# Cliques and Cavities in the Human Connectome

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# Overview

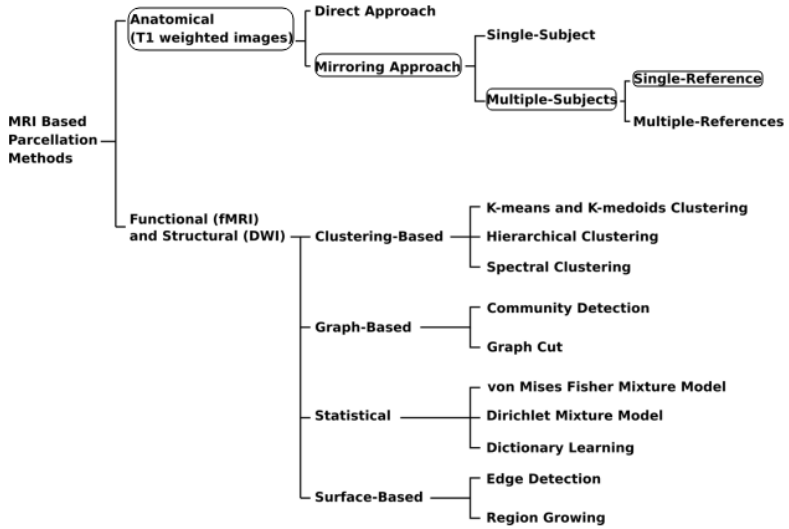

1. Human Brain
2. Cliques
3. Cavities

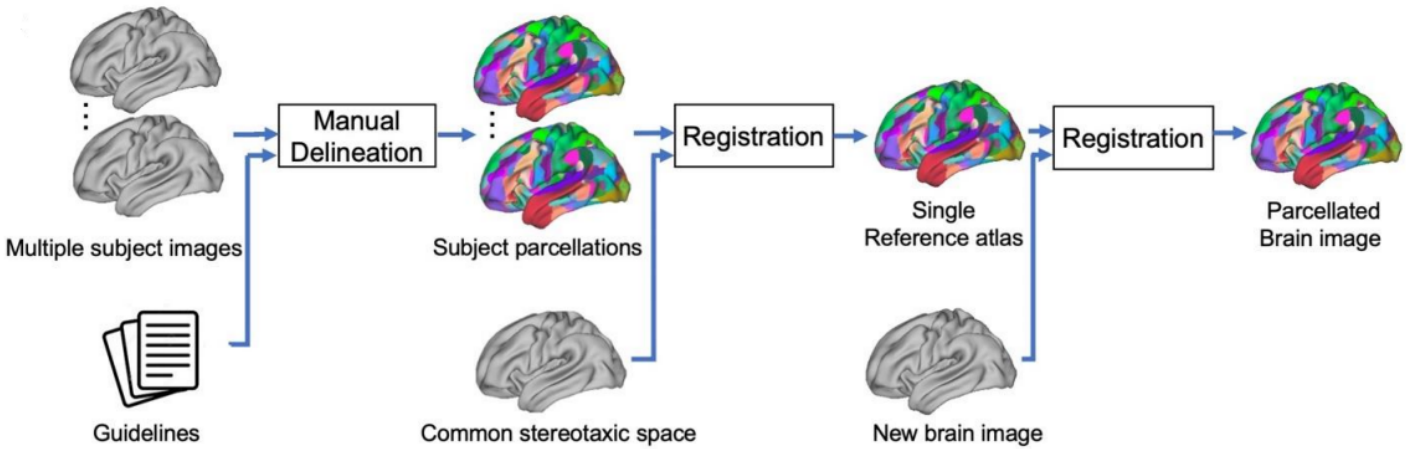
# Overview

- Goal
  - Investigate densely connected group of nodes of the brain to get a fundamental insight into the complexities of brain function
- Experiment & Data
  - Diffusion spectrum imaging (DSI) and T1-weighted anatomical scans (from 8 healthy adult volunteers on 3 separate days)
  - Null model: Minimally wired
- Investigation of Data
  - Weighted graph
  - Cliques of a graph
  - Filtration from a weighted graph
  - Persistence homology
  - Cavities (non-trivial homology classes)

