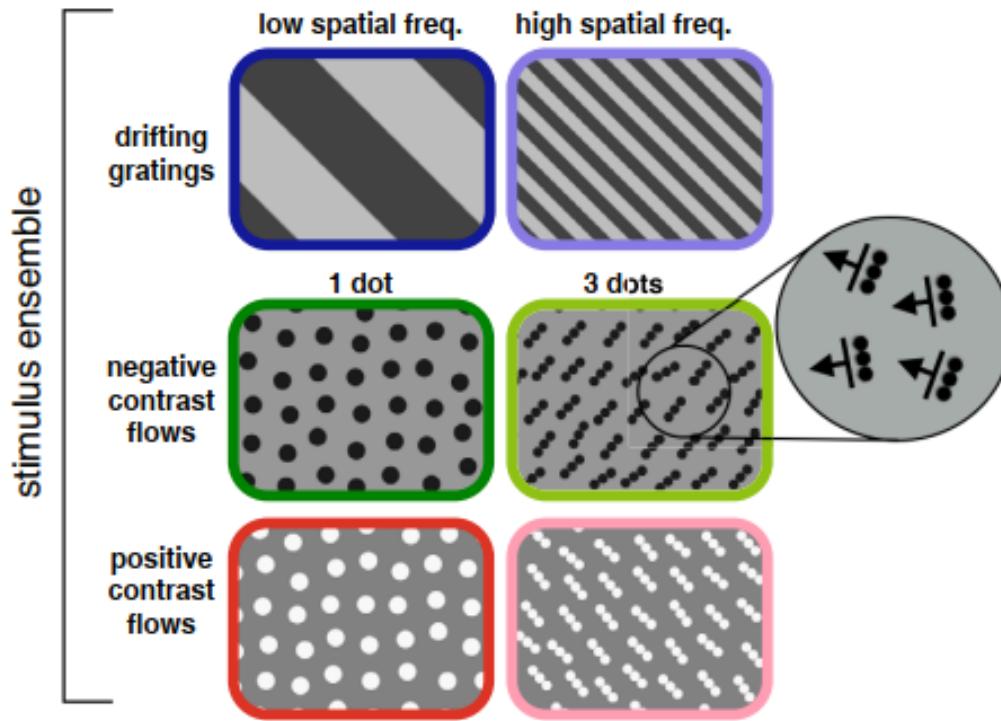


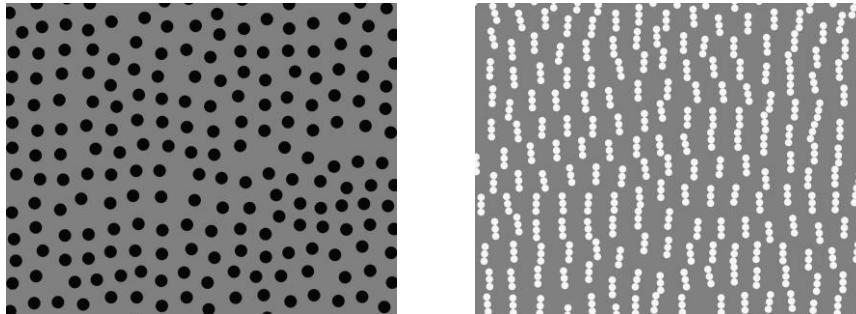
# Embedding Analysis of Neuron Responses under Various Stimuli in Vision Systems

Huimiao Chen

Feb 14, 2025



Luciano et al., 2024

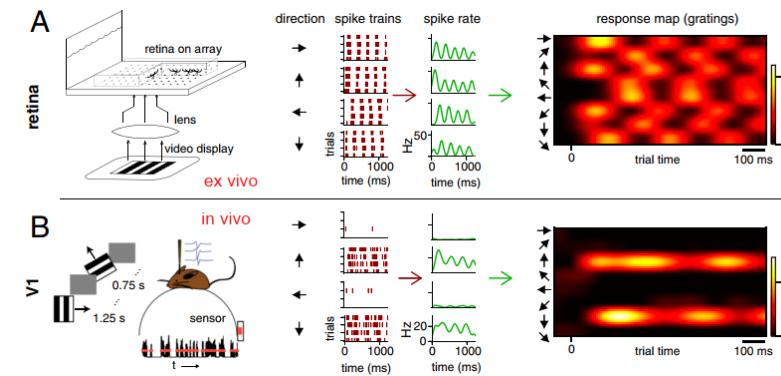


# Stimuli and Data

# dir: 0, 45, 90, 135, 180, 225, 270

Low Freq Gratings  
High Freq Gratings  
Neg 1-dot Flows  
Neg 3-dot Flows  
Pos 1-dot Flows  
Pos 3-dot Flows

In total,  $6 * 8 = 48$  stimuli



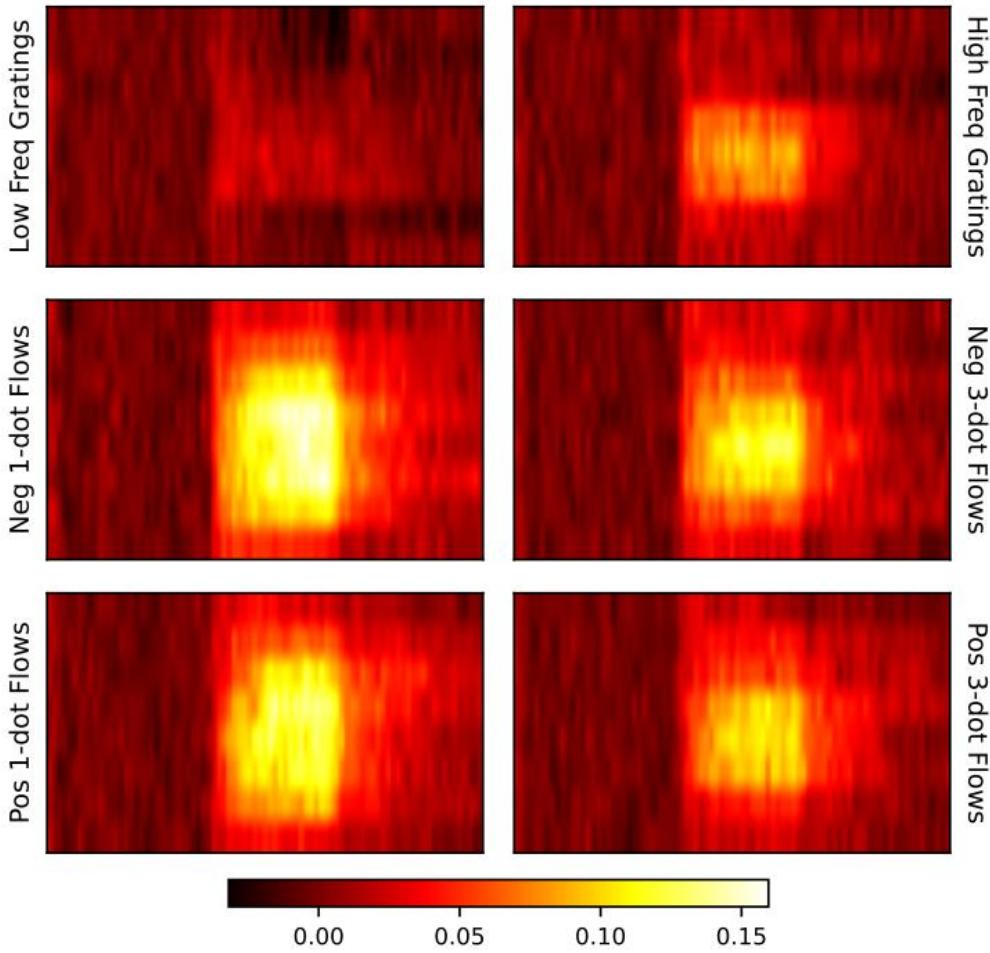
Public dataset

Cells in **dLGN** from **Multiple FOVs** (225 neurons)

Cells in **SC** from **Multiple FOVs** (1000+ boutons)

Data collected by Yue Fei

# Example Response Map of a Neuron



*85 frames is 2s off + 1.5s on + 2s off*

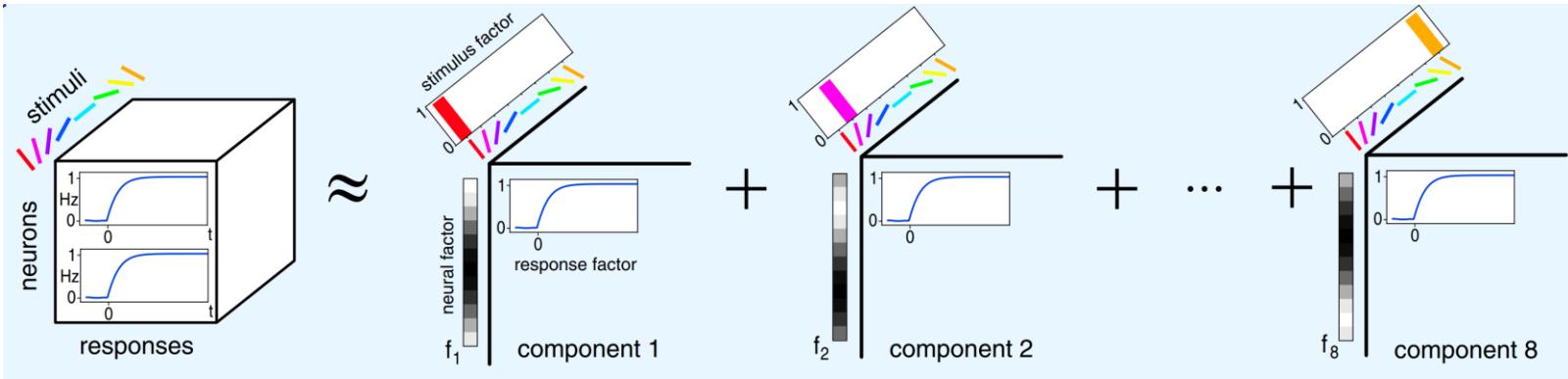
*1-31 frames are off,  
32-54 frames are on, and  
55-85 frames are off*

*For our data, we remove the 1-31 frames to do analysis.*

# **Retina**

# Manifold Embedding

## Tensor Decomposition



Data here is a 3-D tensor (traces):  
Neurons, Stimuli, Responses.

**Neural factors:** How each neuron responds to different stimuli.

**Stimulus factors:** The components of the stimuli that drive the neural responses.

**Response factors:** The temporal dynamics of the neural responses.

L. Dyballa et al 2024

- **Neuron factor matrix**  $N \in \mathbb{R}^{I \times R}$ ,
- **Stimulus factor matrix**  $S \in \mathbb{R}^{J \times R}$ ,
- **Response factor matrix**  $R \in \mathbb{R}^{K \times R}$ ,

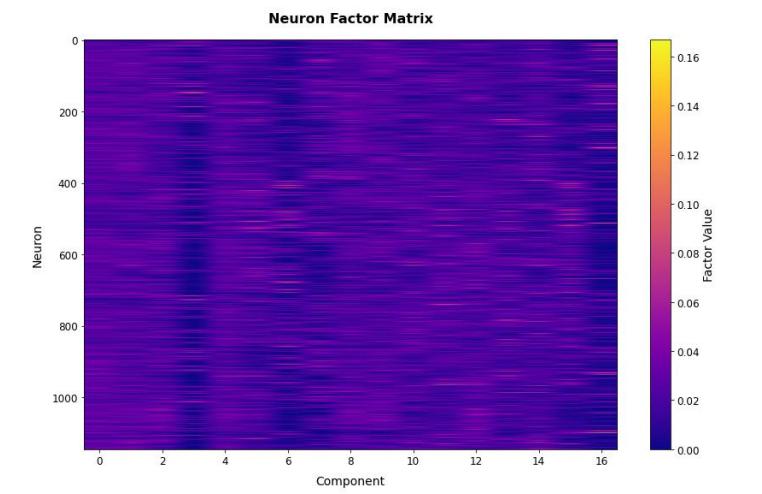
where  $R$  is the rank of the decomposition (i.e., the number of hidden components), and the number of columns  $R$  represents the number of latent factors.

$$\min_{N,S,R} \frac{1}{2} \|T - \sum_{r=1}^R N(:, r) \circ S(:, r) \circ R(:, r)\|_F^2$$

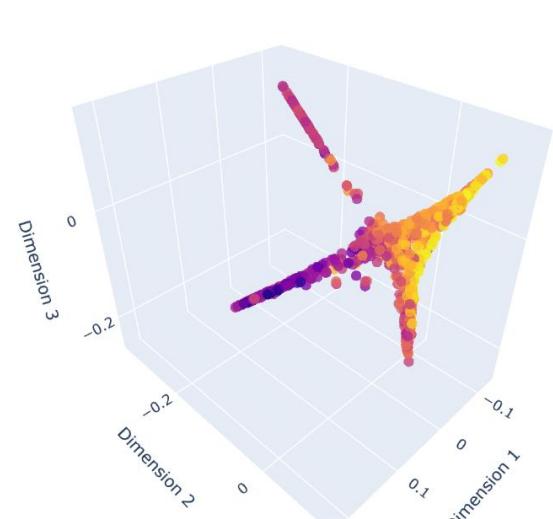
### Iterative Optimization:

Since the problem is non-convex and involves multiple variables, an **iterative optimization** approach is used. A common method is **Alternating Least Squares (ALS)** or **gradient-based methods**. Here's the general idea:

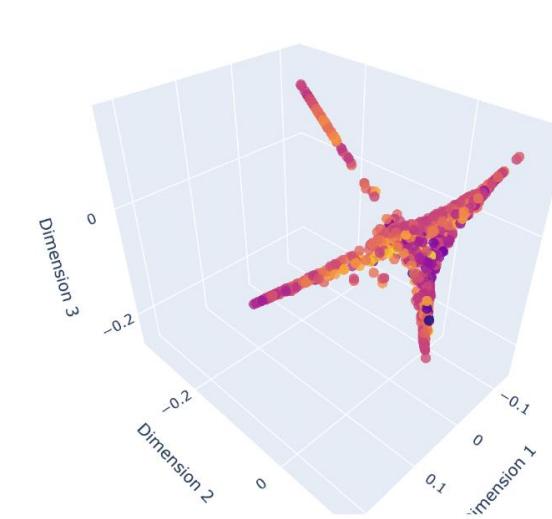
- **Initialization:** Start by initializing the factor matrices  $N$ ,  $S$ , and  $R$  randomly with non-negative values.
- **Iterative Updates:**
  - Fix  $S$  and  $R$ , then solve for  $N$  by minimizing the objective with respect to  $N$ .
  - Fix  $N$  and  $R$ , then solve for  $S$ .
  - Fix  $N$  and  $S$ , then solve for  $R$ .



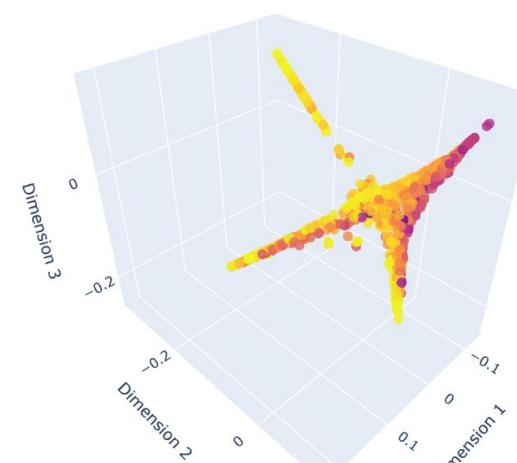
Neuron Diffusion Map (Flow Polarity Index)



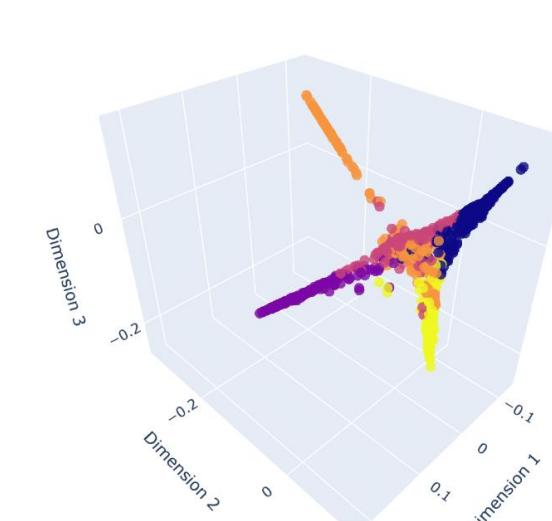
Neuron Diffusion Map (Grating Selectivity Index)



