



Exploring the functional networks of the resting brain with topological data analysis

Rafi Ayub^{1,2}

¹Department of Bioengineering

²Department of Psychiatry and Behavioral Sciences

Introduction

Background

- The brain exhibits **intrinsic activity** with nuanced structure and **rich dynamics** even at rest when it is performing no explicit task [1]
- Consistent patterns of correlations between regions, known as **resting state networks (RSNs)** show diverse interactions at rest
- Psychiatric disorders have been linked to the **dysregulation** of these networks; changes in **mood or arousal** can also affect network dynamics [2][3]

Problem

- Current methods of characterizing **resting state functional connectivity** are **linear** and may fail to reveal important **non-linear structure** and relationships between brain regions and networks
- How does **physiological state**, such as **fasting**, change brain dynamics?

Solution

- Non-linear methods from **topological data analysis (TDA)** may provide unique insight into the brain's functional architecture

Methods

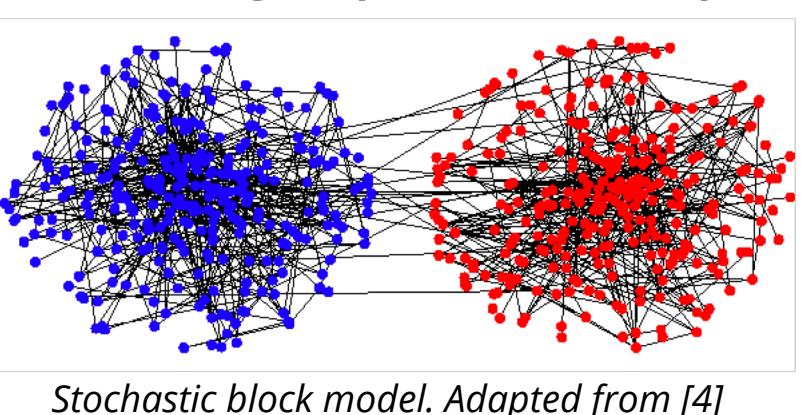
Dataset

- MyConnectome: complete metabolic profile + **84 fMRI scans of a single subject** over a year – 31 in fed state, 40 in fasted state

Mapper

Tool from **TDA/manifold learning** that can capture the structure of the data

- Project data into lower-dimensional embedding using **tSNE**
- Bin points according to resolution parameter
- Bins on lower-dim points guide partial clustering on original high-dim points – we use **hierarchical clustering, HBDSCAN**
- Result is a graph that represents the “shape” of original data



Stochastic block model. Adapted from [4]

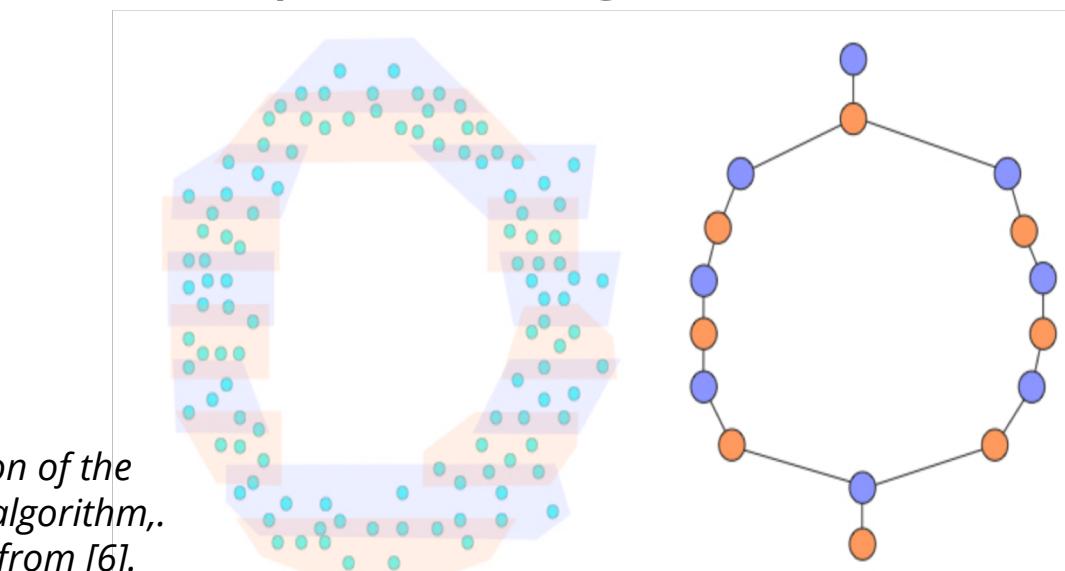
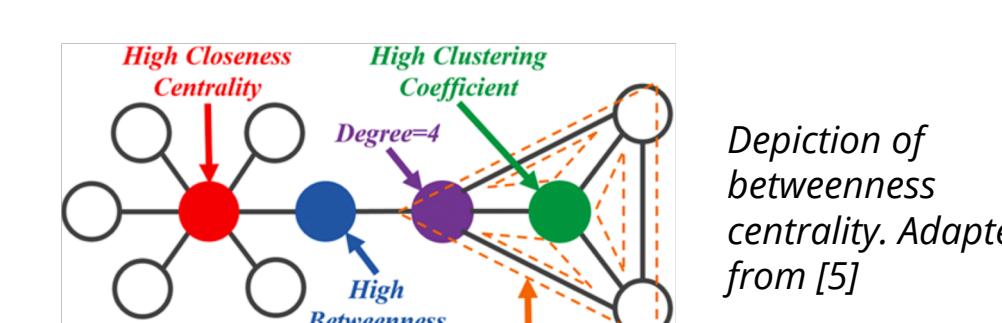