# Data Acquisition

# Brain Parcellation

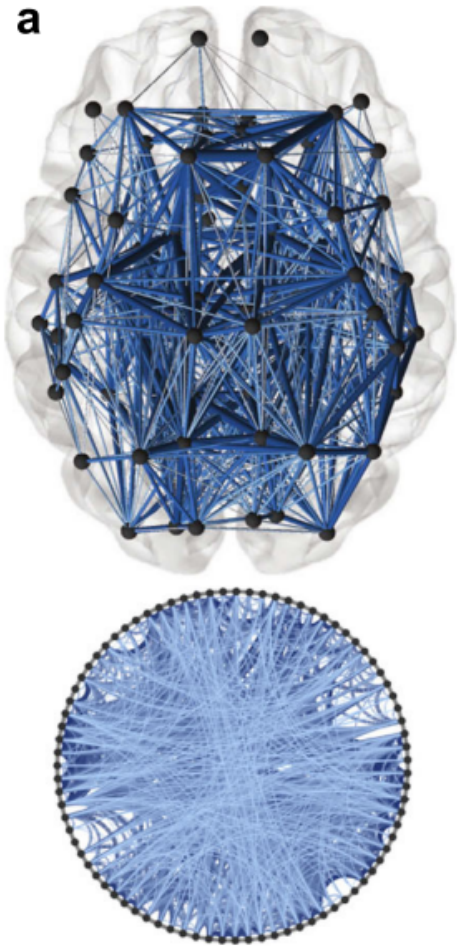


# Representing Brain as a Weighted Network from Scan

Empirical model: DSI

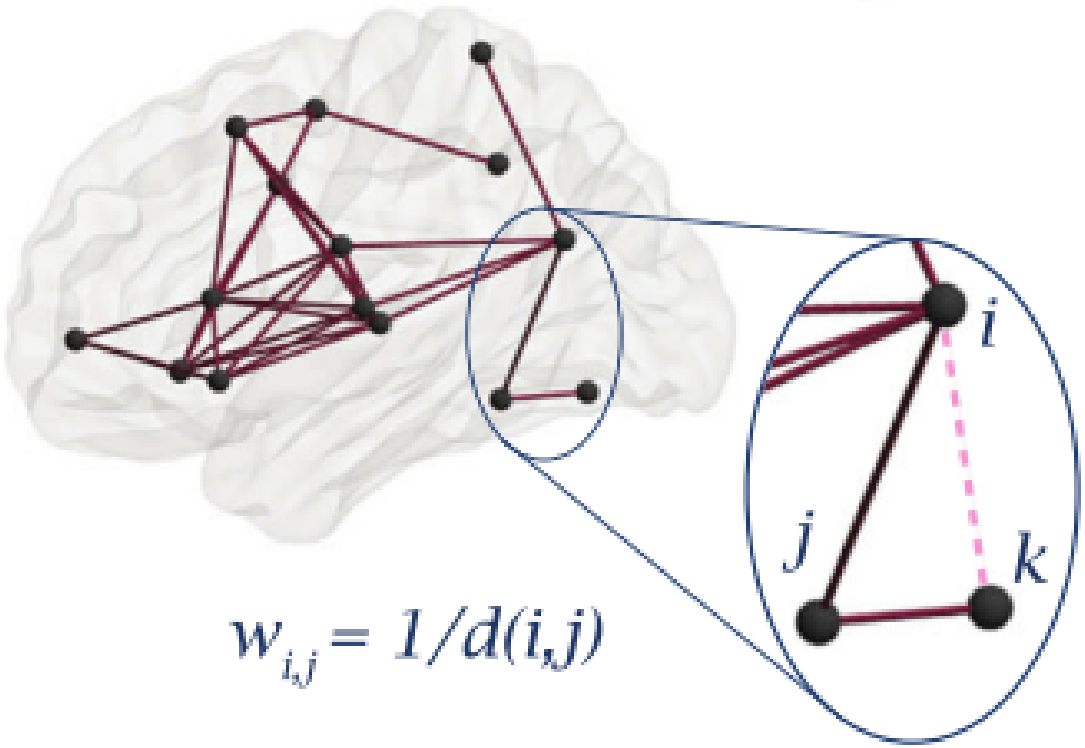
- Divide whole-brain images into 83 regions (network nodes)
- Construct weighted edges between nodes as the density of white matter tracts.



# Representing Brain as a Weighted Network without Scan

Null model: Minimally wired (MW)

- Divide whole-brain images into 83 regions (network nodes)
- Each pair of nodes are then linked by an edge with weight $w_{i,j} = \frac{1}{d(i,j)}$, where $d(i,j)$ is the Euclidean distance between nodes $i$ and $j$.



# Cliques in the Human Structural Connectome

We will use

- Group-averaged network from the scans, (average weights of all scans)
- Minimally wired networks as a null-model,

Both are thresholded at a reasonable edge density (0.25) to remove spurious edges, where

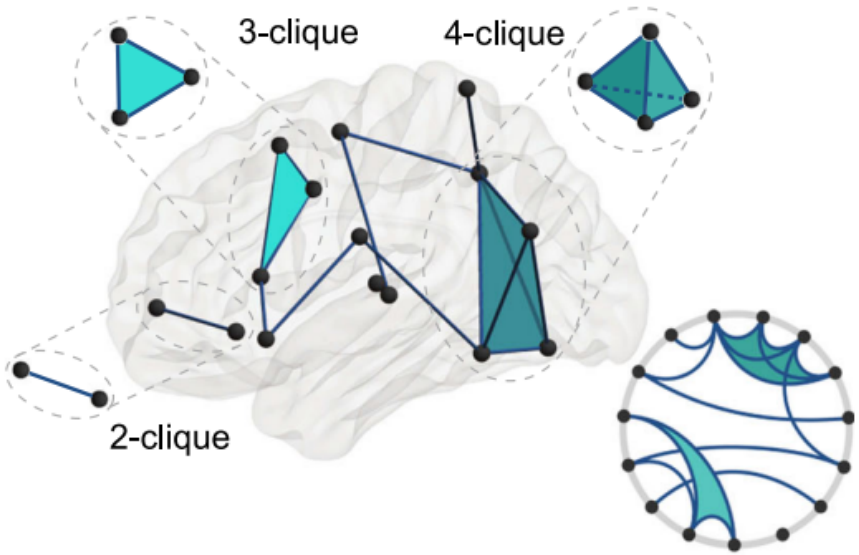
$$\text{edge density} = \frac{\text{number of edges present}}{\text{number of total possible edges}}$$

# Cliques

## Definition

In a graph $G$, a **k-clique** is a set of $k$ all-to-all connected nodes.

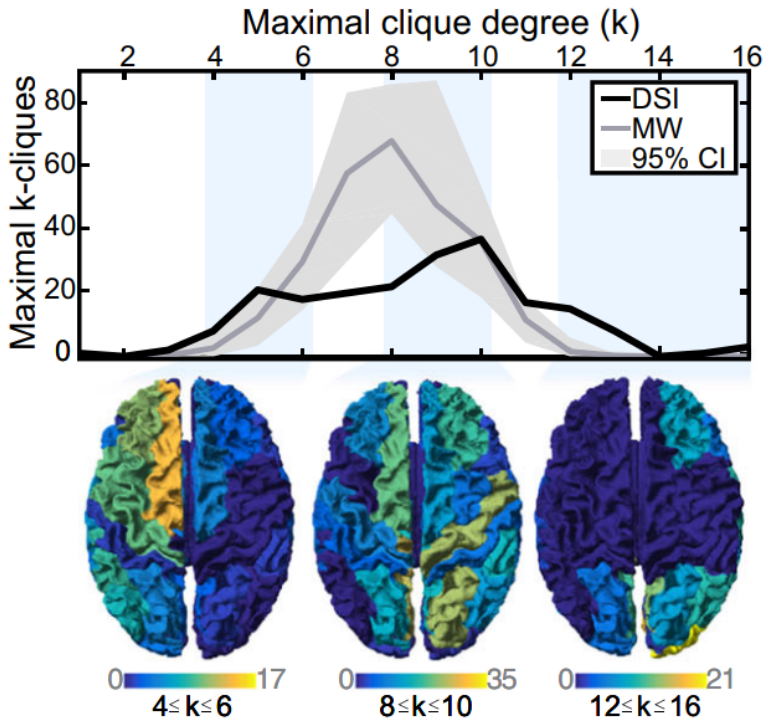
In the context of brain networks, cliques are group of brain regions that are able to rapidly and effectively share information.




- Any subset of a $k$-clique is a cliques of a smaller degree, called a face.
- Any clique that is not a face is called maximal.

# Anatomical Distribution of Maximal Cliques

Let $P_k(v)$ denote the number of maximal $k$-cliques in which $v$ is a node. Let $P(v) = \sum_k P_k(v)$. It is called total participation.