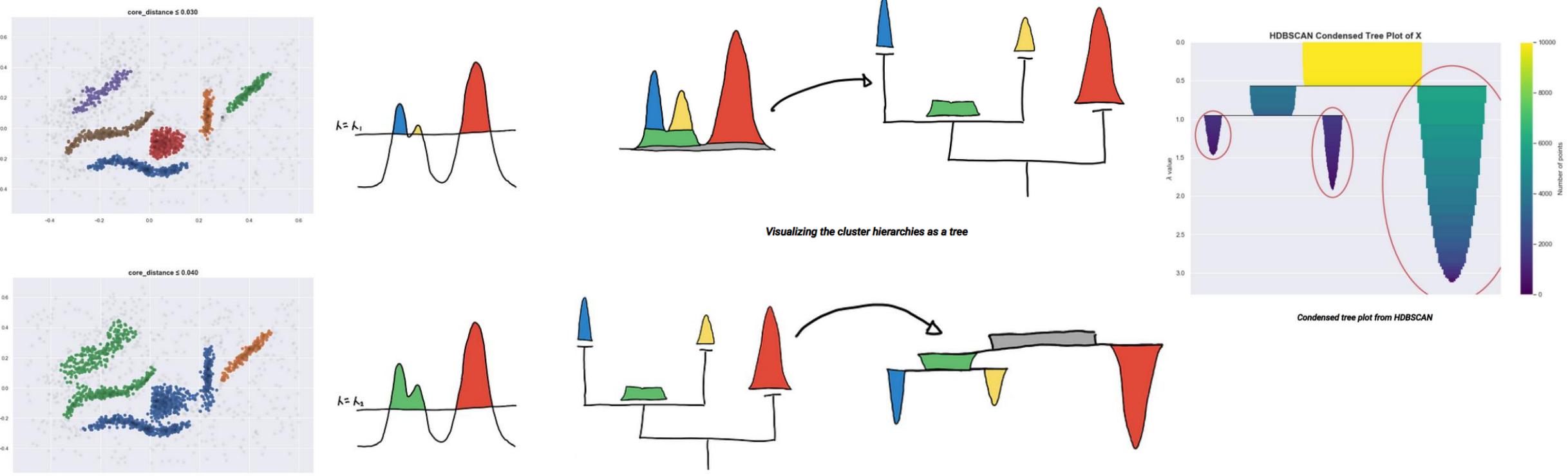
Neuron Diffusion Map (Stimulus Entropy Index)



Neuron Diffusion Map (HDBSCAN Cluster Index)



# HDBSCAN (Hierarchical Density-Based Spatial Clustering of Applications with Noise)



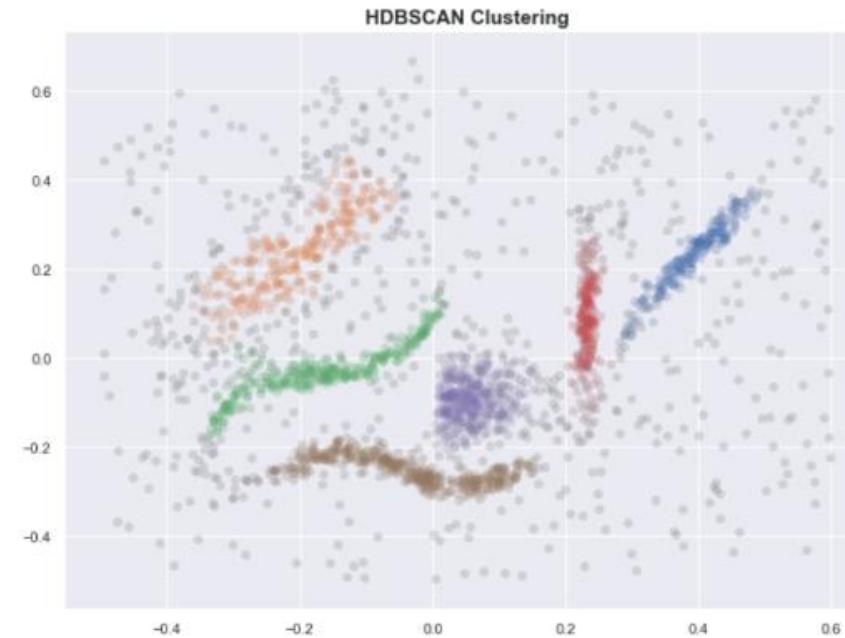
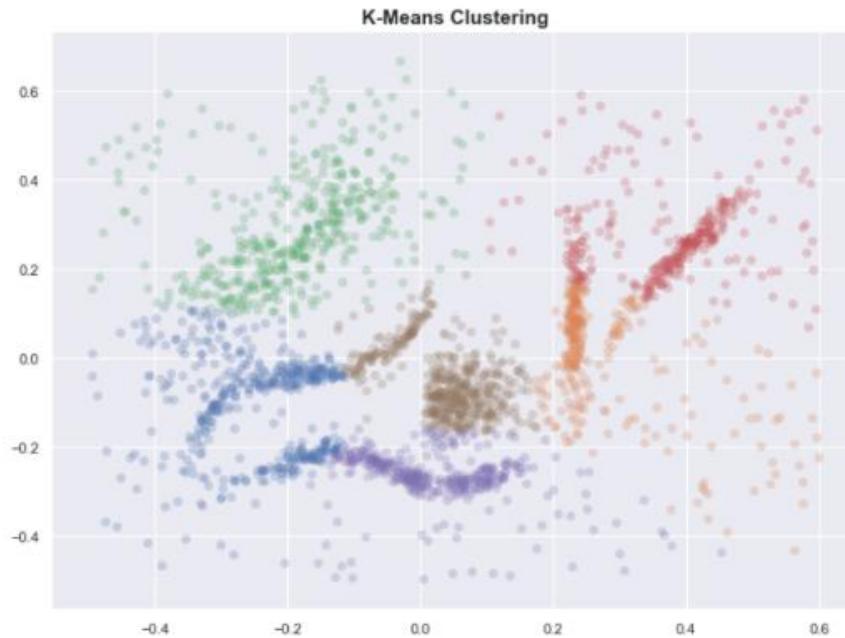
***Visualizing the tree top-down***

$$\lambda = \frac{1}{\text{core distance}}$$

<https://pberba.github.io/stats/2020/01/17/hdbscan/>

- **A larger  $\lambda$  value (Low Core Distance):**  
higher density, meaning the point belongs to a more tightly clustered region.
- **A smaller  $\lambda$  value (High Core Distance):**  
lower density, meaning the point is in a sparser region and may be separated earlier.

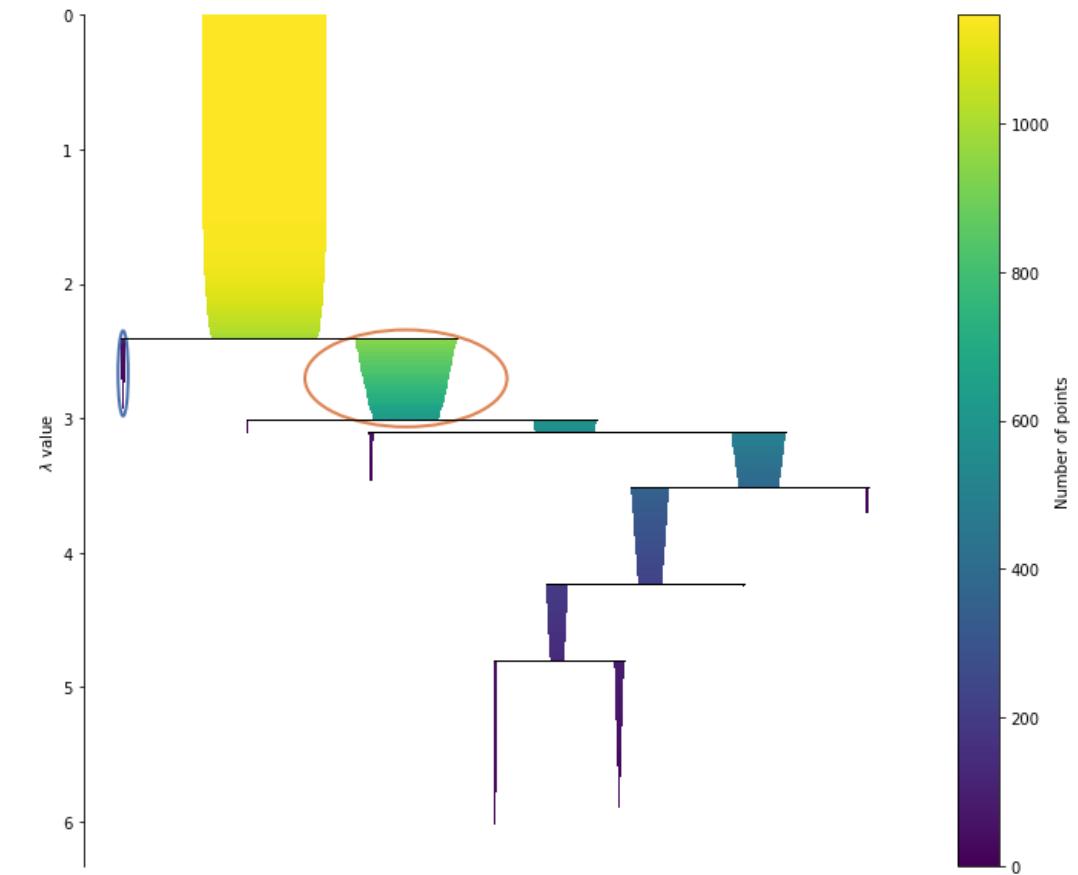
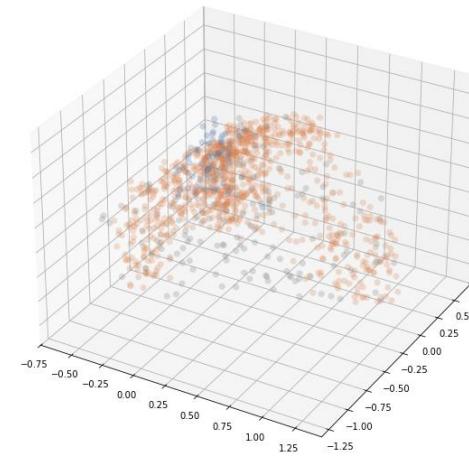
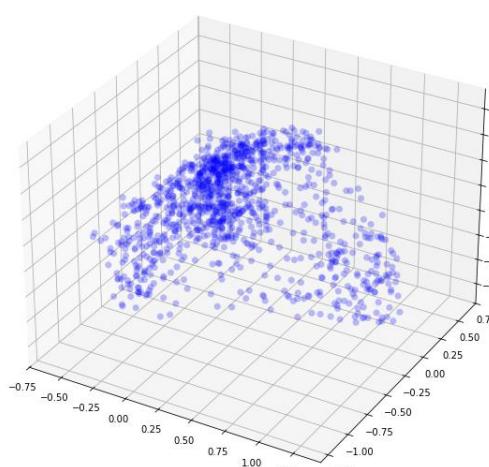
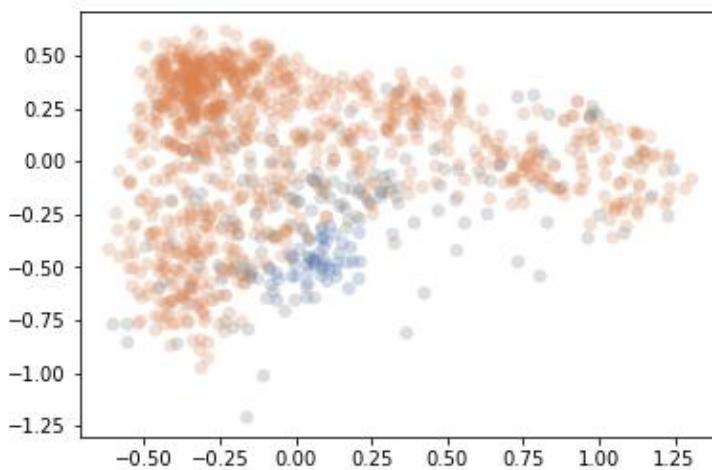
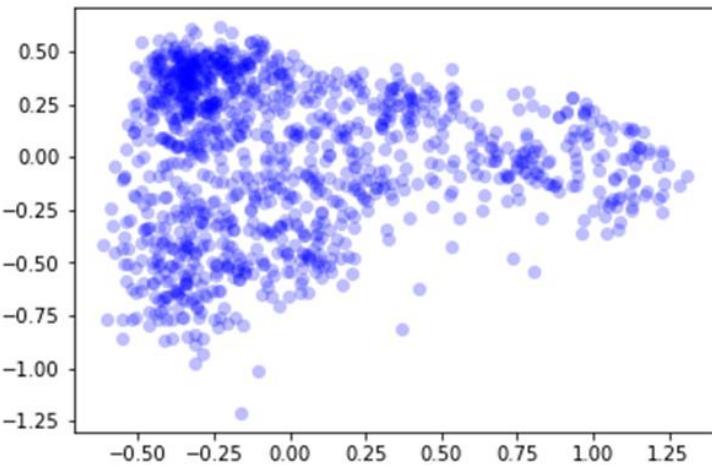
# K-means vs HDBSCAN



- “round” or spherical
- equally sized
- equally dense
- most dense in the center of the sphere
- not contaminated by noise/outliers

**More flexible shape  
Can have outliers (noise)**

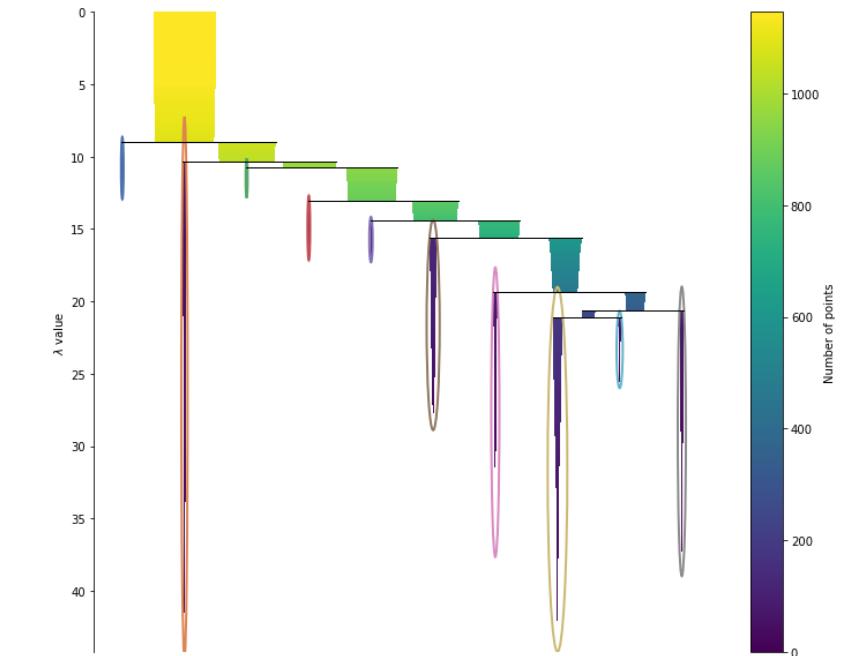
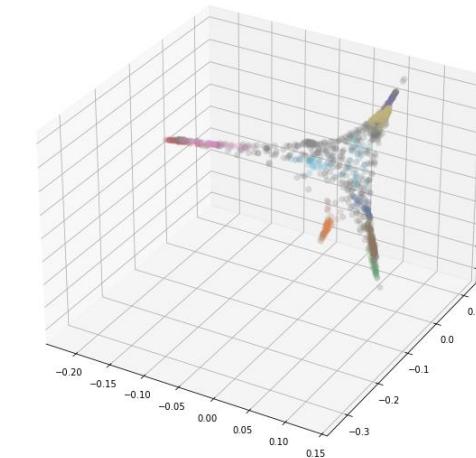
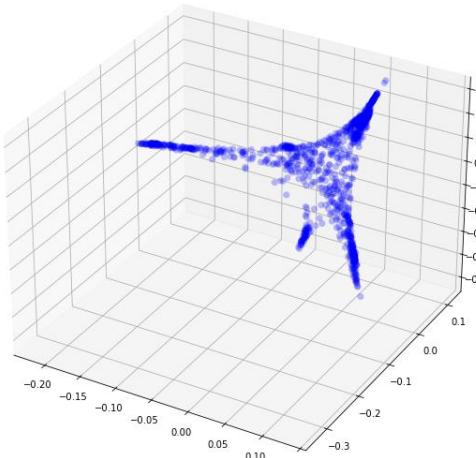
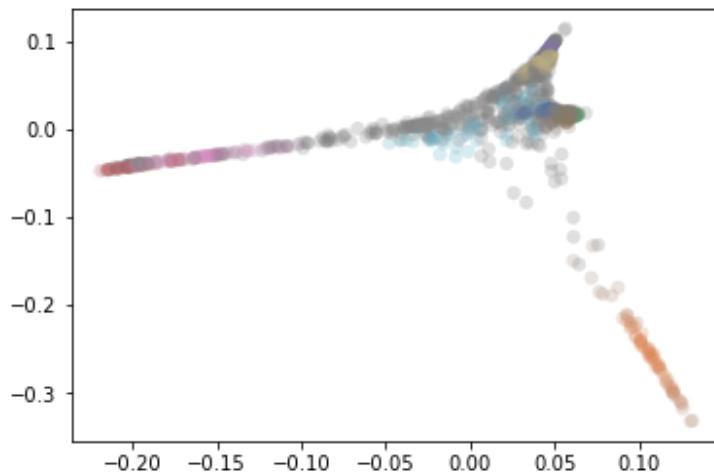
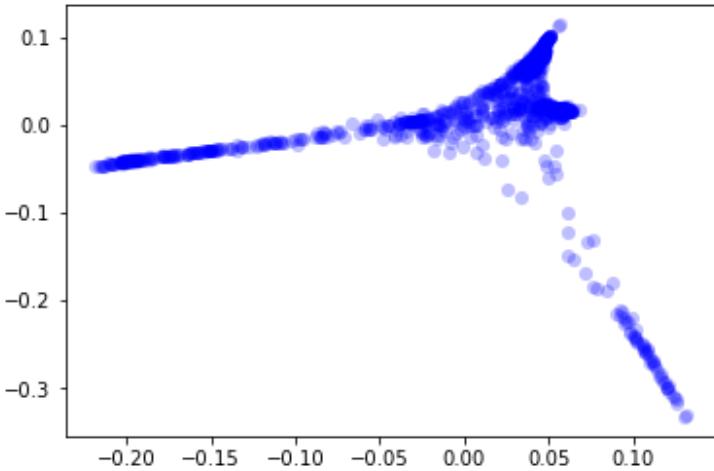
## Before diffusion map



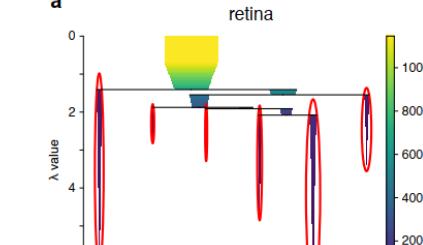
$$\lambda = \frac{1}{\text{core distance}}$$

- **A larger  $\lambda$  value (Low Core Distance):**  
higher density, meaning the point belongs to a more tightly clustered region.
- **A smaller  $\lambda$  value (High Core Distance):**  
lower density, meaning the point is in a sparser region and may be separated earlier.