Illustration of the Mapper algorithm. Adapted from [6].



Depiction of betweenness centrality. Adapted from [5]

Network analysis

- Betweenness centrality
- Within-module degree
- Participation coefficient
- Modularity/community structure
- Stochastic Block Model (SBM)

Results and Discussion

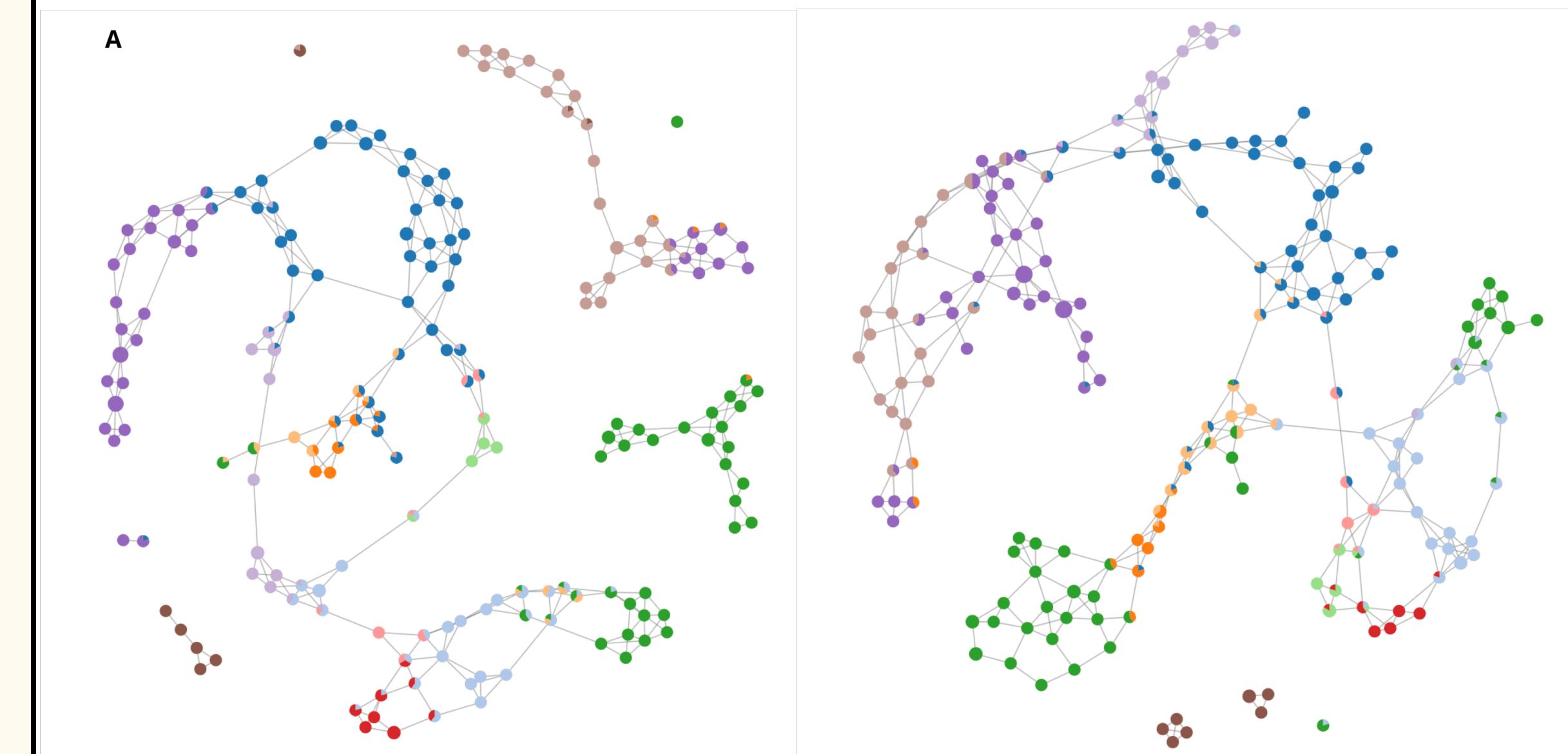


Figure 1: (A) Mapper graphs created by running once on all scans concatenated for fasted state, fed state, and the null SBM, from left to right. (B) Legend assigning each color to an RSN. (C) Comparison of graph modularity by using RSN labels as community assignments.

