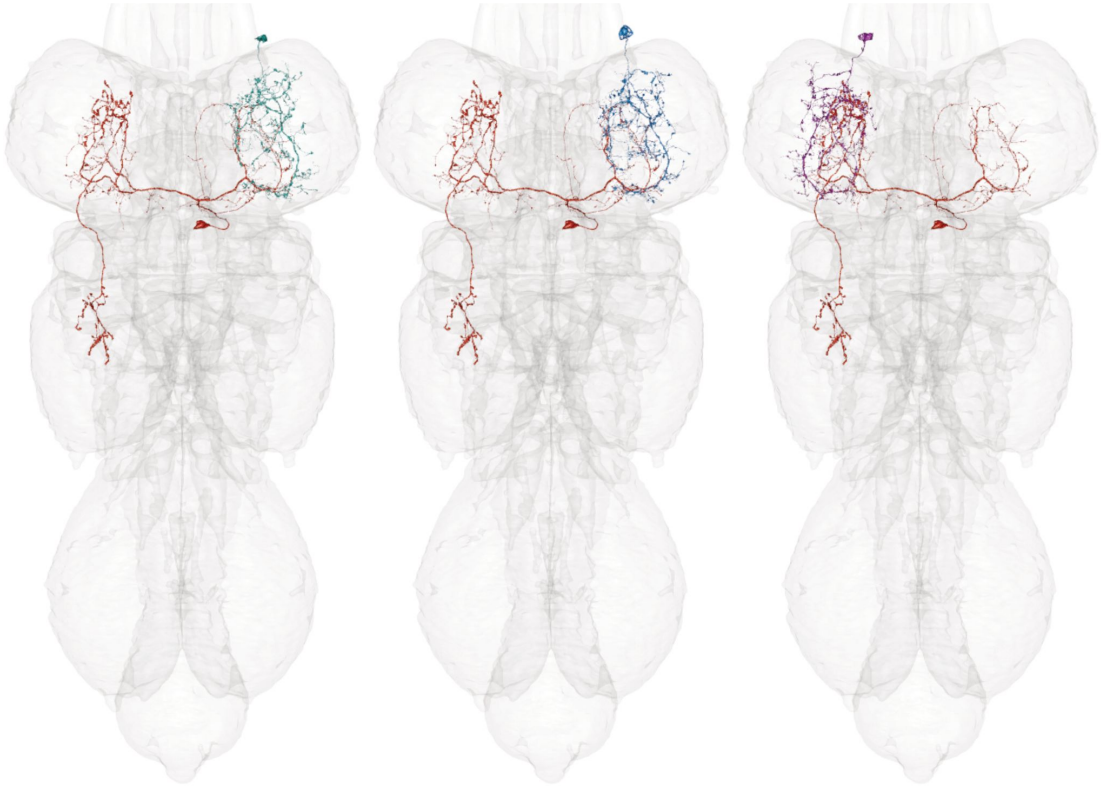
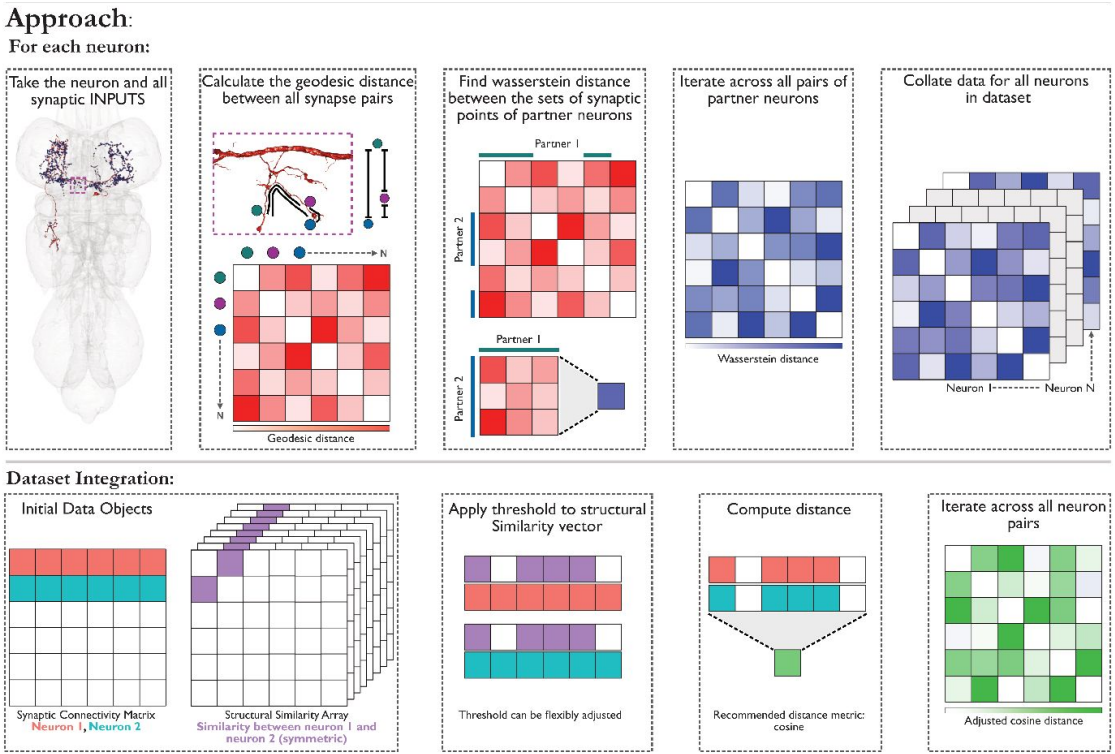
# R club bits

