# 2 populations and 3 populations spiking network model of pDp (zebrafish homolog of olfactory cortex)

$pDp_{sim}$ consists of 5000 sparsely connected integrate-and-fire **neurons**, which receive input from the olfactory bulb. An **odor** is simulated by increasing the firing rate of 10% of the olfactory bulb neurons. We start with a network that is randomly connected and fit the model parameters such that $pDp_{sim}$ reproduces key features of *ex-vivo* Dp during odor presentation. We then reorganize connections to introduce either E assemblies or E-I assemblies, to mimic olfactory learning.

- ➔ Model with 1 excitatory (E) and 1 inhibitory (I) population is described in [1].
- ➔ Model with 1 excitatory, 1 feedforward (FFI) and 1 feedback inhibitory (FBI) population is described in more detail in [2]. Also defined as the 3 populations model.

**Connectivity matrices (connec folders)**

*Variables:*

$w_{XY}$: Binary matrix, where 1 symbolizes a connection between 2 neurons. X are the presynaptic neurons (rows), Y the postsynaptic ones (columns).

Ee: Assembly neurons matrix of size *number of E assemblies x number of assembly neurons*

Ii: Assembly neurons matrix of size *number of I assemblies x number of assembly neurons*

2 populations

Connectivity matrices used in [1] are located in the connec_2pop folder. Connection probability and strength are described in Table 2 of [1].

- Extension _tEI: Tuned E+I networks.
- Extension _tI: Tuned I networks.
- Extension tEI_noA: Tuned[adjust] (Figure 4-fig. supplement 3)
- Extension _matchS: Scaled[adjust] (Figure 4-fig. supplement 3, multiply w_ie by chi)

3 populations

Connectivity matrices used in [2] are located in the connec_3pop folder. Connection probability and strength are described in Table 2 of [2].

- Extension _r: random networks
- Extension _s: structured (tuned I) networks
- Extension _sw: E assemblies (Fig. S7, multiply w_ie(1:500,:) by $\chi$=1.04)
- Extension _halfI: struct[FF assembly] (Fig. S7)
- Extension _mix: struct[FB component] (Fig. S7)

**Connectivity matrices (functions)**

- generate_connectivity.m: generates random connectivity matrices
- introduce_assemblies.m: rewires connections to form assemblies

**Olfactory bulb input (odorset folders)**

*Variables:*
r_olfbs: time x number of olfactory bulb neurons (mitral cells). 1 symbolizes a spike.

2 populations
odorset_10learned.mat: 10 learned, uncorrelated odors. Odors are presented for 2 seconds and separated by 1 second of baseline activity (1 sec of baseline activity at the beginning).

odorset_10novel.mat: 10 novel, uncorrelated odors. Odors are presented for 2 seconds and separated by 1 second of baseline activity (1 sec of baseline activity at the beginning).

odorspace_fig4.mat: odor subspace described in Fig. 4 (A-C)

odorspace_fig6.mat: odor subspace described in Fig. 6 (A)

| | Identity of activated mitral cells | Identity of inhibited mitral cells |
|---|---|---|
| odorset_10learned.mat<br>odorset_10novel.mat | OBinp(odor number,1:150,1) | OBinp(odor number,226:300,1) |
| odorspace_fig4.mat<br>odorspace_fig6.mat | Corner odors<br>MCact(odor number,:,1) | Corner odors<br>MCinh(odor number,:,1) |

3 populations
odorset_20odors.mat: 20 odors. Odors are presented for 2 seconds and separated by 1 second of baseline activity (1 sec of baseline activity at the beginning).

*Odors used to create assemblies (2 different sets of 20 learned odors were used)*

| Odor set | Networks |
|---|---|
| odorslearned_corr.mat | A1, A2, B1, B2, C1, C2, D1, D2 |
| odorslearned_nocorr_thl2C.mat | A3, A4, B3, B4, C3, C4, D3, D4 |

**Olfactory bulb input (function)**

generate_odorset.m: generates a sequence of $x$ random odors (2 seconds presentation, separated by 1 second of baseline activity)

**Simulation**

run_pDpsim.m: simulate $pDp_{sim}$ (main figures)
inputs: 1) number of inhibitory populations
2) connectivity structure (random or assemblies)
3) perform analysis (see next section)
4) For 2 populations: odor set
For 3 populations: with or without partial inactivation of inhibitory neurons

**Analysis:**

- observables.m: calculates the observables used to fit the model (see Methods in [1])
- co-tuning: calculates co-tuning

**Data (data folder)**

2 populations

Each .mat corresponds to the results of the activity of one type of networks (rand, scaled or tuned) in response to the learned (_learned), odor subspace from Fig.4 (_subspace4), or odor subspace from Fig.6 (_subspace6).

The spiking of E neurons is in the cell array ACT, the spiking of I neurons in the cell array ACT_I. Each cell corresponds to one network. 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 0.1 ms (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 x 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
```

3 populations

*data_xxx_xxx.mat:*

-contains the firing rate of each neuron evoked by each odor of the odor set (distinct from learned odors) averaged over the first 1.5 seconds of odor presentation. Control activity (no PIN) or upon partial inactivation of inhibitory neurons (PIN)
Btot_each: Matrix of size *number of networks x number of E neurons x number of odors*
BtotI_each: Matrix of size *number of networks x number of I neurons x number of odors*

*corr_individualdata.xlsx*:

-7 first columns: correlations between activity patterns evoked by two different odors in random networks or corresponding structured networks, with or without inhibiting I neurons.

**References**

[1] Meissner-Bernard C., Zenke F. & Friedrich R. (2024) Geometry and dynamics of representations in a precisely balanced memory network related to olfactory cortex. *eLife* **13**:RP96303.

[2] Meissner-Bernard C., Jenkins B., Rupprecht P., Arn Bouldoires E., Zenke F., Friedrich RW. & Frank T. (2024) Computational functions of precisely balanced neuronal assemblies in an olfactory memory network. *bioRxiv* doi.org/10.1101/2024.04.09.588702