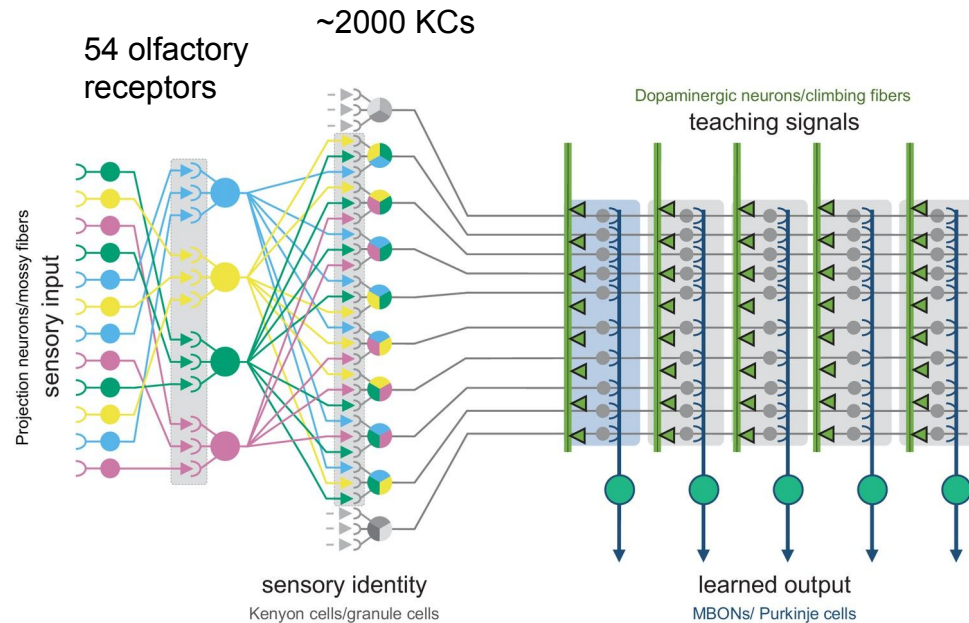
A fluorescence microscopy image of a fruit fly mushroom body. The image shows a central structure with two main lobes, stained in bright yellow. The surrounding tissue is stained in a deep blue. The overall shape is somewhat butterfly-like, with the yellow-stained regions forming the wings and the blue-stained regions forming the body.

# Modeling APL-Mediated Local Inhibition in the Fruit Fly Mushroom Body

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2023/11/29

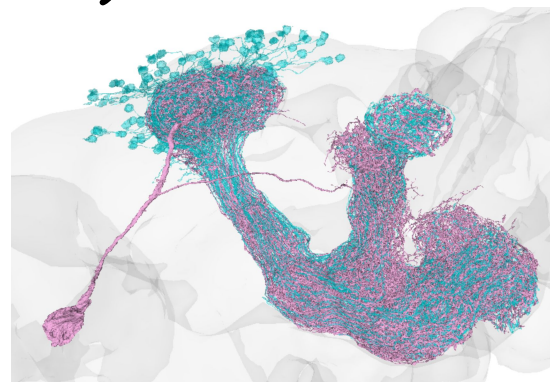
# Introduction: Mushroom body

- Mushroom body is the learning hub of insects:
  - Mushroom body is the analog of hippocampus and cerebellum. The major type of neurons in mushroom body is Kenyon Cells (KC)
  - Kenyon Cells, receiving combinatorial olfactory inputs, are the engrams of olfactory memory
  - Single odor activates an ensemble of Kenyon Cells. The sparsity of Kenyon Cells activity is critical for odor discrimination



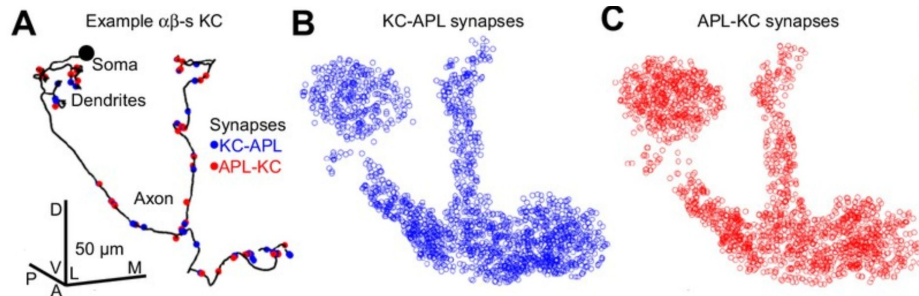
# Anterior Paired Lateral (APL) Neuron

- APL provides lateral inhibition in Mushroom body:
  - APL is a giant GABAergic interneuron (1 neuron per hemisphere)
  - APL neuron integrates inputs from all Kenyon Cells and delivers inhibitory feedback
  - APL is essential for olfactory discrimination
  - The inhibition from APL is not global



KCs

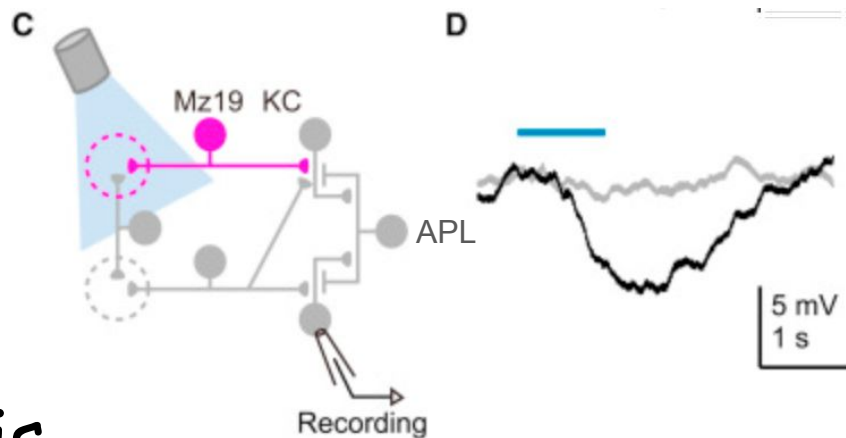
APL



# Inhibition from APL is not Global

- APL provides local lateral inhibition
  - Not all KCs can inhibit each other by APL
  - APL don't have voltage gated ion channels for generating spikes

What is the function of this local inhibition in the mushroom body?

