Graffinity: Visualizing Connectivity in Large Graphs
Supplemental Material

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1. Contents

In this supplemental document, we include an alternative derivation for the connectivity matrix based on properties of the adjacency matrix. This is followed by detailed images of our prototype software being used for connectivity analysis in a retina connectome.

2. Alternative Derivation for the Connectivity Matrix

An alternative derivation of the connectivity matrix follows from properties of adjacency matrices. Let $G = (N, E)$ be a graph with adjacency matrix M. The jth *power* of M is a matrix that represents paths of length j on G; two nodes are connected in M^j if they are connected by a j-hop walk on G [PS01].

If we are interested in searching for paths with length $< k$ on G then the connectivity matrix, C_k can be computed using the adjacency matrix: $C_k = \sum_{i=1}^{k} M^i$. Each entry of C_k will be non-zero if there is a path with length $< k$ connecting its corresponding nodes.

Although this derivation is useful for identifying whether paths exist, we use the query-based path-set technique to create our connectivity matrices. The derivation in our paper provides more information about the possible paths connecting two entities, rather than the presence of paths computed here.

3. Use case: retinal connectomics cone-rod crossover (expanded from paper)

In this section we provide more detailed information about the connectomics analysis described in our paper's use case. See Figures 1, 2, 3, 4, and 5 for details. Please see the paper for a description of the underlying data.
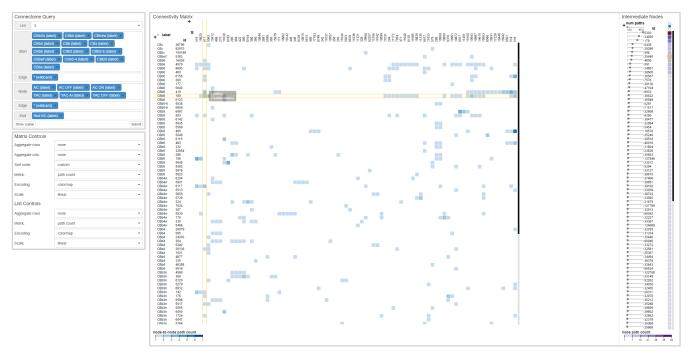
Figure 1: *We queried for cone-rod crossover circuitry using the connectome query interface (top-left). The query returned 272 paths connecting 90 start nodes to 74 end nodes. Highlighting reveals the intermediate nodes used in the paths from node 180 to node 517: nodes 25440 and 5303.*

Figure 2: *We aggregated the source and intermediate nodes by label to reveal patterns of communication between sets of nodes. Here, the bands in the rows of the connectivity matrix reveal some preferences for ON-cone bipolar cells (nodes with label CBb which hyperpolarize in response to light) driving the inhibition of rod bipolar cells (nodes with label Rod BC). We also see that certain labels are less represented than others. Attributes of the nodes, shown in the far left column of the connectivity matrix, provide context for this. For instance, the label CBx contains only two nodes with a relatively small number of annotations as shown by their position on the linear-scale number line.*

Figure 3: *We used the intermediate nodes matrix to inspect the crossover paths passing through nodes with label YAC Ai. We expect these nodes to only form connections with label CBb6. However, here we have hovered over node 179. The connectivity matrix's highlighting reveals that nodes of label CBb3 and CBb6 form paths with node 179.*
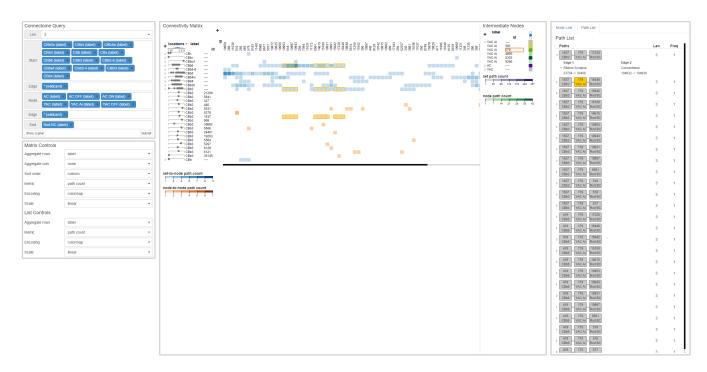