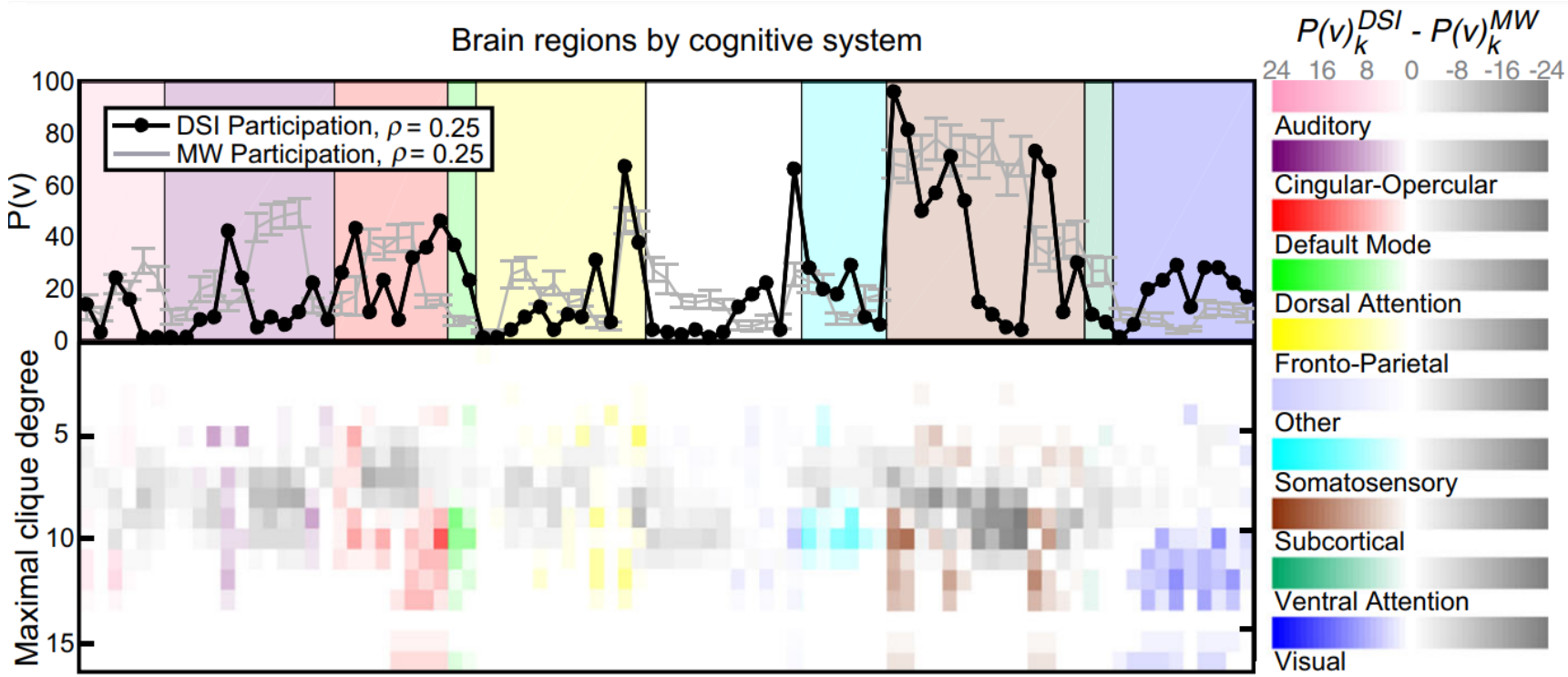



On the bottom: Heat maps of node participation for a range of clique degrees.

## Observations

- Distribution of maximal clique degree is unimodal in MW.
- Distribution of maximal clique degree is bimodal in empirical data.
- General progression of maximal clique participation from anterior to posterior regions of cortex.
- Human brain displays preferences for small (4-6 node), and large (12-16 node) processing units, instead of medium sized (app. 8 node) units as in the MW null model.

# Node participation in maximal cliques in specific cognitive systems




The largest maximal cliques are formed by nodes located almost exclusively in the subcortical, dorsal attention, visual and default mode systems, suggesting that these systems are tightly interconnected.

# Graph Statistics

- The summed edge weight of connections emanating from a node is called **node strength**.

$$s(v) = \sum_{v \in e} w(e)$$

- The **weighted communicability** between nodes $i$ and $j$ is

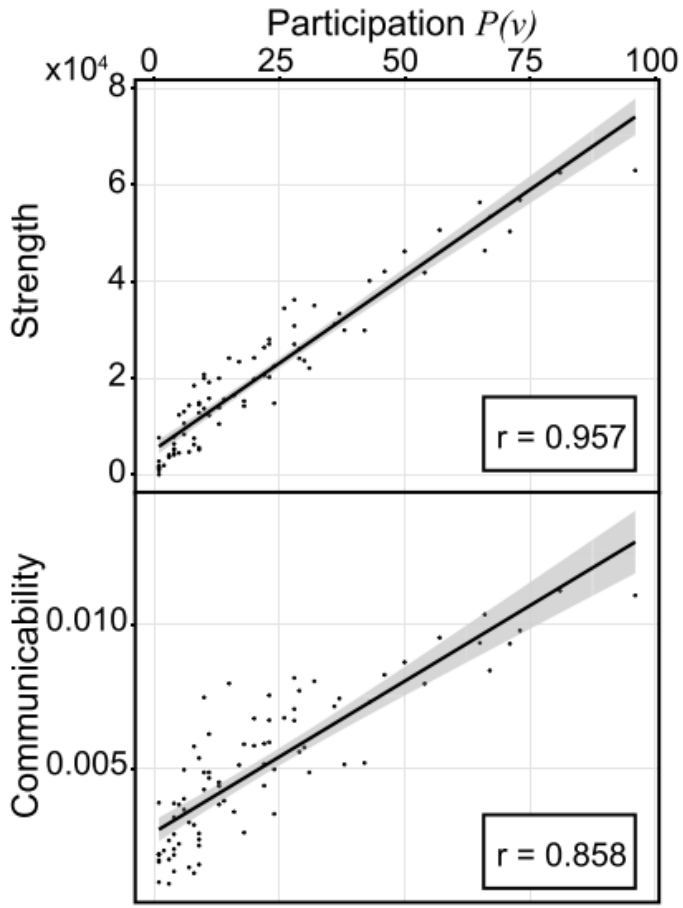
$$C_{ij} = (exp(D^{-1/2} A D^{-1/2}))_{ij}$$

where $A$ is the adjacency matrix (with weights) and $D = diag(s(i))$

- The **node communicability** of the node $i$ is

$$C_i = \sum_j C_{ij}$$

# Node Participation vs Strength and Communicability



# Cavities in the Human Structural Connectome

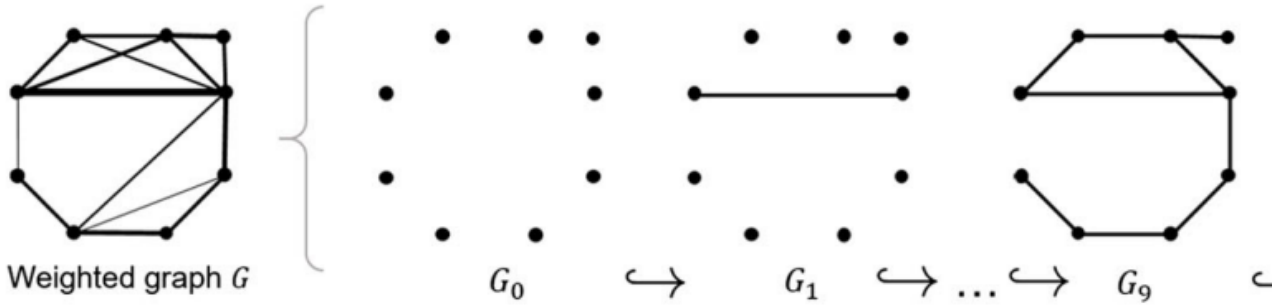
Cliques $\leftrightarrow$ neighborhood-scale building block for the computational structure of the brain.