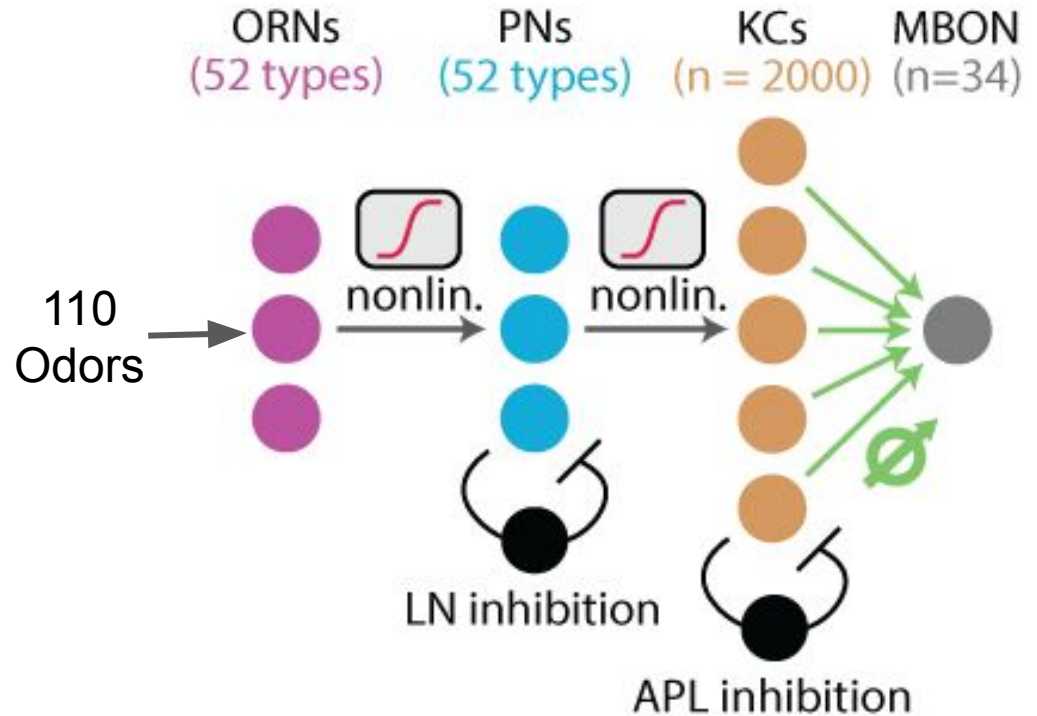


# Research Motivation and Objectives

- Our project aims to explore how APL imposes local inhibition on Kenyon Cells and how this inhibition affects olfactory perception and learning processes by building and analyzing computational models.
- We seek to understand the impact of APL's inhibitory mechanisms on the sparsity of sensory representations and the accuracy of learning by simulating these inhibitory processes.

# Previous Model

- Kennedy-MB model
  - Simplified LIF model for KCs
  - Input from experimental recording of 110 odors in ORNs
  - Uniform APL inhibition to all KCs
  - We aim to construct local inhibition model based on Kennedy-MB model

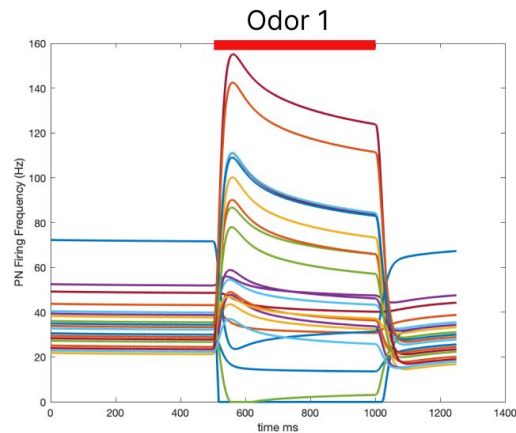
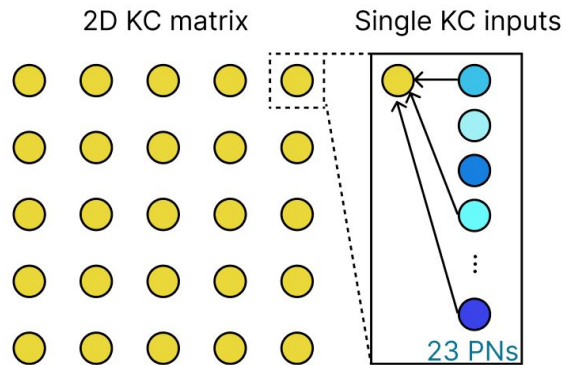


Modeling



# 2D KC grid

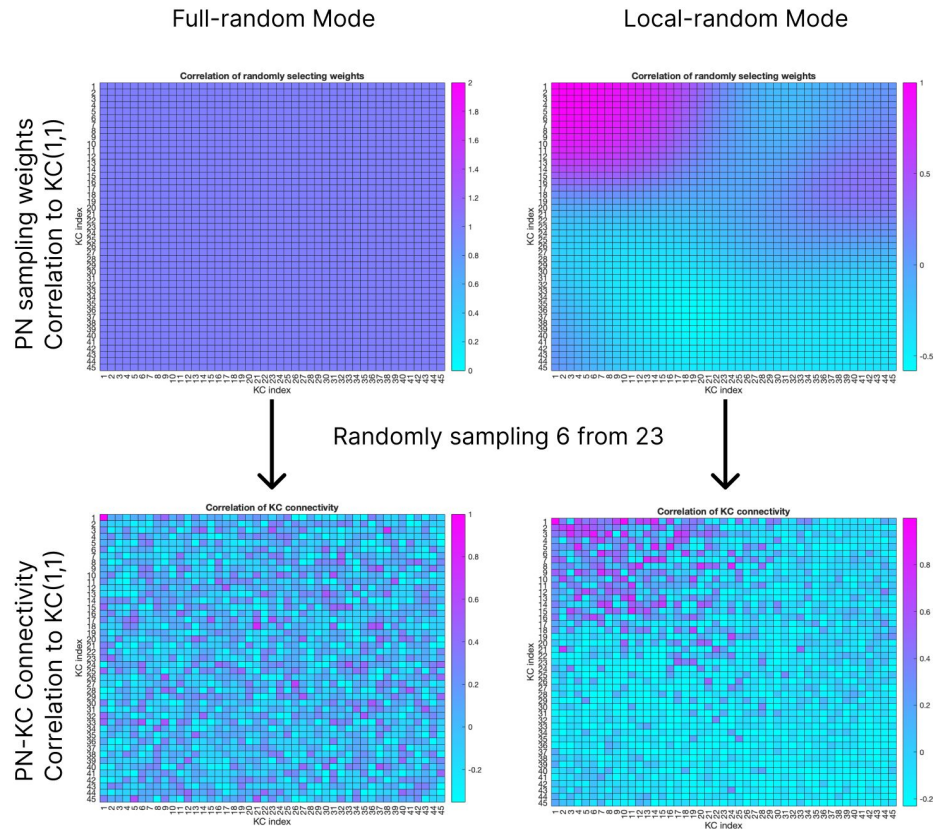
- KC receive excitatory input from Projection Neurons (PNs)
  - 2025 KCs arranged as 45\*45 2-D KC matrix to simulate their spatial relationships
  - Each KC randomly receives 6 inputs from 23 PNs; PNs firing rate is from the Kennedy-MB model





