GraSPy: an Open Source Python Package for Statistical Connectomics

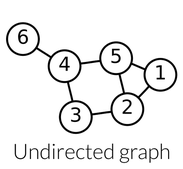
Benjamin D. Pedigo[1], Jaewon Chung[1], Eric W. Bridgeford[2], Bijan Varjavand[3], Carey E. Priebe[3], Joshua T. Vogelstein[1]

[1]Department of Biomedical Engineering, Johns Hopkins University [2]Department of Biostatistics, Johns Hopkins University [3]Department of Applied Mathematics and Statistics, Johns Hopkins University

Summary

- Connectome datasets are growing in size
- Analysis is a current bottleneck
- Graphs (networks) are natural models
- Require specific statistical tools and implementations [1]
- `GraSPy`: open source python toolkit [2]
- Graph sampling, estimation, embedding, testing
- Accelerate understanding of connectomes with valid graph inference
- Available at neurodata.io/graspy

Graphs



Undirected graph

$$\begin{pmatrix} 0 & 1 & 0 & 0 & 1 & 0 \\ 1 & 0 & 1 & 0 & 1 & 0 \\ 0 & 1 & 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 & 1 & 1 \\ 1 & 1 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 \end{pmatrix}$$

Adjacency matrix A

- Model adjacency matrices as samples from a matrix of probabilities P:

$$A \sim Bernoulli(P) \quad P \in \mathbb{R}^{n \times n}$$

- Latent position random graphs: latent vector for each node determining probability of connections
- Find P using the dot product of the latent positions

$$P = XX^T, \quad X \in \mathbb{R}^{n \times d}$$

where row i of X is a latent vector for node j [1]

Random Graph Models

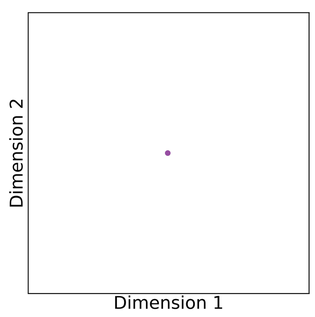
Graph model	Latent representation	Realization (sample)

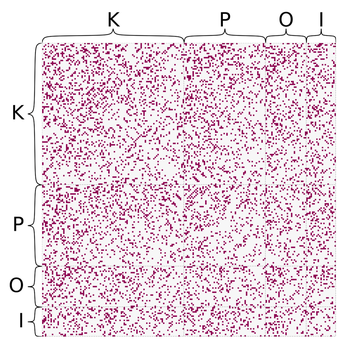
Ernyos-Reyni (ER):

$$p_{ij} = p$$

p is overall connection probability

Latent representation: all nodes share same latent position



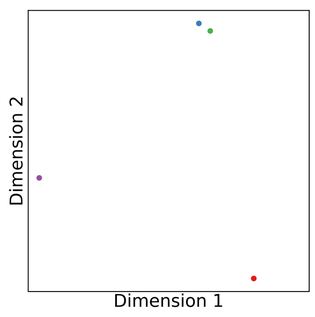


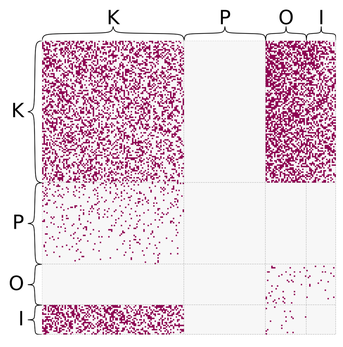
Stochastic block model (SBM):

$$p_{ij} = B_{\tau_i, \tau_j}$$
$$B \in [0,1]^{K \times K}, \tau \in \mathbb{R}^n$$

B contains block-block connection probabilities, τ block assignments

Latent representation: nodes in a block share same latent position.



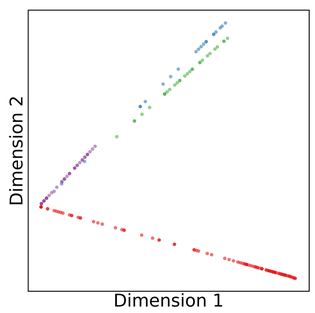


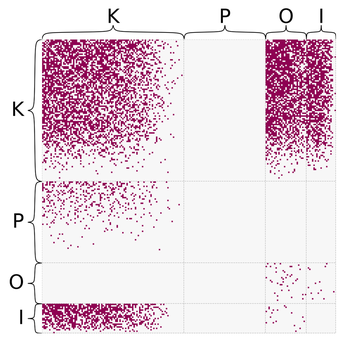
Degree-corrected SBM (DCSBM):

$$p_{ij} = B_{\tau_i, \tau_j} d_i d_j$$
$$d \in \mathbb{R}^n$$

$d \in \mathbb{R}^n$ represents expected degree for each node

Latent representation: nodes in block live on a line, expected degree determines their position on line