- Structural connectivity
- WNN integration
- Pseudo-alignment topology/morphological metrics

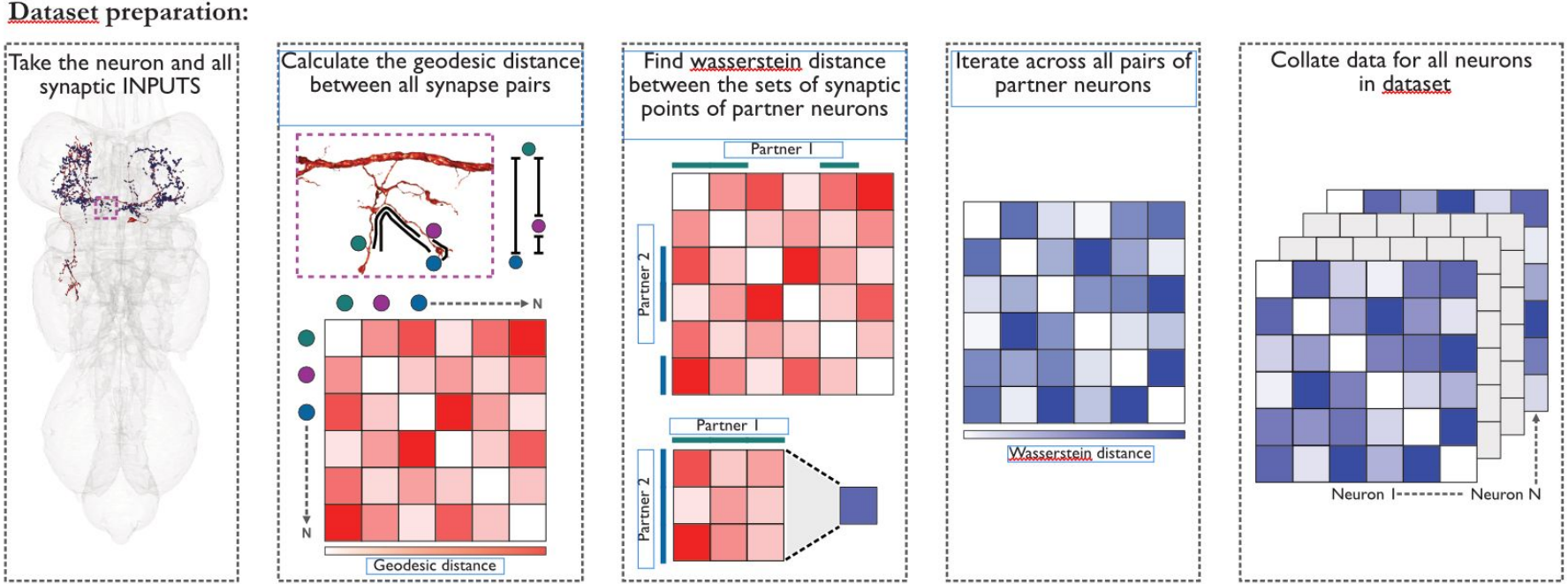
- Structural connectivity