The relationship between these blocks can be investigated by studying the unexpected absence of strong connections, which can be detected as topological cavities in the structure of brain network.

# Filtration from a Weighted Graph

- Start with the empty graph $G_0$, i.e. no edges
- Add 1 edge at a time in order of decreasing edge weight.

$$G_0 \subset G_1 \subset \ldots \subset G_{|E|}$$

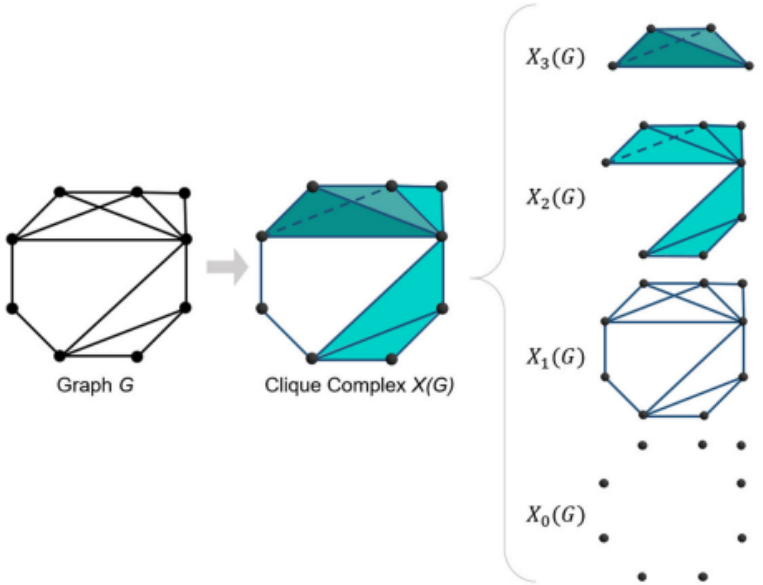


# Clique Complex

The **clique complex** of a graph G, denoted $X(G)$ is the collection of all cliques on $G$

$$X(G) = \{X_0(G), X_1(G), ..., X_N(G)\}$$

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

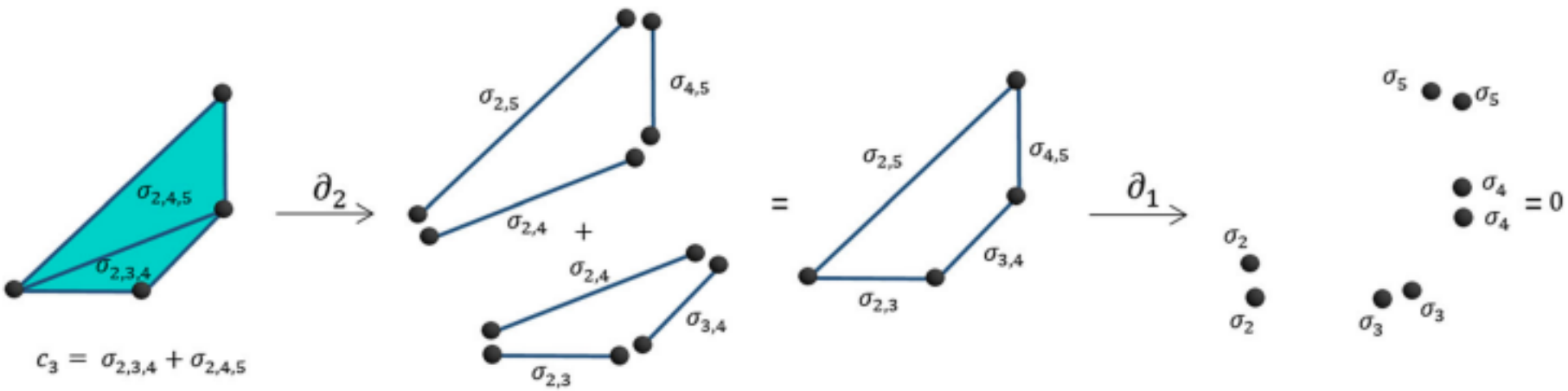


# Boundary Operator and Chain Complex

The **chain group**, $C_k(X(G))$ is the vector space with basis $X_k(G)$.

Define the **boundary operator** (with coefficients in $\mathbb{F}_2$) on the basis $X_k(G)$ to be

$$\partial_k(\sigma_{0,1,\ldots,k}) = \sum_{i=0}^{k} \sigma_{0,1,\ldots,\hat{i},\ldots,k}$$

