Identifying Predictive Features in Brain Connectome Data

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DIMACS REU at Rutgers University

June 2022

Brain Connectome Data

What is brain connectome data?
Brain networks can be described as graphs where edges are between regions that "fire together".

- fMRI measures activation of voxels over time
- Calculate time dependent activation correlations
- Pick threshold correlation to define "fire together"
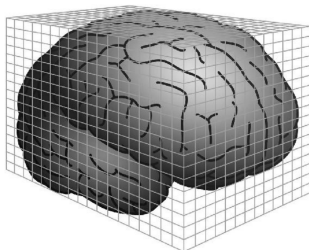- Create graph

Figure 1-7: The human brain divided into voxels

(1)

Goals

Our goal is to find **novel features** of the connectome that can predict various behavioral, psychological, and demographic information.

E.g. Can we predict whether a participant is male or female from their connectome data?

Our analysis is partitioned into two themes:

- **local** connectome features (via motifs)
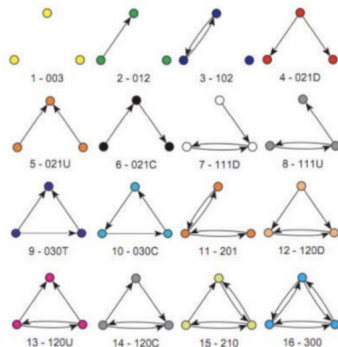- **global** connectome features (via persistent homology)

Motifs

Motifs: Sub-graphs that occur more often than would be expected in a random graph

- Triangle graph in social networks
- Triad motifs predict conscious state[2]

Motifs are going to be a proxy for local structure.

- Frequency of particular motifs
- Proportion of structural-function motifs
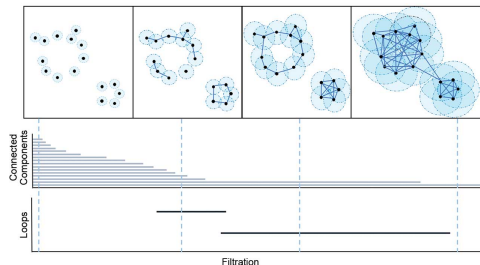

(3)

Persistent Homology

We want to learn how to abstract the global connectivity for graph learning

Process

- obtain time series data of fMRI scans
- construct graphs for each data set
- construct the node representation vectors
- identify a proper filtration
- apply persistent homology methods to obtain persistent bar codes $\rightarrow$ help expose significant features

(4)

References

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(3) Braines, D., Felmlee, D., Towsley, D., Tu, K., Whitaker, R. M., & Turner, L. D. (2018). The role of motifs in understanding behavior in social and engineered networks. In J. Llinas, & T. P. Hanratty (Eds.), Next-Generation Analyst VI [106530W] (Proceedings of SPIE - The International Society for Optical Engineering; Vol. 10653). SPIE. https://doi.org/10.1117/12.2309471

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Acknowledgements

- Thank you to our mentor Dr. Jie Gao!
- Additional thanks to Rutgers University for hosting us as part of the 2022 DIMACS REU program
- This research is funded by NSF HDR TRIPODS award CCF-1934924