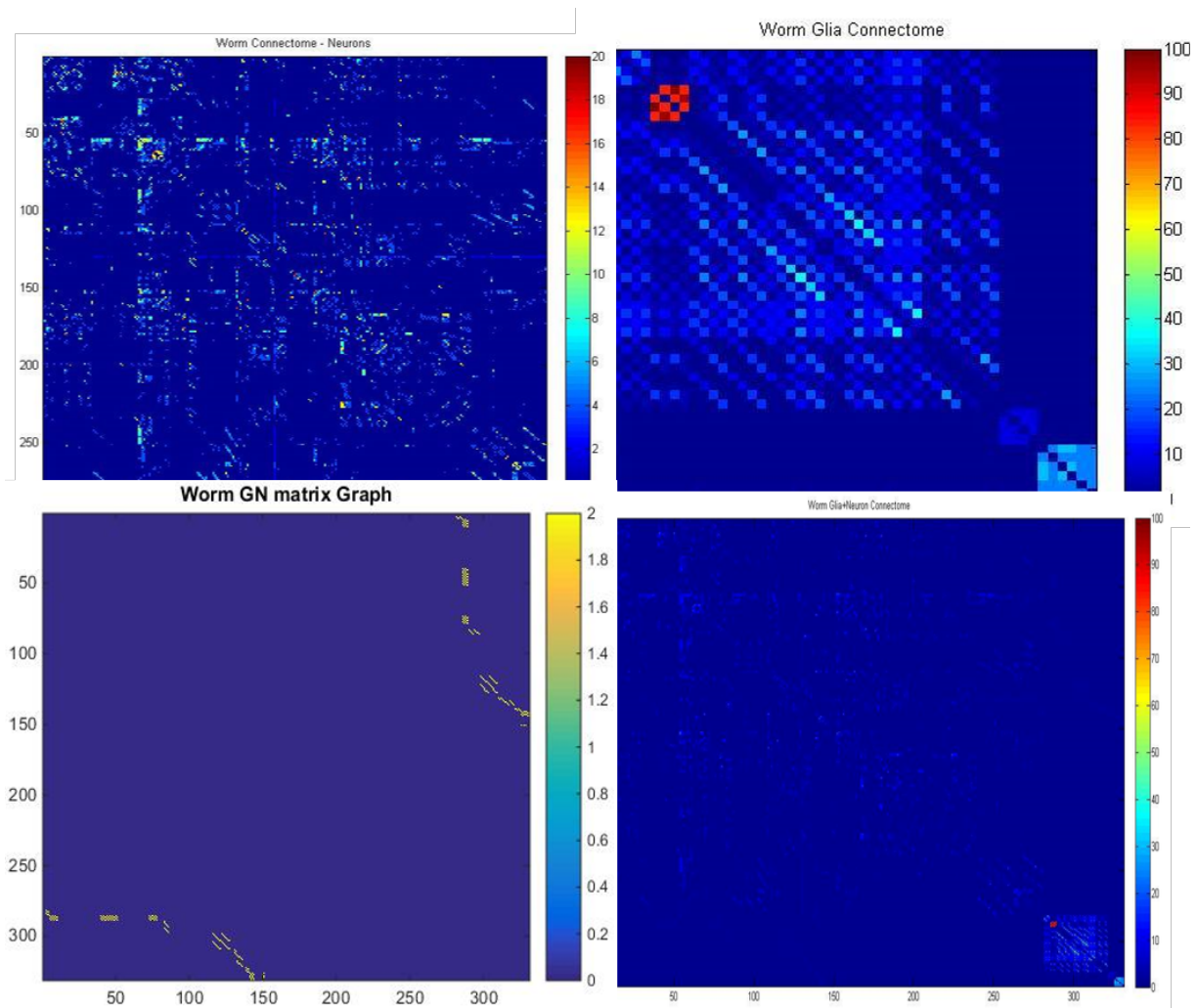


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Final Project Report

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Comparison of SBM and biSBM for the inferred C. elegans glia network



Opportunity The idea of including non-neuronal cell types in Connectomics have been posed by some authors, who claim that the exclusion of glia from the BRAIN Initiative makes the quest of Connectomics of understanding the brain futile [1]. These same authors have proposed the use of the *C. elegans* connectome data as starting point for the inclusion of glia in cell wiring studies. However, no action has been taken in the matter, and it remains uncertain whether their claims are valid or not. Do glia play a role in the *C. elegans* connectome? Are their roles important enough to consider them in connectivity studies? Does their exclusion make current Connectomics studies invalid? How are they organized? Many questions remain unanswered.

Challenge The precise *C. elegans* glia-glia wiring has never been investigated, which in terms slows down the study of the interactions of glial cells. However, the WormAtlas Project [2] does report a detailed neuron-glia adjacency list (with images included) and neuron-neuron connectivity data, from which the glia-glia network can be inferred.

Action The glia-glia adjacency matrix was inferred from the data available and the 'Worm Glial Connectome' was constructed. Additionally, the matrices for neuron glia, neuron neuron glia and neuron neuron connections were constructed too. A failed attempt of inferring the underlying block structure of the matrices was also carried out.

Resolution The matrices obtained are shown on the previous page and the adjacency lists obtained are available at <http://sandragomez21.weebly.com/txt-files—raw-adjacency-lists-and-matrices.html>. The glia population in the neuron neuron glia matrix appear to be clustered in a small community, with glial members that interact with the neurons interacting little with other glial cells (see glia neuron matrix for comparison).

Future Work Statistical analysis must be performed on the inferred networks to determine whether or not their structure is product of assumptions made when constructing the network, or errors in the algorithm used to produce the data. Additionally, permutation testing should be carried out to determine whether the observed structure in communities can be obtained by chance. We hope that this first step in computing the glial connectivity data can help to answer the questions posed above.

Bibliography

1. Nature 501, 2527 (05 September 2013), doi:10.1038/501025a
2. WormAtlas, Altun, Z.F., Herndon, L.A., Crocker, C., Lints, R. and Hall, D.H. (ed.s) 2002-2015. <http://www.wormatlas.org>