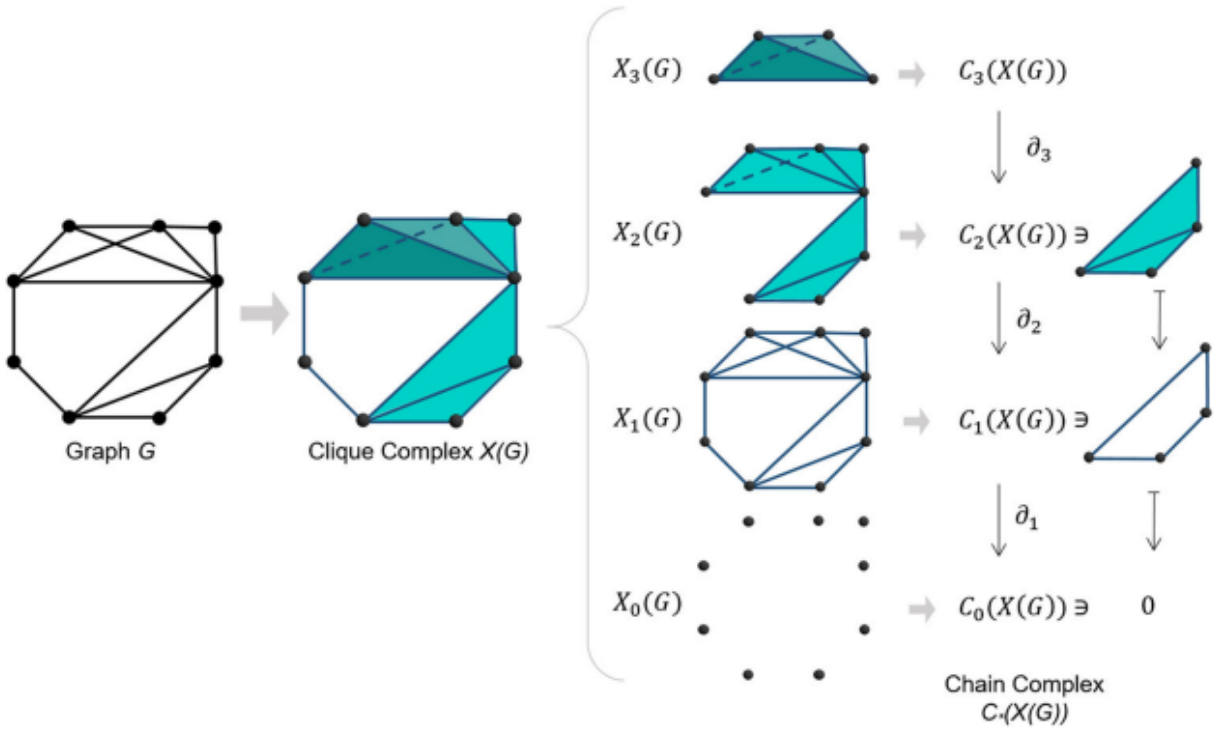


# Boundary Operator and Chain Complex

These operators link together the chain groups into a sequence

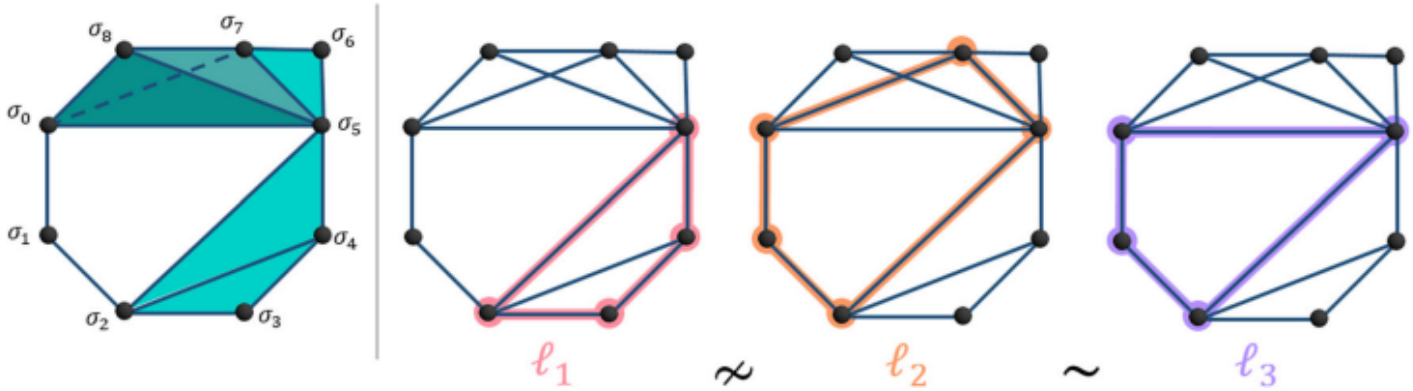
$$C_k \xrightarrow{\partial_k} C_{k-1} \xrightarrow{\partial_{k-1}} \dots \xrightarrow{\partial_2} C_1 \xrightarrow{\partial_1} C_0 \xrightarrow{\partial_0=0} 0$$

called the **chain complex** for $X(G)$.



