Towards a new approach to reveal dynamical organization of the brain using topological data analysis

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- They observe that the revealed individual differences in the dynamical organization of the subject were predictors of the task performance

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- The previous approaches have been unable to reveal the optimal temporal and spatial scales which best probe clinically and behaviorally relevant brain dynamics
- Additionally, they are unable to determine if the brain dynamics are best thought of as continuous or discrete or able to tell whether a particular brain activity is healthy or not

Pipeline

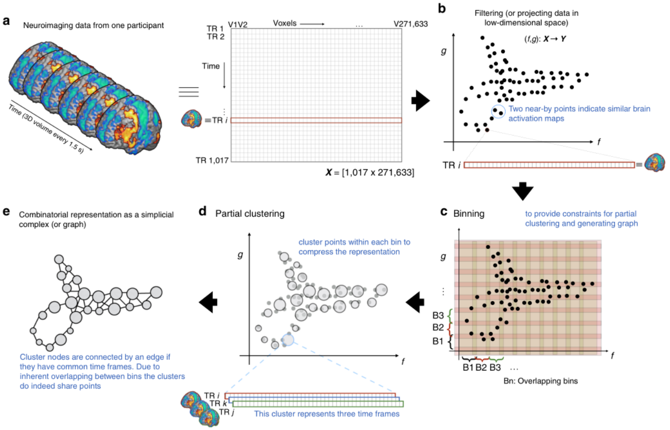

Figure: The method used to convert the 4-dimensional fMRI data into a simplicial complex. Steps b-e are a part of Mapper (the TDA-based algorithm/tool the authors used).

How Mapper works

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- Step 4 treats each cluster as a vertex of a graph and adds an edge between two vertices if they shared a point[4]

Filtering in Mapper

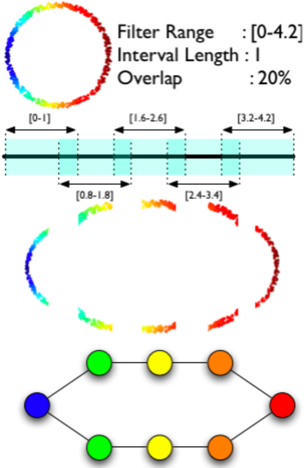

Figure: Toy example of applying a filter to data[4]. The data is sampled from a noisy circle, and the filter used is $f(x) = ||x - p||^2$, where p is the left most point in the data. We divide the range of the filter into 5 intervals which have length 1 and a 20% overlap. For each interval we compute the clustering of the points lying within the domain of the filter restricted to the interval, and connect the clusters whenever they have non-empty intersection. At the bottom is the simplicial complex which we recover whose vertices are colored by the average filter value.

Diagram of the Filtering process

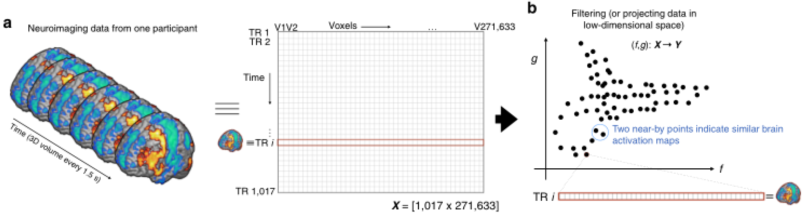

Figure: Our paper uses a very different filter function than the previous example. They use something called the Neighborhood Lens function to take their 271633-dimensional data into $\mathbb{R}^2$. This function is part of a patented software that appears to be standard.

Clustering

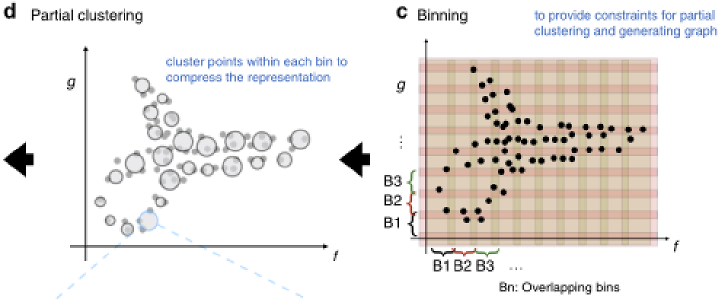

Figure: Mapper take two parameters when binning the data: Resolution and Gain. Resolution controls the number of bins and Gain controls the overlap between bins.