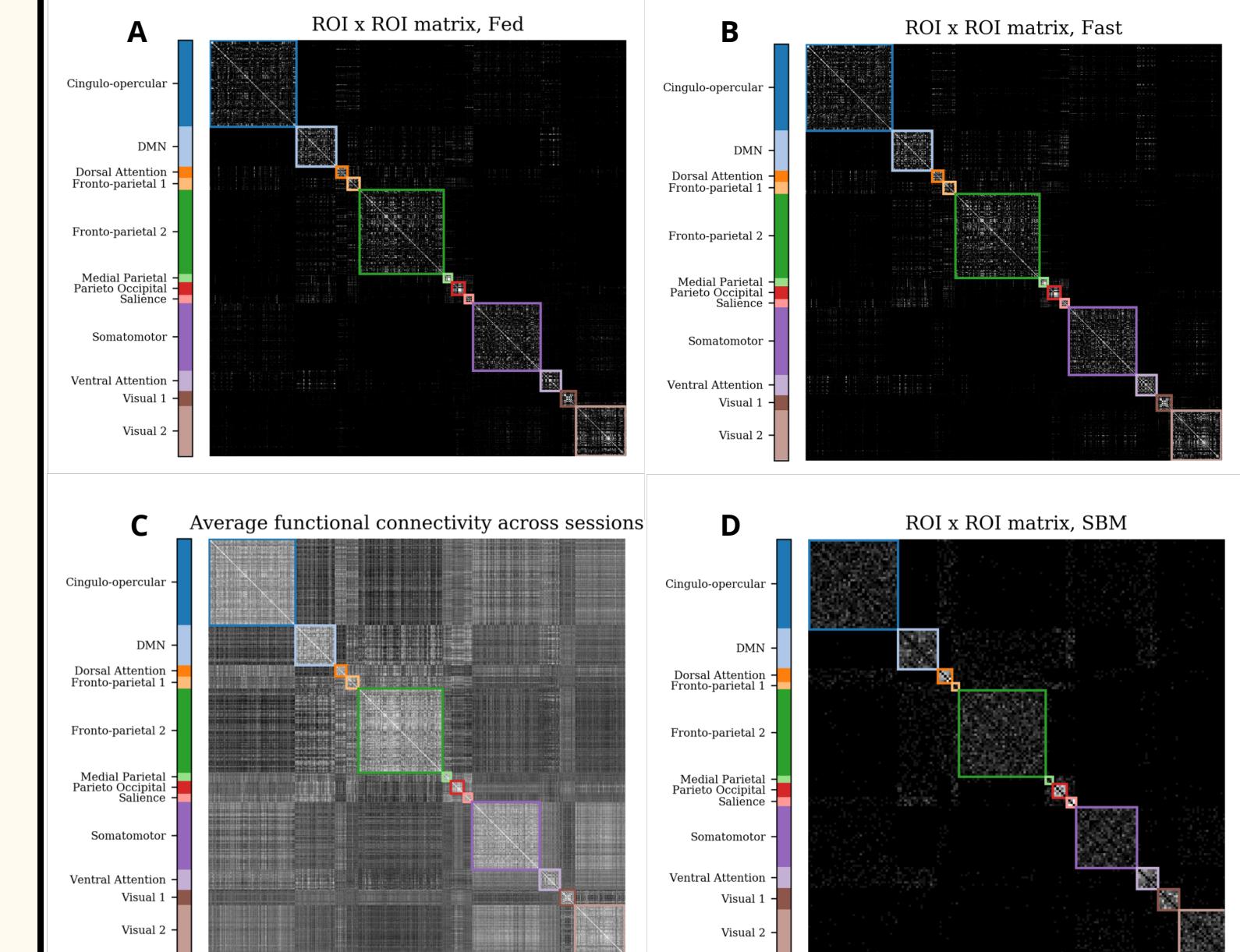


Figure 2: ROI x ROI adjacency matrix (ROI = region-of-interest), where each row or column is a subject-specific parcellated brain region. A matrix element is 1 if the ROIs corresponding to the row and column are found in the same node or are in two connected nodes. The matrix was averaged across all scans – 31 for fed (A), 40 for fasted (B), all 84 for SBM (D). These are compared to the average correlation matrix of the ROIs' timeseries across all scans, showing that the Mapper graph can embody these relationships.