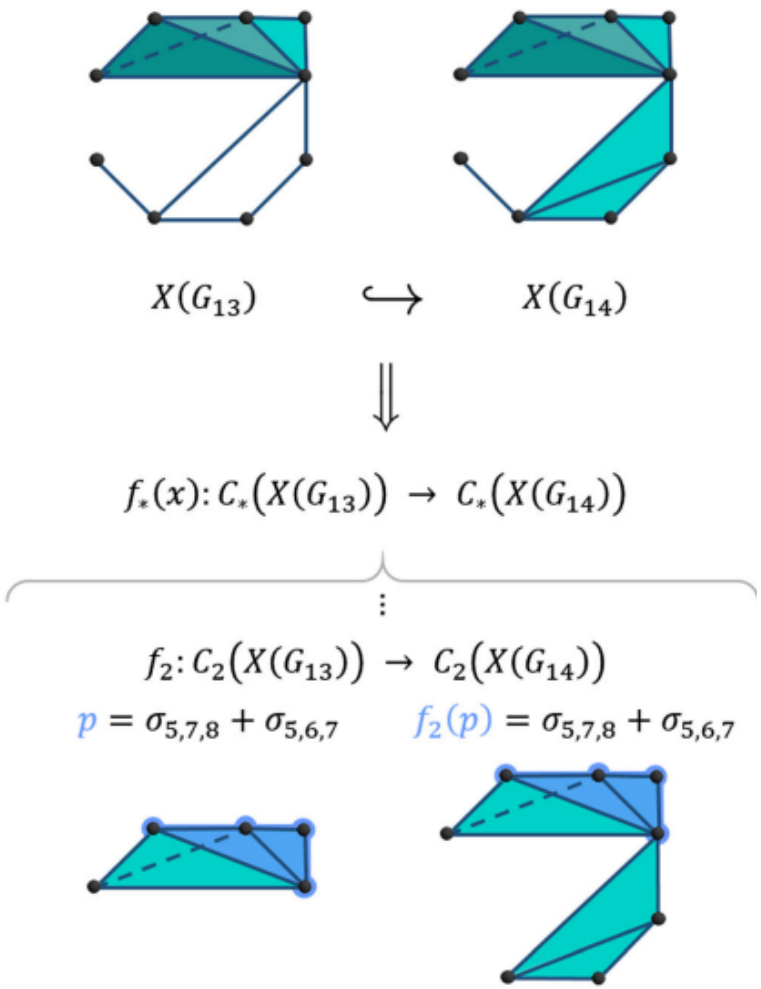
# Homology

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

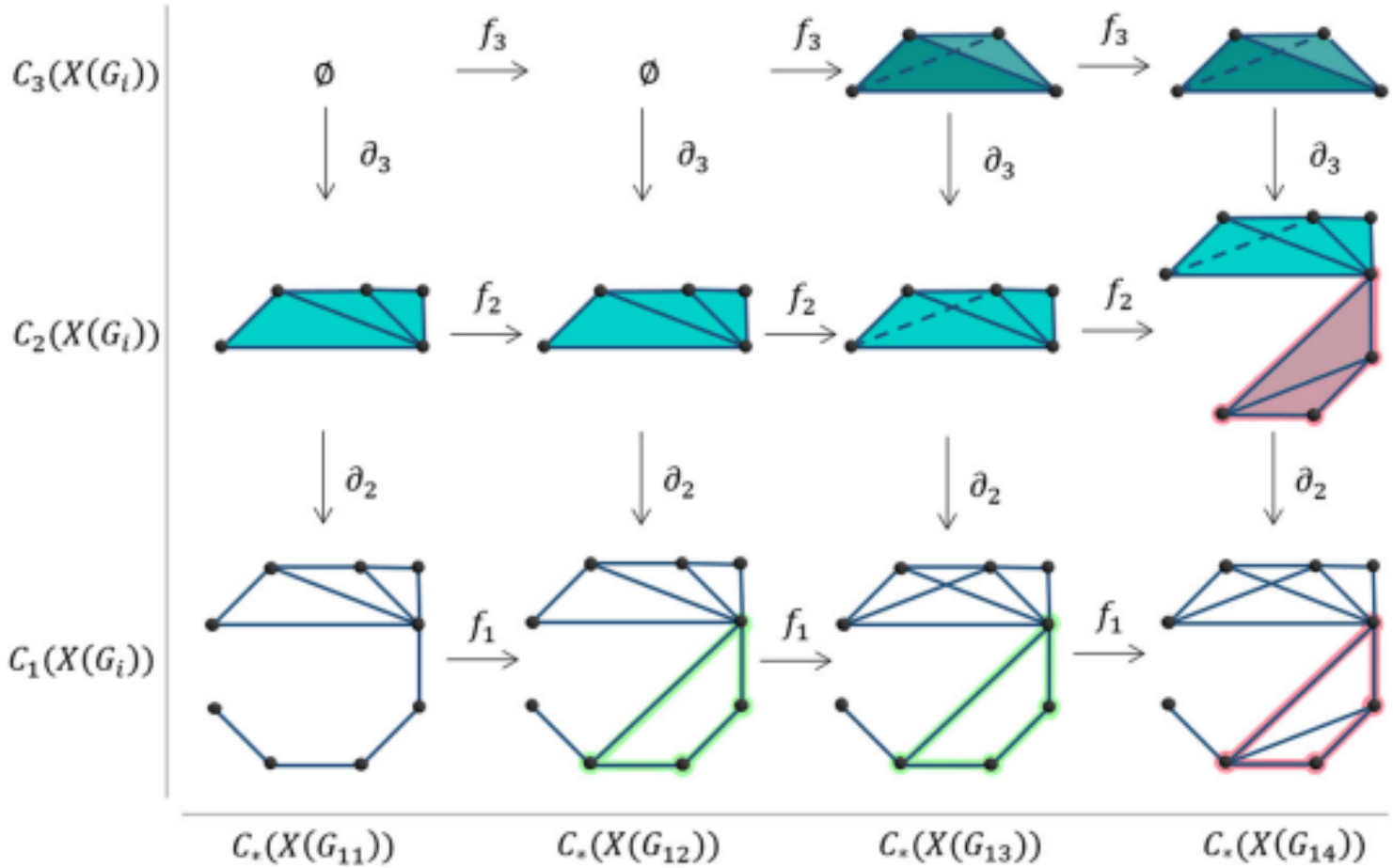


# Induced maps between chain complexes

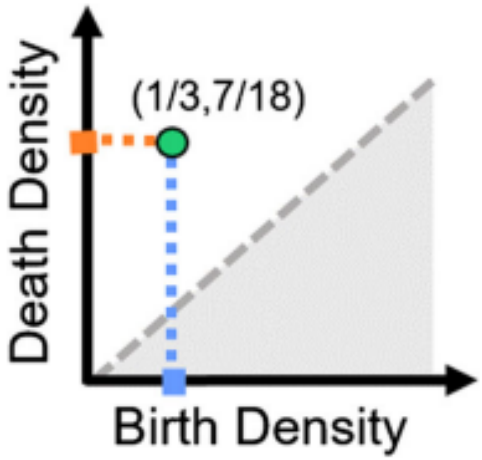
Inclusion maps between clique complexes induce maps between the corresponding chain complexes.



# Persistence Complex of a Weighted Graph



# Birth and Death Density and Persistence Diagram




$$\rho_{\text{birth}} := \frac{\text{number of edges present during birth}}{\text{number of all possible edges}}$$

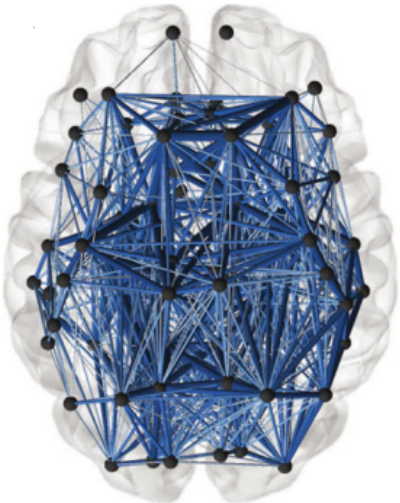
$$\rho_{\text{death}} := \frac{\text{number of edges present during death}}{\text{number of all possible edges}}$$

We record $\rho_{\text{birth}}$ and $\rho_{\text{birth}}$ for all topological cavities (e.g. non-trivial homology classes) and display them on a *persistence diagram*.

# Recall

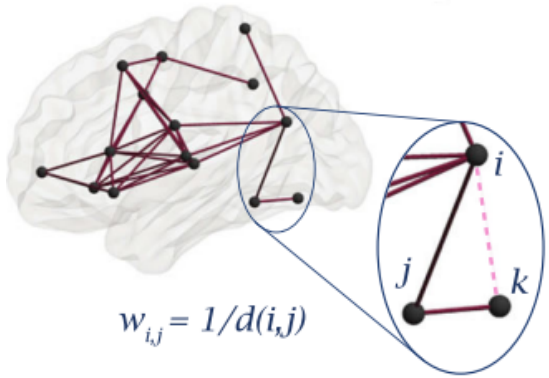
Empirical model:

- Construct weighted edges between nodes as the density of the white matter tracts.
- Thresholded at edge density 0.25