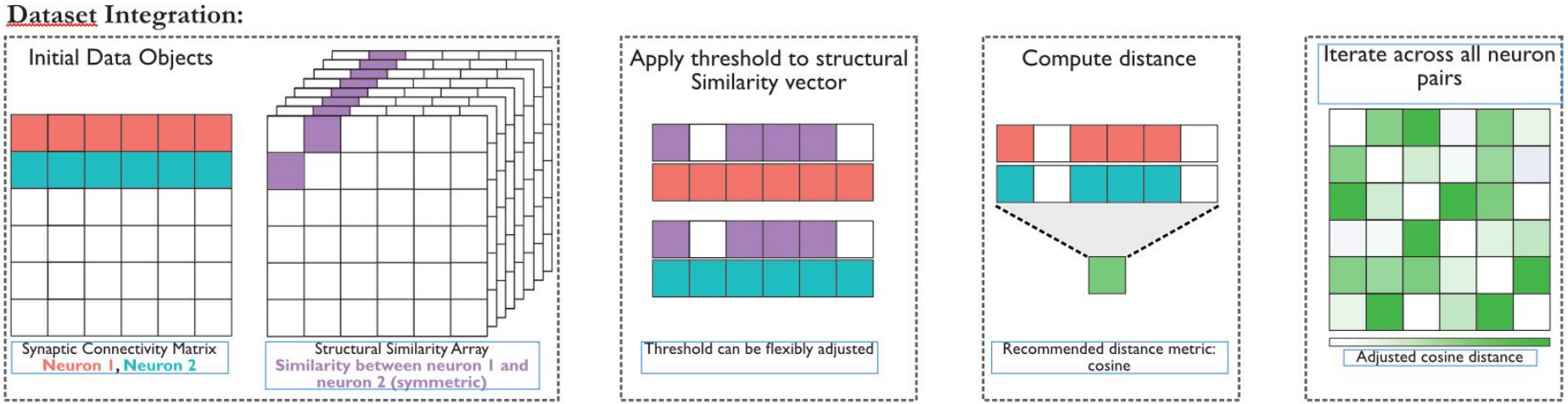
- Structural connectivity



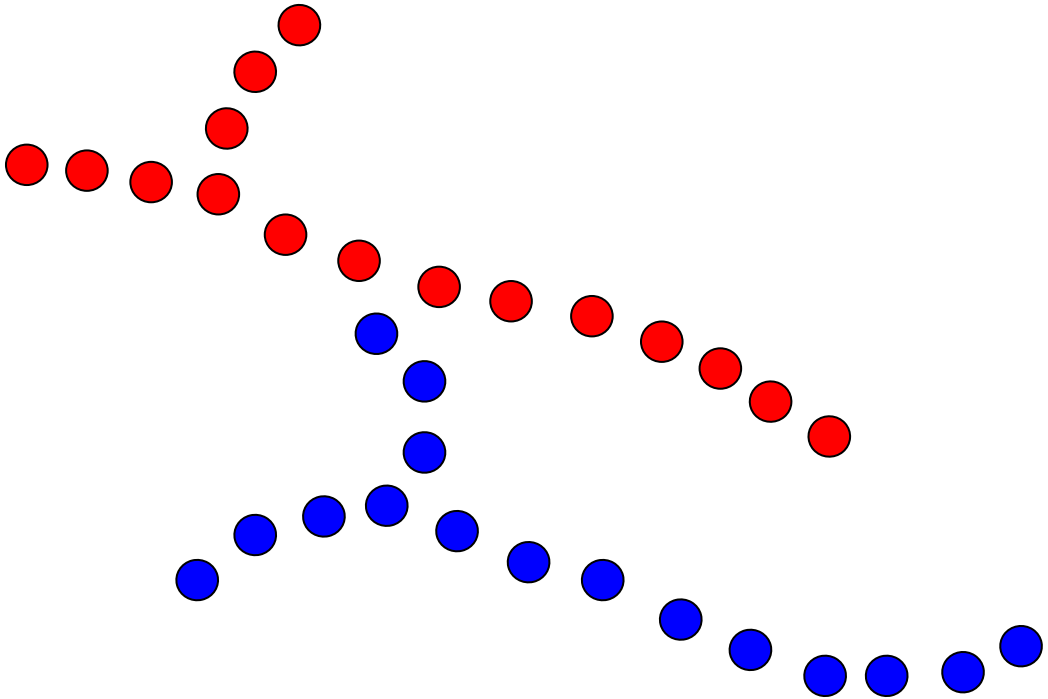
- Structural connectivity



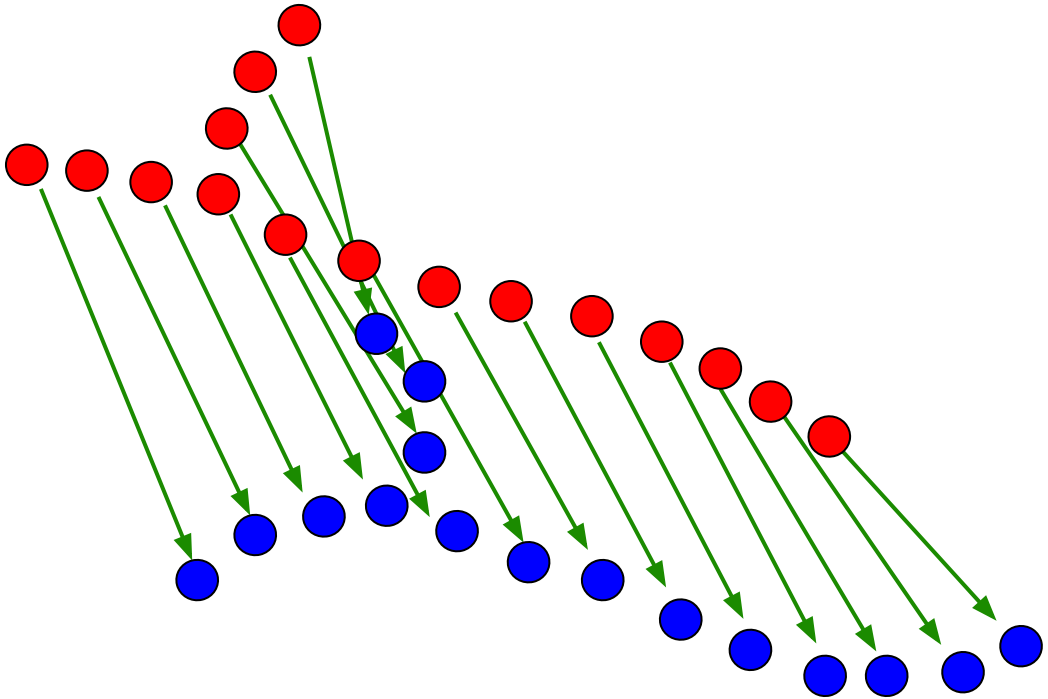