# PN-KC connectivity

- Each KC randomly sample 6 inputs from 23 PNs with replacement
  - Full(uniform)-random mode: All PN have the same weight to be sampled
  - Recent connectome analysis suggests closer KC share similar PN-KC connectivity
  - Local-random mode: The sampling weight of each PN is assigned by gaussian distributions in the 2-D KC space



# Input current to KC

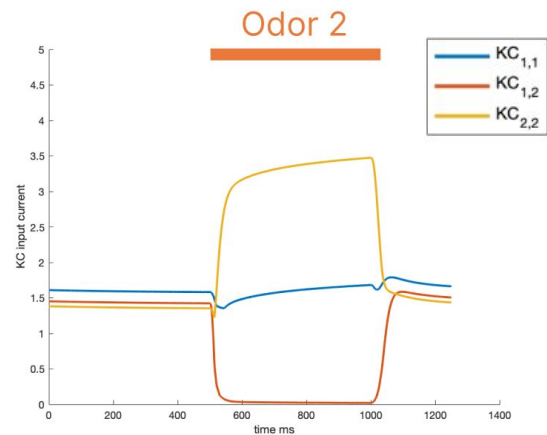
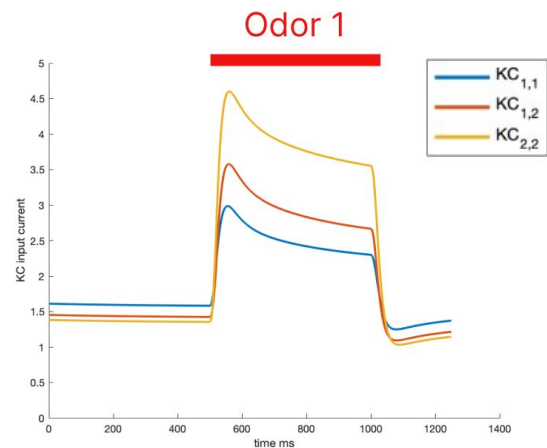
- At each time step, the input current to KC from PN is:

$$I_{i,j}(t) = A * w_{PN \rightarrow KC_{i,j}} * PN(t)$$

$w_{(PN \rightarrow KC_{i,j})}$ : Connectivity of KC  $i,j$

$PN$ : Firing rate of PN

$A$ : Scaling factor



# Response of KC

- Each KC is implemented as Izhikevich 2D LIF model

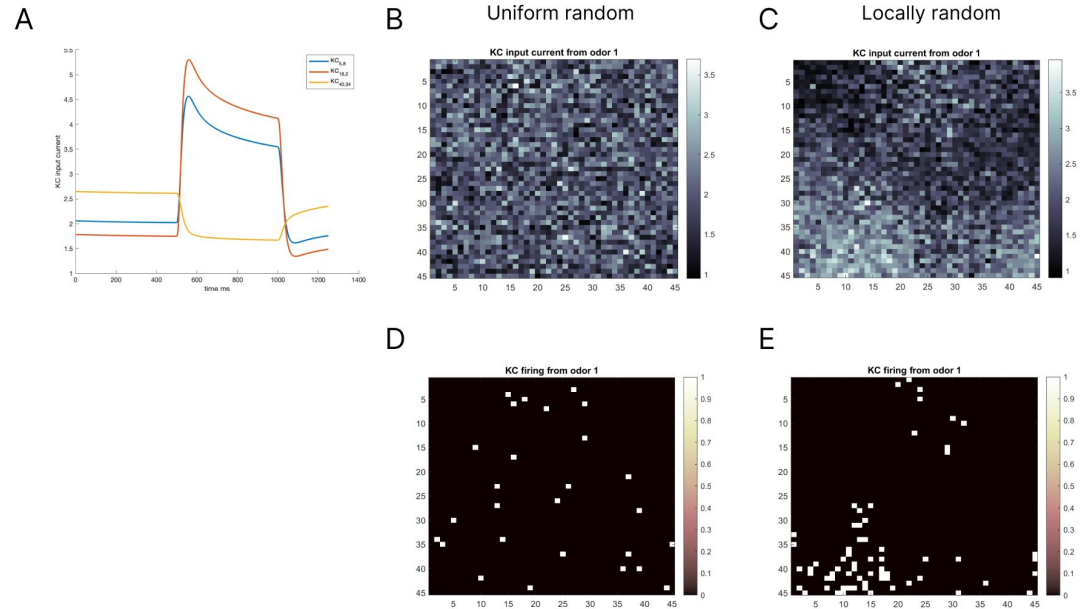
$$\frac{dV}{dt} = 0.04 V^2 + 5V + 140 - u + I$$

$$\frac{du}{dt} = a(bV - u)$$

Reset condition: If  $V \geq 30$ , then set  $V = c$  and  $u = u + d$

Parameter values:  $a = 0.02$ ,  $b = 0.2$ ,  $c = -65$ ,  $d = 8$

- For odor1, the input current to KC and the respective firing rates is visualized for a disconnected network
- It's compared between uniformly random and locally random connectivity between PN and KC

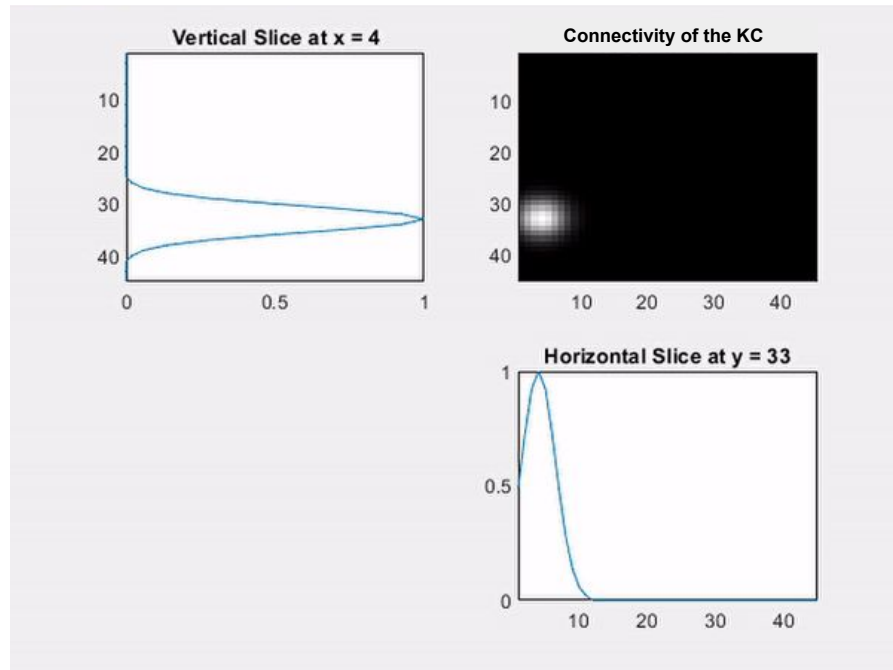


**Figure.** A) Input currents for odor 1 visualized for three sample KC  
 B, C) Input currents (max) visualized as a raster plot for all KC for uniform and local connectivity  
 D, E) The output firing rate of KC in a disconnected network

