## Previous results

There are numerous papers that discuss neural circuits present in C. elegans, and their correlation with its functional behaviors. Those are usually verified by removing particular circuits from C. elegans and recording behavioral changes. Even for this well-known organism, very few work has been done in computationally analyzing the network structure using a general framework for understanding the correlation between network and functionalities, and discovering/verifying subnetwork circuits.

Recent paper (Towlson et al. 2013) has addressed the issue of finding important neurons (rich club) in the network by analyzing graph parameters including degree, clustering coefficient and network motifs. However, it only provides information about these important neurons, with no system view on organization of the entire network.

Topological clustering done by (Sohn et al. 2011) is so far the only comprehensive clustering analysis. It uses the method of simulated annealing to maximize intra-cluster synapses and minimize inter-cluster synapses. It belongs to the class of MCMC algorithms, which has the disadvantage of instability, i.e. there exist multiple convergent solutions for a network using different initial values. Additionally as shown in discussion, the inherent property of C. elegans connectome makes it hard to assign some neurons to a fixed cluster deterministically, especially the hub neurons. Thus we aim to find an algorithm that is more computationally efficient, stable and reproducible that characterizes both the important hub neurons and the role of all neurons in the entire connectome network.

# Discussion

## Functional significance

Our spectral analysis proves to be a useful tool in exploring the structure of a neural network by providing hub information and the sub-modules of the network of the respective hubs.

The minimum klinotaxis circuit identified (Izquierdo and Beer 2013), for example, is a typical circuit that resides in the left arm of the embedding.

The top arm contains circuits that requires coordination of relatively large amount of motor neurons corresponding to complex physical responses

The touch circuit as elaborated in (Chalfie et al. 1985) is a good example for cross-arm communication

## Structural significance

As can be seen in the above analysis, it is difficult to do a clear clustering of C-elegans neurons, primarily because (1) the hub analysis shows that neuron network lacks deep hierarchy: the hub neurons commonly acts globally (eg. AVA, AVB neurons) in the network, acting as the command neuron for a variety of behaviors. They cannot be effectively clustered. (2)

Instead, we propose a new model based on information flow analysis.

## Connection with spatial locations

In general our graph embedding is independent of spatial structure. However given that the synaptic connections are more likely to exist between neurons that are close together, the connectivity also encodes spatial information, though to a less extent.

The distinction between the top arm and right arm is largely spatial-based.

Izquierdo, Eduardo J., and Randall D. Beer. 2013. “Connecting a Connectome to Behavior: An Ensemble of Neuroanatomical Models of C. Elegans Klinotaxis.” Edited by Lyle J. Graham. *PLoS Computational Biology* 9 (2): e1002890. doi:10.1371/journal.pcbi.1002890.

Chalfie, M, J E Sulston, J G White, E Southgate, J N Thomson, and S Brenner. 1985. “The Neural Circuit for Touch Sensitivity in Caenorhabditis Elegans.” *The Journal of Neuroscience: The Official Journal of the Society for Neuroscience* 5 (4): 956–64.