- Structural connectivity



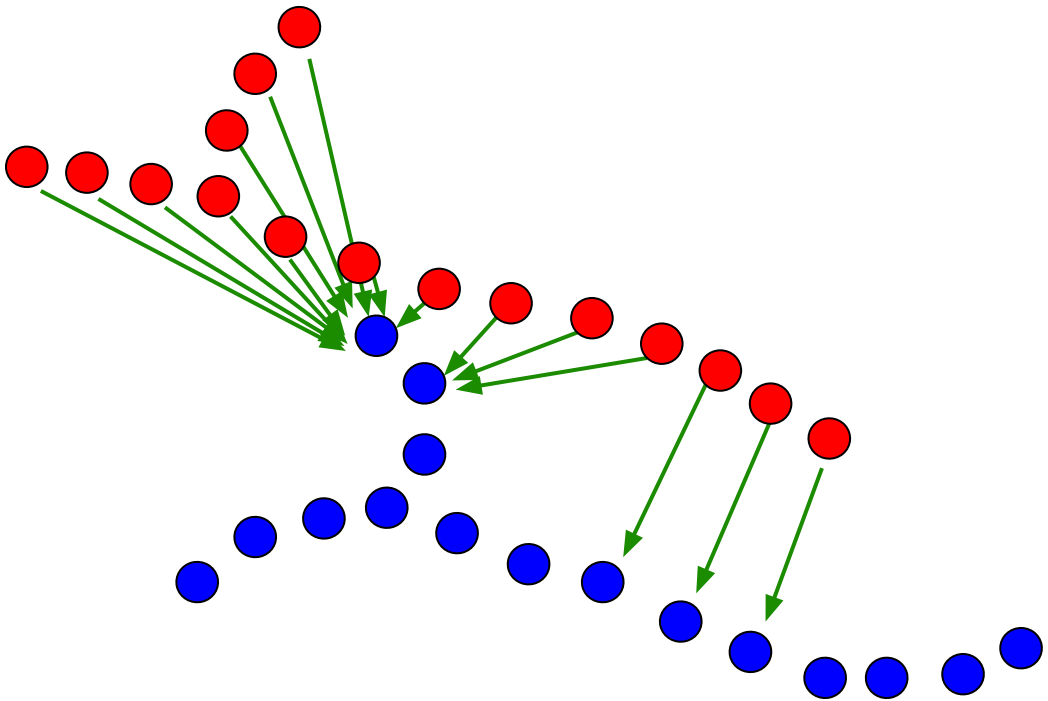
- Structural connectivity



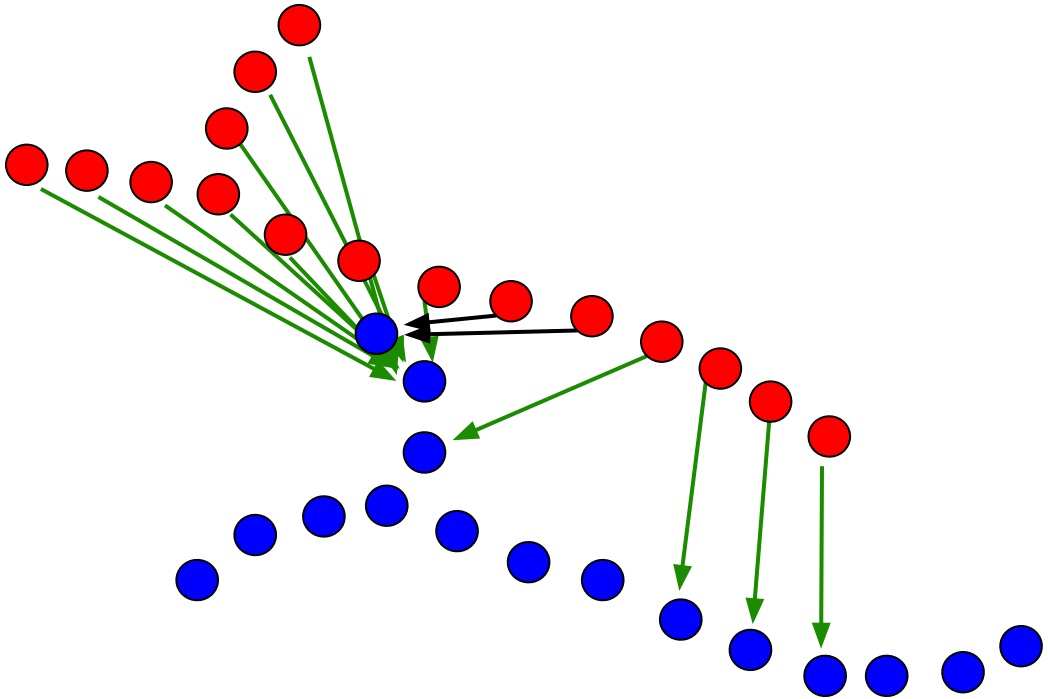
# Structural connectivity - Wasserstein Distance