## After diffusion map



a

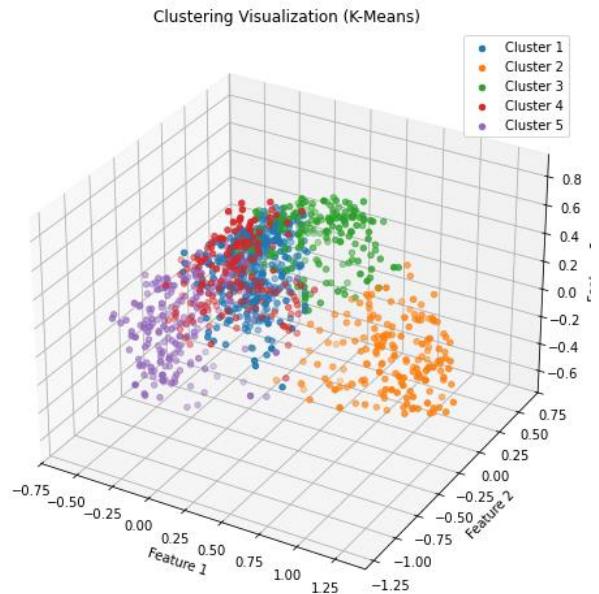


Compare to fig from Luciano et al., 2024

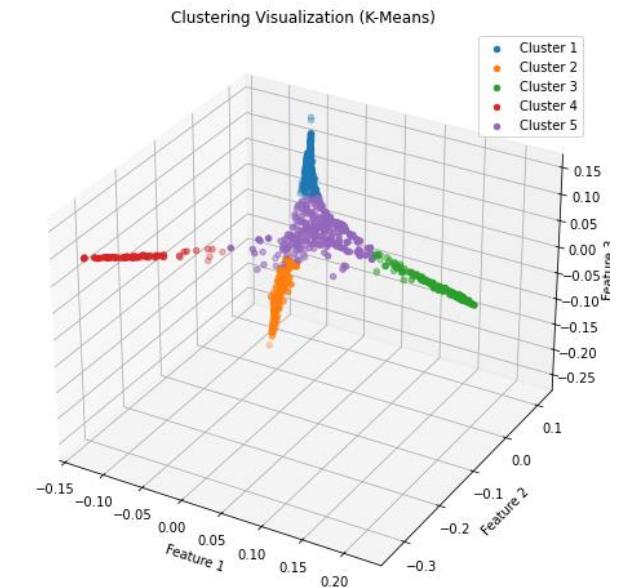
$$\lambda = \frac{1}{\text{core distance}}$$

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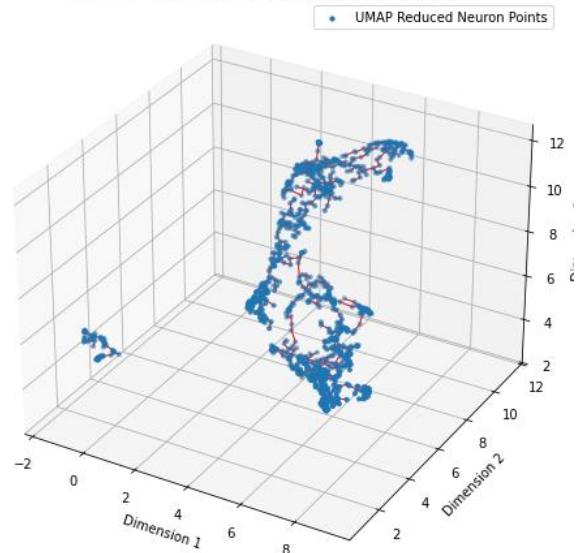
## Before diffusion map



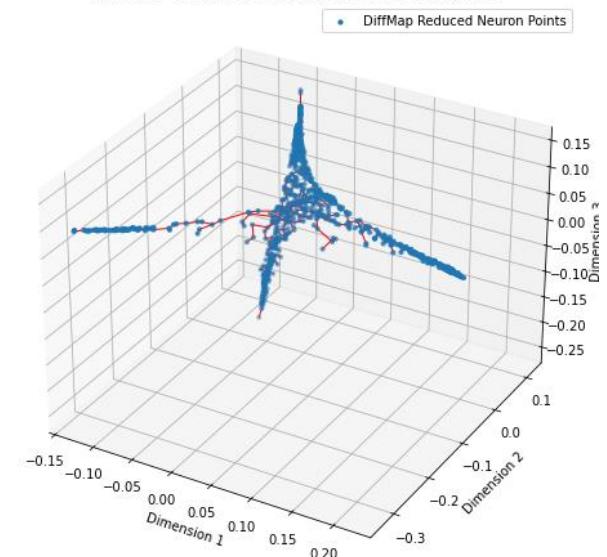
## After diffusion map



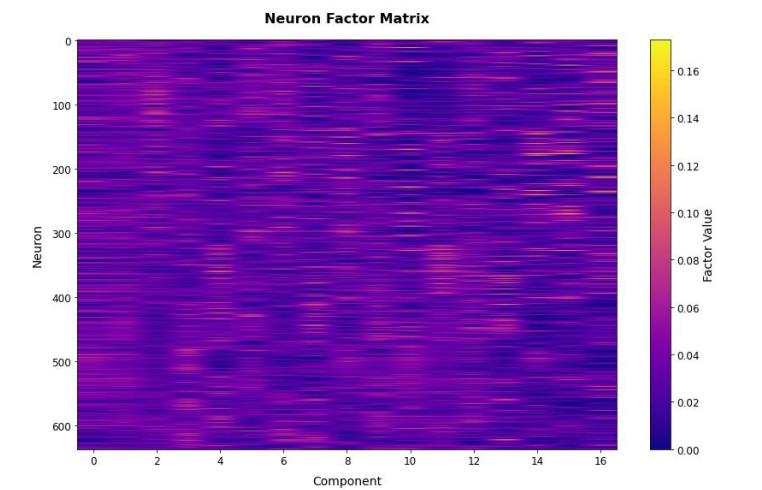
Trajectory Visualization with minimum spanning tree



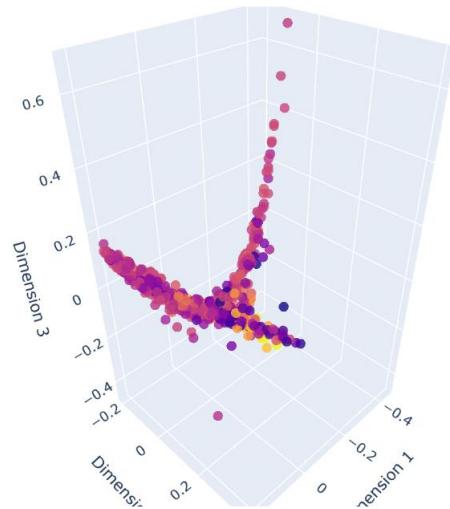
Trajectory Visualization with minimum spanning tree



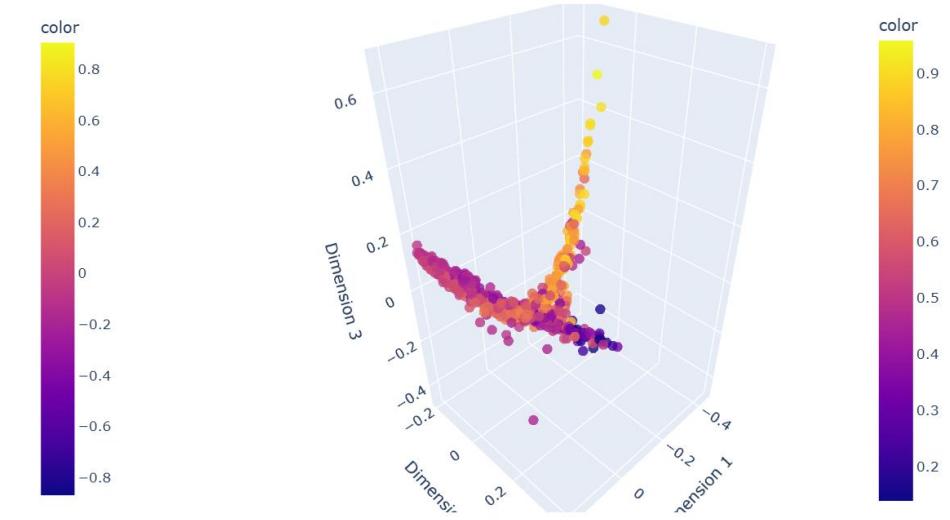
**V1**



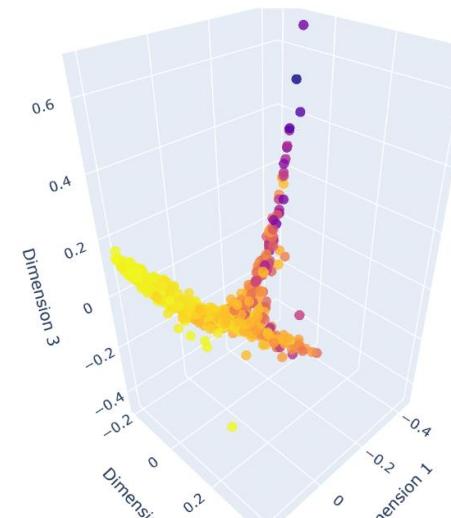
Neuron Diffusion Map (Flow Polarity Index)



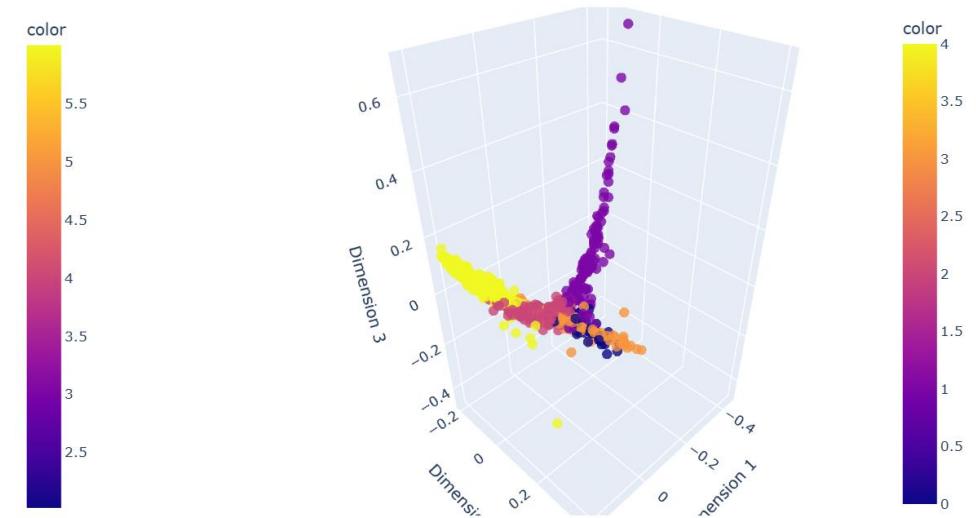
Neuron Diffusion Map (Grating Selectivity Index)



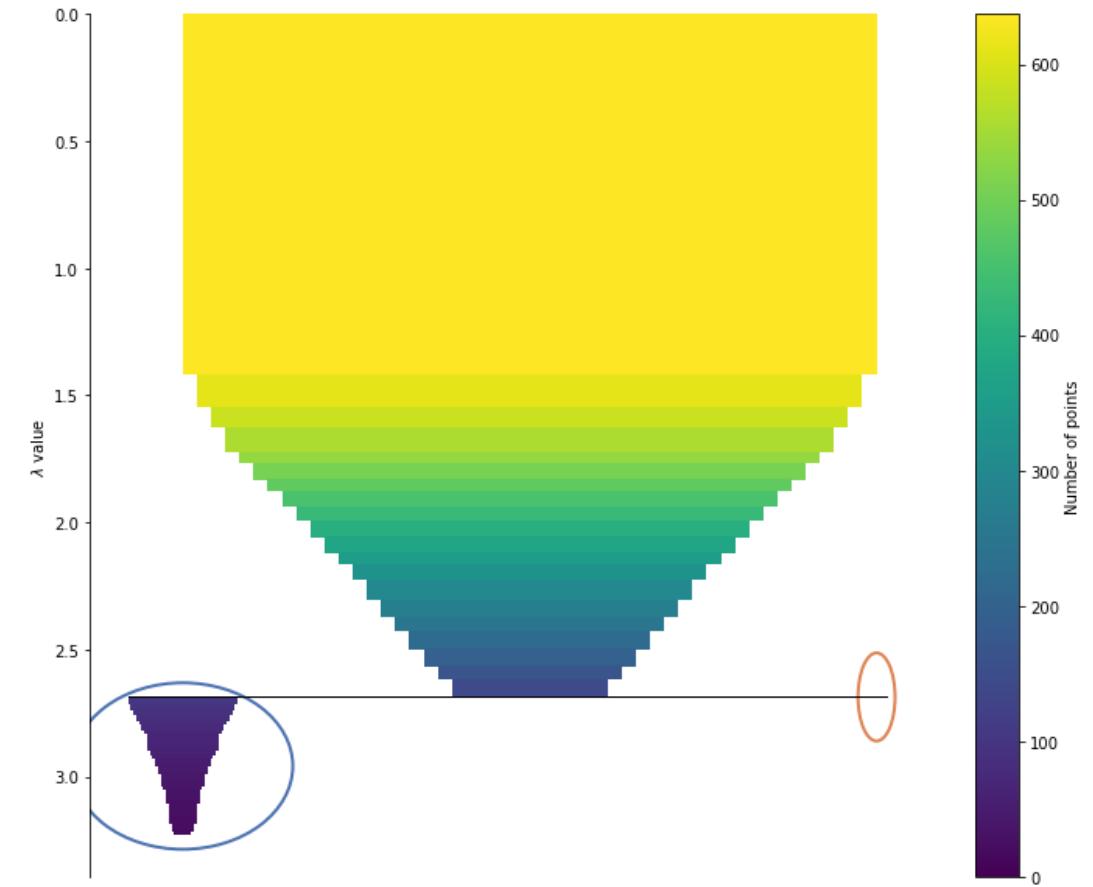
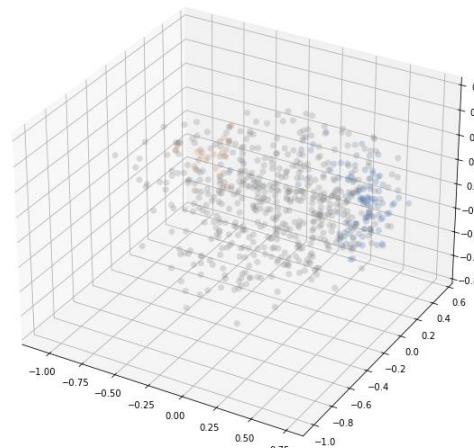
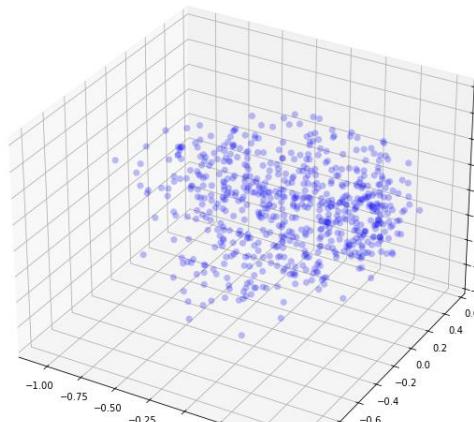
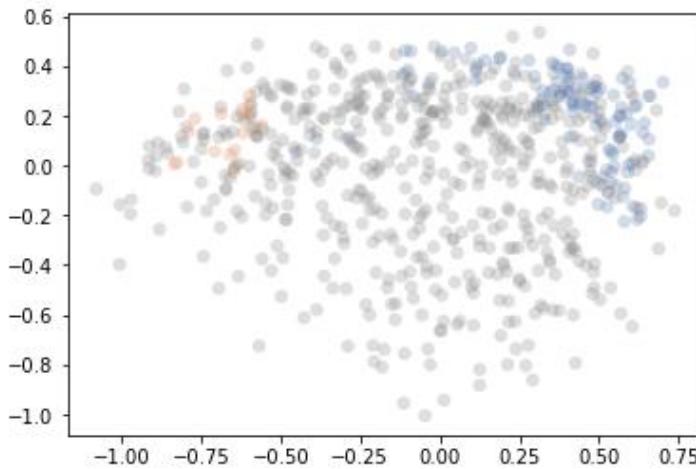
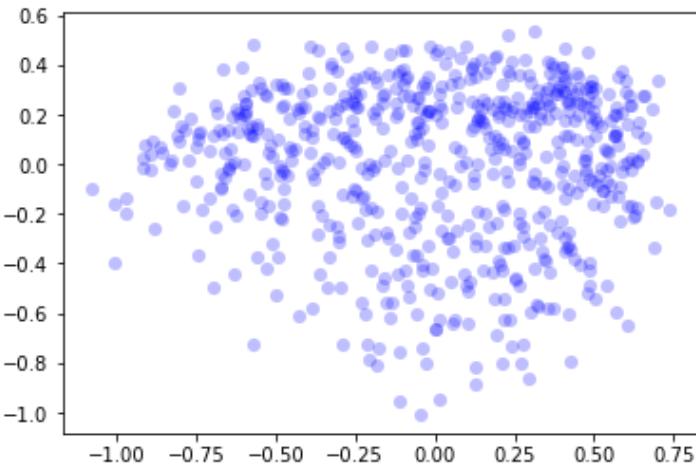
Neuron Diffusion Map (Stimulus Entropy Index)



