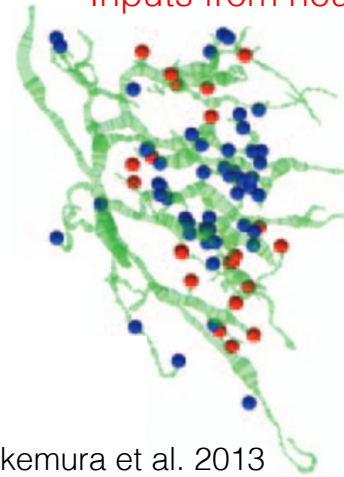


Introduction to fly connectomics

Some details about the data format

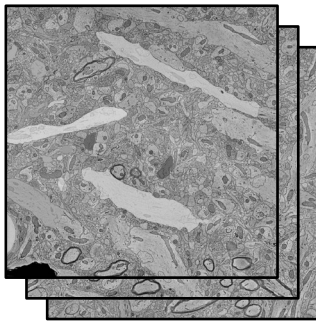
Potential directions

Inputs from neuron j
Inputs from neuron k

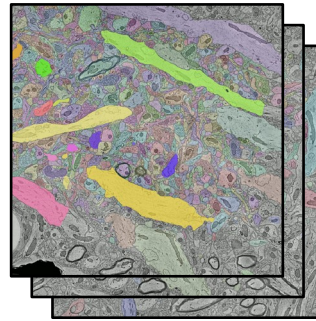


Takemura et al. 2013

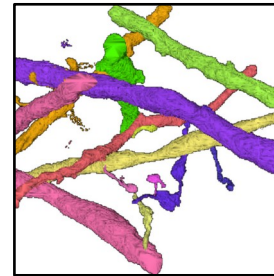
Electron microscopy images



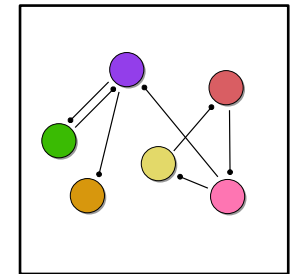
Segmentation



3D reconstruction



Graph



Cell types
"Names"

Neurotransmitter types
Size/number of synaptic
connections
Recordings/effects of
activation/inactivation
Transcriptomic

C. elegans



~300 neurons

1986

wormwiring.org

Drosophila
larva

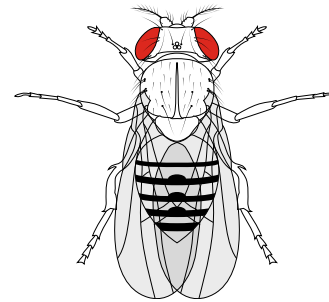


~2,000 neurons

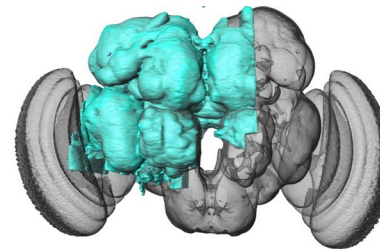
~2010-2023

[llem.catmaid.
virtualflybrain.org](http://llem.catmaid.virtualflybrain.org)

Drosophila
adult

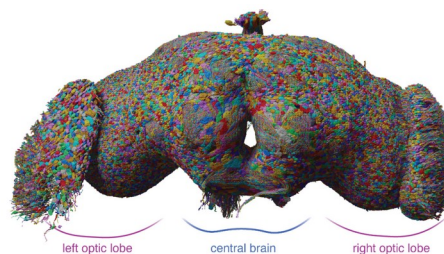


~20,000 neurons
2020



neuprint.janelia.org

~120,000 neurons
2023



codex.flywire.ai

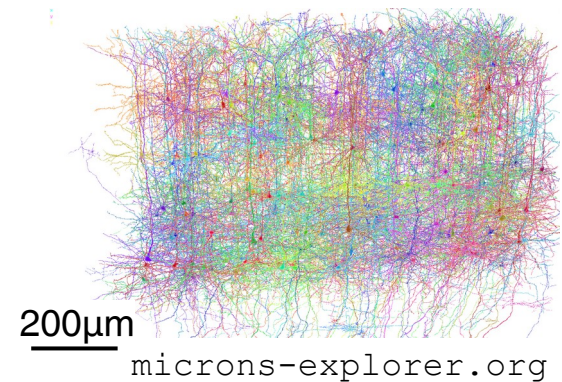
?

Mouse



~75,000,000 neurons

~200,000 neurons
2021



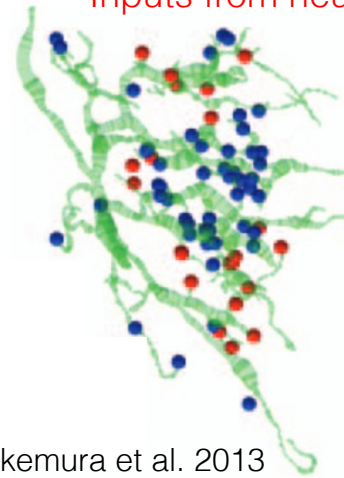
200µm

microns-explorer.org

Upcoming: complete male fly brain, ventral nerve cord

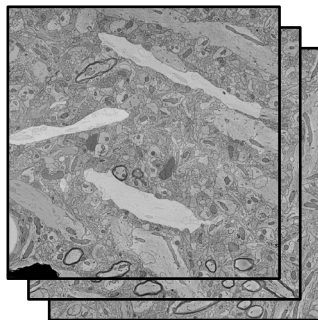
Inputs from neuron j

Inputs from neuron k

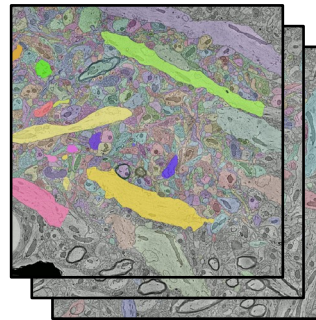


Takemura et al. 2013

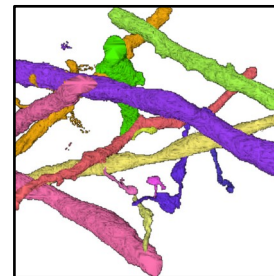
Electron microscopy images



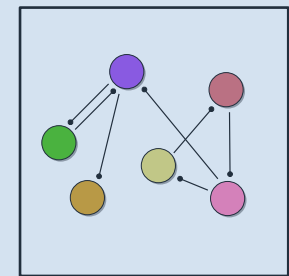
Segmentation



3D reconstruction



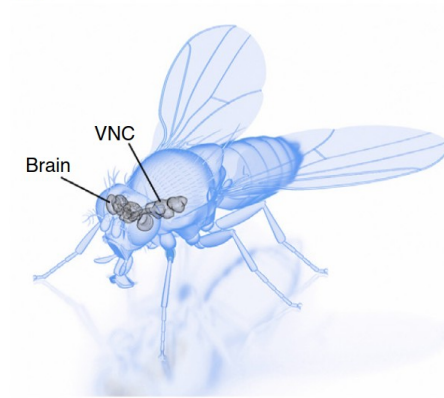
Graph



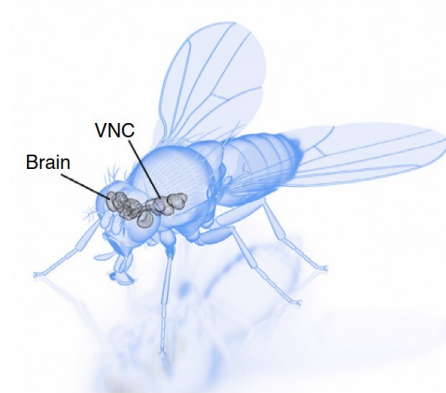
Cell types
"Names"

Neurotransmitter types
Size/number of synaptic
connections
Recordings/effects of
activation/inactivation
Transcriptomic