# KC Network - Connectivity

- The local forward/feedback inhibition of APL is modelled as a local lateral inhibition among Kenyon Cells
- The connection weight of a presynaptic-KC to a postsynaptic KC is modeled to decay with distance (as a gaussian function)

$$w_{syn}(r) = e^{-\frac{r^2}{2\sigma^2}}$$



Each frame shows the connection weight of a given KC with other KCs

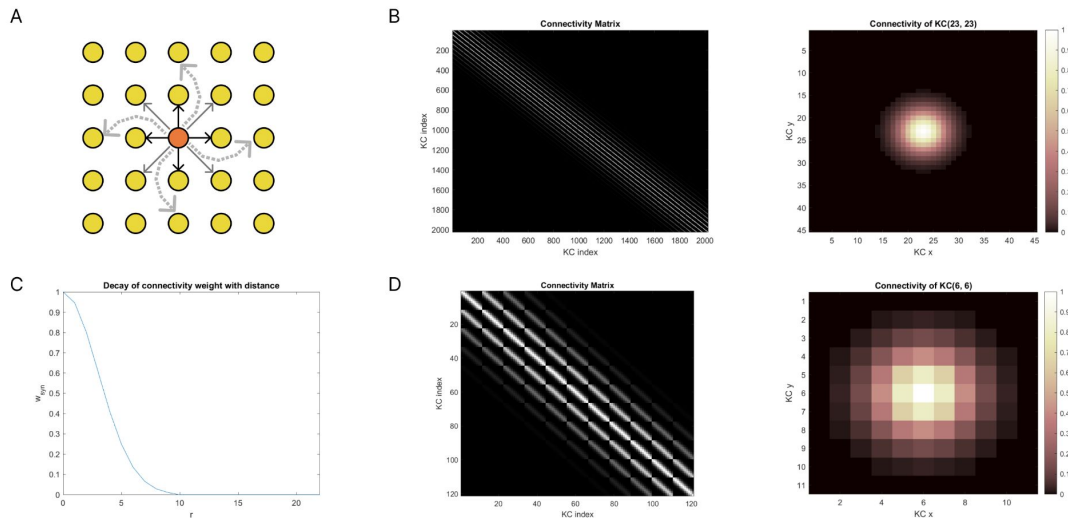
# KC Network - Connectivity

A) This figure illustrates how KC cells are connected in a 2D grid. The center cell (orange) is connected to all its neighboring cells but the strength decays with distance.

B) Adjacency matrix showing how the KC cells are connected ( $n=2025$  [45x45],  $\sigma = 3$ )

C) Plot showing the connectivity strength decaying with spatial distance.

D) Adjacency matrix of a smaller network for visualization purpose ( $n=121$  [11x11],  $\sigma = 1.5$ )



# KC Network - How connection params affect sparsity

These figures visualize how varying inhibition strength and range affects the sparsity of KC firing. Analysed for odor 1, unif random,  $A = 0.035$ ,  $\tau_{\text{syn}} = 50$ .

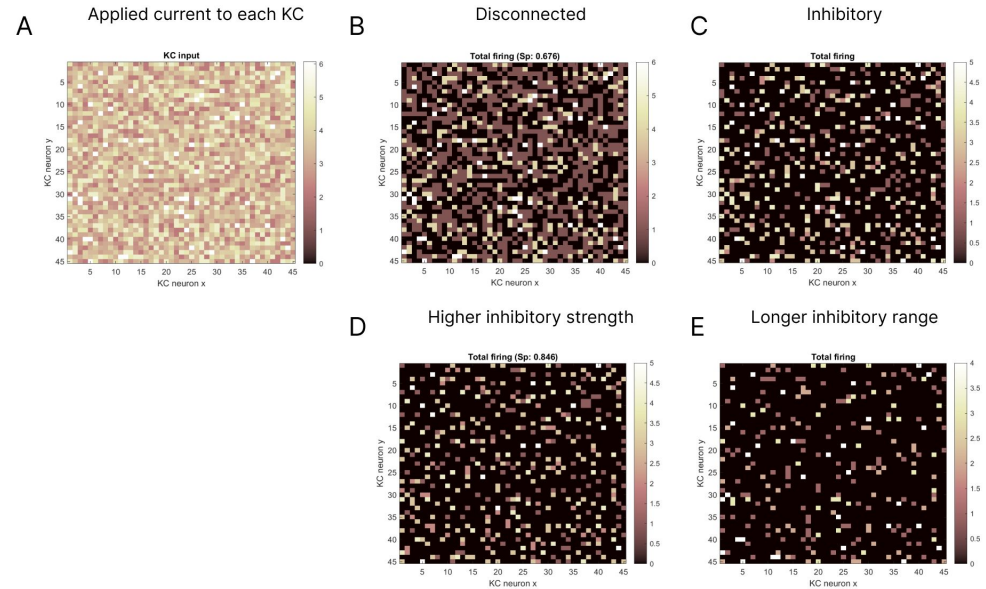
A) visualizes the maximum input current across the time for each of the KC cells.