Neuron Diffusion Map (HDBSCAN Cluster Index)



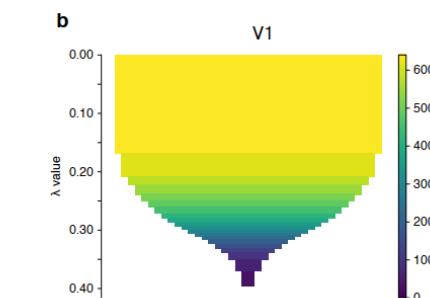
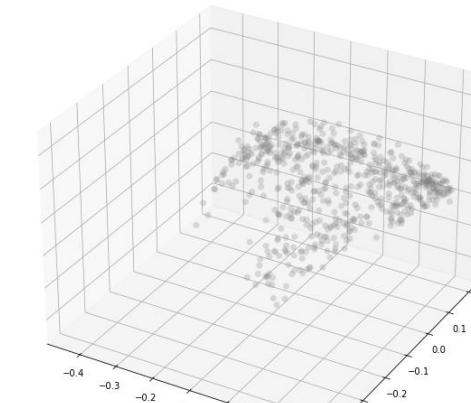
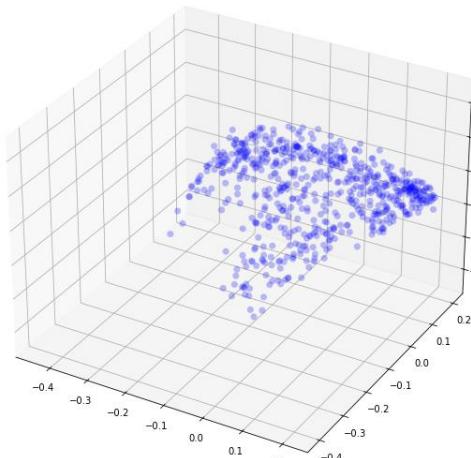
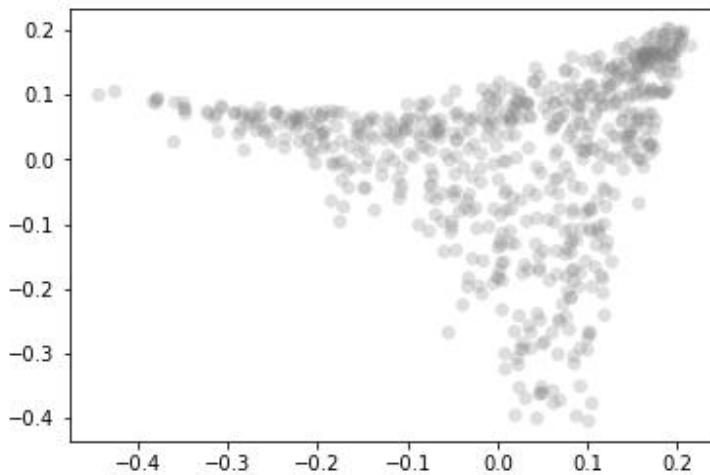
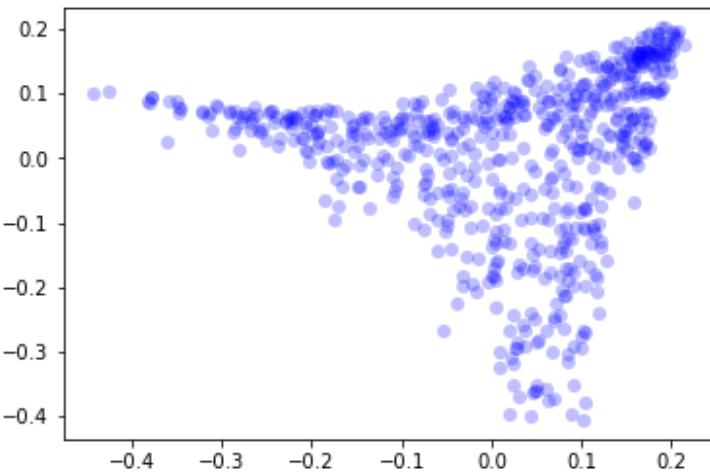
## Before diffusion map



$$\lambda = \frac{1}{\text{core distance}}$$

- **A larger  $\lambda$  value (Low Core Distance):**  
higher density, meaning the point belongs to a more tightly clustered region.
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lower density, meaning the point is in a sparser region and may be separated earlier.

## After diffusion map

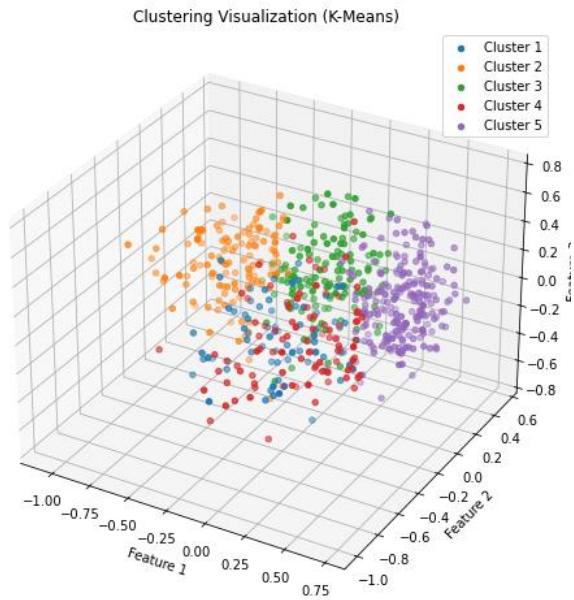


Compare to fig from Luciano et al., 2024

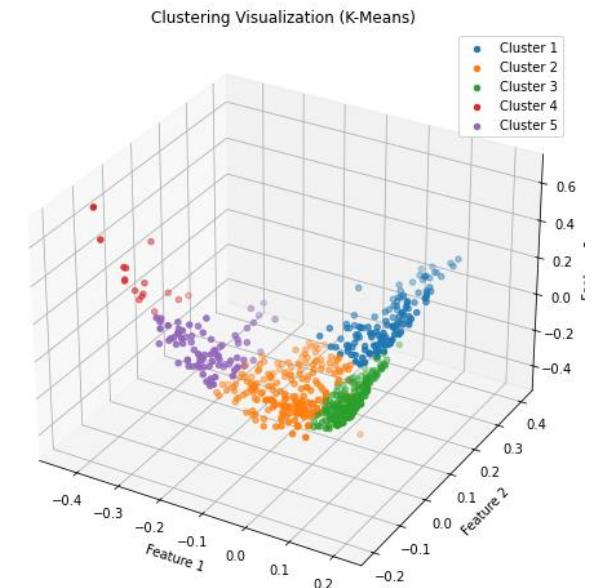
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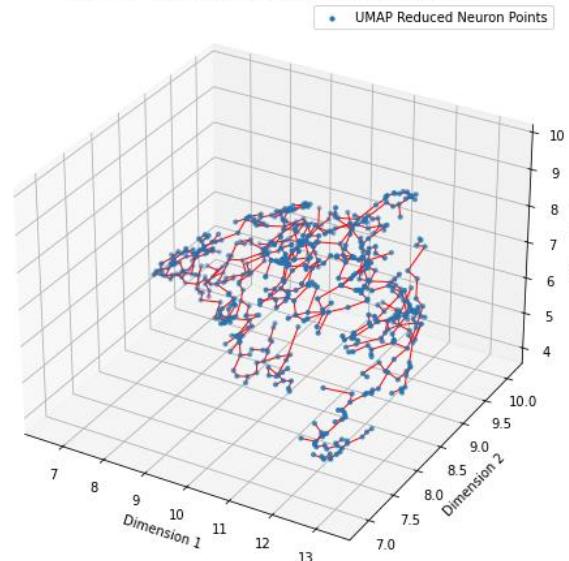
## Before diffusion map



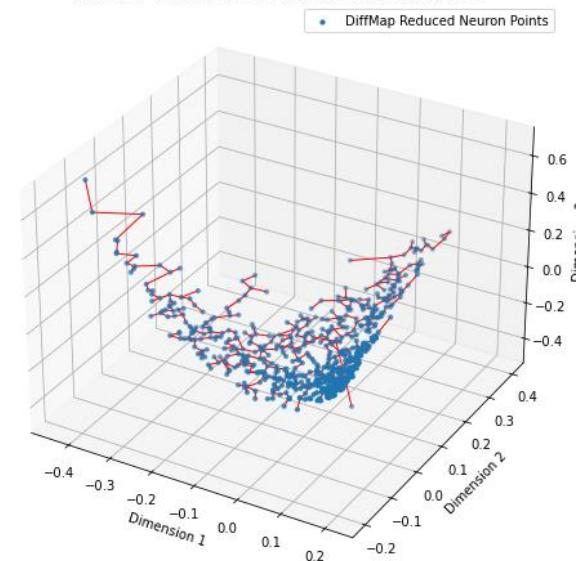
## After diffusion map



Trajectory Visualization with minimum spanning tree

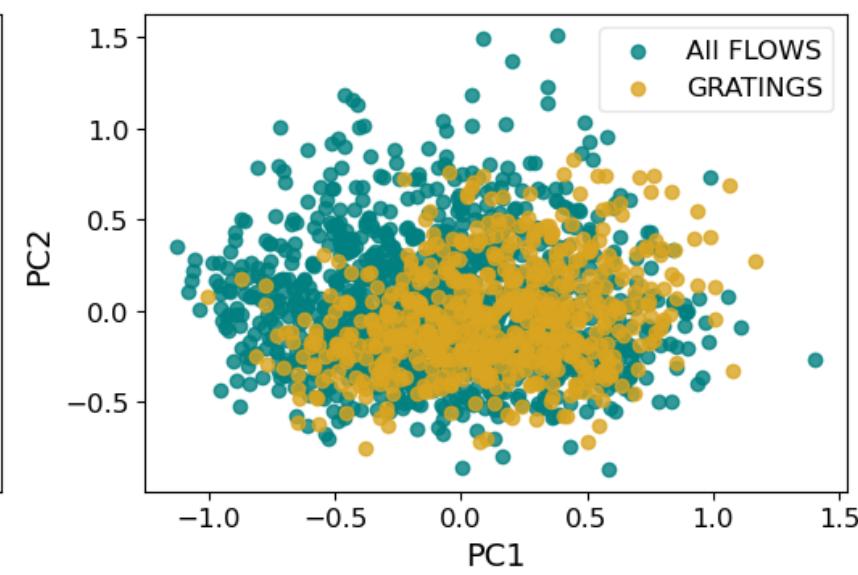
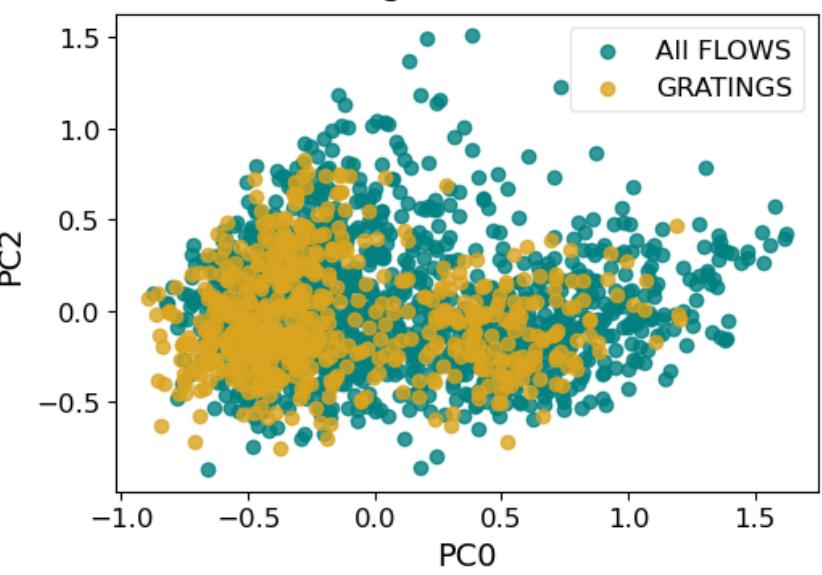
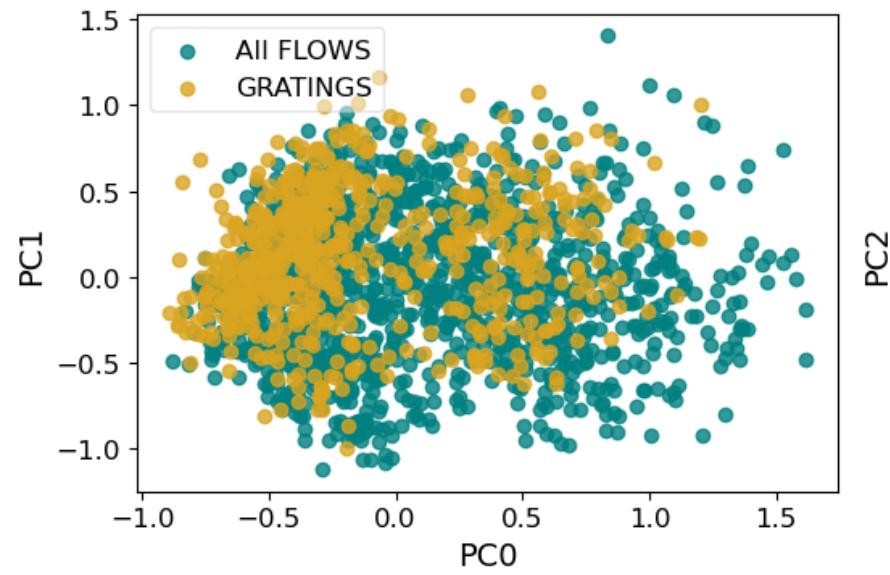


Trajectory Visualization with minimum spanning tree

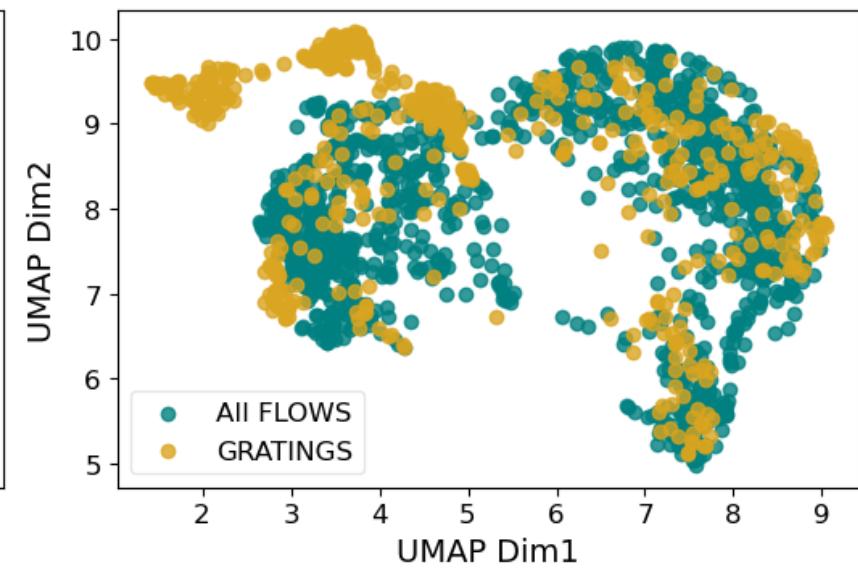
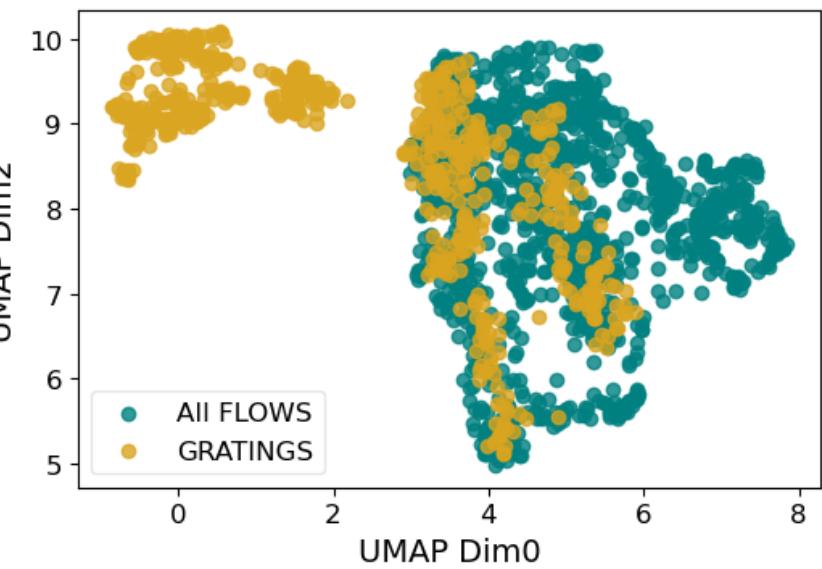
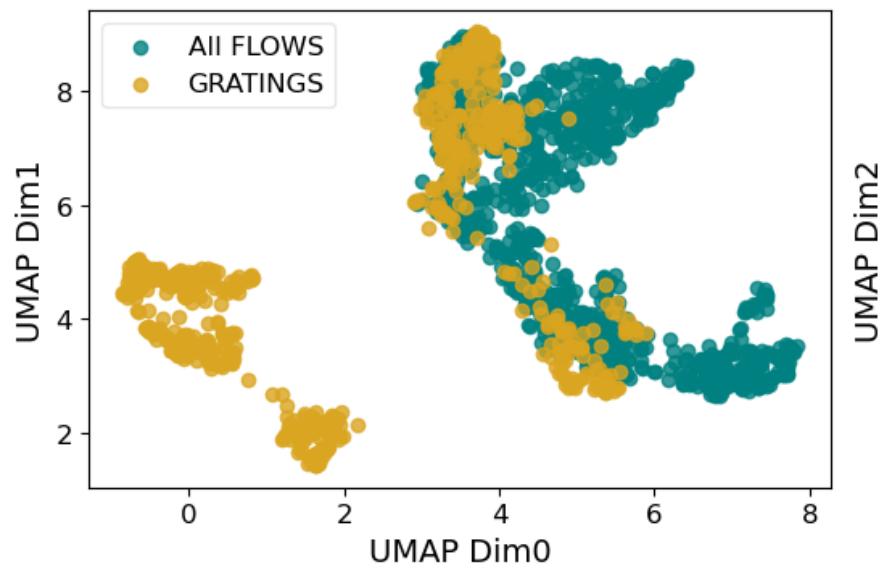