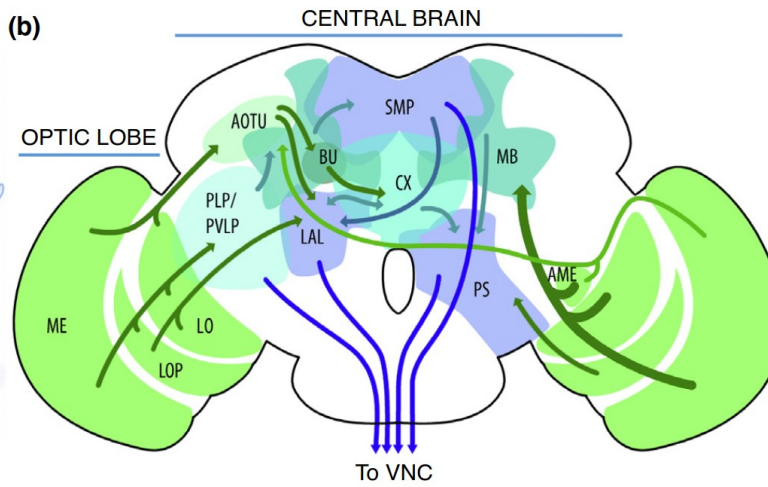
(a)



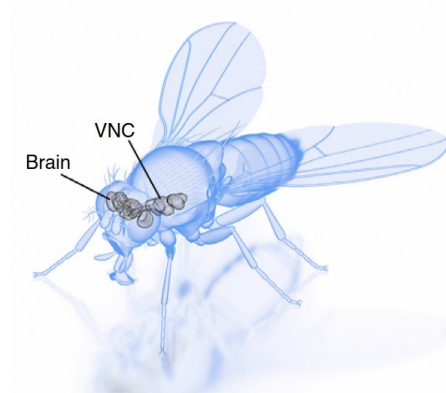
(a)



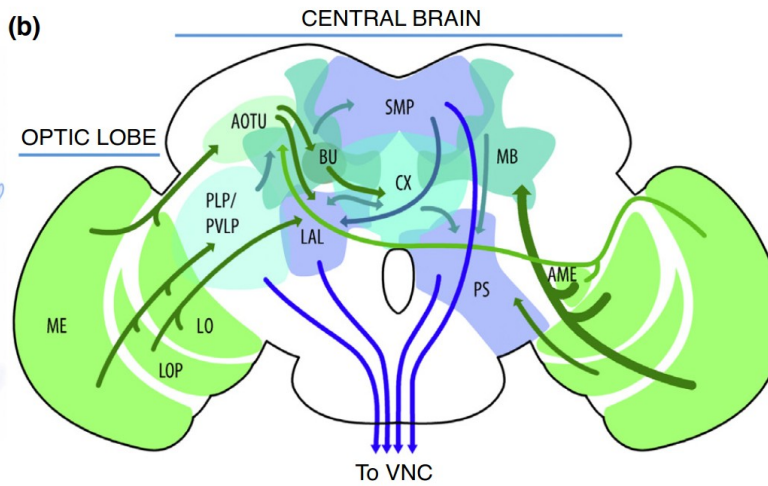
(b)



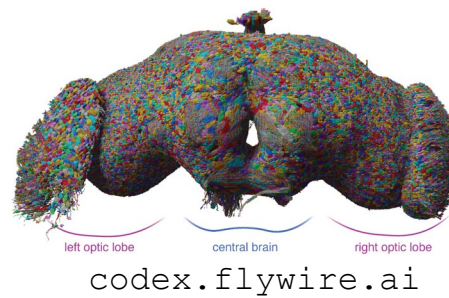
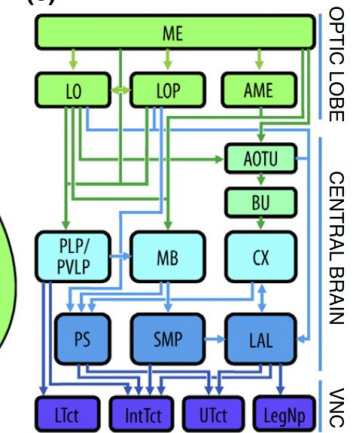
(a)



(b)



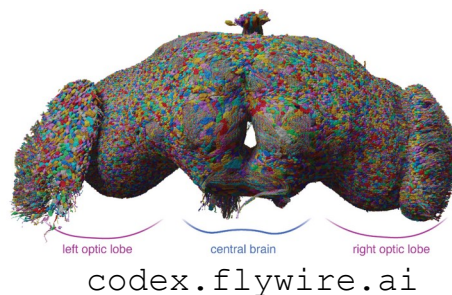
(c)



$$N = 139255$$

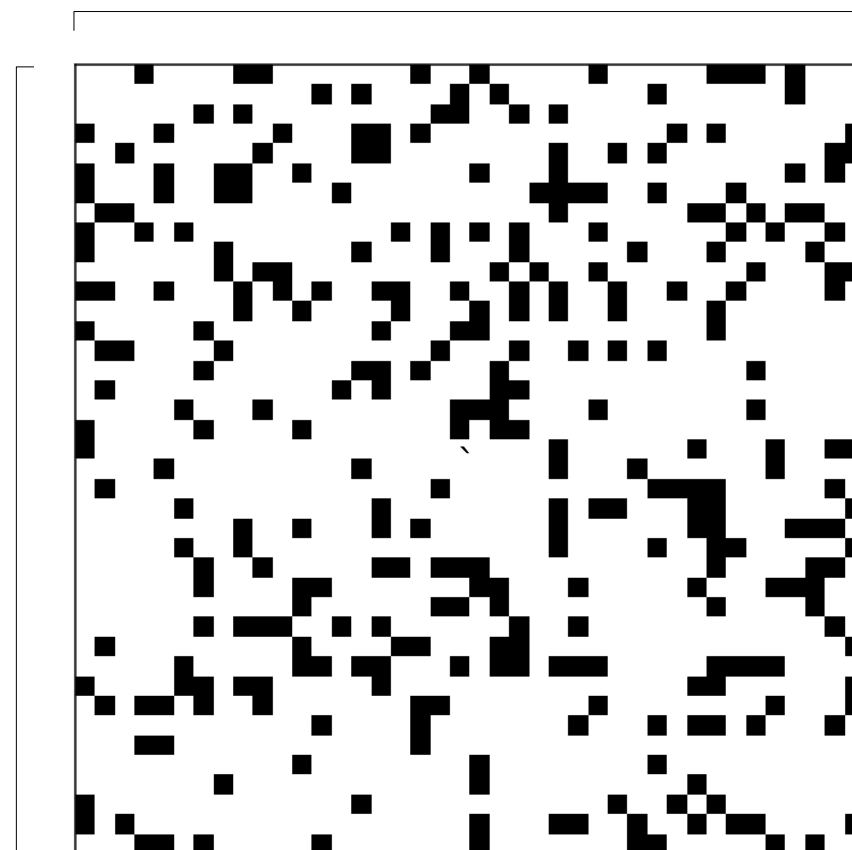
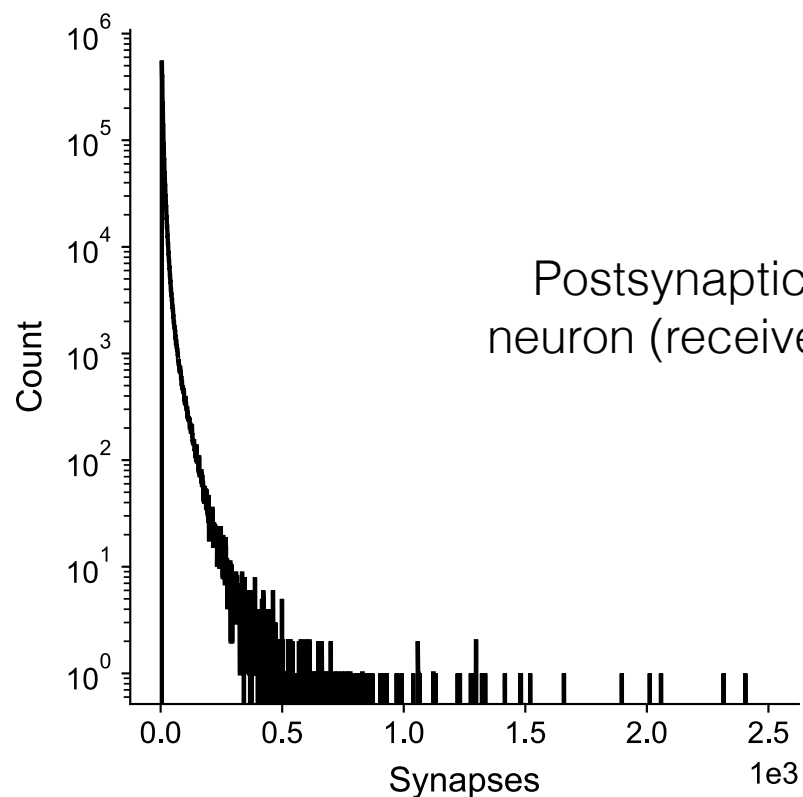
$$p(\geq 5) = 0.00014$$

$$p(\geq 10) = 0.000055$$



Presynaptic neuron (sender)

