EN.580.694: Statistical Connectomics
Final Project Report

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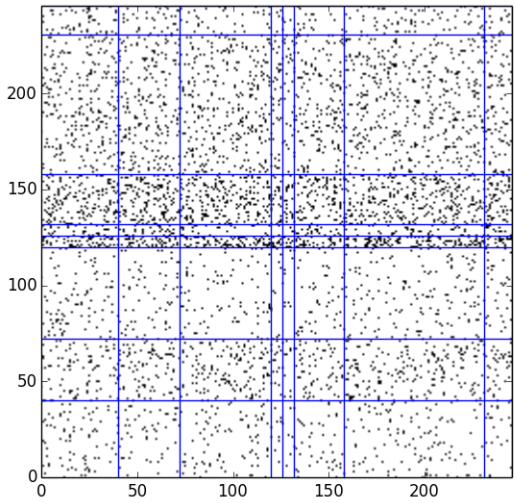
Title



Opportunity Graph Models allow us to generate similar graphs from a smaller amount of parameters. If we can model connectomes well, then a good model allows us to generate similar connectomes to perform statistical analysis on similar graphs. The paper by Pavlovic [**?**] used the Erdos Reyni mixture model as an approximation of the C. Elegans connectome. Using other graph models to perform the same analysis will aid future researchers in selecting tools for connectomics work.

Challenge

Action The Random Dot Product Graph Model (RDPG) represents

Resolution Shown above is the TRT result for each atlas using graphs from the KKI2009 dataset. We can see here that with the provided graphs, the Desikan and Harvard-Oxford atlases correctly match 41 of 42 scans and have 70 and 48 regions, respectively. The Juelich and Talairach atlases both correctly matched all subjects and have 121 and 1106 regions, respectively. It can also be seen that the Talairach atlas has much higher discrimination across subjects than the other three atlases, as indicated by the larger dynamic range of image intensities. This suggests that parcelation schemes with too few regions may discard useful information about the brain graphs.

Future Work Moving forward, it we will evaluate whether or not specific atlas region labels matter when performing comparing graphs, or rather the scale/number of regions. Randomly permuted atlases could be generated over a large range of scales and a peak operating point determined. This information can aide in building better, more interpretable classifiers for inference and diagnosis.

References

[1] Pavlovic DM, Vrtes PE, Bullmore ET, Schafer WR, Nichols TE (2014) Stochastic Blockmodeling of the Modules and Core of the Caenorhabditis elegans Connectome. PLoS ONE 9(7): e97584. doi: 10.1371/journal.pone.0097584