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1 General remarks

- Starting with a white matter structure, the authors looked into cliques and cycles. Cliques are sets of regions that possess similar function, operate in unison, or share information rapidly. The authors also investigated cycles that correspond to paths of potential information transmission along which computations can be performed serially to affect cognition in either divergent or convergent manner.
- Cycles are observed in subcortical-cortical loops particularly engaging weakly connected areas in the evolutionarily more recent structures of the prefrontal cortex.
- Cliques are observed in high densities in the rich-club linking network hubs at the brain’s structural core.

2 Materials

- DSI data from 8 healthy adult volunteers, 3 days (24 total scans).
- Lausanne parcellation of 83 regions used for nodes.
- Edges between nodes using the number of streamlines (also normalized).
- Symmetric weighted adjacency matrices, thresholded at $\rho = 0.25$ for consistency with previous work; see here <http://arxiv.org/abs/1512.06457>.

3 Methods

1. A $k + 1$ -clique: set of $(k + 1)$ -nodes such that all pairwise edges exist (nodes, edges, triangles, and so on).
2. For a graph of size N , its clique complex is the set of set of cliques:

$$X(G) = \{X_0(G), X_1(G), \dots, X_N(G)\} \quad (1)$$

where $X_k(G)$ is the set of all $k + 1$ -cliques.

¹The paper can be found here <https://arxiv.org/abs/1608.03520>.

3. Consider now $C_k(X(G))$ ², the chain group with basis element $k + 1$ -cliques

$$\sigma_{i_1}, \sigma_{i_2}, \dots, \sigma_{i_k} \in C_k(X(G)) \quad (2)$$

This is a basis of a vector space and therefore linear combinations of these produce collections of $k + 1$ -cliques (consider these as chains that produce cliques). Here, vector spaces are over the field $\mathbb{F}_2 = \{0, 1\}$.

4. Alright, so now consider the boundary operator which is an operator that maps elements of C_{k+1} to elements of C_k :

$$\partial_k : C_k \rightarrow C_{k-1} \quad (3)$$

and defined as

$$\partial_k(\sigma_{0,1,\dots,k}) = \sum_{i=0}^k \sigma_{0,1,\dots,\widehat{i},\dots,k} \quad (4)$$

The symbol \widehat{i} stands for the vertex i not included in the set of vertices that form the clique (basically you want to go to a lower dimension).

5. Now, the chain complex is defined as

$$\xrightarrow{\partial_{k+1}=0} C_k \xrightarrow{\partial_k} C_{k-1} \dots \xrightarrow{\partial_2} C_1 \xrightarrow{\partial_1} C_0 \xrightarrow{\partial_0=0} 0 \quad (5)$$

This lets us move from k -chains to $k - 1$ -chains for all k (with the boundary being moving from 0-chains to zero).

6. In turn, (as with every operator) it useful to define the kernel of ∂_k , $ker(\partial_k)$, i.e., the elements of C_k that are mapped to 0. One can write

$$ker(\partial_k) \subset C(X_k(G)) \quad (6)$$

These are called the k -cycles

$$l \in C_k \text{ s.t. } \partial_k(l) = 0 \quad (7)$$

The 1-cycle (one-dimensional cycle) is the well known circuit. Crucially, cycles can contain either cavities or collection of cliques.

7. Also, consider the image $im(\partial_k)$ of the operator where it holds

$$im(\partial_k) \subseteq ker(\partial_k) \quad (8)$$

²attention! later the $C_k(X(G))$ will be replaced by the simpler C_k considering the $X(G)$ is well-defined

8. Now, one needs to look for cycles surrounding cavities; basically we need to consider only the second category of cycles, i.e., cycles that do not contain a collection of cliques. To do so, define k -boundaries as elements in

$$im(\partial_{k+1}) \subseteq C_k(X(G)) \quad (9)$$

9. However, not all cycles are boundaries. The final refinement considers k -cycles l_i and l_j that are equivalent if their sum (defined over \mathbb{F}_2) is the boundary of $k+1$ -chain. The equivalent class of a k -cycle is the set $[l] = \{\nu \in Z_k | \nu \sim l\}$.³ Also, cycles differing by boundaries are equivalent.

10. Alright, now the homology is the number of the proper cycles (the ones enclosing cavities) as we defined previously

$$H_n := ker(\partial_n)/im(\partial_{n+1}) \quad (10)$$

11. Now, we want to talk about persistent homology (how homology is applied to weighted data like the one stemming from white matter structure). Basically, one can create a chain of graphs by adding one edge at a time. This creates a filtration

$$G_0 \subset G_1 \subset \dots \subset G_{|E|} = G \quad (11)$$

where each G_i has an edge less from G_{i+1} . This creates a mapping of cliques from $X(G_i)$ to $X(G_{i+1})$

$$f_* : C_*(X(G_i)) \rightarrow C_*(X(G_{i+1})) \quad (12)$$

where the $*$ refers to the function indexed by dimension.