N

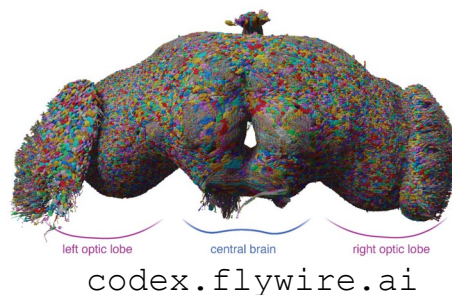


■ Connected
□ Disconnected

$$N = 139255$$

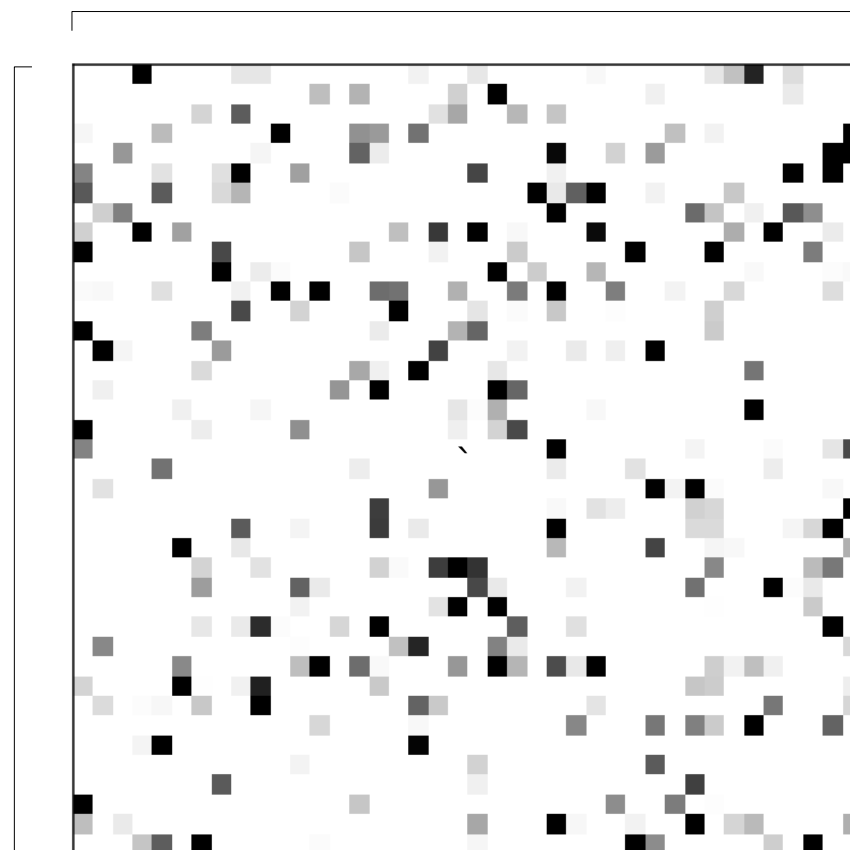
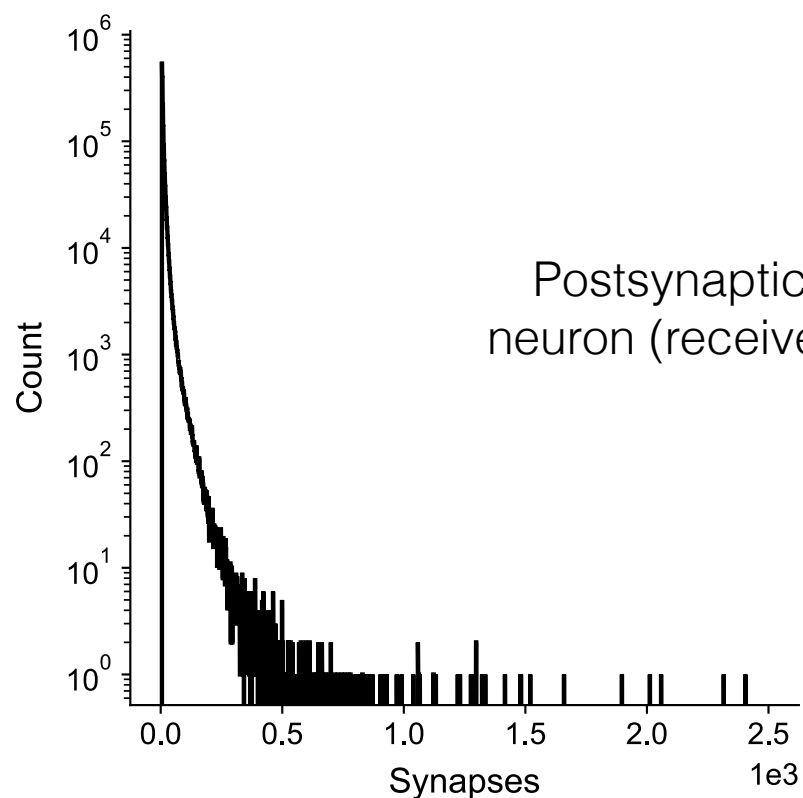
$$p(\geq 5) = 0.00014$$

$$p(\geq 10) = 0.000055$$



Presynaptic neuron (sender)

N

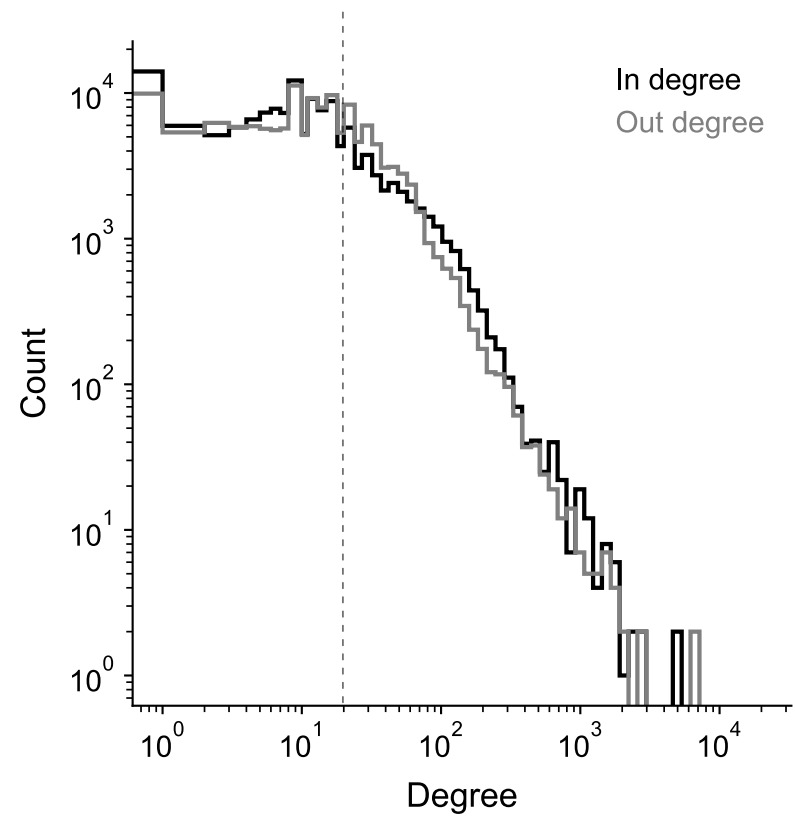
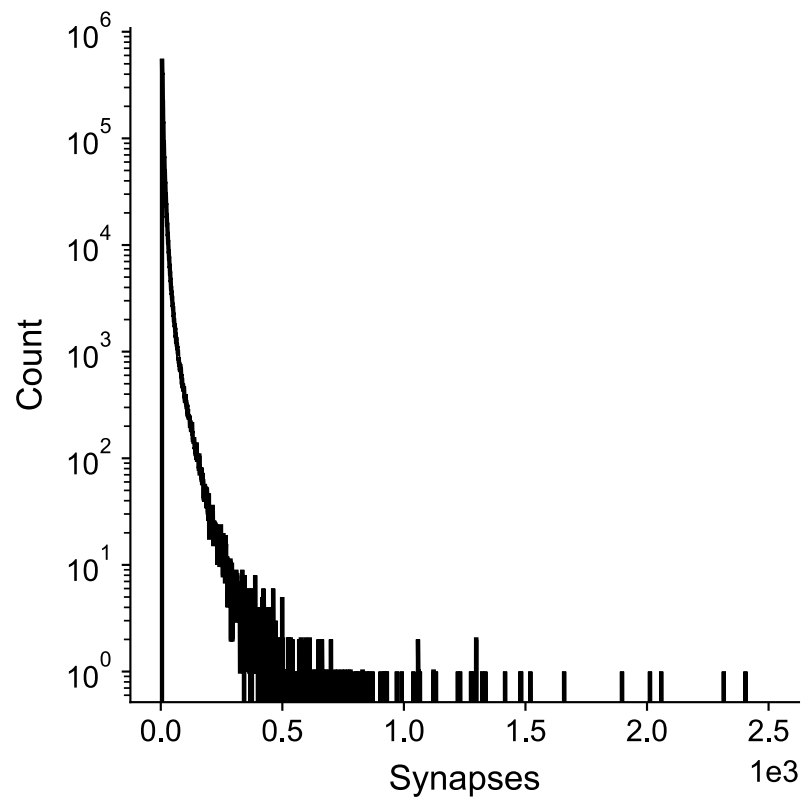