- Networks tend to have their **own roles** and **connect to other networks preferentially**. Ex: DMN tends to connect with many RSNs, FP1 tends to hang in periphery
- Real brain graphs exhibits higher **modularity**, **participation coefficient**, **within-module connectivity** than SBM
- RSNs in fasted state show **higher participation** across the board
- RSNs in real brain graphs show **more internal structure** than SBM, demonstrating that structure is **not solely due to self-preference**

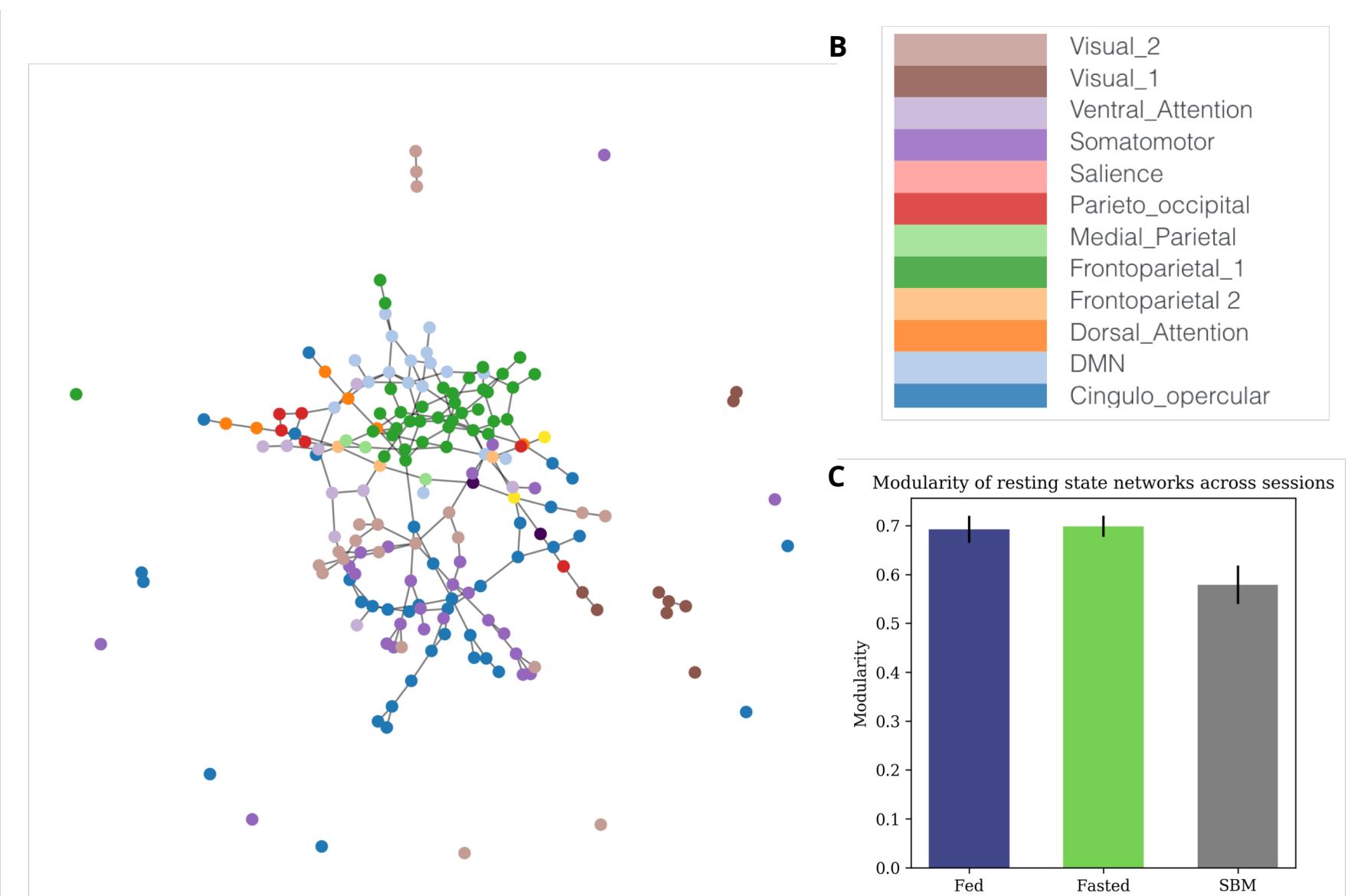


Figure 3: Comparison of participation coefficient (A), within-module connectivity (B), and betweenness centrality (C) among the three types of graphs. Values were averaged across all nodes within an RSN within a scan, and then averaged across all scans.

References

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Conclusions

- Brain networks have high participation coefficient yet maintain high within-module degree. The brain is **modular** and **optimizes integration and segregation of function**
- In the fasted state, brain networks **communicate with one another more often** than in the fed state