Example

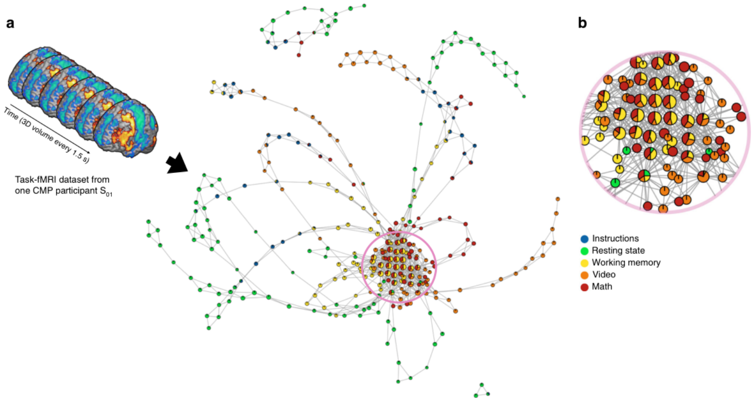

Figure: After running Mapper on an individual's fMRI data, we are left with a graph like the above. The fMRI datasets (1017 $\times$ 271633) matrix) were compressed to 279 $\pm$ 60 points.

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- This paper doesn't describe how they acquire weights on the edges and there is no canonical way to assign weights from mapper
- Two likely possibilities: the weight between two nodes is the number of timeframes they shared, or the weight is something that depends on the mean distance between the timeframes constituting the nodes

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$$Q_{\mathrm{mod}} = \sum_{i,j} (A_{ij} - P_{ij})\,\delta(g_i, g_j)$$

where A is the adjacency matrix, $P_{ij} = \frac{k_i k_j}{\sum_{ij} A_{ij}}$, k_i is degree of i, g_i is the community that i belongs to, and δ is the Kronecker delta.

Some intuition for Q_{mod}

- It is based on the idea that a random graph is not expected to have a cluster structure, so the possible existence of clusters is revealed by the comparison between the actual density of edges in a subgraph and the density one would expect to have in the subgraph if the vertices of the graph were attached regardless of community structure
- This expected edge density ($P_{ij} = \frac{k_i k_j}{2m}$ where $m = \sum_{ij} A_{ij}$) depends on the chosen null model, i.e. a copy of the original graph keeping some of its structural properties but without community structure[1]

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- In this case, the null model that produces the above expected edge density is called the configuration model. This a very standard type of model in network science because, as opposed to the Erdős-Renyi model, this model allows us to give the network arbitrary degree distributions. (The Erdős-Renyi model only allows for Poisson distribution for the degree sequence).

How Q_{mod} scales

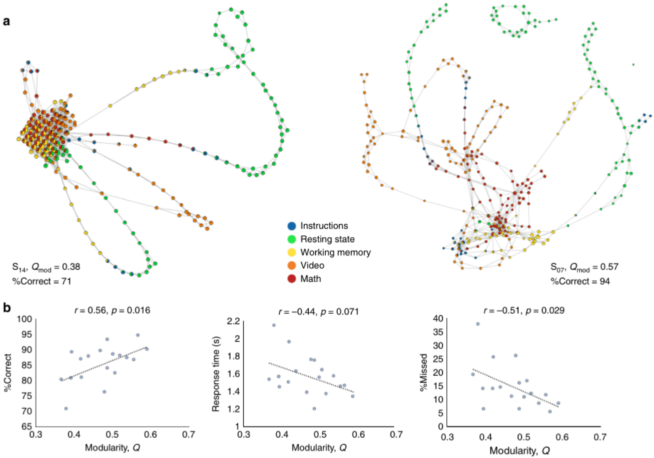


Figure: There are two different participants' shape graphs and the relations between modularity and various metrics