**dLGN**

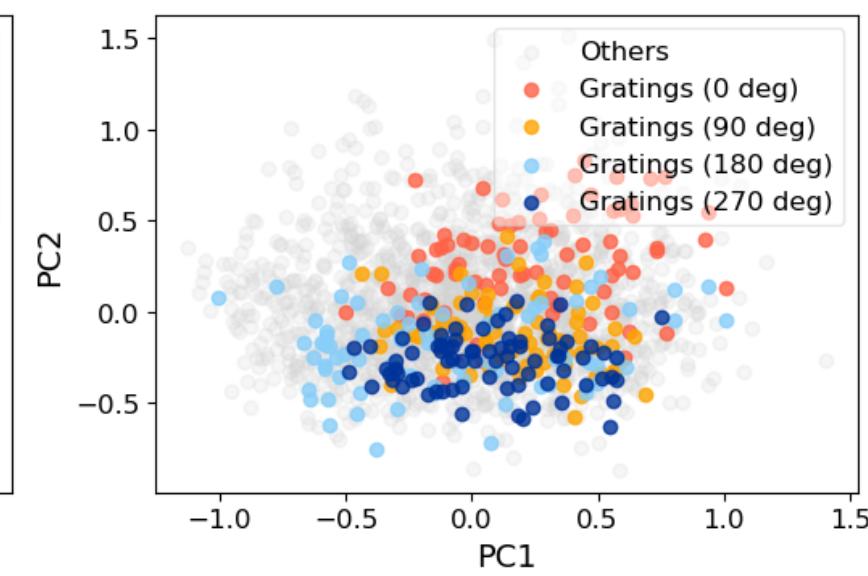
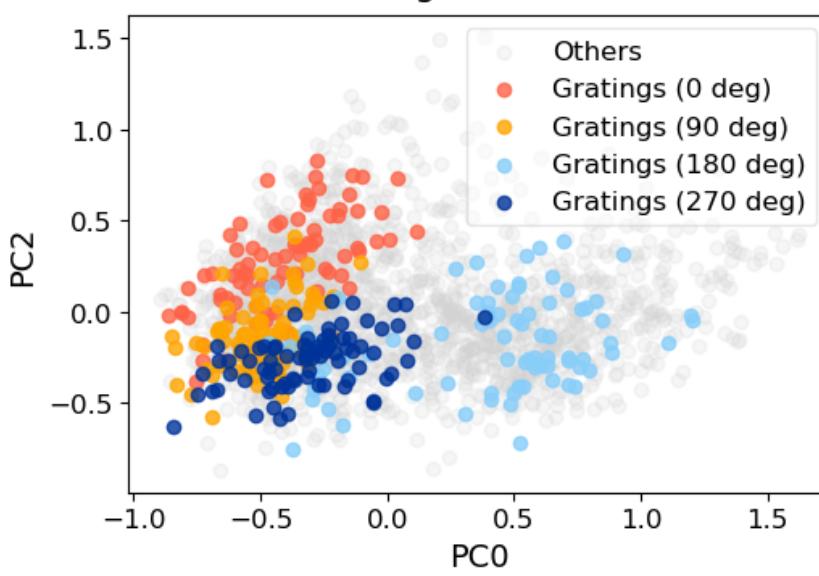
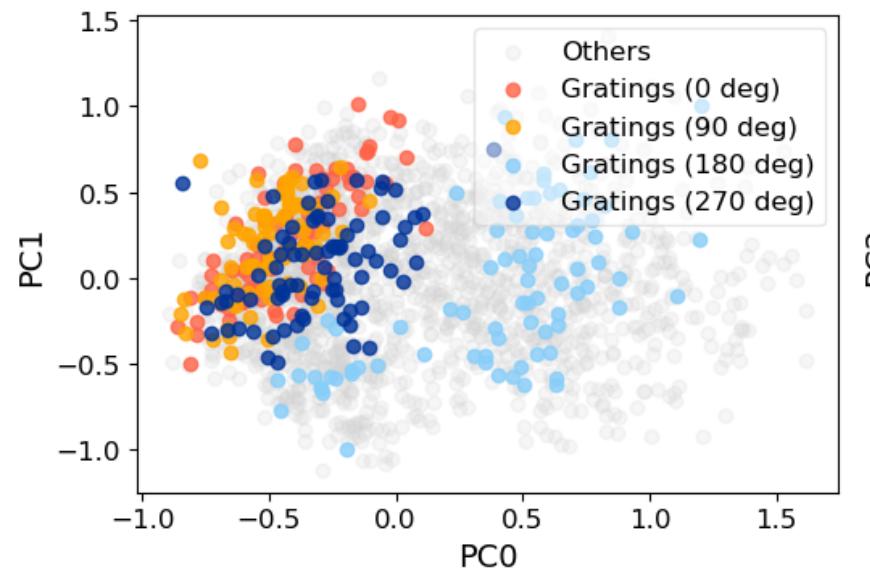
PCA: Gratings vs. All Flows



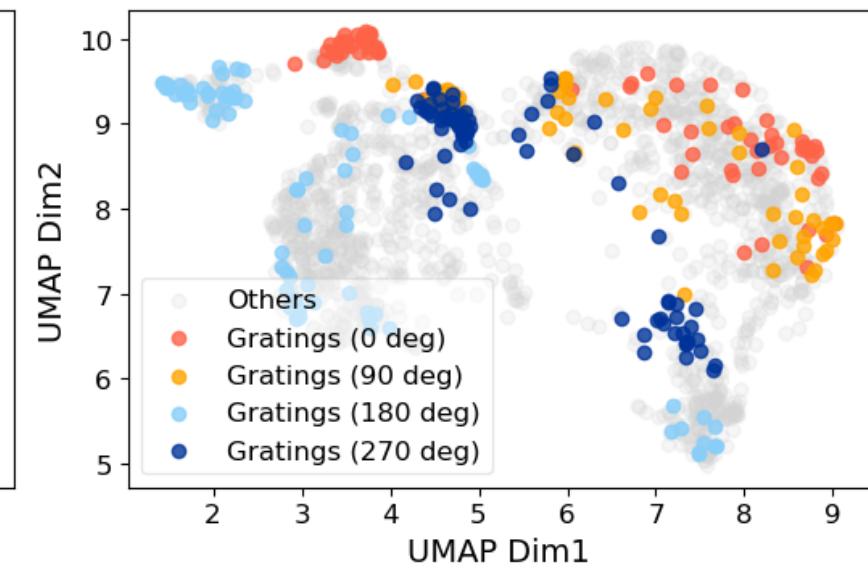
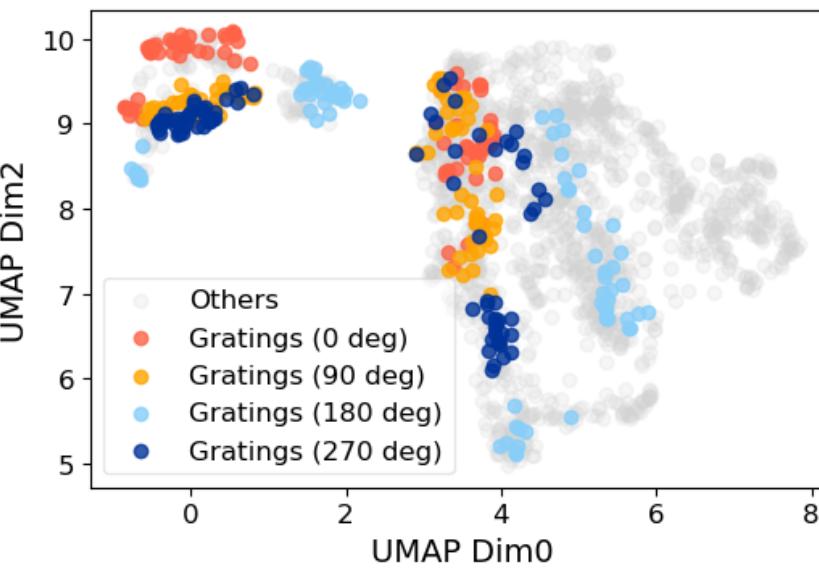
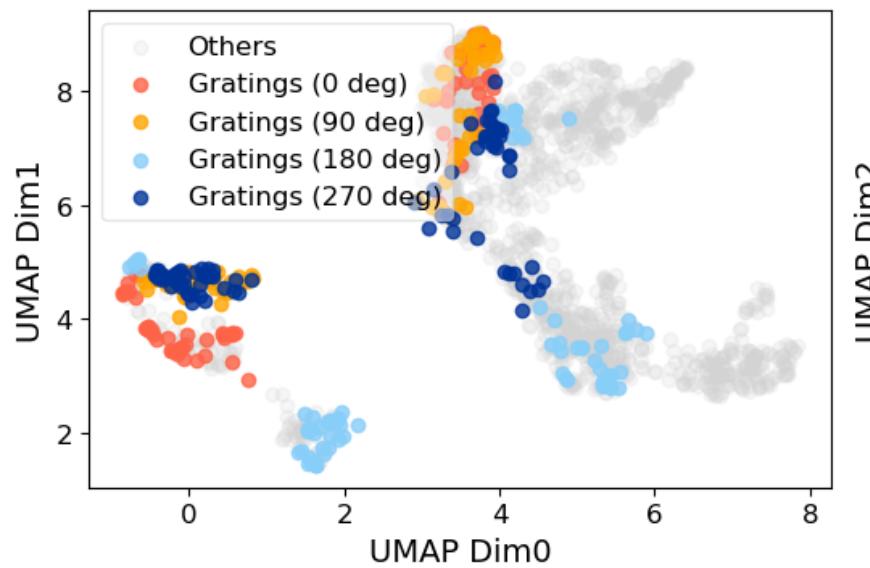
UMAP: Gratings vs. All Flows



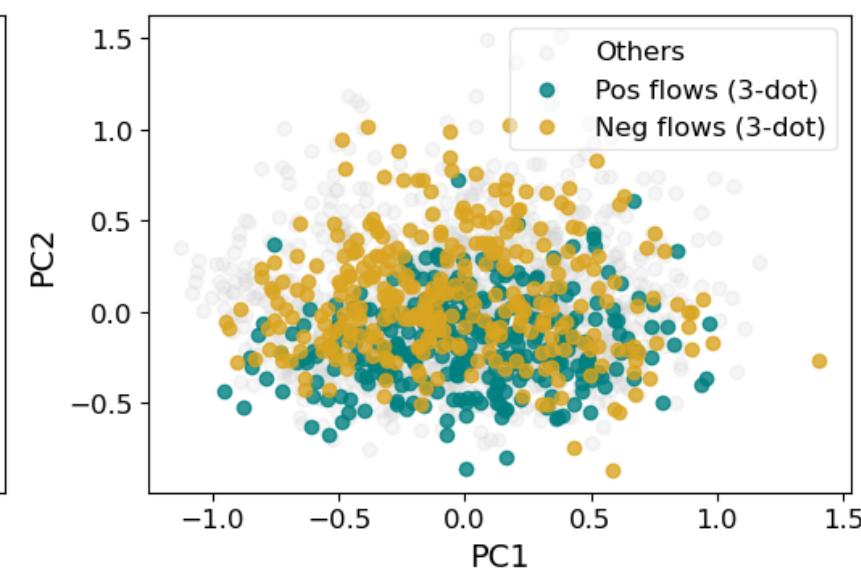
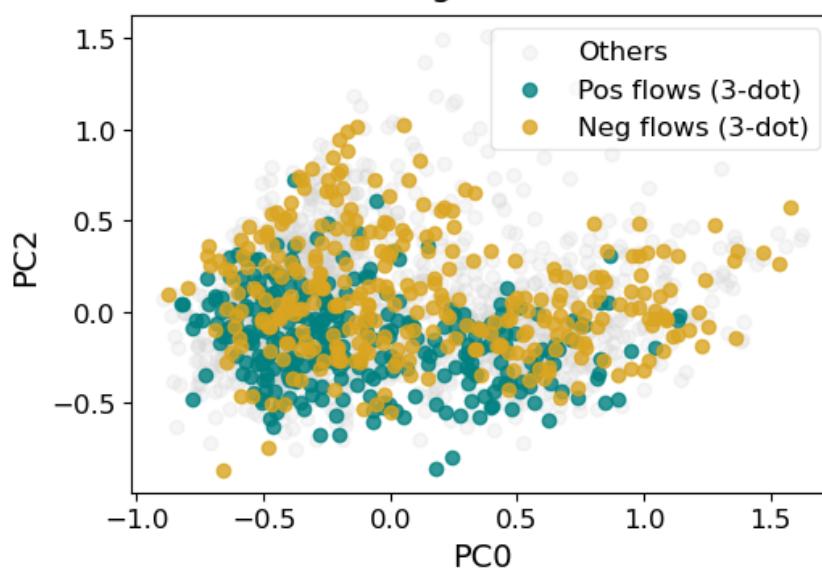
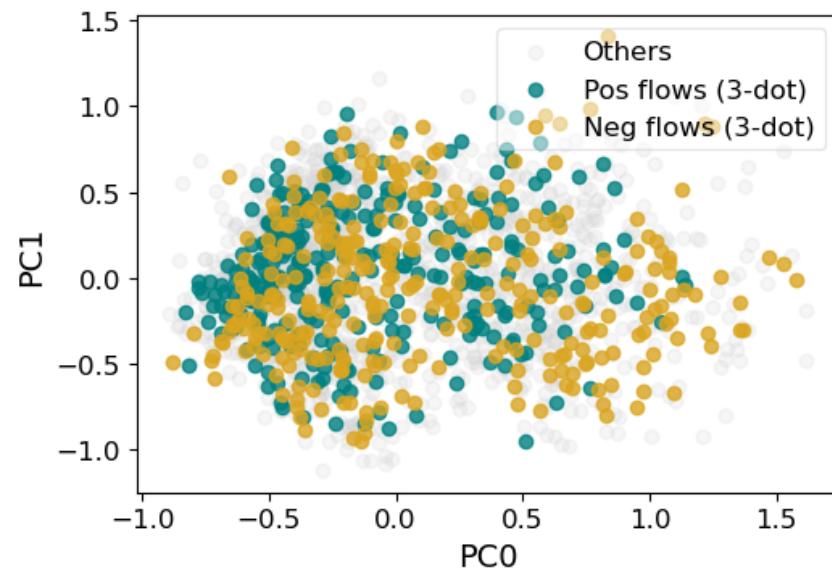
PCA: Gratings directions



