

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 and 1 inhibitory population is described in more detail in [1].
- ➔ Model with 1 excitatory, 1 feedforward and 1 feedback inhibitory population (3 populations) is described in more detail in [2].

Connectivity matrices (connec folders)

Variables:

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

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.

3 populations

Connectivity matrices used in [2] are located in the connec_3pop folder.

- Extension_r: random networks
- Extension_s: structured (tuned I) networks

Olfactory bulb input (odorset folders)

Variables:

r_olfbs: time x number of olfactory bulb neurons. 1 symbolizes a spike.

OBinp(1:10,1:150,1):

OBinp(1:10,225:300,1):

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)

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).

Assemblies

[Generate random connectivity matrices .m](#)

[Rewire connections to create assemblies .m](#)

Simulation

run_pDpsim.m

Analysis:

- [observables](#)
- [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) or odor subspace from Fig.4 (_subspace4).

3 populations

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. (2023) Geometry and dynamics of representations in a precisely balanced memory network related to olfactory cortex. *bioRxiv* doi.org/10.1101/2023.12.12.571272

[2] Meissner-Bernard C., Rupprecht P., Friedrich R. & Frank T. (*in preparation*) Computational functions of precisely balanced neuronal assemblies in an olfactory memory network