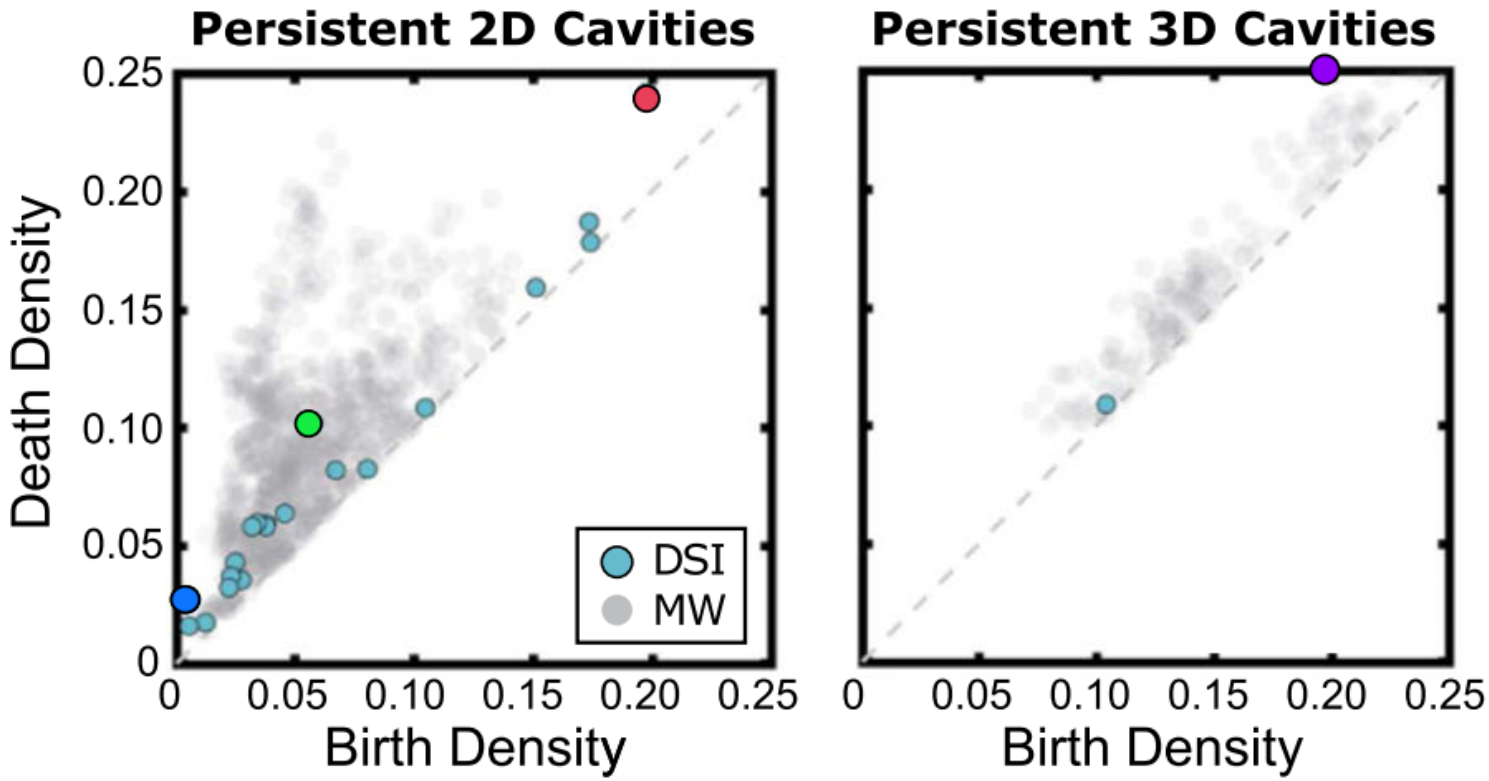


Null model:

- Weight of each edge is $\frac{1}{d(i,j)}$, where $d(i,j)$ is the Euclidean distance.
- Thresholded at edge density 0.25.



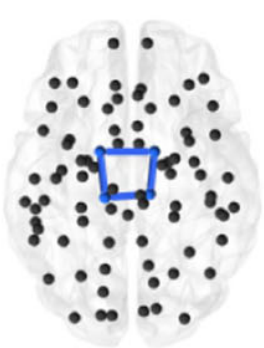
# Persistent 2D-3D Cavities

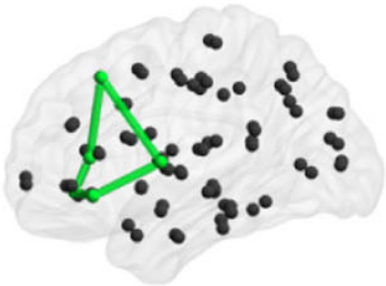


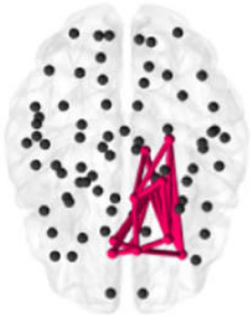

Persistence diagrams for the group-averaged DSI and MW null network in dimensions 1 and 2.

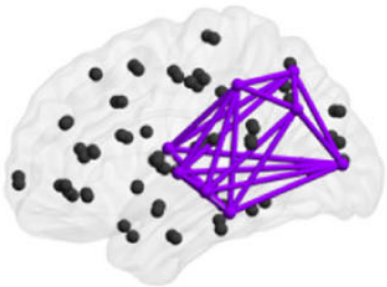
$H_1 \leftrightarrow$ 2D cavities, $H_2 \leftrightarrow$ 3D cavities