Analyzing the core-periphery structure of the graph

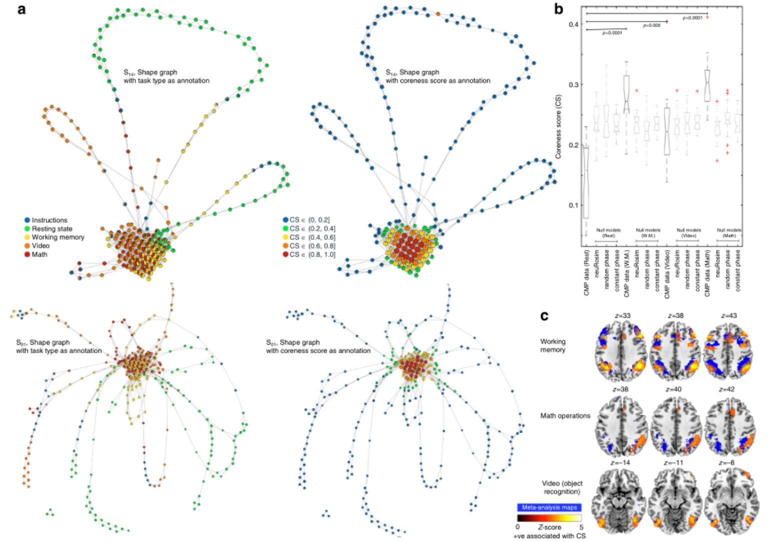
- We assign each node a coreness score (CS) by giving higher scores to nodes which lie deeper in the network
- The Borgatti-Everett algorithm is an algorithm that assigns coreness scores to each vertex of the shape graph. If we call C_i is the coreness of vertex i, then we can define the core matrix C by $C_{ij} = C_i C_j$. We can define a quality function

$$R_{(\alpha,\beta)} = \sum_{i,j} A_{ij} C_{ij}$$

where (α, β) are the two parameters which determines the boundary between the core and periphery and size of the core respectively. A large α indicates a sharp transition.
-
$$CS(i) = Z \sum_{(\alpha,\beta)} C_i(\alpha, \beta) \times R(\alpha, \beta)$$

where Z is a normalization factor to make the maximum CS be 1 and this sum is not actually over all α, β but instead over a uniform

How coreness score (CS) scales



Trying to explain the topological features using anatomy

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Connectivity in the shape graph for different times

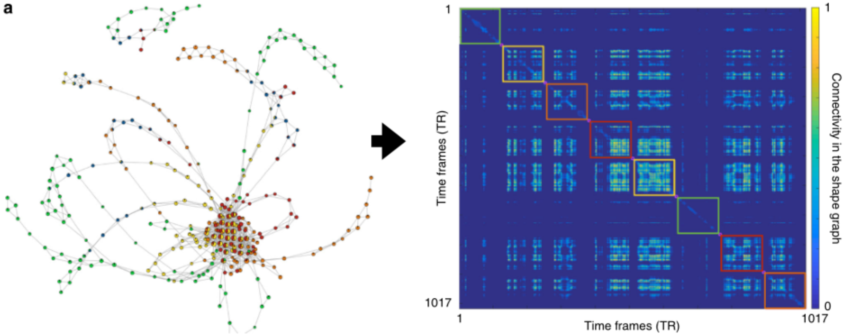

Figure: Shows which times during the scan were similar to other times by looking at the connections between times in the shape graph.

Brains are typically more connected during strenuous tasks

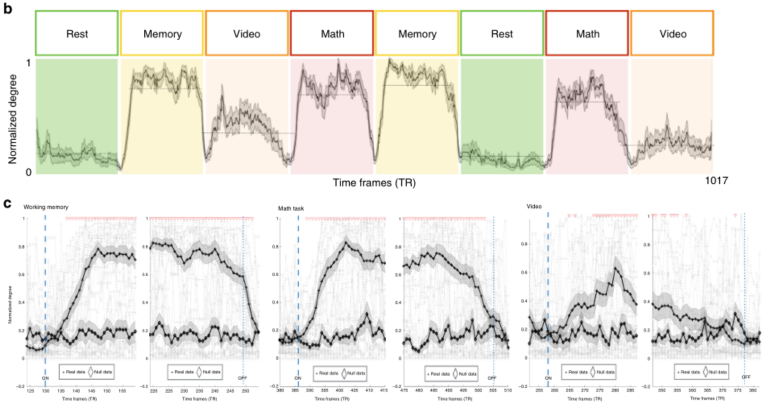

Figure: When there is a transition between tasks, this is captured by a dramatic change in the degree of the corresponding nodes. This phenomenon of nodes taken during strenuous activity having high degree is significant

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[4] Gurjeet Kaur Chatar Singh, Facundo Mémoli, and Gunnar E. Carlsson. "Topological Methods for the Analysis of High Dimensional Data Sets and 3D Object Recognition". In: (2007).

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