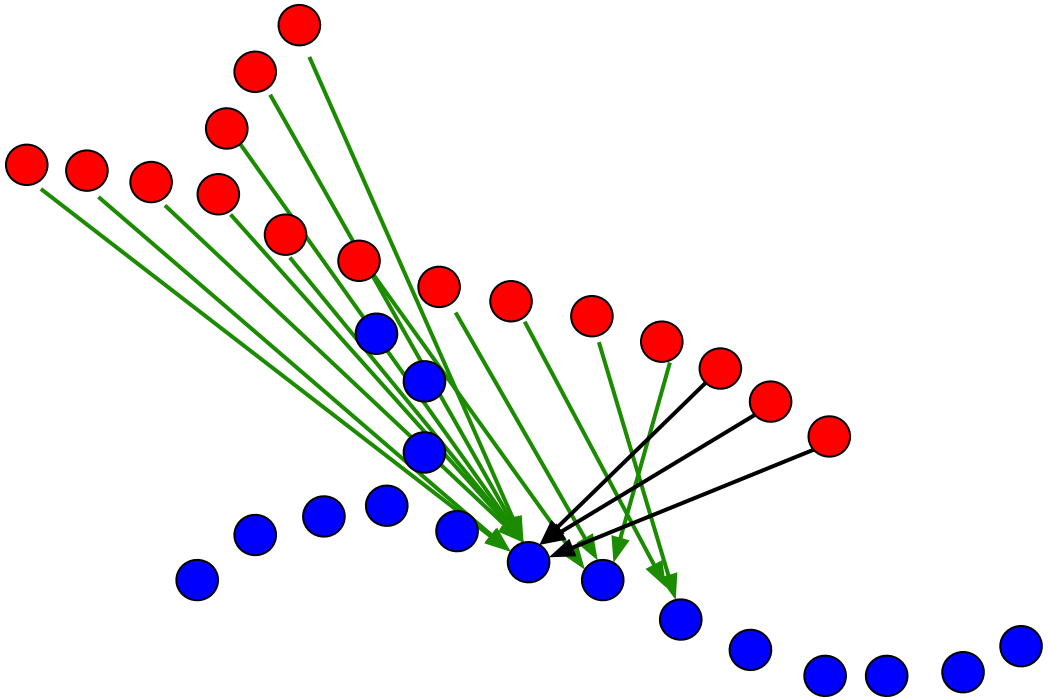
# Structural connectivity - Minimium



# Structural connectivity - 0.1 Quantile

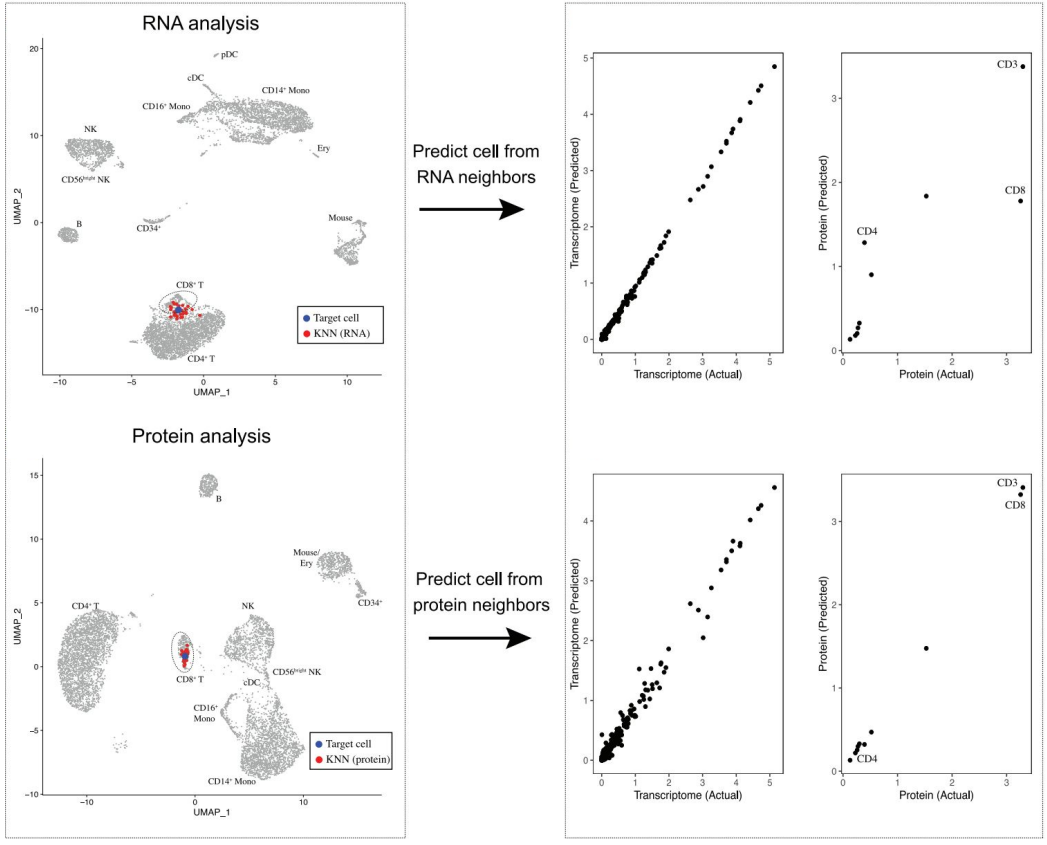


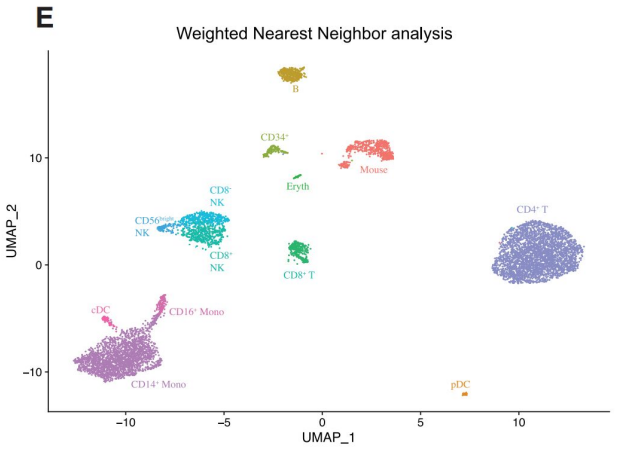
# Structural connectivity - Median



- WNN integration

# Billy - WNN

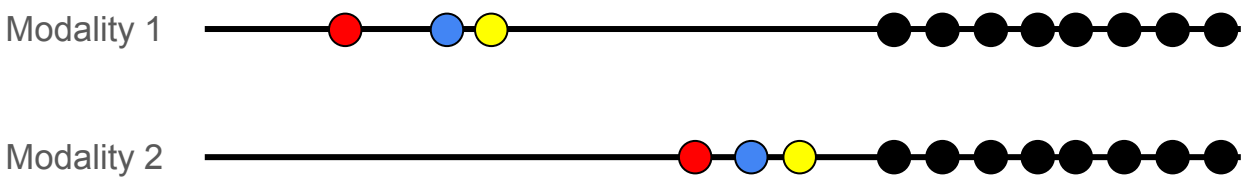