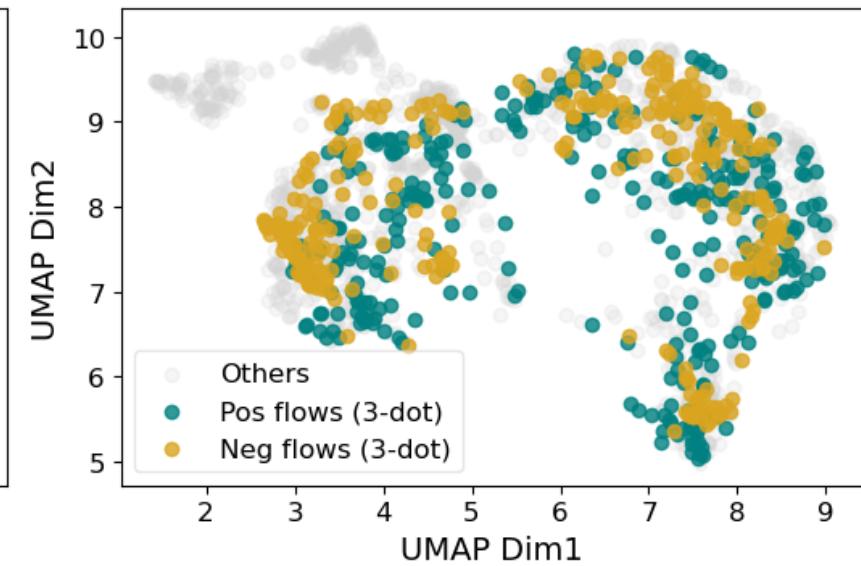
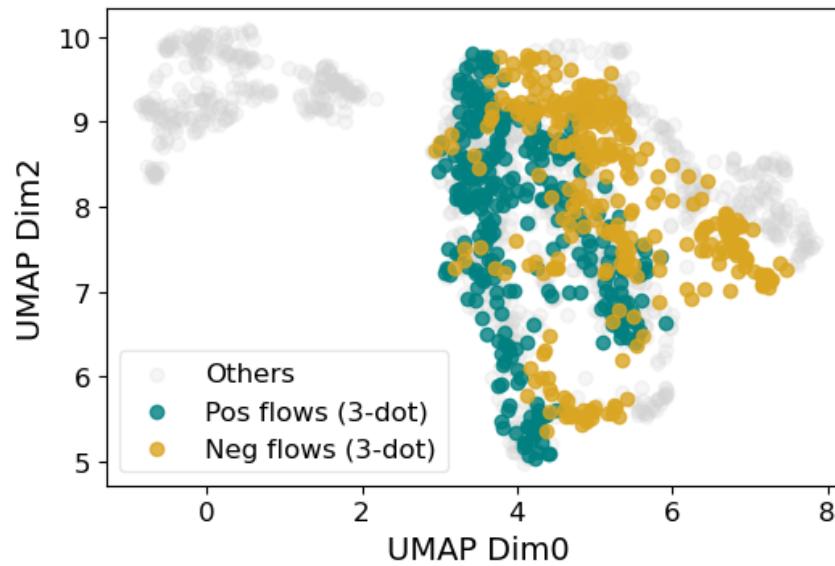
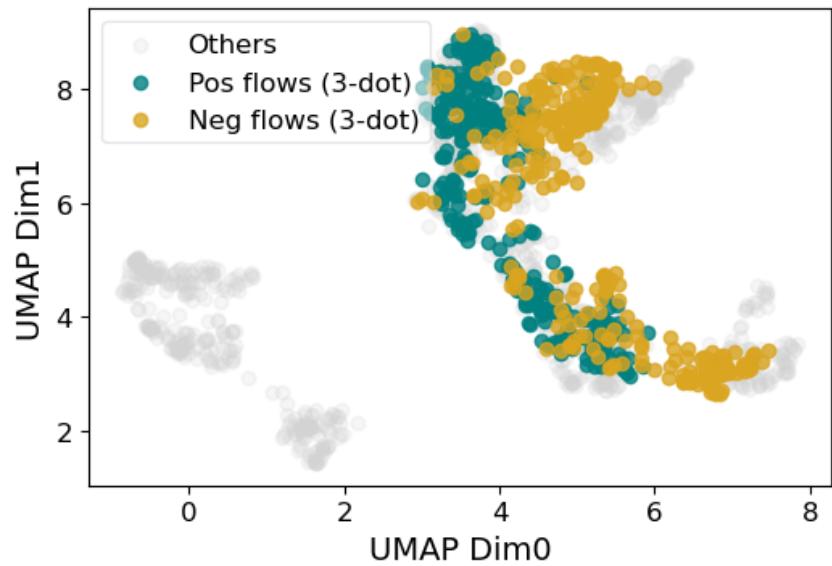
UMAP: Gratings directions

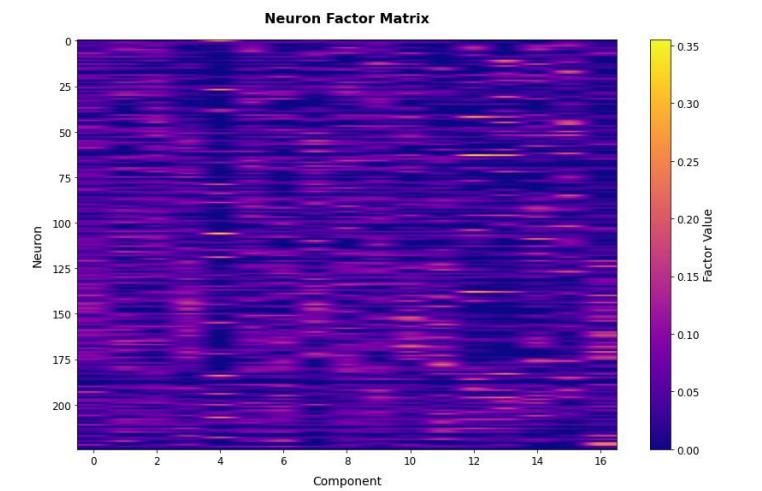


PCA: Pos vs neg flows (3-dot)

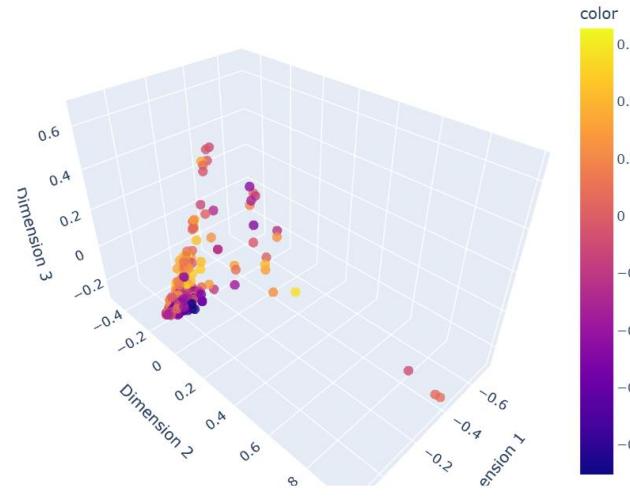


UMAP: Pos vs neg flows (3-dot)

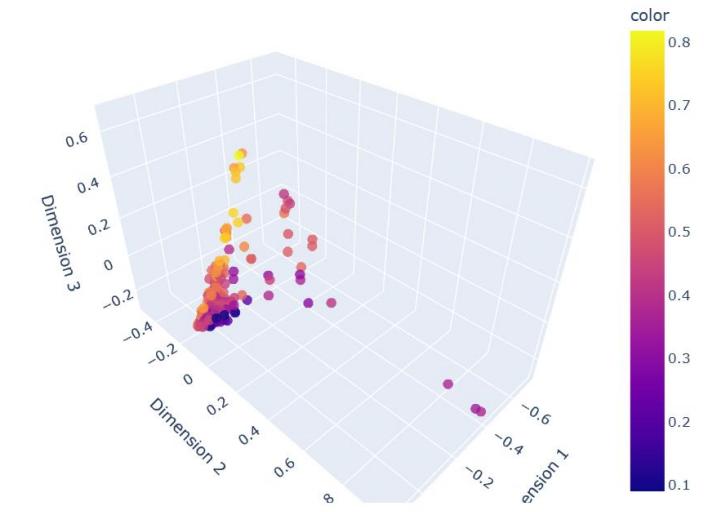




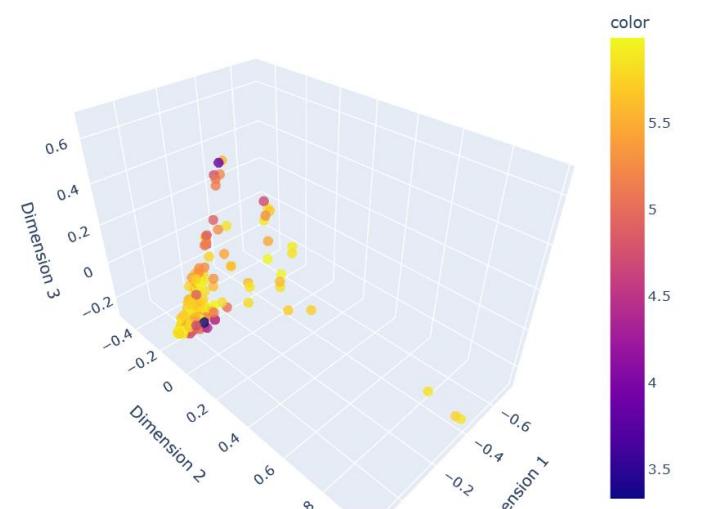
Neuron Diffusion Map (Flow Polarity Index)



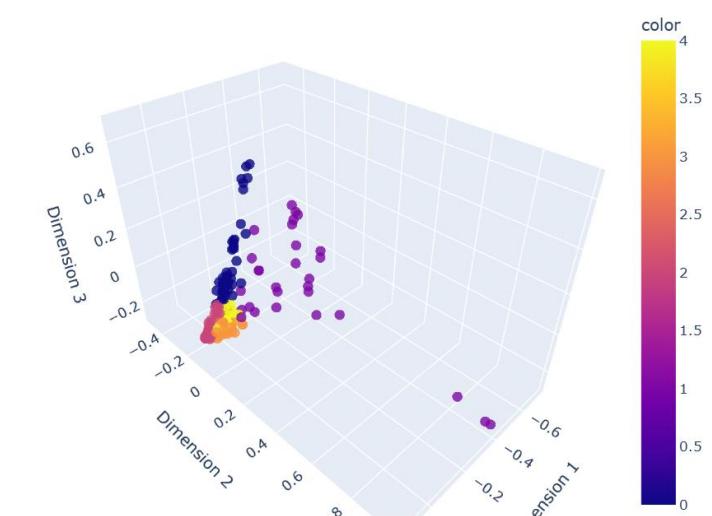
Neuron Diffusion Map (Grating Selectivity Index)



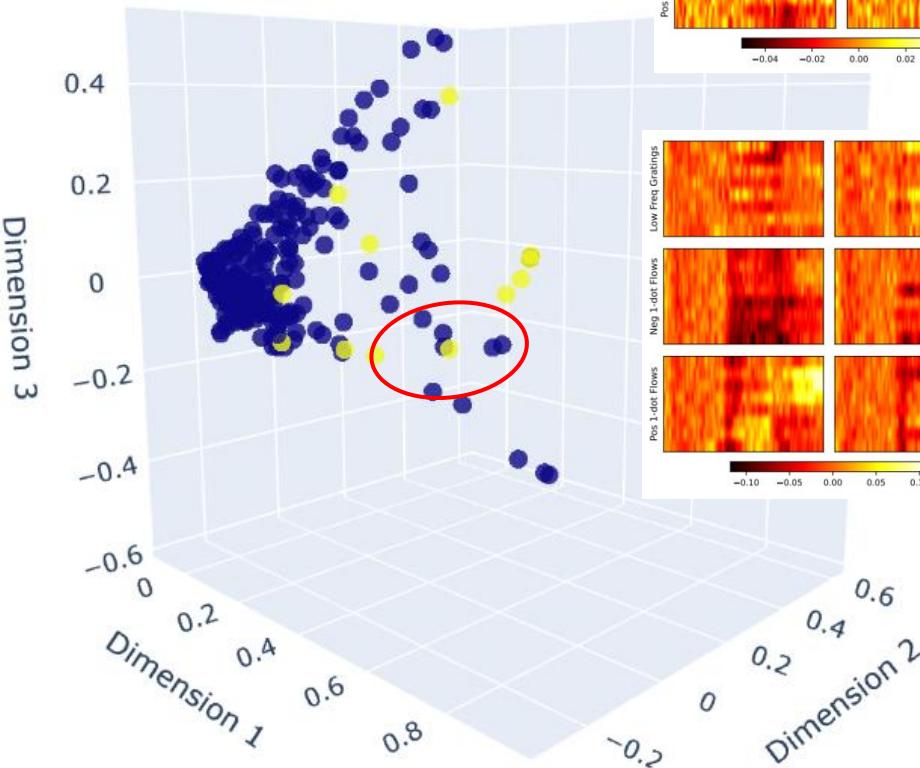
Neuron Diffusion Map (Stimulus Entropy Index)



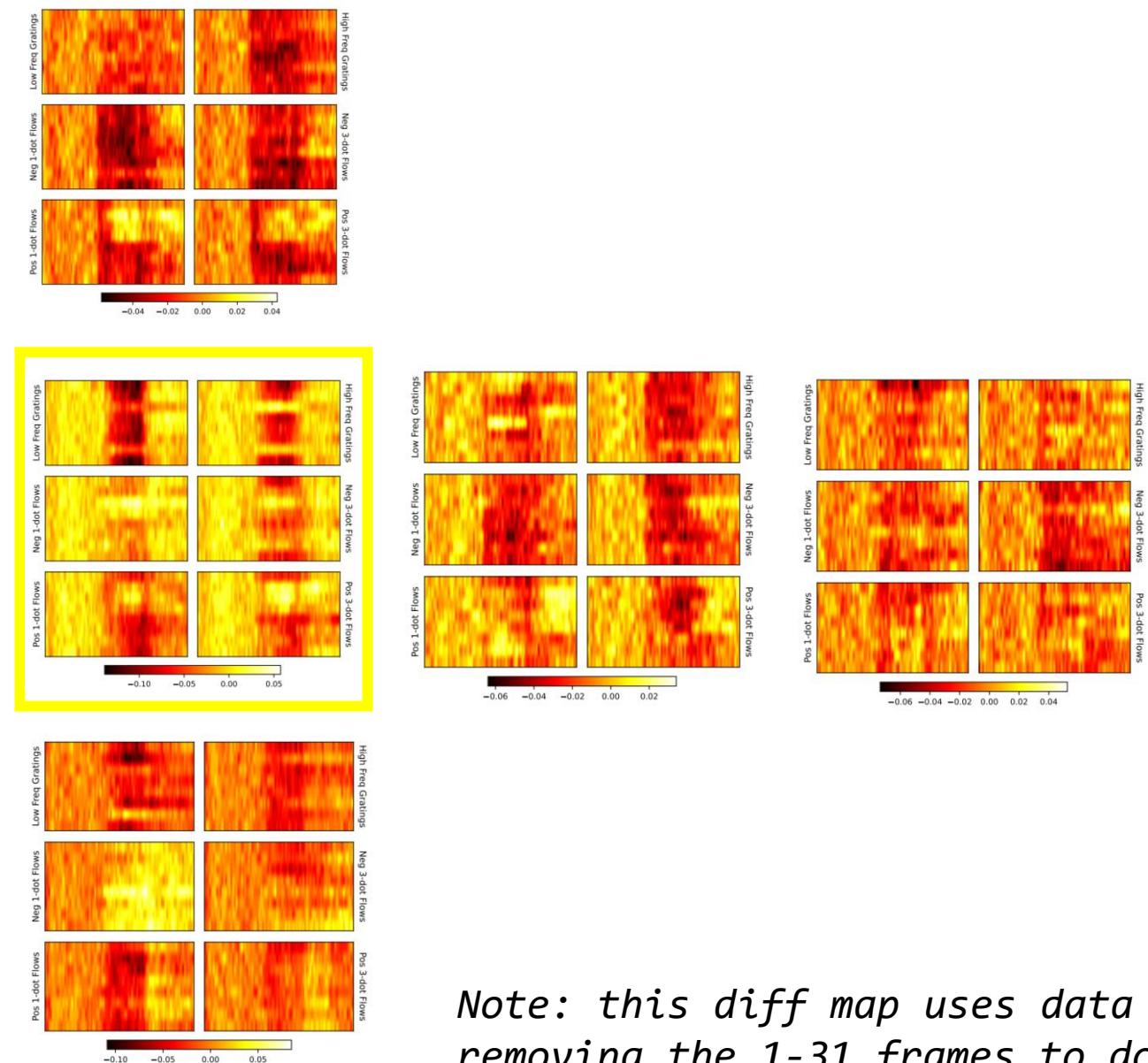
Neuron Diffusion Map (HDBSCAN Cluster Index)