B)  $g_{\text{syn}} = 0 \rightarrow$  sparseness: 0.68

C)  $g_{\text{syn}} = -2$ ,  $\sigma = 1 \rightarrow$  sparseness: 0.82

D)  $g_{\text{syn}} = -5$ ,  $\sigma = 1 \rightarrow$  sparseness: 0.856

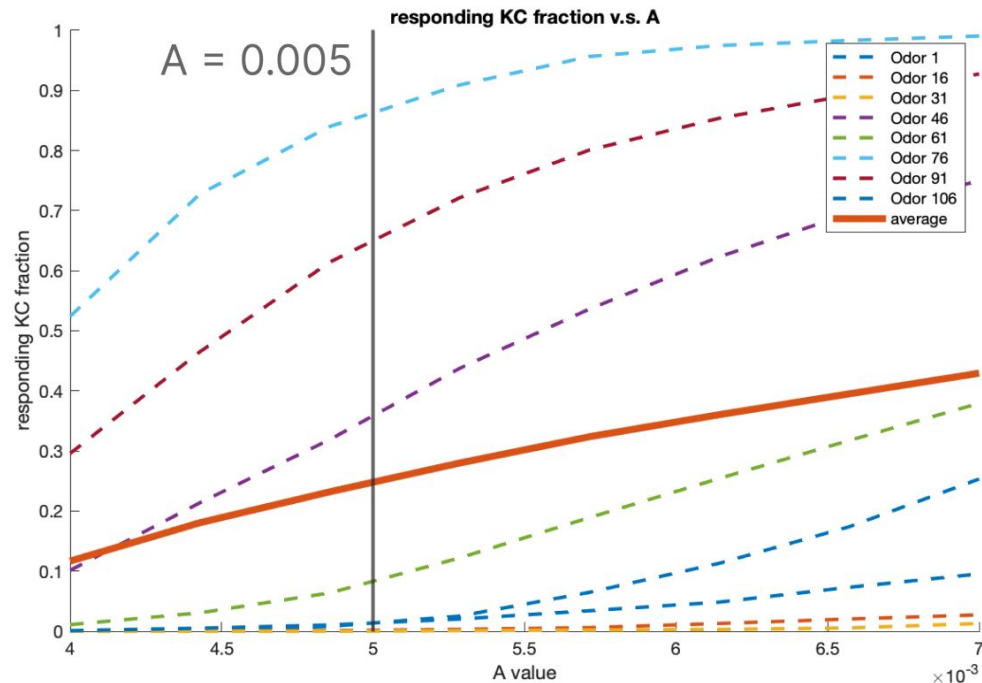
E)  $g_{\text{syn}} = -2$ ,  $\sigma = 3 \rightarrow$  sparseness: 0.91



**Figure.** These figures visualize how varying inhibition strength and range affects the sparsity of KC firing. Analysed for odor 1, full random,  $A = 0.035$ ,  $\tau_{\text{syn}} = 50$ . A) visualizes the maximum input current across the time for each of the KC cells. B)  $g_{\text{syn}} = 0$ , result: sparseness: 0.676 C)  $g_{\text{syn}} = -2$ ,  $\sigma = 1$ , result: sparseness: 0.822 D)  $g_{\text{syn}} = -5$ ,  $\sigma = 1$ , result: sparseness: 0.846 E)  $g_{\text{syn}} = -2$ ,  $\sigma = 3$ , result: sparseness: 0.912

# Tuning parameter: Input strength

- In Kennedy-MB model, a model without APL have ~25% KC responding to a odor on average
- We randomly select 8 odors and tuning  $A$  value to achieve this sparsity
- When  $A = 0.005$ , there are 25% KC responding on average





# Results

# Result 1: Local inhibition sparsen odor responses

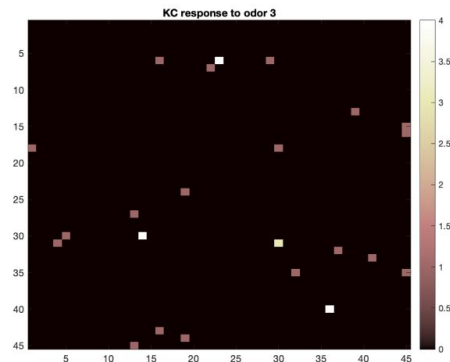
The lifetime sparseness is measured by:

$$S_{KC} = \left(1 - \left(\frac{(\sum_{j=1}^N r_j / N)^2}{\sum_{j=1}^N r_j^2 / N}\right)\right) / (1 - 1/N)$$

- **N**: KC number
- $r_j$ :  $KC_j$  spikes counts

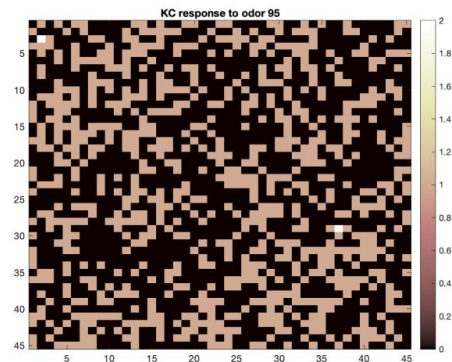
If all KC respond to the odor homogeneously,  $S_{KC} = 0$

## Sparse Responses



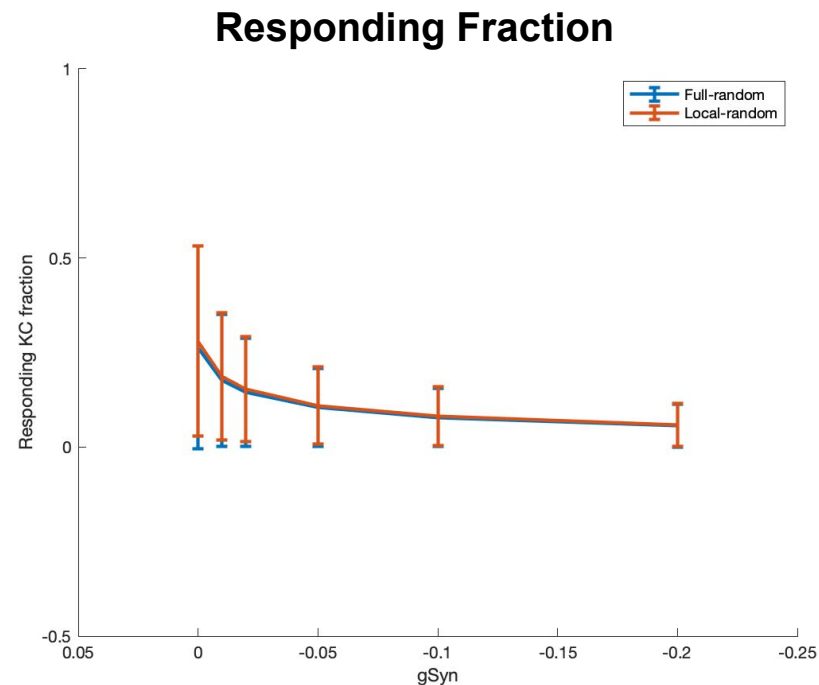
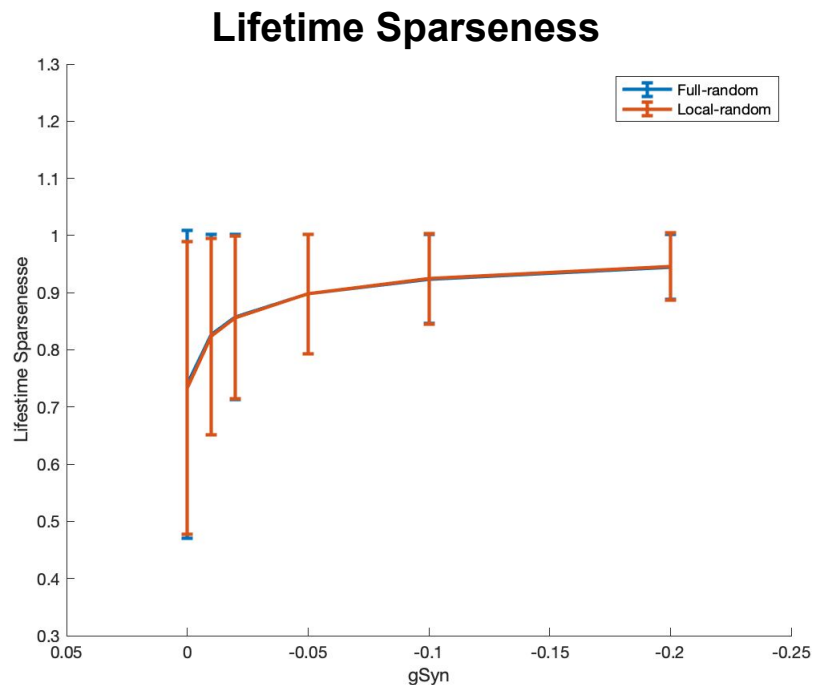
Responding KC: 1.14%  
Lifetime Sparseness: 0.99