Number/size of connections

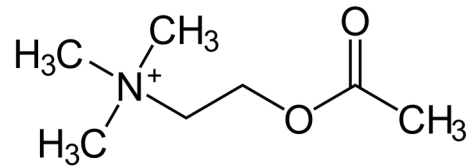
$$N = 139255$$

$$p(\geq 5) = 0.00014$$

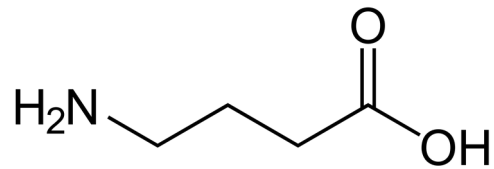
$$p(\geq 10) = 0.000055$$



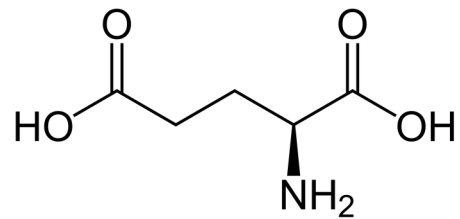
Acetylcholine (excitatory)



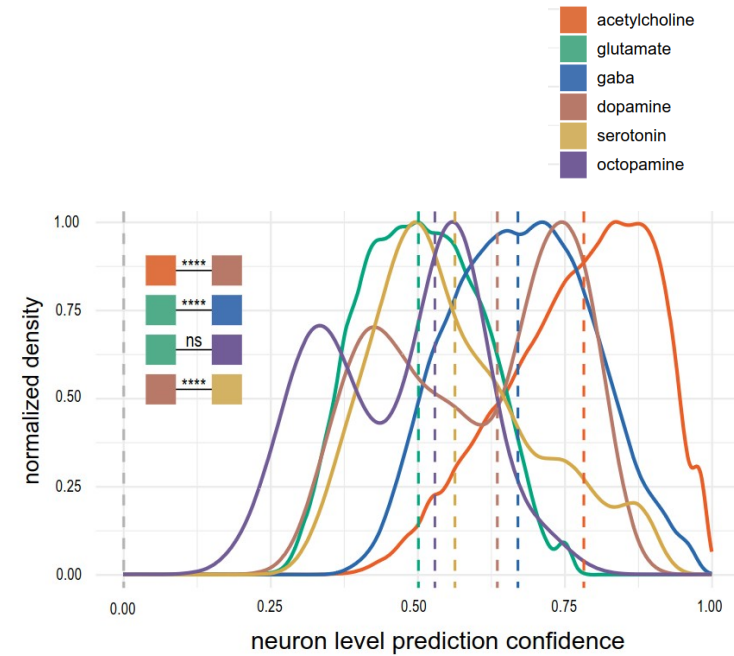
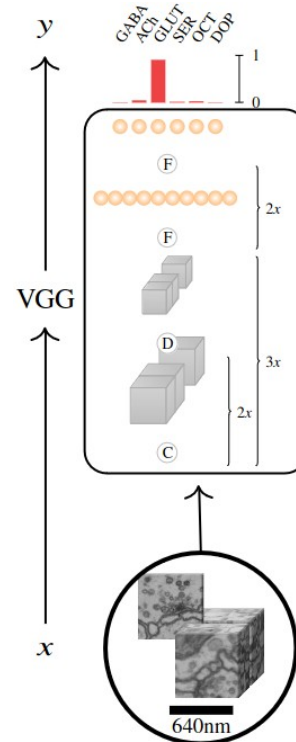
GABA (inhibitory)