# Negative Response

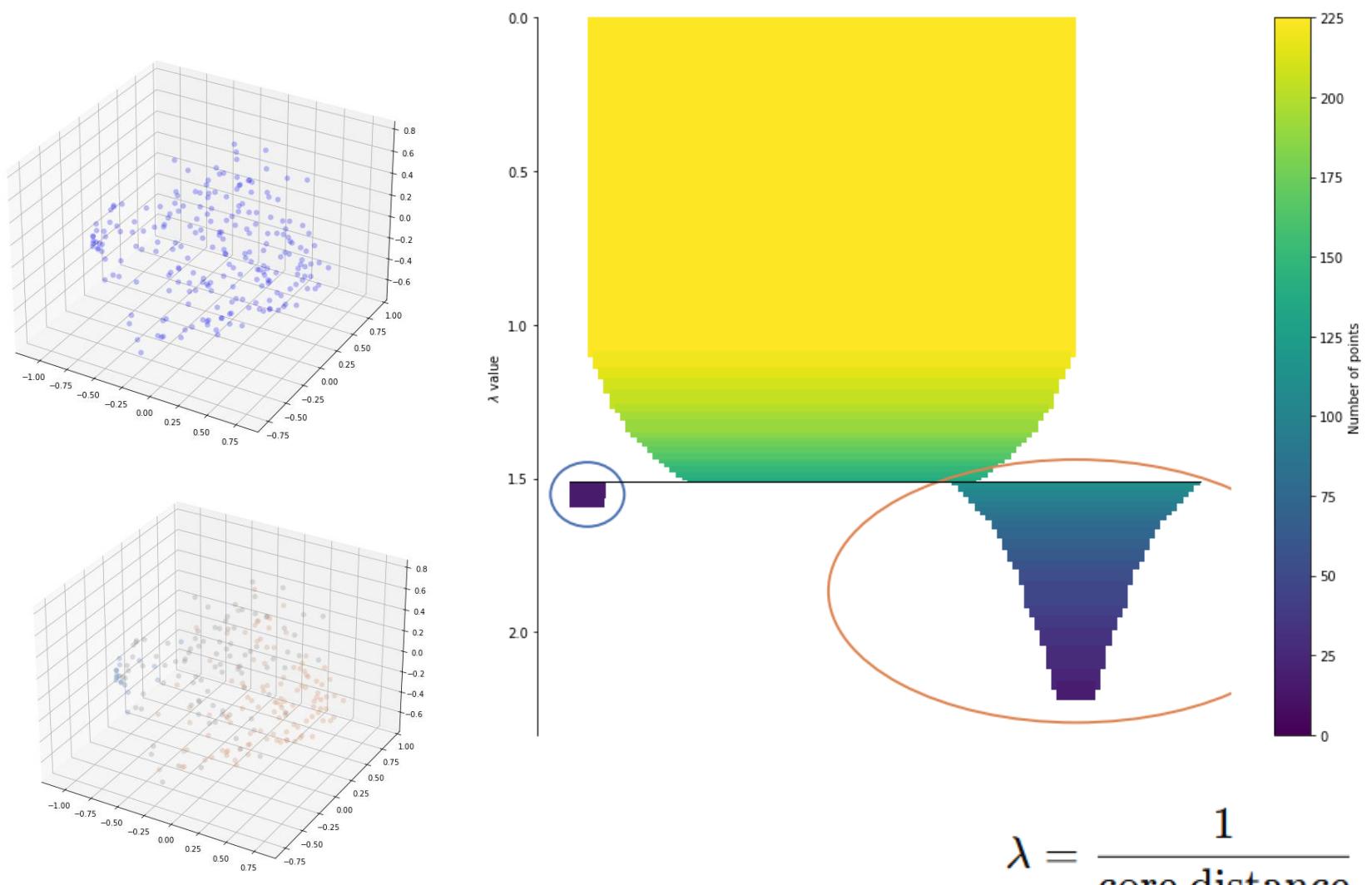
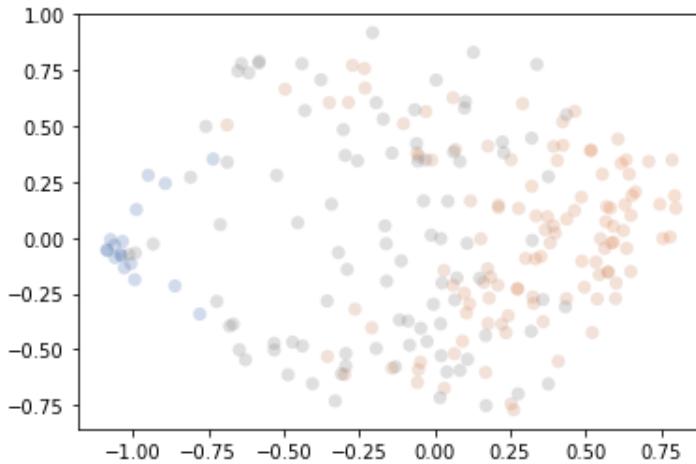
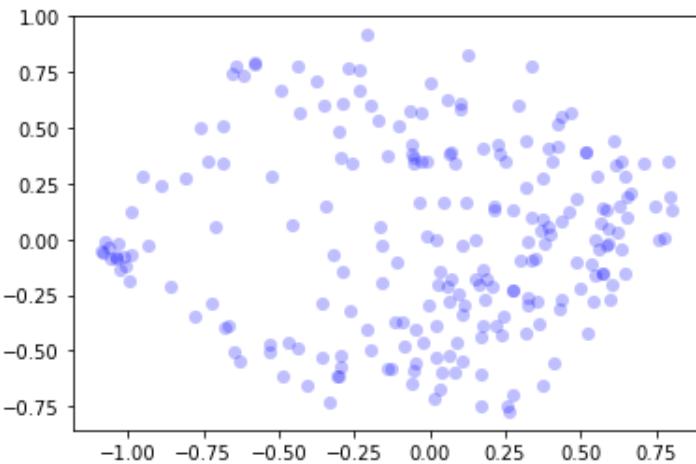


```
threshold = -0.1
min_count = 10 # Set the required count
# Count values < threshold along axis (1, 2, 3)
count_below_threshold = (data < threshold).sum(axis=(1, 2, 3))
# Create a binary mask (1 if count >= min_count, else 0)
negative_response_index = (count_below_threshold >= min_count).astype(int)
```



*Note: this diff map uses data not removing the 1-31 frames to do analysis.*

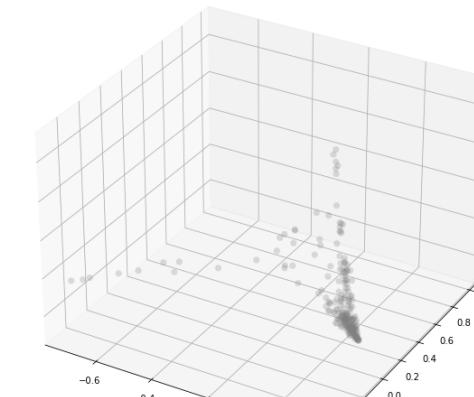
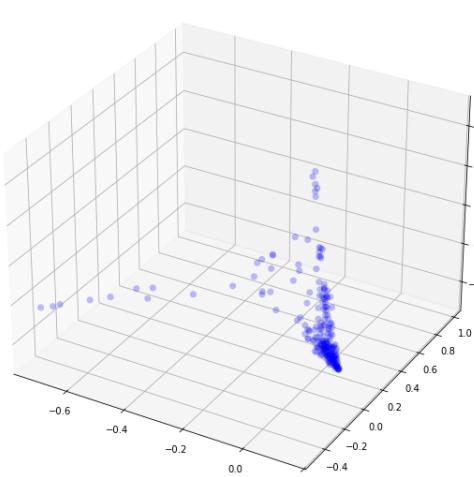
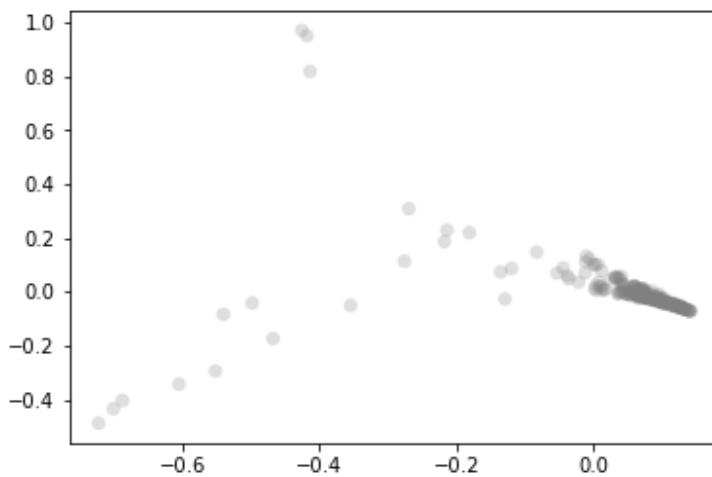
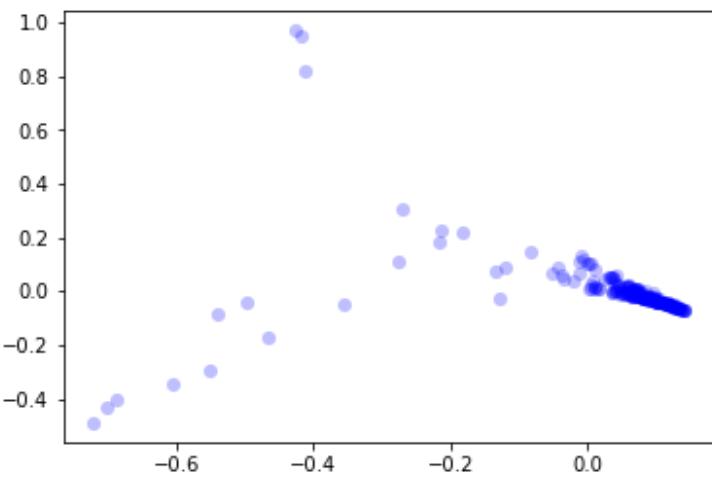
## Before diffusion map



$$\lambda = \frac{1}{\text{core distance}}$$

- **A larger  $\lambda$  value (Low Core Distance):**  
higher density, meaning the point belongs to a more tightly clustered region.
- **A smaller  $\lambda$  value (High Core Distance):**  
lower density, meaning the point is in a sparser region and may be separated earlier.

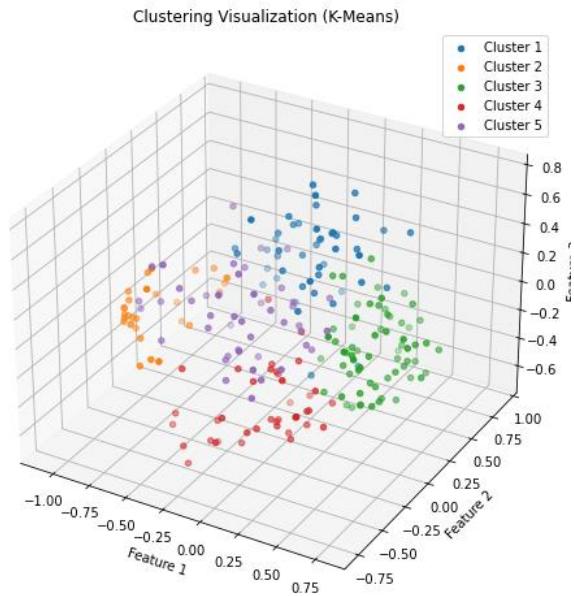
## After diffusion map



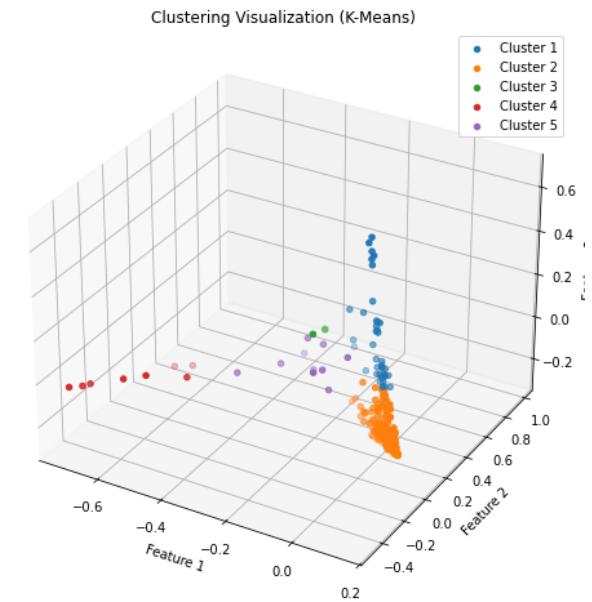
$$\lambda = \frac{1}{\text{core distance}}$$

- **A larger  $\lambda$  value (Low Core Distance):**  
higher density, meaning the point belongs to a more tightly clustered region.
- **A smaller  $\lambda$  value (High Core Distance):**  
lower density, meaning the point is in a sparser region and may be separated earlier.

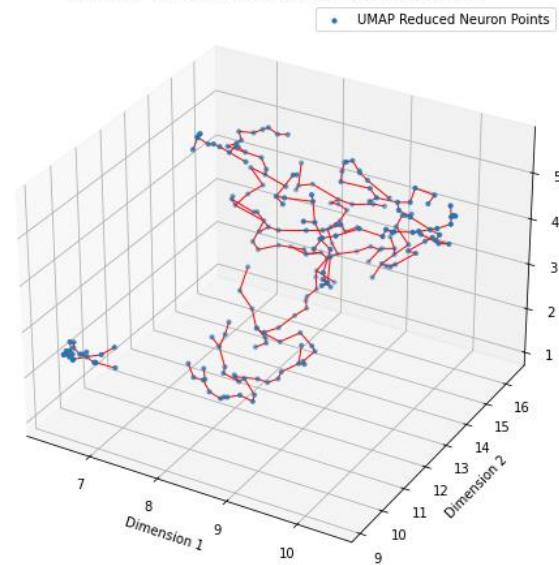
## Before diffusion map



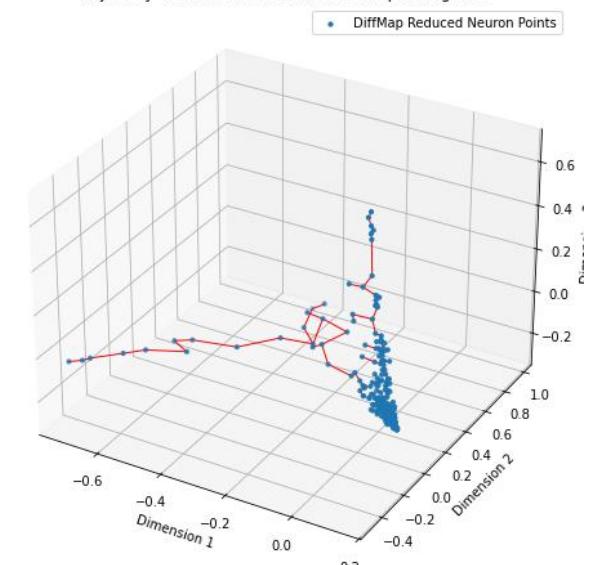
## After diffusion map



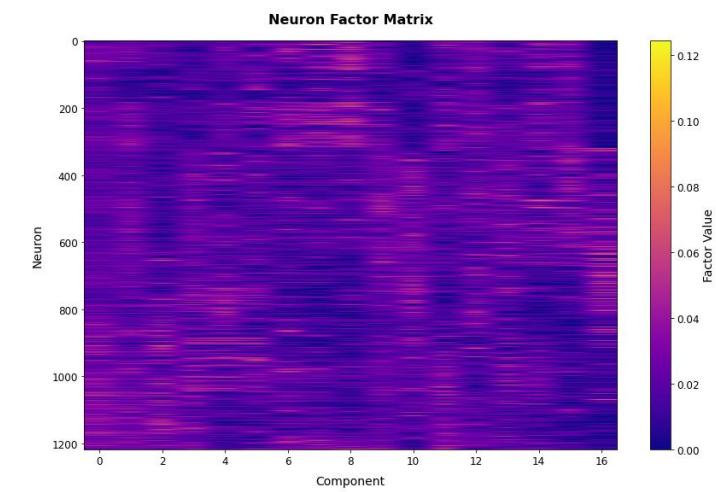
Trajectory Visualization with minimum spanning tree



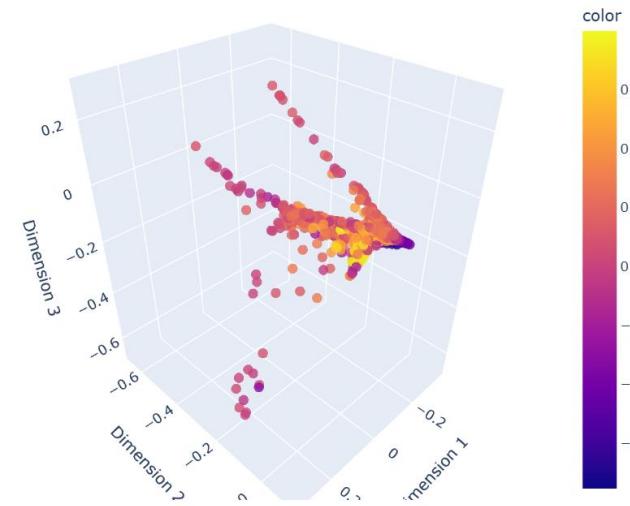
Trajectory Visualization with minimum spanning tree



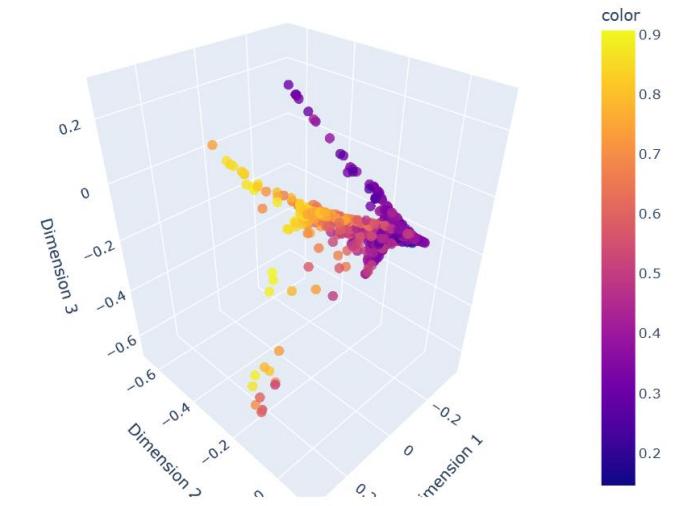
**SC**



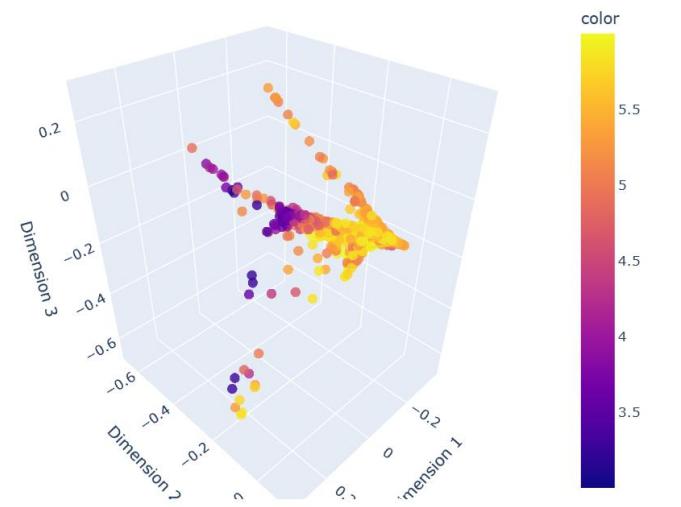
Neuron Diffusion Map (Flow Polarity Index)



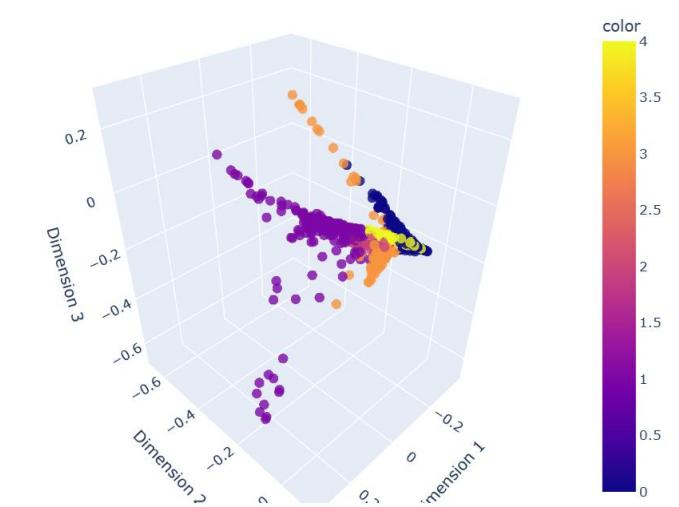
Neuron Diffusion Map (Grating Selectivity Index)