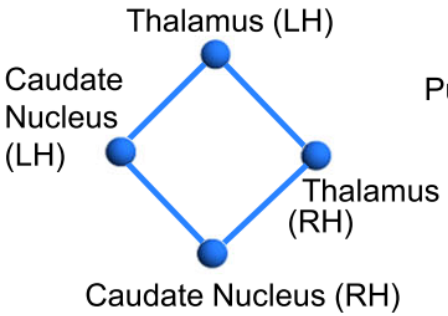
# Persistent 2D-3D Cavities

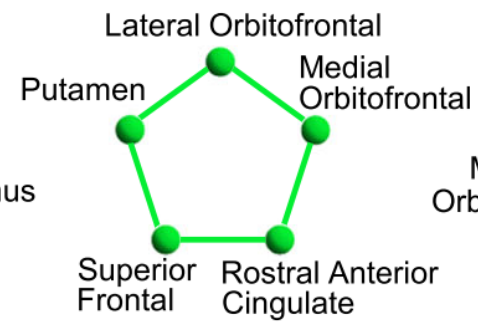


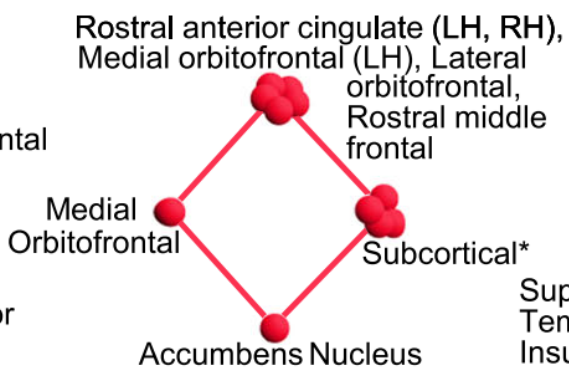


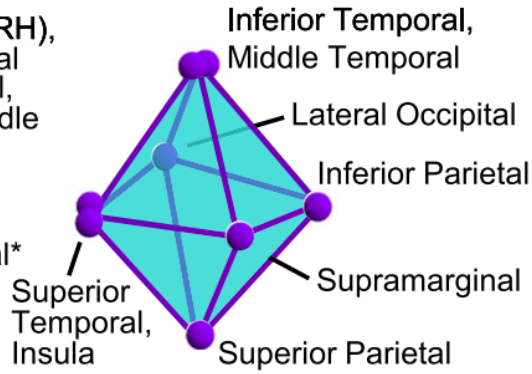






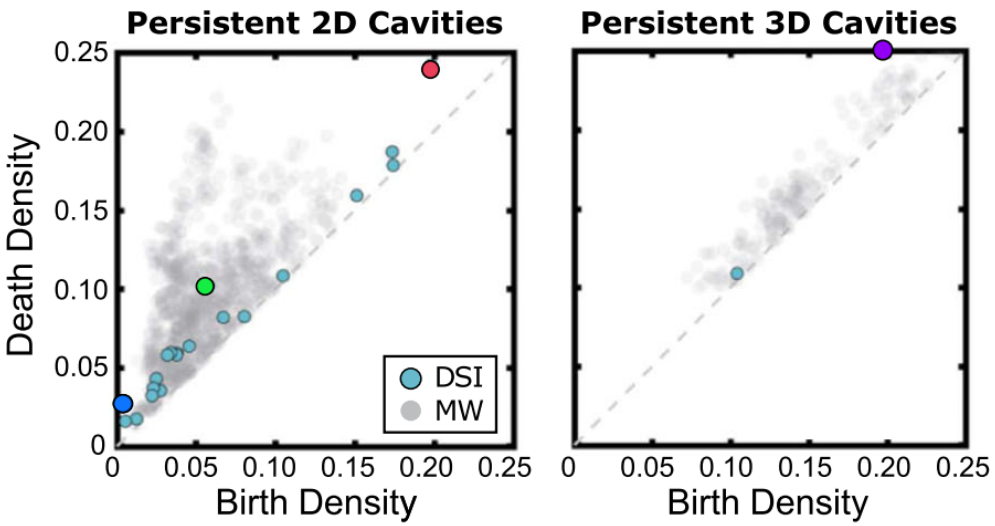
# Consistency Across Subjects

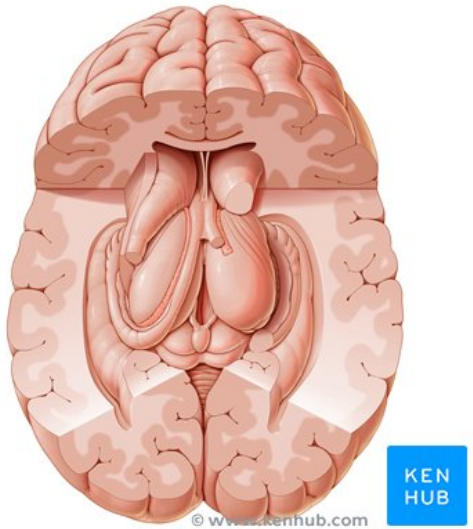
- The blue  green cycles exist in at least one scan of all individuals.
- The red cycle exists in 7 seven of the 8 individuals in at least one scan.
- The octahedral connection is present at least once in 7 of 8 individuals. And, these regions enclose cavity at least once in 6 of these individuals.

## Summary

Topological cavities observed in the group-averaged DSI network appear consistently across individuals.

# Observation

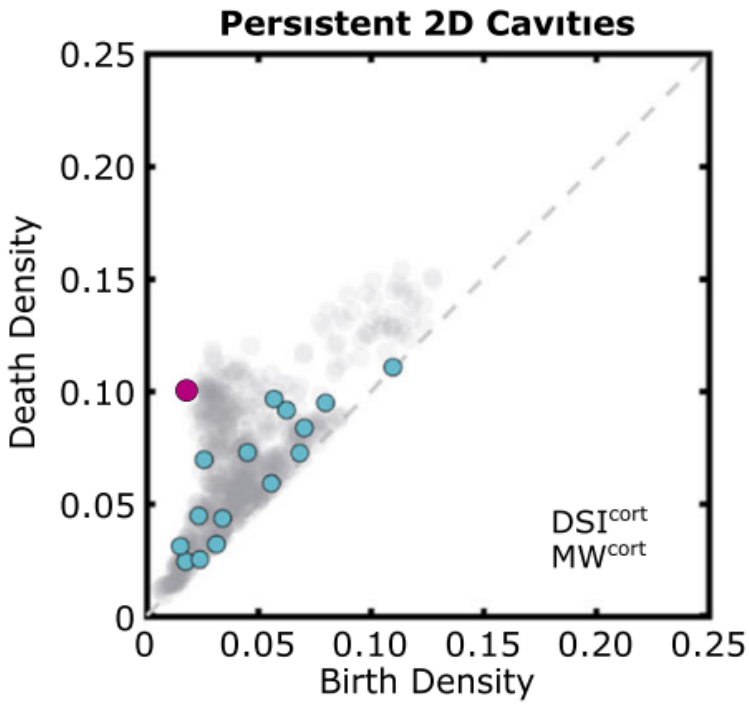


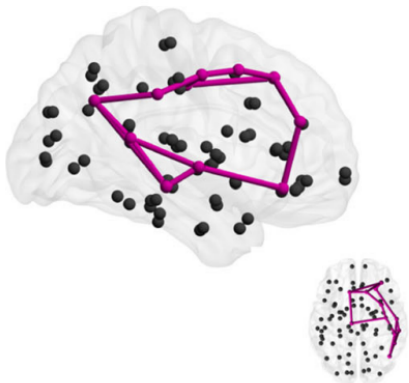



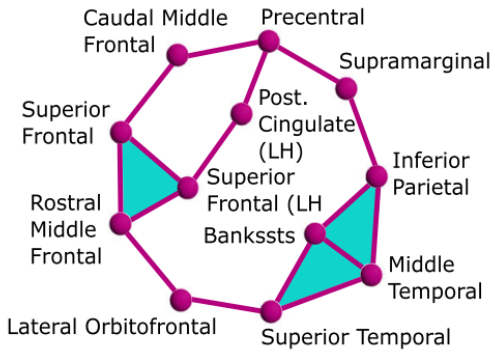

There is a pattern of subcortical-cortical connections within cycles. Indeed, 18 of 20 1-cycles and both 2-cycles contain this motif.

# Focus Only on Cortical Region

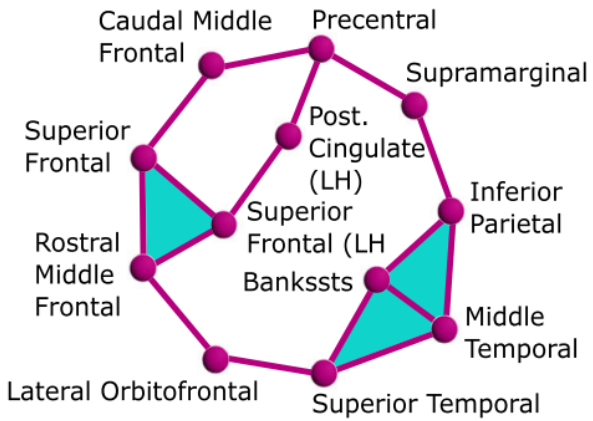
Examine the 66-node group-averaged DSI network composed only of cortical regions:





# Focus only on Cortical Region




- The birth edge was between lateral orbitofrontal and superior temporal regions.
- We get 4 cycles with minimal number of edges.
- At least one of these minimal cycles and corresponding cavity was observed in each scan of every individual.

## Conclusion

Cortico-cortical cycles are indeed present

# References


Main article:

- Sizemore, A.E., Giusti, C., Kahn, A. et al. Cliques and cavities in the human connectome. J Comput Neurosci 44, 115–145 (2018).

Auxiliary articles:

- Cammoun, L., Gigandet, X., Meskaldji, D., Thiran, J.P., Sporns, O., Do, K.Q., Maeder, P., Meuli, R., Hagmann, P. (2012). Mapping the human connectome at multiple scales with diffusion spectrum MRI. Journal of Neuroscience Methods, 203(2), 386–397
- Crofts Jonathan J and Higham Desmond J 2009A weighted communicability measure applied to complex brain networksJ. R. Soc. Interface.6411–414
- Hagmann P, Cammoun L, Gigandet X, Meuli R, Honey CJ, Wedeen VJ, et al. (2008) Mapping the Structural Core of Human Cerebral Cortex. PLoS Biol 6(7): e159.

# The End

Thank you!