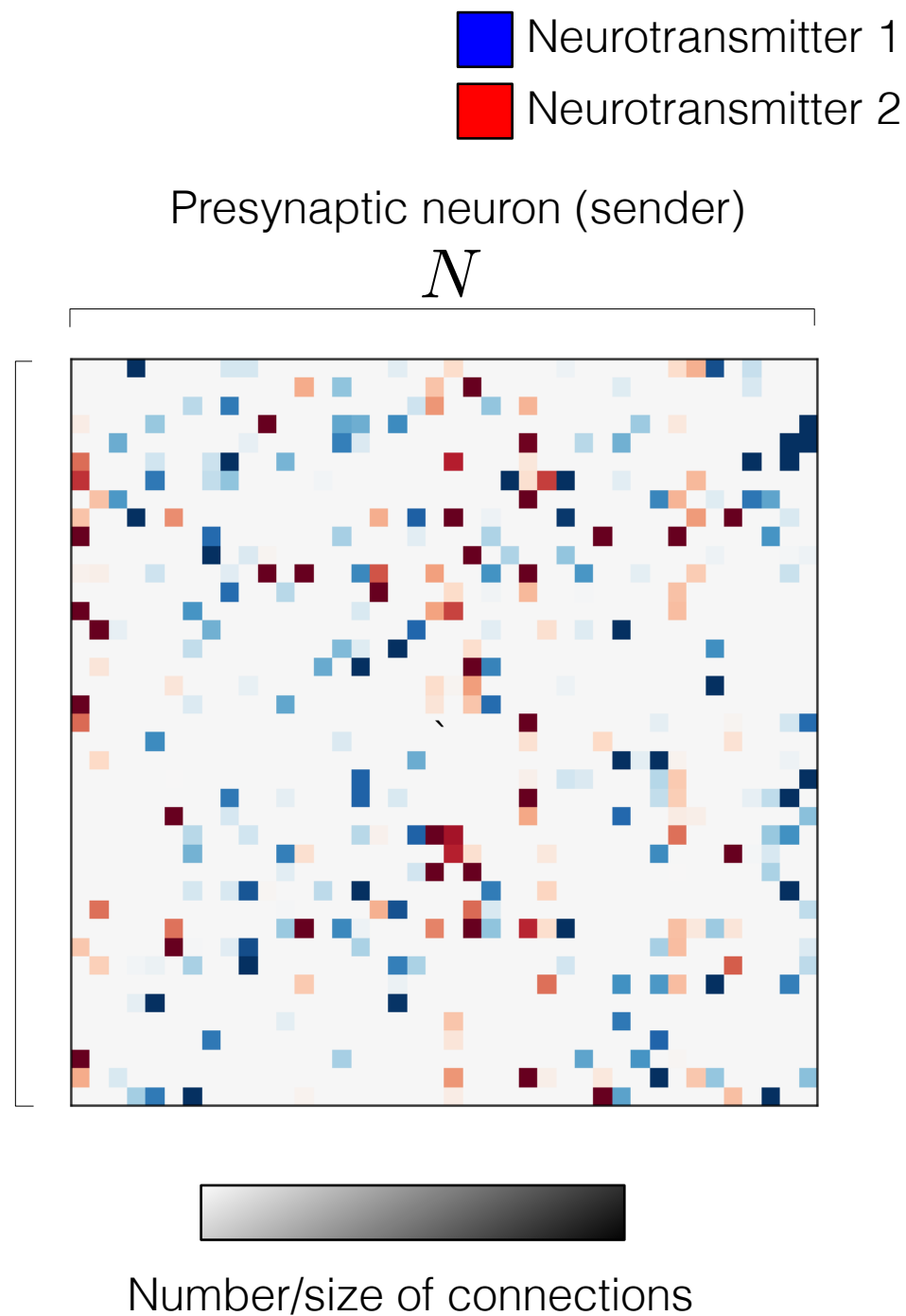
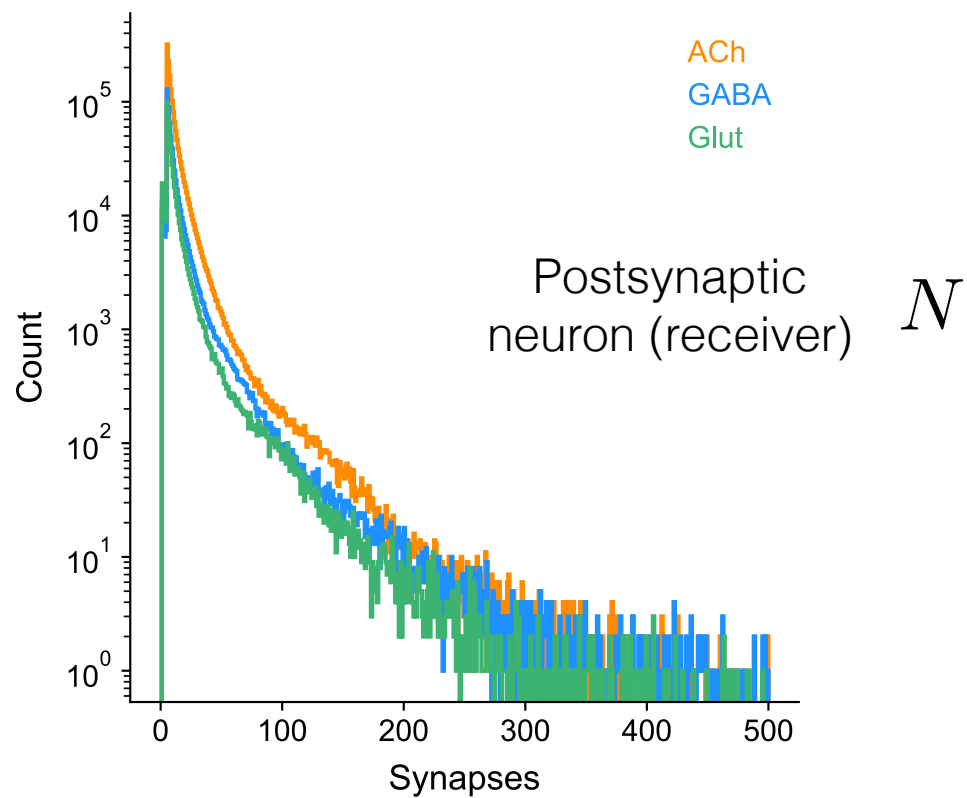
Glutamate (probably inhibitory)



Predicted neurotransmitter



Eckstein et al. 2024



$$\tau_i \frac{dx_i(t)}{dt} = -x_i(t) + \sum_j W_{ij} f_j(x_j(t)) + I_i(t)$$

$$W_{ij} \propto g_{ij} A_{ij}$$

$$g_{ij} = g$$

Global scale factor

$$g_{ij} = \pm g$$

Excitatory/inhibitory

$$g_{ij} = \pm g / \sum_j A_{ij}$$

Normalized by incoming weights

$$g_{ij} = \pm g_{(\text{NT})} / \sum_j A_{ij}$$

Neurotransmitter-specific gain

Introduction to fly connectomics

Some details about the data format

Potential directions

Inspecting neurons

```
In [5]: print(neurons.columns)
neurons
```

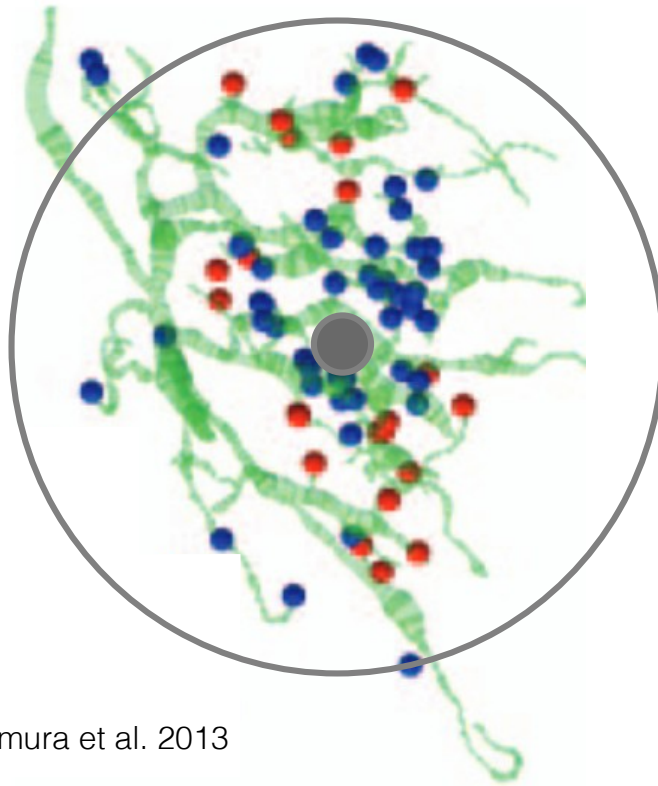
```
Index(['root_id', 'group', 'nt_type', 'nt_type_score', 'da_avg', 'ser_avg',
      'gaba_avg', 'glut_avg', 'ach_avg', 'oct_avg', 'flow', 'super_class',
      'class', 'sub_class', 'cell_type', 'hemibrain_type', 'hemilineage',
      'side', 'nerve', 'x', 'y', 'z', 'x_presyn', 'y_presyn', 'z_presyn',
      'rho_presyn', 'x_postsyn', 'y_postsyn', 'z_postsyn', 'rho_postsyn',
      'J_idx', 'J_idx_post', 'J_idx_pre'],
      dtype='object')
```

```
Out[5]:
```

	root_id	group	nt_type	nt_type_score	da_avg	ser_avg	gaba_avg	glut_avg	ach_avg	oct_avg	...	y_pr
0	720575940596125868	LO.LOP	ACH	0.57	0.03	0.00	0.05	0.28	0.57	0.07	...	272101.65
1	720575940597856265	ME	ACH	0.85	0.01	0.00	0.03	0.04	0.85	0.07	...	332566.47
2	720575940597944841	ME.LO	ACH	0.82	0.02	0.00	0.01	0.05	0.82	0.09	...	315764.23
3	720575940598267657	ME	GABA	0.74	0.01	0.01	0.74	0.19	0.03	0.02	...	291869.89
4	720575940599333574	ME	ACH	0.61	0.02	0.00	0.13	0.13	0.61	0.11	...	301811.97
...
139250	720575940661335681	GNG	GABA	0.71	0.00	0.00	0.71	0.17	0.11	0.00	...	332268.83
139251	720575940661336193	ME.LO	ACH	0.62	0.02	0.00	0.18	0.16	0.62	0.03	...	187984.46
139252	720575940661337217	SCL.MB_ML	ACH	1.00	0.00	0.00	0.00	0.00	1.00	0.00	...	163719.61
139253	720575940661338497	GNG	NaN	0.00	0.00	0.00	0.00	0.00	0.00	0.00
139254	720575940661339777	NO_CONS	NaN	0.00	0.00	0.00	0.00	0.00	0.00	0.00