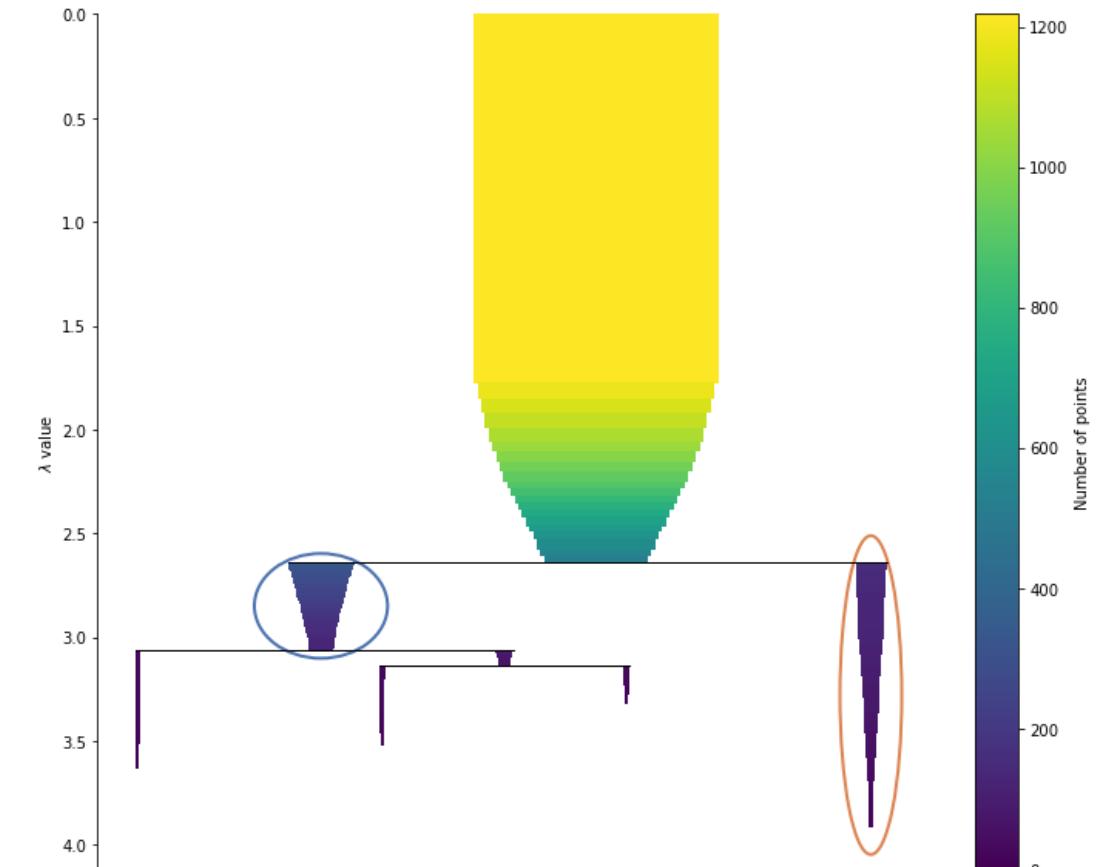
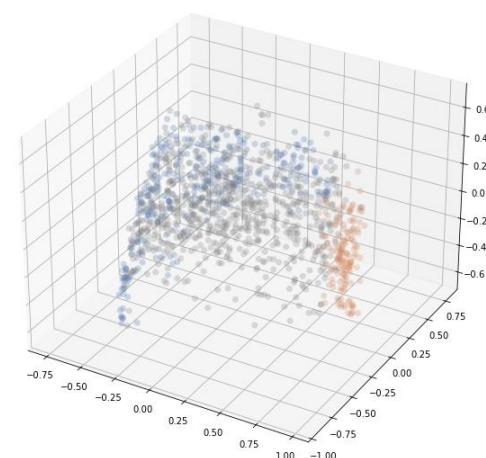
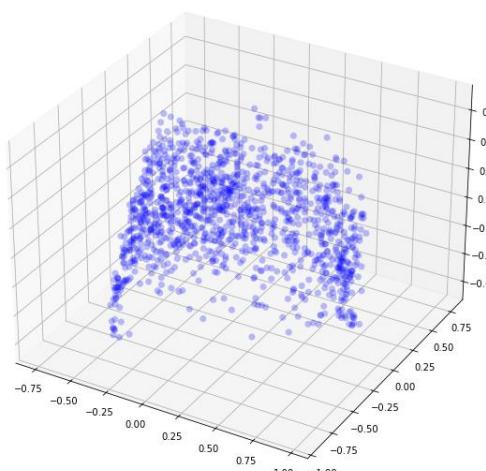
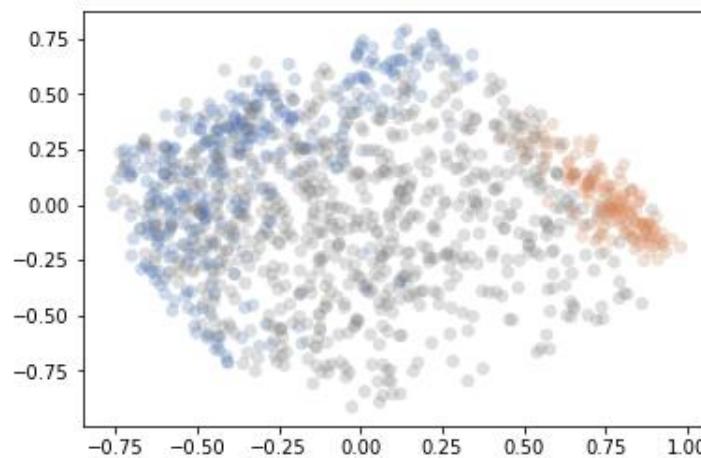
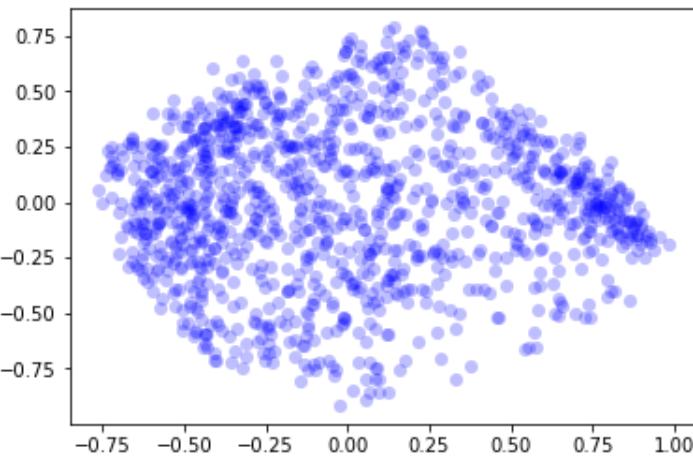
Neuron Diffusion Map (Stimulus Entropy Index)



Neuron Diffusion Map (HDBSCAN Cluster Index)



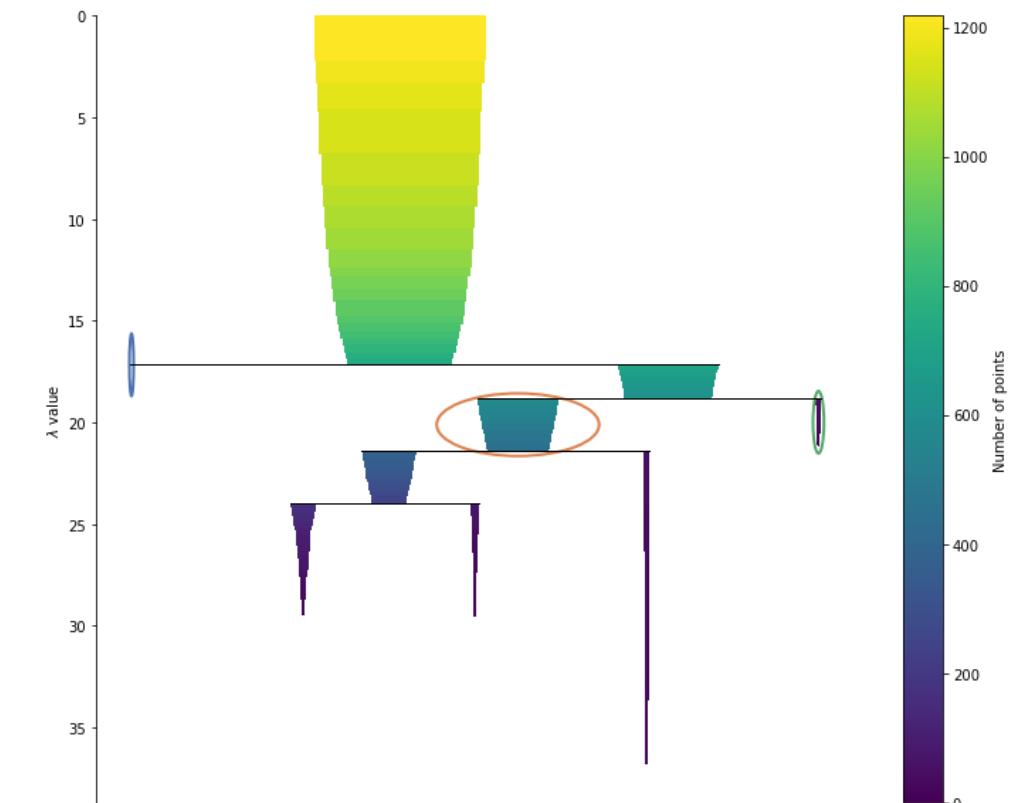
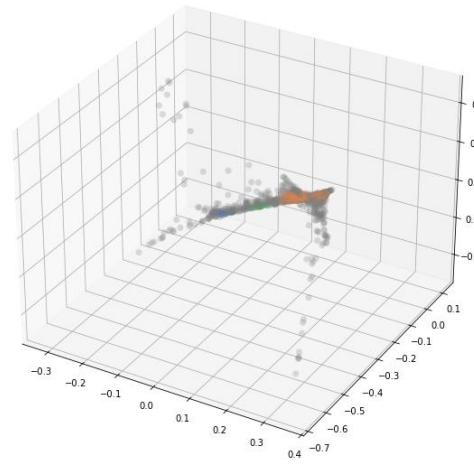
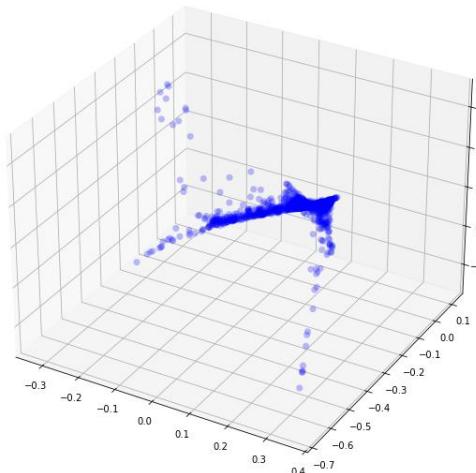
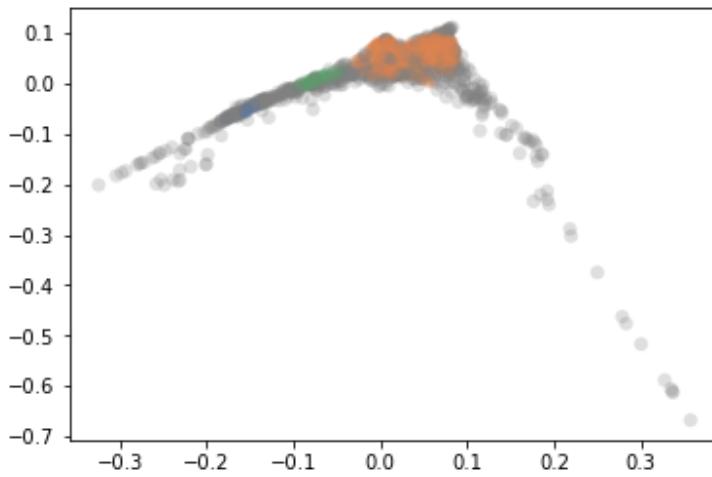
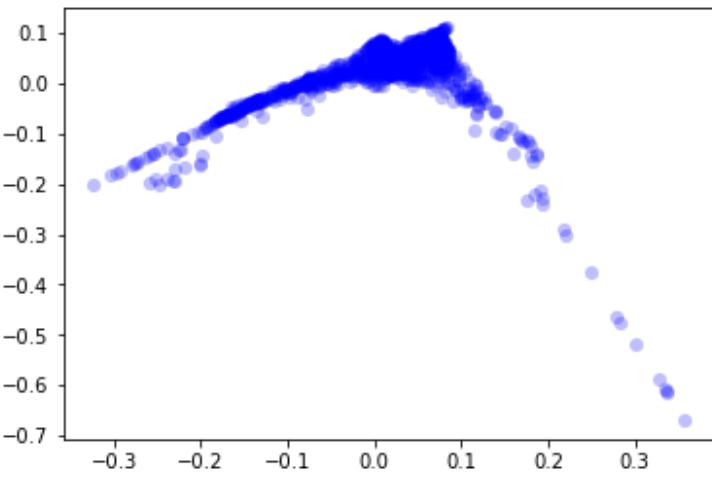
## Before diffusion map



$$\lambda = \frac{1}{\text{core distance}}$$

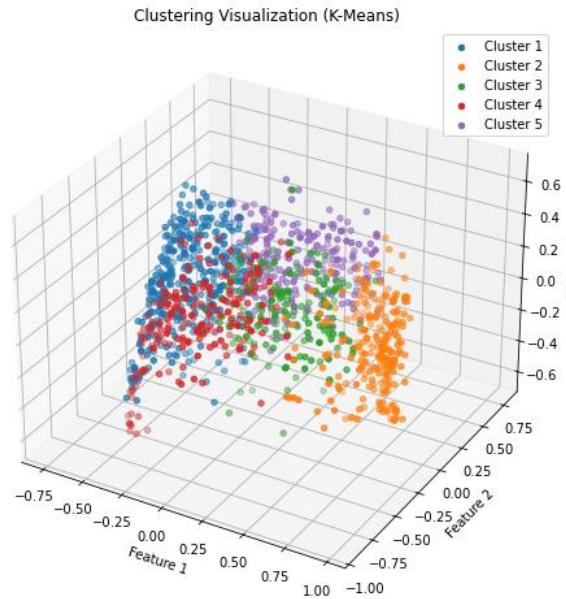
- **A larger  $\lambda$  value (Low Core Distance):**  
higher density, meaning the point belongs to a more tightly clustered region.
- **A smaller  $\lambda$  value (High Core Distance):**  
lower density, meaning the point is in a sparser region and may be separated earlier.

## After diffusion map

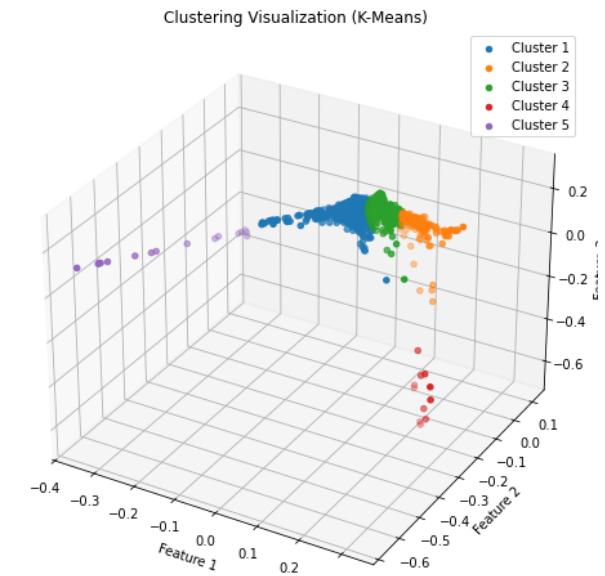


- **A larger  $\lambda$  value (Low Core Distance):**  
higher density, meaning the point belongs to a more tightly clustered region.
- **A smaller  $\lambda$  value (High Core Distance):**  
lower density, meaning the point is in a sparser region and may be separated earlier.

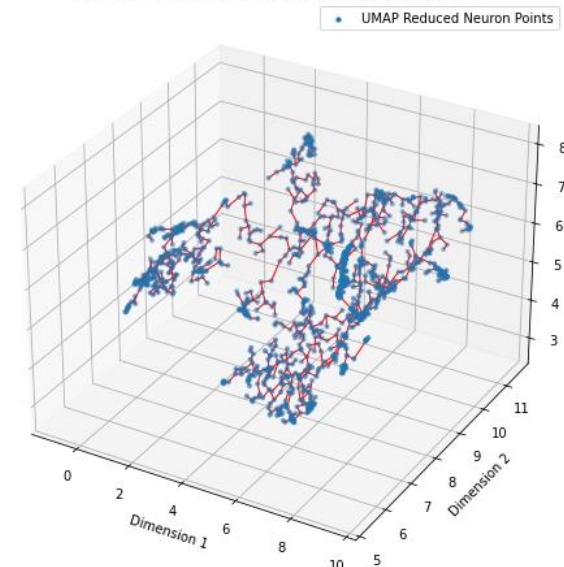
## Before diffusion map



## After diffusion map



Trajectory Visualization with minimum spanning tree



Trajectory Visualization with minimum spanning tree