12. As one can see this is a two-dimensional “game”: imagine on the y-axis going from $C_{j+1}(X(G_i))$ to $C_j(X(G_i))$ and in the x-axis going from $X(G_i)$ to $X(G_{i+1})$. Therefore one can obtain all the homologies in this xy “plane”.

13. It is interesting now how cycles persist throughout this procedure. Cycles that are born and survive edge additions are important. The density of the edges during the birth of an edge is defined as

$$\rho_{birth} = \frac{|edges\ present|}{|edges\ possible|} \quad (13)$$

Similarly, as we keep adding edges, we look for the density of the graph when the cycle disappears (ρ_{death}).

³We will now refer to equivalence classes of k -cycles as k -cycles.

The lifetime of a cycle l is defined as

$$lifetime\ l = \rho_{death} - \rho_{birth} \tag{14}$$

Auxiliary methodological remark. What does it mean for two cycles to be the same when different clique complexes are considered? This question appears when one wants to look whether cycles in the average DSI matrix appear in individual scans.

The first rational question is whether this pattern can exist in the different individual scans' networks (whether this pattern can enclose the same cavity in the individual scan). Firstly, it is asked at which weight w_0 (corresponding to an edge density ρ_0) does the original cyclic connectivity pattern exist first. Then, the authors looked for cross-cycle edges (edges that are not involved in this pattern) which have weight $> w_0$ and thus would appear earlier in the filtration (these edges can besmirch the possibility of enclosing a cavity). For these loops that survived, the authors looked at the cycle in the persistent homology of the complex formed from that scan. They calculated birth and death edges (edges corresponding to ρ_{birth} and ρ_{death}). If a birth edge contained at least one of the original cycle nodes, then a minimal generator l of that cycle at ρ_{birth} is found by querying the network thresholded at that density. There are three cases for this generator:

1. l is the one exactly expected from the cyclic connection pattern. Then the cycle is the same or it is a part of the same equivalence class.
2. If not, we go to the second case. We ask whether l may collapse onto the cyclic pattern of these nodes in the individual scan. We look for $\rho_{birth} \leq \rho_0 \leq \rho_{death}$; then the cavity is enclosed at some point by this cyclic pattern. We consider l the same with the pattern and we are done.
3. If not for the previous two, the cycle and the pattern are not the same surrounding the cavity. We ask if l is "similar" to the pattern in a loose way (e.g. containing all but one nodes).

4 Results

- The participation coefficient is the number of k -cliques in which a node is a member. Participation progresses from anterior to posterior. This means that areas in the frontal cortex that require high-order processing are formed in small clusters whereas early information areas are formed in large groups.
- The spatial distribution of the participation differs from the minimally wired null model, particularly in the cingulo-opercular and subcortical areas.

- Regions that are strongly connected to the rest of the brain by both direct and indirect walks also participate in many maximal cliques.
- The cycle consisting of thalamus, caudate nucleus of both hemispheres appears early.
- The second cycle appears at a later network density and consists of medial orbitofrontal, accumbens nucleus, any of the rostral anterior cingulate (RH, LH) , medial orbitofrontal (LH), lateral orbitofrontal, rostral middle frontal and any of the subcortical regions hippocampus, caudate nucleus, putamen, thalamus, amygdala.
- The final essential 1-cycle consists of medial and lateral orbitofrontal and rostral anterior cingulate to which it is added the nucleus accumbens and rostral middle frontal cortex.
- The longest 2-cycle is an octahedral connection pattern composed of the insula, the inferior and middle temporal cortices, the supramarginal gyrus, the superior and inferior parietal cortex, and the lateral occipital cortex.
- When removing the subcortical areas, the persistent homology of the brain comes closer to the one of the minimally wired null model.
- Additional longevity when subcortical regions are included.

5 General conclusions

- The cavities may reflect the relative paucity of direct connections between regions that evolved to perform different functions.
- The wiring of cortical regions may be more heavily influenced by energy conservation than the wiring of the subcortical regions.
- Subcortical regions could be points that kill the cortical cycle to which they are attached.

6 Methodological considerations

- Comparison with other loop-detecting algorithms. Other loop-detecting algorithms will find loops that are boundaries of higher cliques. Persistent homology is also robust to edge ordering.
- Cycle consistency across individuals and scans. The subcortical cycle exists in at least one scan of all individuals. The earlier-arriving subcortical-frontal cycle exists in at least once in all individuals. The octahedral pattern in

posterior parietal and occipital cortex is present at least once in six of eight individuals.

- Cycles formed without considering subcortical nodes. Discovery of 1-cycle composed of 10 nodes connecting temporal, parietal, and frontal regions (observed in each scan and individual).
- Cycles with different brain areas' sizes (checked).
- Comparison between cycles (as described above).