139255 rows × 33 columns

Inputs from neuron j
Inputs from neuron k

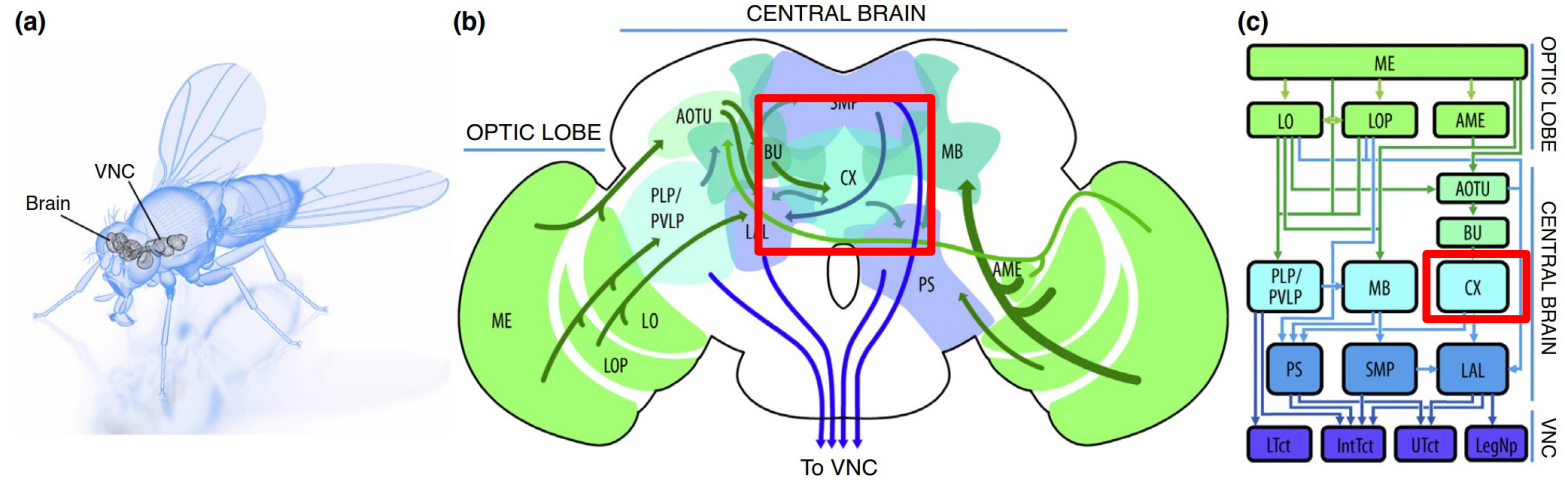


Takemura et al. 2013

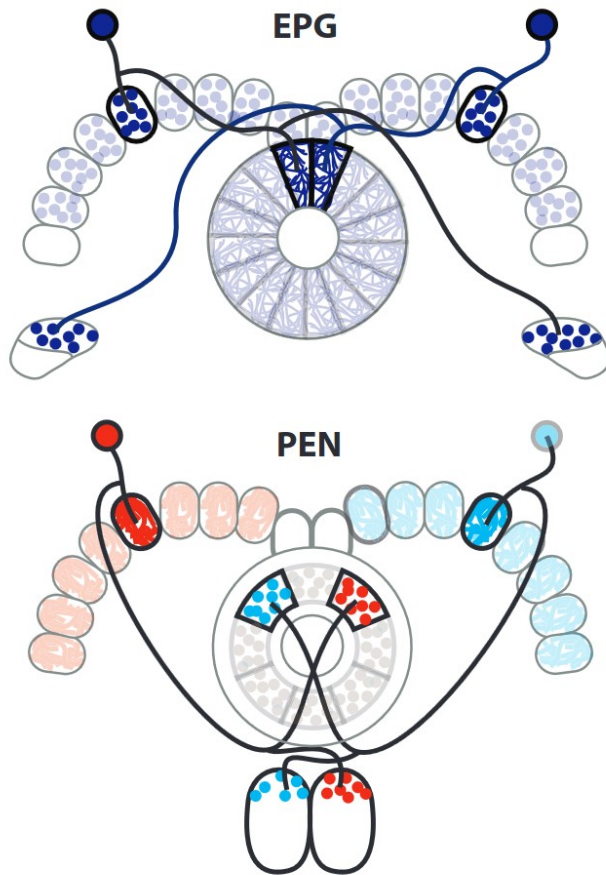
Introduction to fly connectomics

Some details about the data format

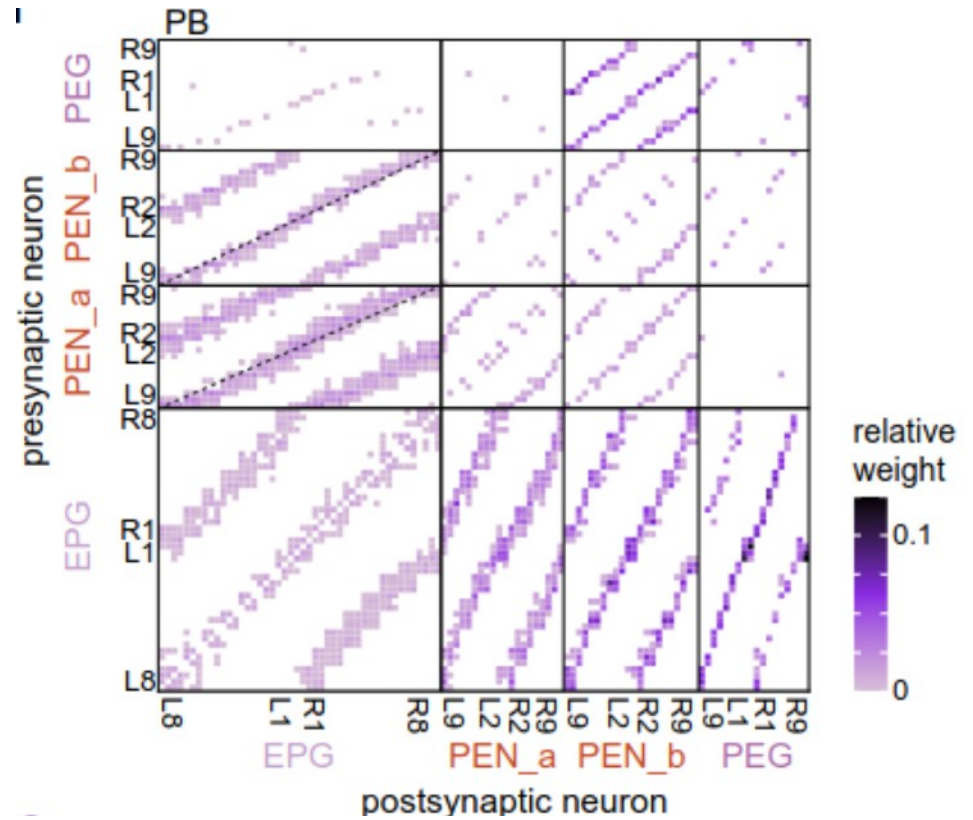
Potential directions



Chiang, Siwanowicz, Card 2020



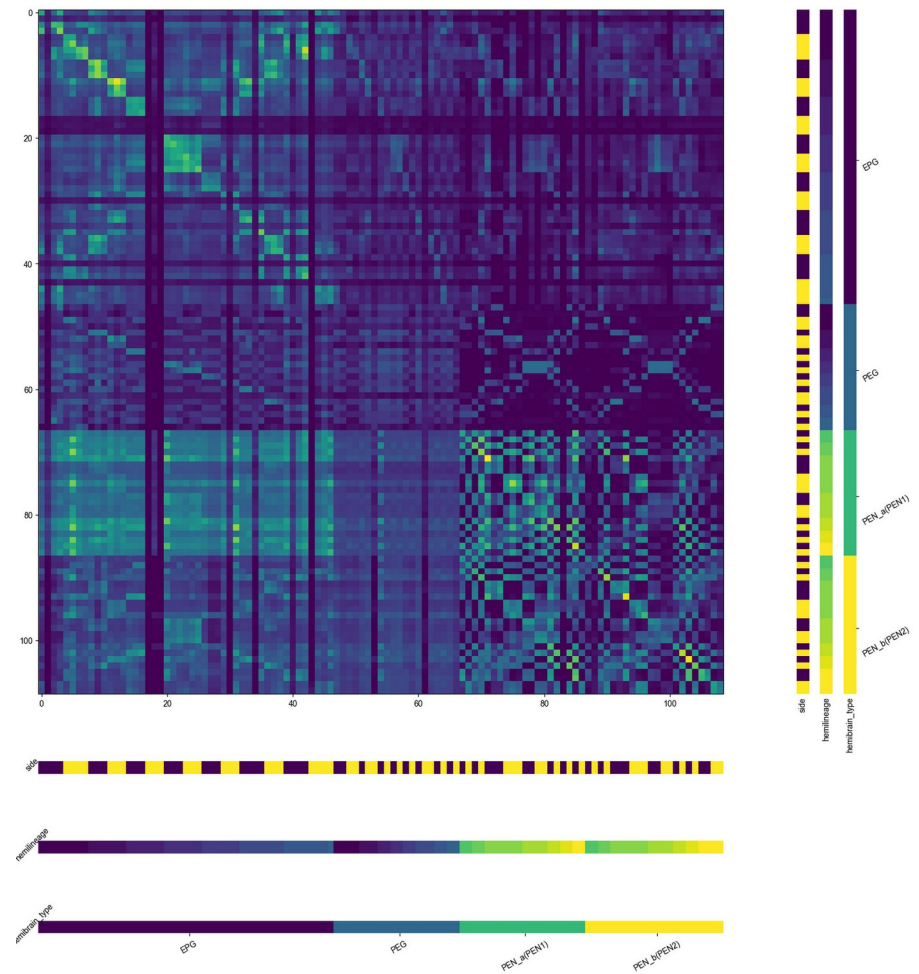
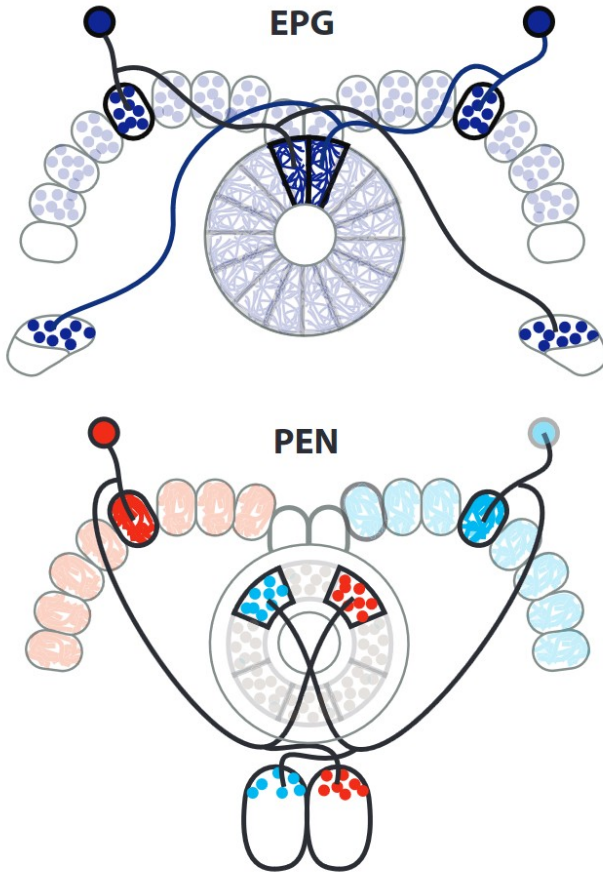
Hulse & Jayaraman 2020