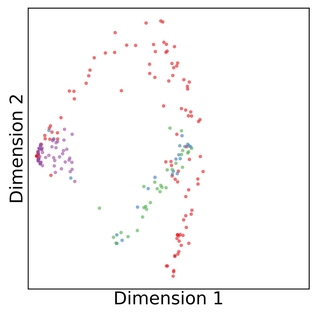


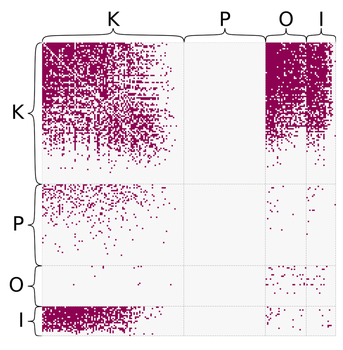
Random dot product graph (RDPG):

$$p_{ij} = \langle x_i, y_j \rangle$$
$$x_i, y_i \in \mathbb{R}^d$$

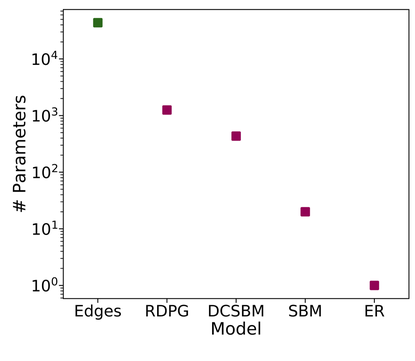
x_i, y_j are latent positions for node i, j

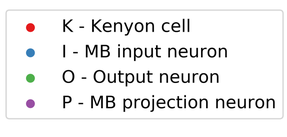
Latent representation point in $\mathbb{R}^d$ for each node





Model parameters	Cell type legend	Original graph





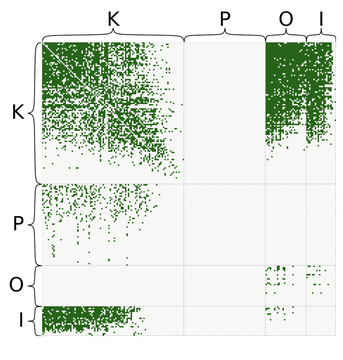


Figure 1. Four random graph models displayed with their corresponding representations in latent space and a sample from the graph model. All graph models are fit to the *Drosophila* left mushroom body from Eichner et al [4]. The latent space representations are calculated by computing an adjacency spectral embedding of the estimated probability matrix from each model.

Graph embeddings

- Embeddings convert graphs into Euclidian representations, allowing subsequent inference and estimation
- Multigraph embeddings can place a population of graphs in the same latent dimensions
- Embeddings such as adjacency spectral embedding (ASE) can be generative models for random graphs (Figure 1).

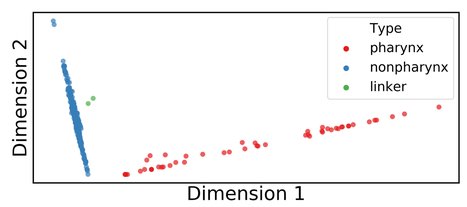


Figure 2. Laplacian spectral embedding (LSE) on the hermaphrodite C. elegans connectome [3], showing pharynx/nonpharynx division

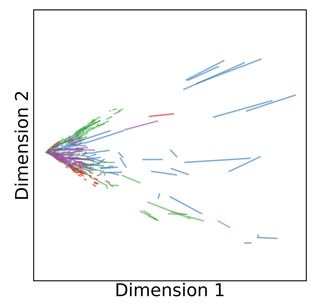


Figure 3. Omnibus embedding of the male and hermaphrodite *C. elegans* connectome, lines show disparity between sex for each node

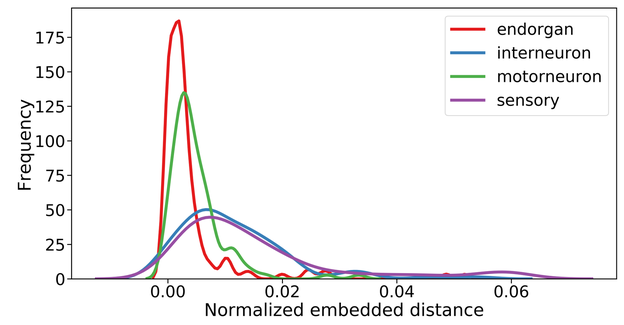


Figure 4. Kernel density estimates (KDEs) of distances in the embedding plotted by cell type, color coded as in Figure 3

Graph hypothesis testing

- How to test if two graphs (G_1 and G_2) were generated from same distribution?