RNA analysis
pDC
cDC
CD14+ Mono
CD16+ Mono
NK
Ery
CD56high NK
B
CD34+
Mouse
CD8+ T
CD4+ T
Target cell
KNN (RNA)
UMAP_1
UMAP_2
Predict cell from RNA neighbors
Transcriptome (Predicted)
Transcriptome (Actual)
Protein (Predicted)
Protein (Actual)
CD3
CD8
CD4
Protein analysis
Mouse/ Ery
Target cell
KNN (protein)
Predict cell from protein neighbors


E
Weighted Nearest Neighbor analysis
B
CD34+
Eryth
Mouse
CD8+ NK
CD56high NK
CD8+ NK
CD8+ T
CD4+ T
cDC
CD16+ Mono
CD14+ Mono
pDC
UMAP_1
UMAP_2

# Billy - WNN

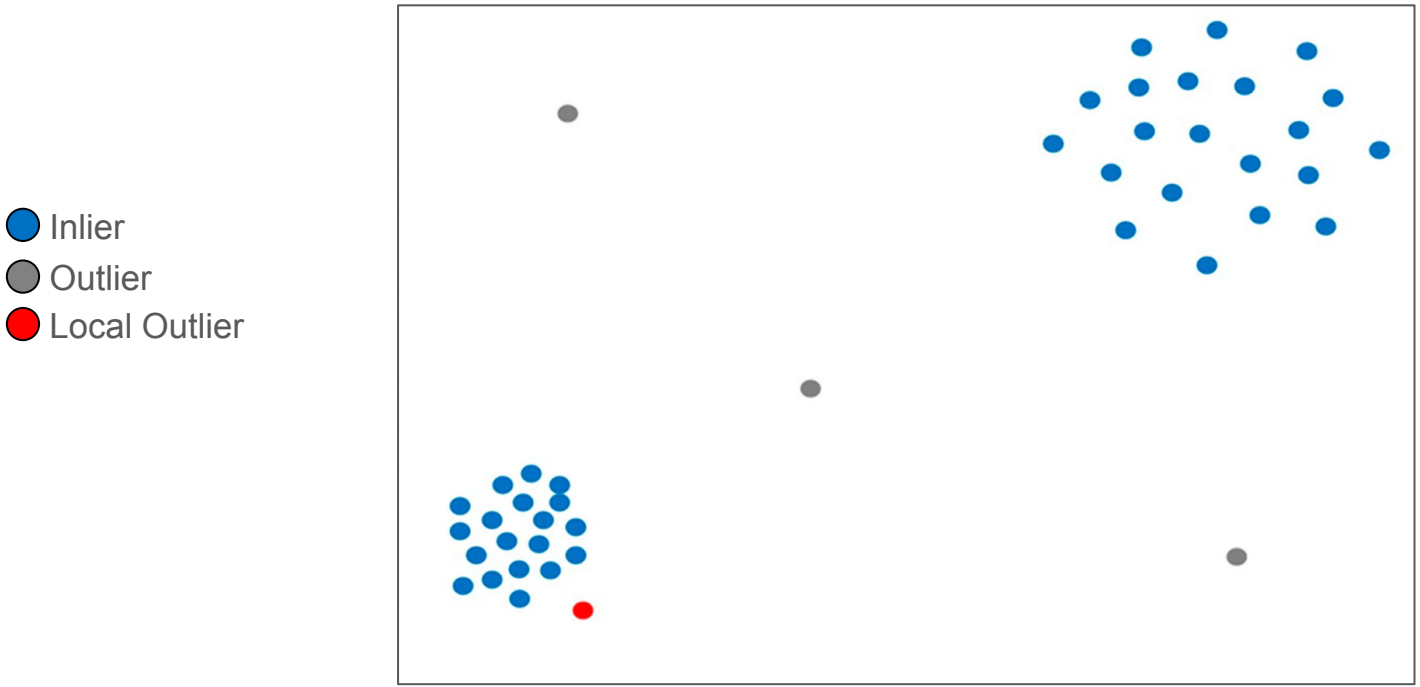
Complex:

- Assumes that the “information” content of differing modalities is the same.