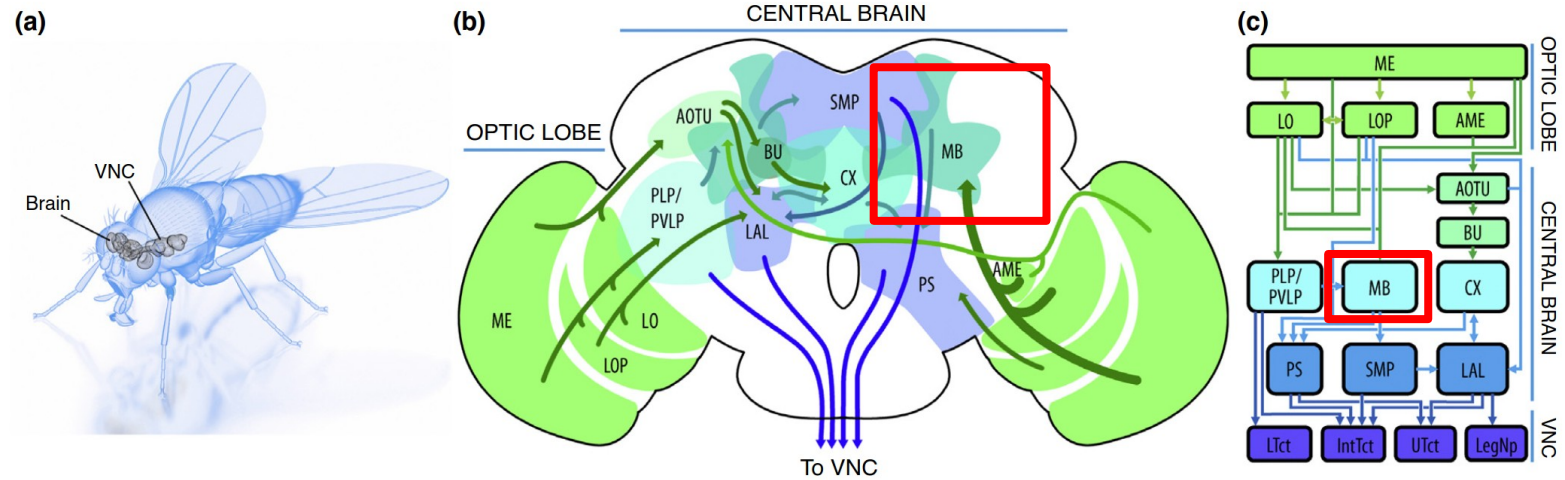
Hulse et al. 2021

hello_flywire.ipynb

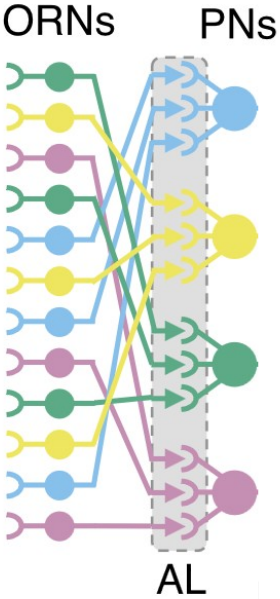
```
In [20]: hulse_fig17=neurons[(neurons['hemibrain_type']=='EPG') | (neurons['hemibrain_type']=='PEG') | neurons.hemibrain_type]
hulse_fig17_neurons, hulse_fig17_J, hulse_fig17_neurons_pre, hulse_fig17_neurons_post, hulse_fig17_nts Js = filter
plot_connectivity(hulse_fig17_neurons_pre, hulse_fig17_neurons_post, hulse_fig17_J.todense(), input_tick_labels=1,
```