## Dense Responses



Responding KC: 38.77%  
Lifetime Sparseness: 0.61

# Result 1: Local inhibition sparsen odor responses

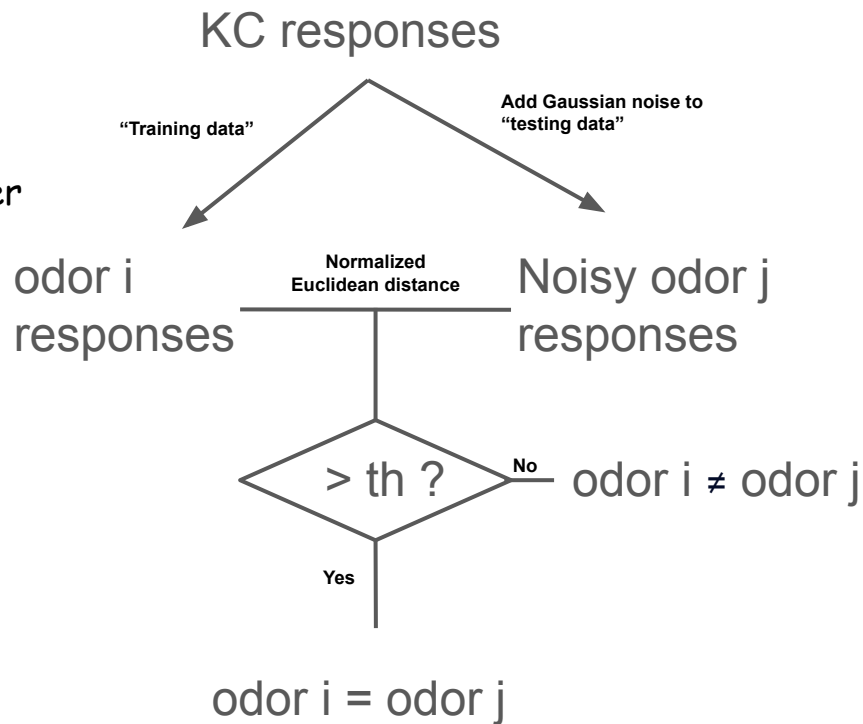
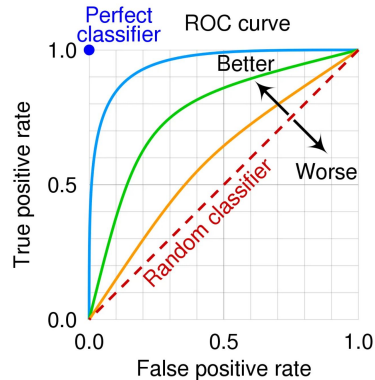


gSyn: Inhibition strength

A = 0.005,  $\sigma = 10$ , average of 110 odors

# Result 1: Local inhibition increases odor separability

- Simplified linear classifier
- ROC curve

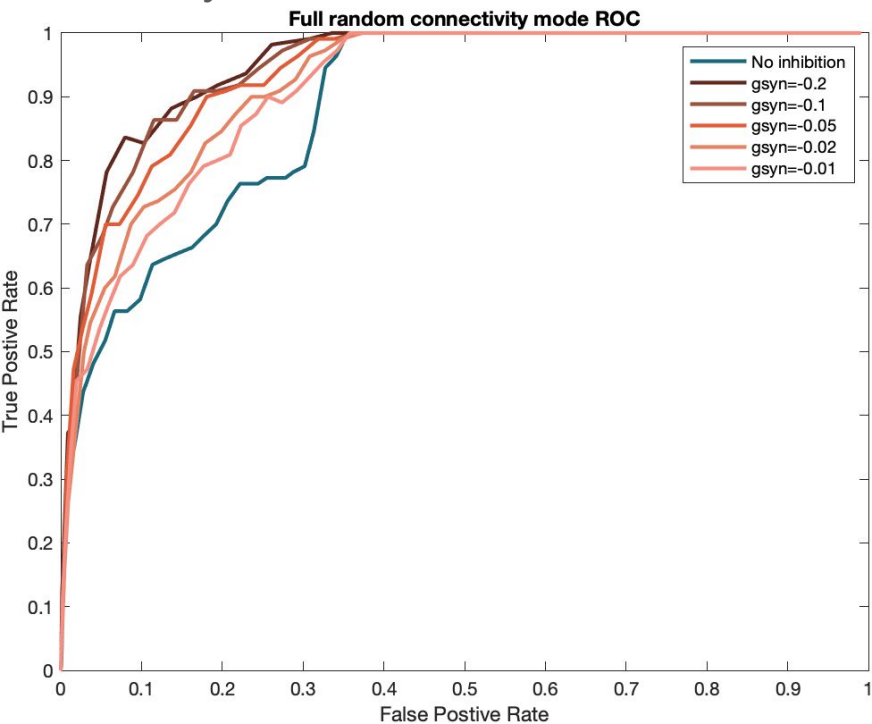


ROC figure:

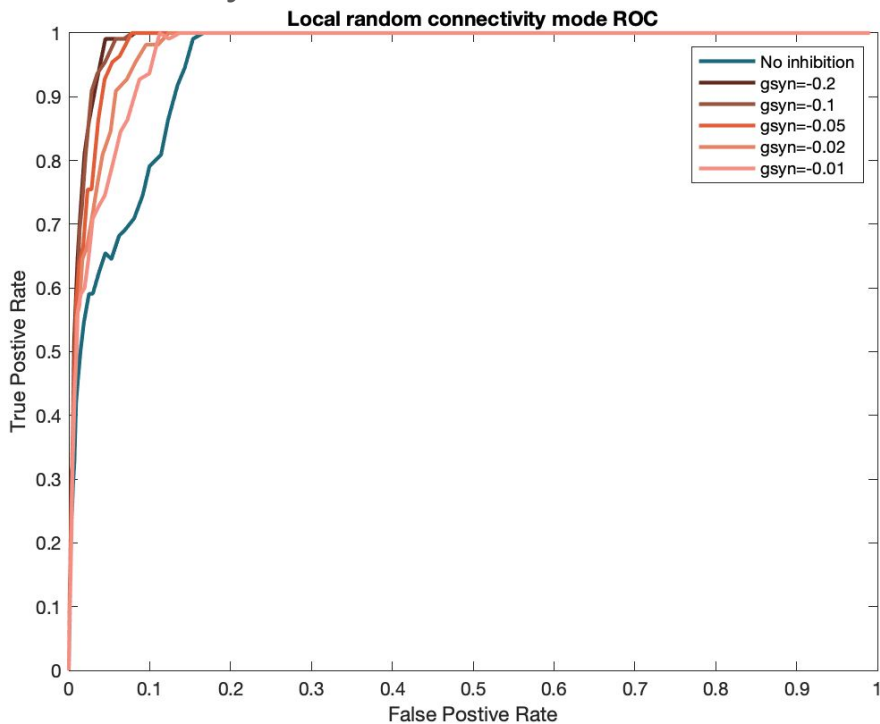
<https://medium.com/@ilyurek/roc-curve-and-auc-evaluating-model-performance-c2178008b02>

# Result 1: Local inhibition increases odor separability

## Fully random PN-KC connection

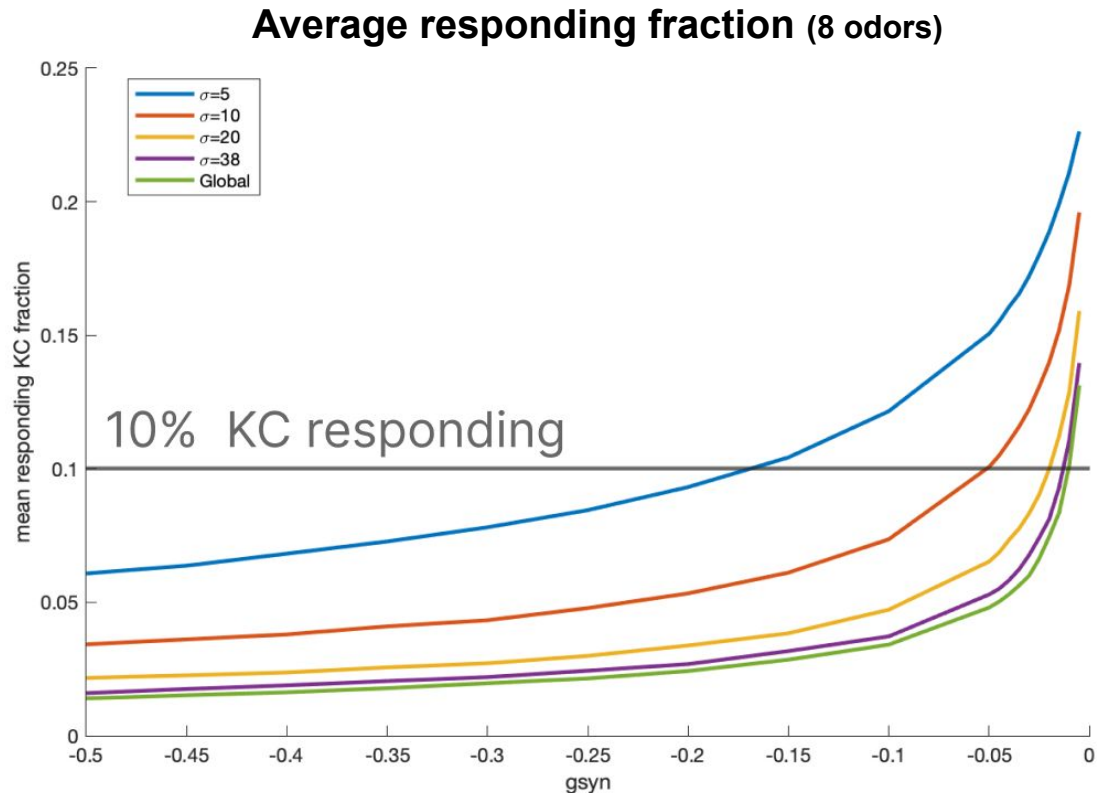


## Locally random PN-KC connection



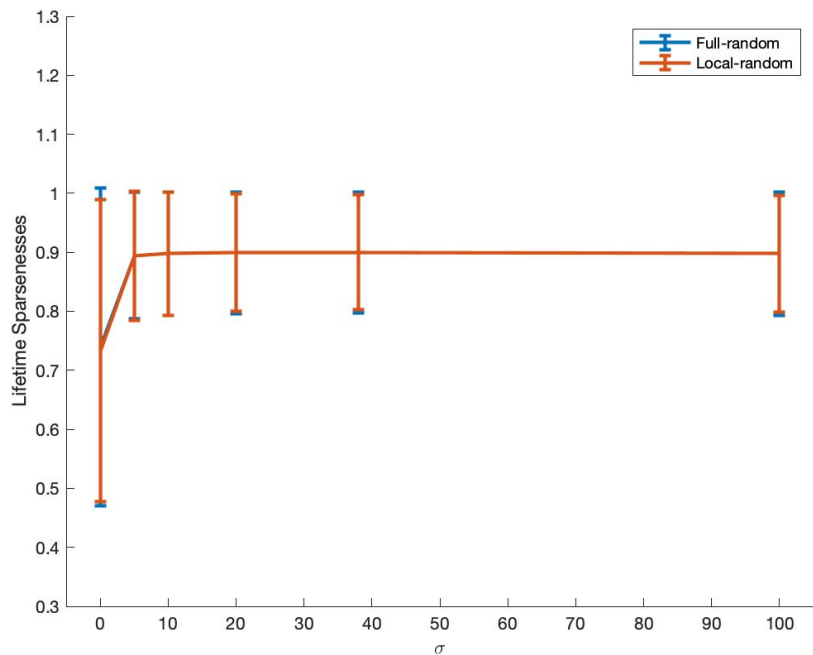
## Result 2: Exploring the effect of inhibition range