# Billy - WNN LOF

LOF (local outlier factor)

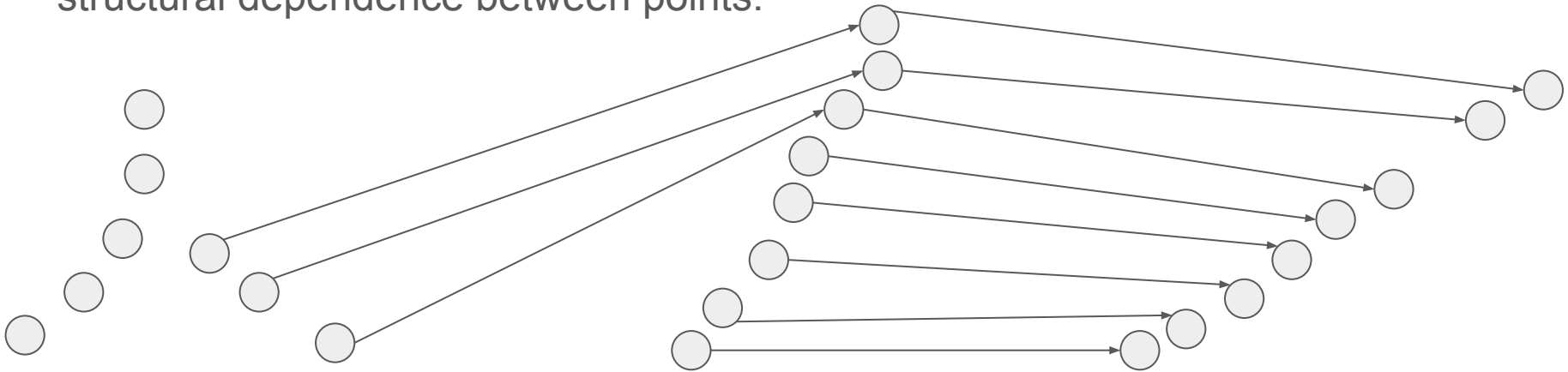


- Pseudo-alignment topology/morphological metrics

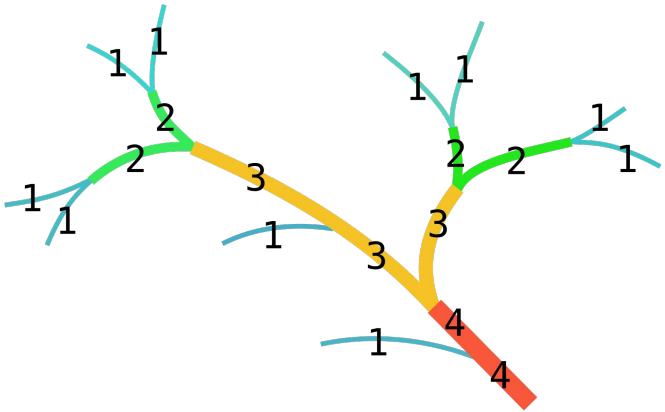
# Billy - Morphological similarity

Previous efforts have looked to transform between neuromeres, but unfortunately have been fairly inconsistent.

Initially planned for a optimal transport (OT) based approach, however lacks structural dependence between points.

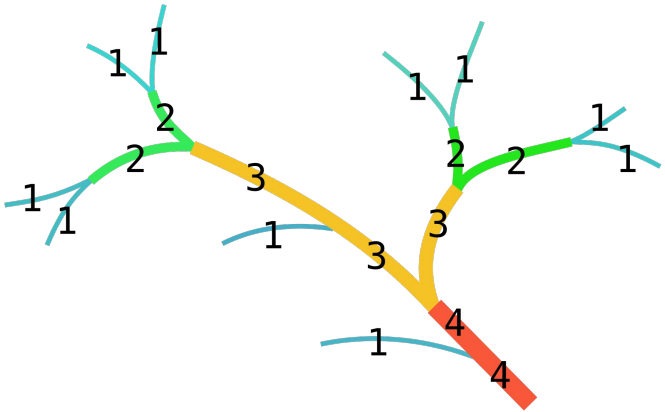


- Pseudo-alignment topology/morphological metrics




Strahler order - False lead

- Pseudo-alignment topology/morphological metrics




Strahler order - False lead