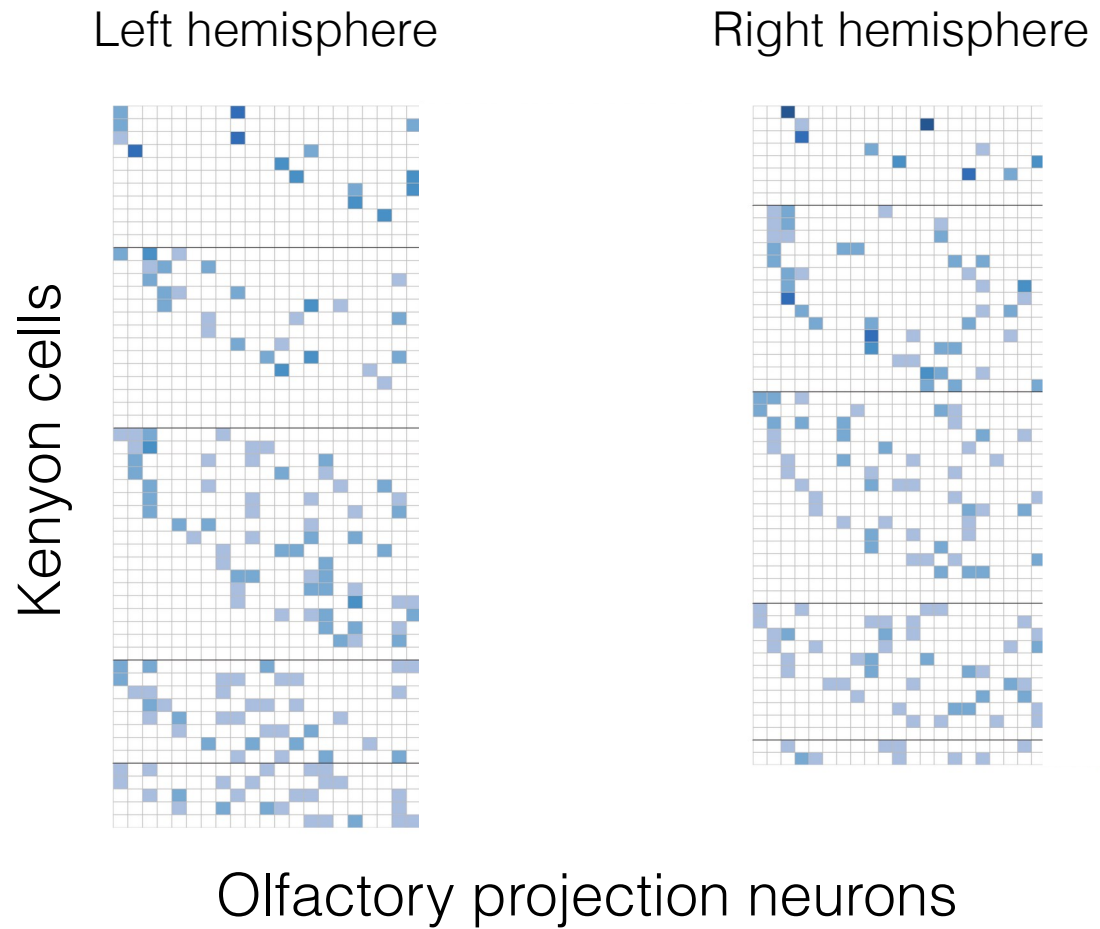
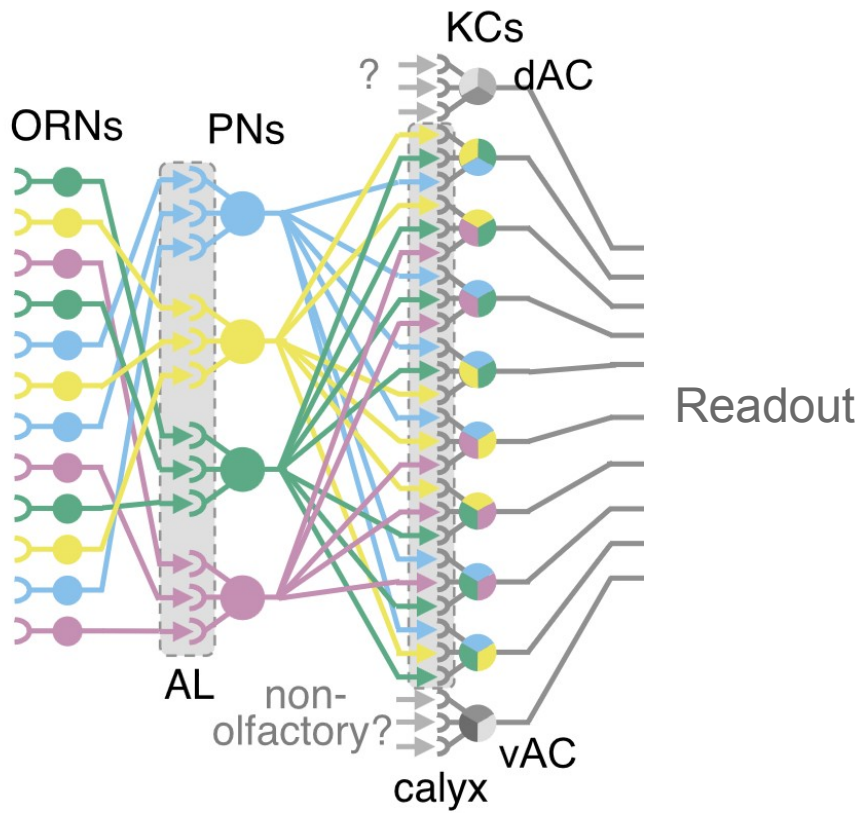


Hulse & Jayaraman 2020



Chiang, Siwanowicz, Card 2020

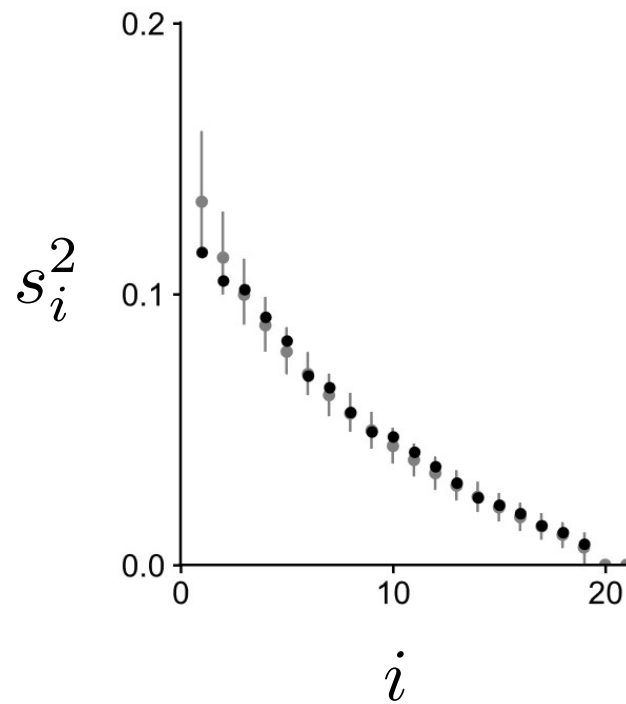




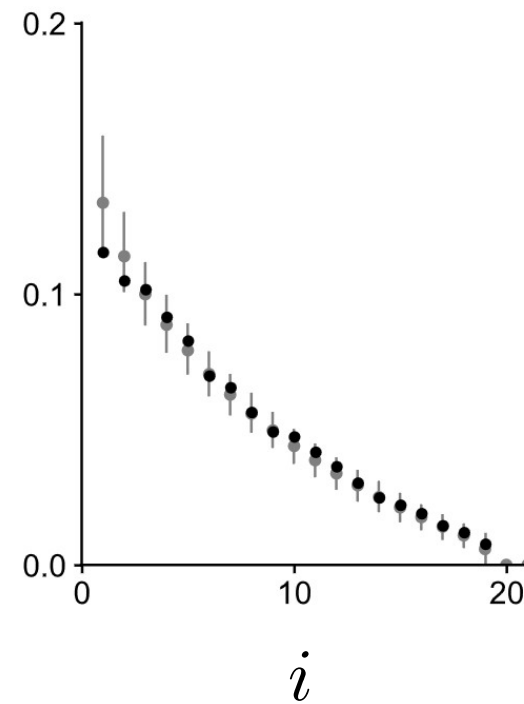
Adjacency matrix (unweighted)
Degree-matched random matrices

$$A = USV^T$$

Left



Right





alitwinkumar / connectome_examples

hello_flywire.ipynb: Loading data, selecting interesting subsets of neurons.

basic_pandas_tutorial.ipynb: Pandas tutorial.

flywire_spatial_analysis.ipynb: Analyzing synapse locations.

gnn_tutorial.ipynb: Using graph neural networks to predict synapses.

$$h_v^{(k)} = f^{(k)} \left(W^{(k)} \cdot \frac{\sum_{u \in \mathcal{N}(v)} h_u^{(k-1)}}{|\mathcal{N}(v)|} + B^{(k)} \cdot h_v^{(k-1)} \right) \quad \text{for all } v \in V.$$

Node v 's embedding at step k . Nonlinearity (ReLU) Learnable weights Mean of v 's neighbour's embeddings at step $k-1$. Learnable bias Node v 's embedding at step $k-1$.

Adapted from Daigavane, et al., "Understanding Convolutions on Graphs", Distill, 2021

