## EN.580.694: Statistical Connectomics Final Project Proposal

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## Using a Random Dot Product Model to Approximate the (clustering?) of the C. Elegans Connectome

**Opportunity** The Paper by [1] contains an analysis of ERMM, SBM, [other two methods] for C. Elegans. There's an opportunity to do the same level analysis comparing ERMM as a baseline to a Random Dot Product Graph Model (RDP) on C. Elegans, and comparing the results. If using this method provides statistically significant results, then it may be a useful tool for connectomics.

**Challenge** The challenge to this problem is formulating the problem correctly, performing a correct statistical test on the connectome, and validating the results.

**Action** Random Dot Product Graph Model is a graph model that can be used in place of other models. I will test the Random Dot Product Graph Model using C. Elegans Data.

**Resolution** We will show whether the Random Dot Product Graph Model is able to cluster the connectome into similar modules as ERMM.

**Future Work** The results of this paper will give insight to when a Random Dot Product Graph Model could be used in a graph statistical problem.

REFERENCES

## Statistical Decision Theoretic

Sample Space The sample space is the connectome of C. Elegans.

**Model** The model is the RDP Graph Model. ERMM will also be used in a separate test as a comparison.

**Action Space** The Action Space is the distribution of all possible Random Dot Product Graphs.

Decision Rule Class The decision rule is block assignments for each vertex.

**Loss Function** The loss function is the Integrated Classification Likelihood so we can compare across different blocks. [1] equation (7).

$$ICL(\mathcal{M}_q) = max \log |\mathcal{L}(x, \tilde{z}|\mathcal{M}_q; \phi) - \frac{1}{2} \frac{Q(Q+1)}{2} \log \left[\frac{n(n-1)}{2}\right] - \frac{Q-1}{2} \log [n]$$

**Risk Function** The risk function is the expected value of the loss function R = E[].

## References

[1] D. M. Pavlovic, P. E. Vértes, E. T. Bullmore, W. R. Schafer, and T. E. Nichols. Stochastic Blockmodeling of the Modules and Core of the Caenorhabditis elegans Connectome. *PLoS ONE*, 9:97584, July 2014.