme

Juvenile model ("Small" networks: 1000 excitatory neurons, 250 inhibitory neurons)

OB

6 odors, 4 trials. 3 first odors correspond to "amino-acids", 3 last to "bile acids".
Odors are presented for **2 seconds** and separated by 1 second of baseline activity (1 sec of baseline activity at the beginning). **Structure: odor1 trial1 odor2 trial1 … odor1 trial2 odor 2 trial2 … odor1 trial4 odor2 trial4.** Total of 72 seconds (simulation with 0.1 ms timestep).
The **odorseq_bo_poisson.mat** file contains the OB input:

- r_olfbs is a matrix time x number of olfactory bulb neurons. 1 symbolizes a spike.
-OBinp(x, 1:150,1): gives the identity of the 150 activated Mitral cells during presentation of odor x ($1 \leq x \leq 6$).
-OBinp(x, 251:300,1): gives the identity of the 50 inhibited Mitral cells during presentation of odor x ($1 \leq x \leq 6$).

Dp

2 categories of networks (**n=8** per category: 2 A, 2 B, 2 C, 2 D; for parameters value see Table 2 in the Methods section of the paper Meissner-Bernard et al., 2025, eLife)

1) *Random* network (extension "_small")
2) Network which has "learned" odor 1 & 2 (*E-I assemblies*, extension "tboth")
Hypothesis: E-I assembly forms for both CS+ and CS-.

Connectivity matrices are located in the **connec_matrices** folder.
Variables of each .mat file:

w_{XY}: Binary matrix, where 1 symbolizes a connection between 2 neurons. X are the presynaptic neurons, Y the postsynaptic ones.
Ee: Matrix number of E assemblies x number of assembly neurons
Ii: number of I assemblies x number of assembly neurons

Dpsmall_rand and Dpsmall_tboth corresponds to the simulated Dp activity in response to the OB input previously described:
_rand corresponds to the random networks and _tboth to the networks with E-I assemblies.
Variables of each .mat file:

The spiking of E neurons is in the cell array ACT, spiking of I neurons in the cell array ACT_I. Each cell corresponds to one network (see above, n=8 per category). To store the **sparse matrix** corresponding to network 1 in a new array, just type nameofvariable=ACT{1}. You will get a matrix in which the first column corresponds to **when** a spike occurs, and the second column indicates **which neuron spiked**. The time is 0.1ms (e.g. 1000=100 ms). The following line of code would for example average the number of spikes within time bins of 200 ms for each neuron, resulting in a time*neurons matrix.

```
spike_E=ACT{1};
FR=zeros(360,4000);
for i=1:360
    times(:,i)=[200/dt*(i-1)+1;200/dt*i];

    spikeE_temp=sort(spike_E((spike_E(:,1)>times(1,i))&(spike_E(:,1)<times(2,i)),2));

     if ~isempty(spikeE_temp)
        [NspikE,EdspikE]=histcounts(spikeE_temp,'BinMethod','integers');
        FR(i,round(EdspikE(1)):floor(EdspikE(length(EdspikE))))=
                                                    NspikE/(times(2,i)-times(1,i))/dt*1000;
    end
end
```

mfr sponta= mean baseline firing rate
mfr E= mean odor-evoked firing rate of E neurons
mfr E= mean odor-evoked firing rate of I neurons
CC= correlation coefficient (see eLife 2024 CMB FZ RF)
g_oe= mean afferent conductance during odor stimulation
% rec = average contribution of the recurrentexcitatory input to the total excitatory input in E neurons
gsyn = total synaptic conductance change due to odor stimulation

	mfr sponta	mfr E	mfr I	CC	goe	rec	gsyn
rand_small	0.011689	0.833819	1.640556	0.054102	0.137028	45.1244	0.34346
tboth_small	0.012022	1.009431	2.242389	0.059591	0.137062	52.25458	0.421059