$$G_1 \sim P_1, G_2 \sim P_2$$
$$H_0 : P_1 = P_2, \quad H_a : P_1 \neq P_2$$

- `GraSPy` implements two such hypothesis tests
  - **Matched test**: correspondence between node identities is known
  - **Unmatched test**: correspondence between nodes is unknown or does not exist

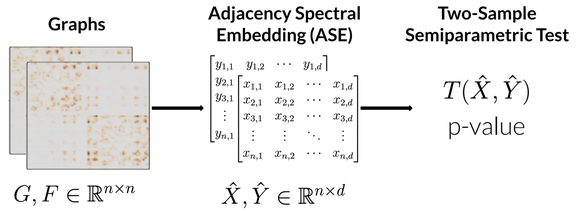


Figure 5. Procedure for the matched test of Tang et al. [5]. Two graphs are embedded using ASE, embeddings are aligned, test statistic is computed as distance between the aligned embeddings.

- Different ways to compare latent positions:
  - Exact:

$$H_0 : X = YW$$
$$H_a : X \neq YW$$

$W \in \mathbb{R}^{d \times d}$ and $WW^T = I$

  - Scaling:

$$H_0 : X = cYW$$
$$H_a : X \neq cYW$$

for some $c > 0$

  - Diagonal:

$$H_0 : X = DYW$$
$$H_a : X \neq DYW$$

for some diagonal $D \in \mathbb{R}^{n \times n}$

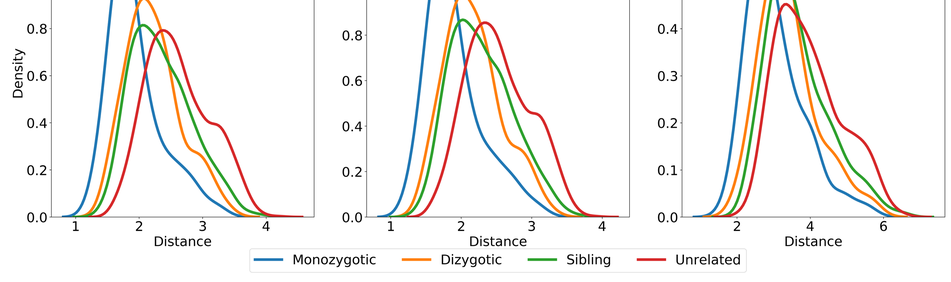


Figure 6. KDEs of matched test statistics for dMRI connectomes from Human Connectome Project Young Adult study [6], compared for different levels of relatedness

Conclusion

- `GraSPy` provides tools for graph hypothesis testing and estimation
- Tools will allow neuroscientists to make claims about graph-value data
- `GraSPy` will continue to grow and add functionality - in particular, we aim to consider node and edge attributes

References

[1] Avanti Athreya, Donniell E. Fishkind, Minh Tang, Carey E. Priebe, Youngser Park, Joshua T. Vogelstein, Keith Levin, Vince Lyzinski, Yichen Qin, and Daniel L Sussman. Statistical inference on random dot product graphs: a survey. *Journal of Machine Learning Research*, 18(226):1–92, 2018.

[2] Jaewon Chung*, Benjamin D Pedigo*, Eric W Bridgeford, Bijan K Varjavand, and Joshua T Vogelstein. GraSPy: Graph statistics in python. March 2019.

[3] Cook, S. J., Jarrell, T. A., Brittin, C., Wang, Y., Bloniarz, A. E., Yakovlev, M. A., Nguyen, K. C. Q., Tang, L. T.-H., Bayer, E. A., Duerr, J. S., Buelow, H., Hobert, O., Hall, D. H., and Emmons, S. W. Whole-animal connectomes of both c. elegans sexes. *Nature*, 2019.

[4] Katharina Eichler, Feng Li, Ashok Litwin-Kumar, Youngser Park, Ingrid Andrade, Casey M Schneider-Mizell, Timo Saumweber, Annina Huser, Claire Eschbach, Bertram Gerber, et al. The complete connectome of a learning and memory centre in an insect brain. *Nature*, 548(7666):175, 2017.

[5] Minh Tang, Avanti Athreya, Daniel L. Sussman, Vince Lyzinski, Youngser Park, and Carey E. Priebe. A semiparametric two-sample hypothesis testing problem for random graphs. *Journal of Computational and Graphical Statistics*, 26(2):344–354, 2017.

[6] David C Van Essen, Stephen M Smith, Deanna M Barch, Timothy EJ Behrens, Essa Yacoub, Kamil Ugurbil, Wu-Minn HCP Consortium, et al. The wu-minn human connectome project: an overview. *Neuroimage*, 80:62–79, 2013.