- To change inhibition range( $\sigma$ ), we control the sparsity of odor responses consistent. In Kennedy-MB model, APL will suppress KC responding fraction to 10%
- We randomly select 8 odors and tuning  $g_{\text{Syn}}$  value to achieve this sparsity for each model with different inhibition range
- For the same sparsity, model with smaller inhibition range requires larger  $g_{\text{Syn}}$  value



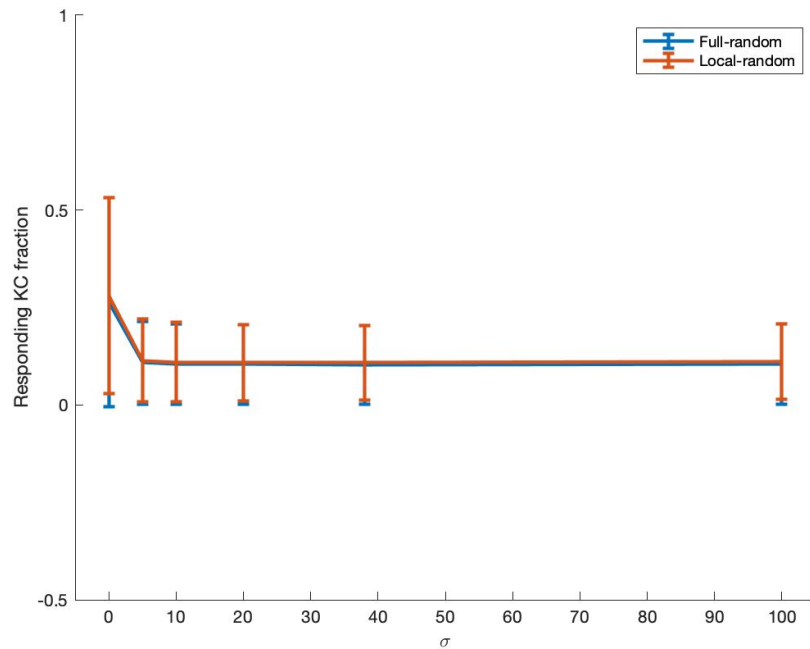
# Result 2: Exploring the effect of inhibition range

## Lifetime Sparseness



$\sigma$ : Inhibition range

## Responding Fraction

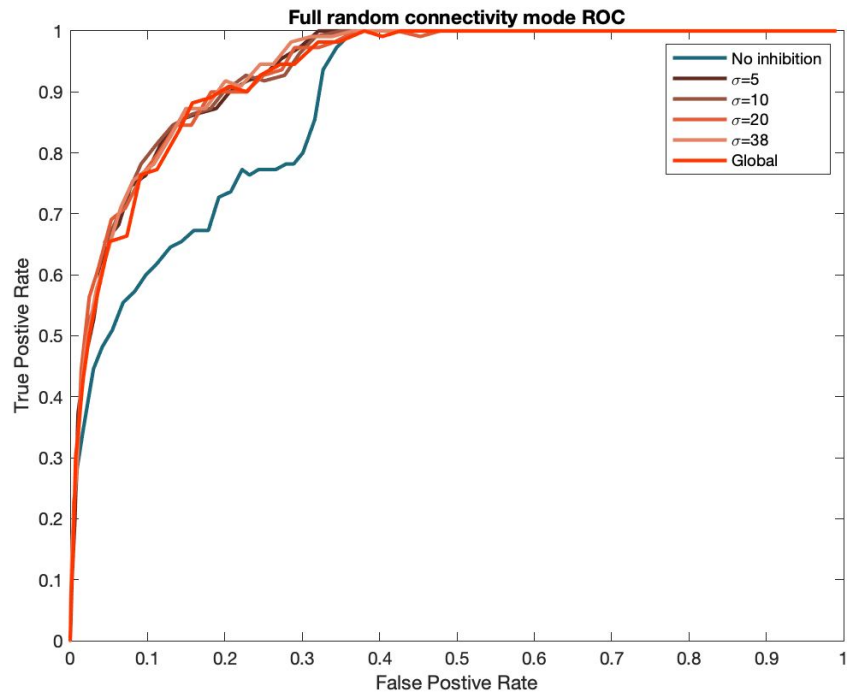


A = 0.005, average of 110 odors

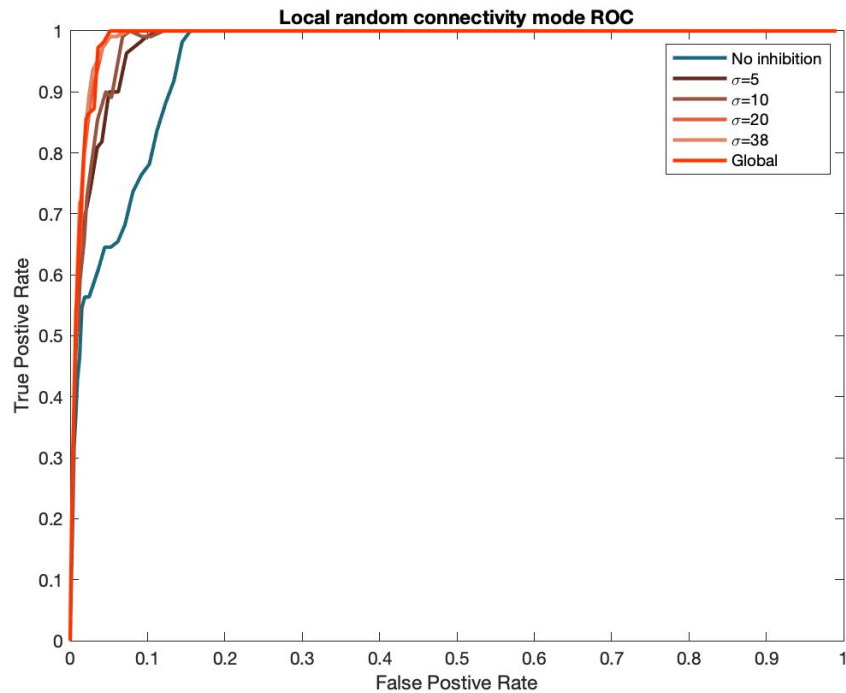


# Result 2: Exploring the effect of inhibition range

Fully random PN-KC connection



Locally random PN-KC connection



# Conclusion

- Local inhibition, a more realistic assumption based on recent findings, is able to perform on par with global inhibition models in regulating the sparsity of KC outputs
- Stronger inhibition will increase the sparsity, and make the odor representations more separable, hence the animal will be able to recognise the source odor with higher accuracy
- Controlling the sparsity and changing inhibition range do not alter prediction performance for full random PN-KC connectivity
- Local-random PN-KC connectivity improves the model performance compared to uniform/full random connectivity

**Through simulations, we have shown that a more physiologically realistic model is able to better predict the odors, and thereby explain the evolutionary advantage of its existence**

Thank you!



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