Figure 4: *We unrolled the connectivity matrix row containing cells with label CBb3. The connectivity matrix shows us that node 1673 forms connections with node 179. The path list view allows us to identify the ribbon synapses responsible for those paths.*
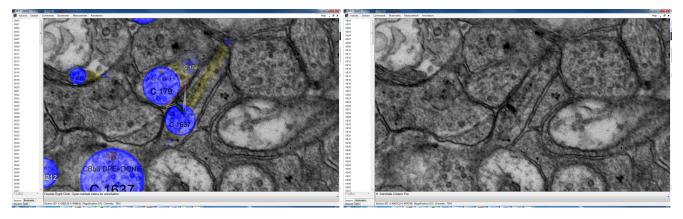
Figure 5: *We used connectome annotation software to examine the synapse connecting cell 1673 with cell 179. Here is the synapse with annotations (left) and with annotations hidden (right). In the right image, we see that this connection is not actually a ribbon synapse.*

4. Use Case: Retinal Connectomics Cone-bipolar Cell Tilling

We also used Graffinity to analyze direct connections of ON cone bipolar cells. Here, we demonstrate the cypher query interface, node aggregation, and sorting. See Figures 6, 7, and 8 for details. The resulting insight will influence future analysis of these cells.
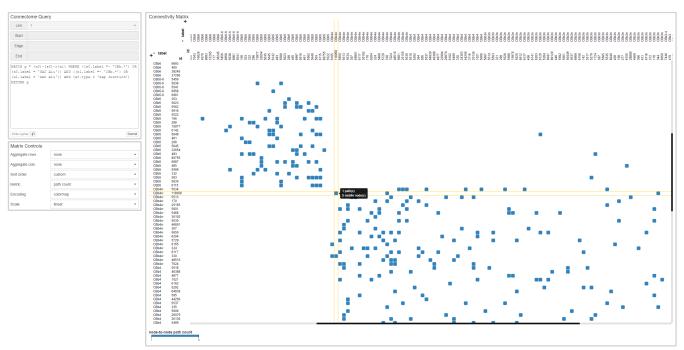
Figure 6: *We queried for direct connections of type Gap Junction between ON cone bipolar cells and a certain class of amacrine cell. Here are 1382 edges between 236 start/end nodes. We have sorted the rows and columns according to label, and we are particularly interested in the connections of nodes within and between labels. These connections are shown in the connectivity matrix as regions of square blocks (top-left vs bottom-right).*
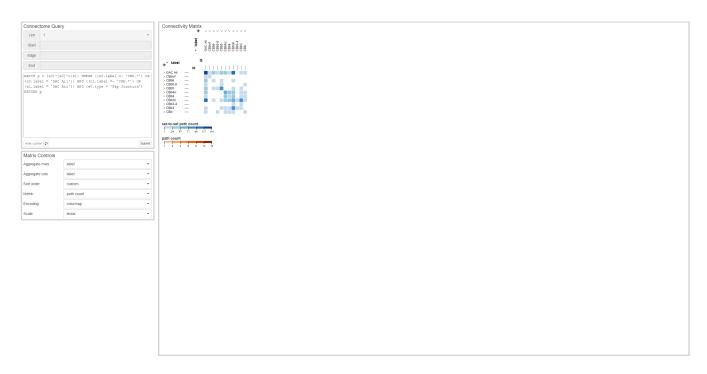

Figure 7: *We aggregated the start and end nodes by their labels to reveal connections between node types. This resulted in a symmetric matrix because gap junctions are bidirectional connections between cells. Uncertainty remains in the classification of some cells. For instance, cells with label CBb5-6 may actually belong to label CBb5 or CBb6, but more information is needed to resolve their classification.*

Figure 8: *We unrolled the row with label CBb5-6 to view the connections of individual cells in this label with other cone bipolar cell classes. Cells 5638 and 6958 form gap junctions with CBb5. Although more analysis is needed, this provides information valuable to identifying the correct label for these cells.*

References

[PS01] PEMMARAJU S., SKIENA S.: *Computational Discrete Mathematics: Combinatorics and Graph Theory with Mathematica*. Cambridge University Press, 2001. 1