

Location, Location, Location!

Homological scaffolds and gene mapper
Application to neuroscience

Paul Expert/Giovanni Petri

Centre for the Mathematics of Precision Healthcare
Global Digital Health Unit
ISI Foundation

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The « so what ?» question

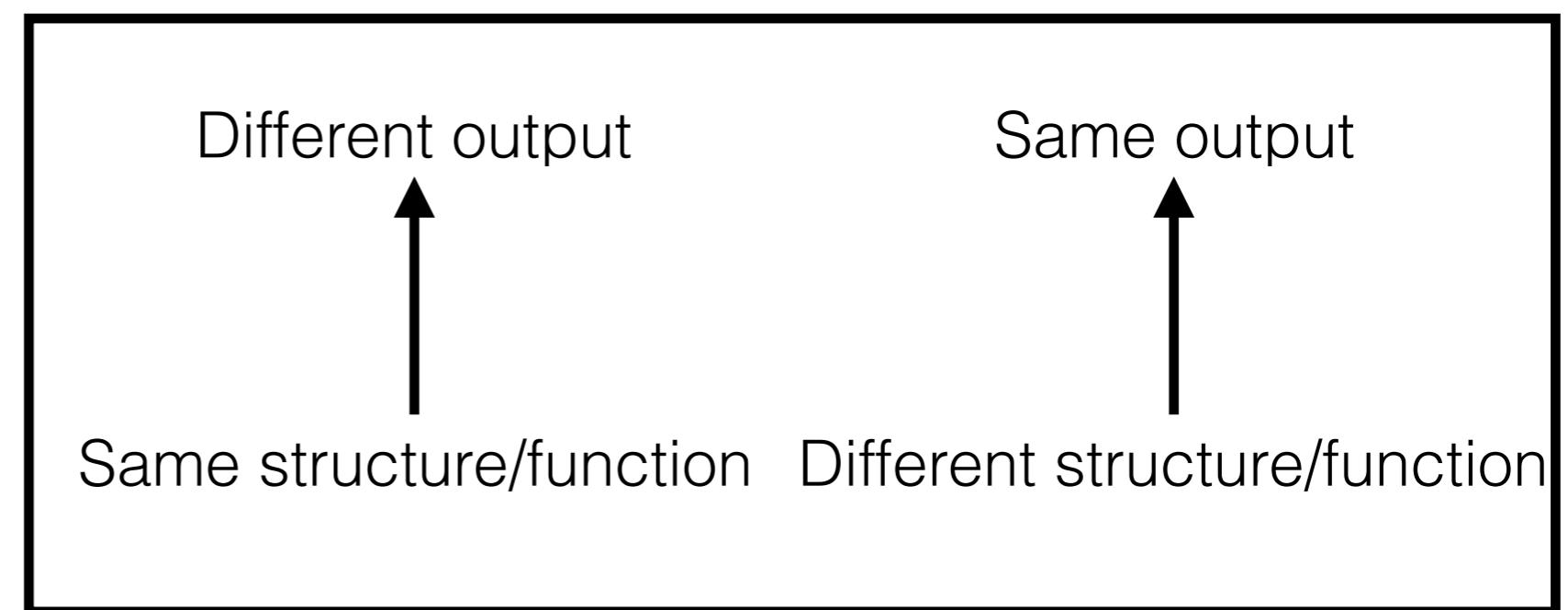
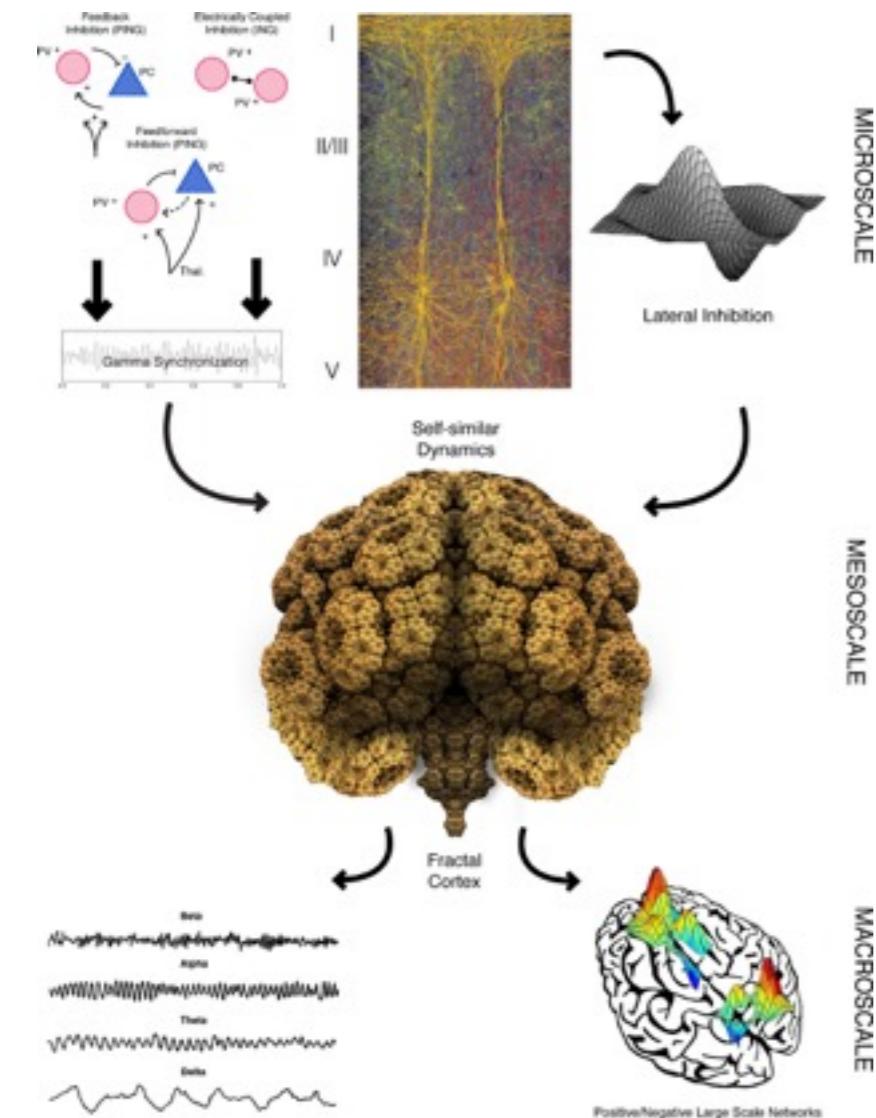
A synergy between new methodology and « clinical » questions is needed.

How to relate, i.e. validate, new findings with existing knowledge while providing added value?

New methodologies are needed:

- i) to integrate large and complex data coming from different modalities, meta-data
- ii) to interpret results from topological methods.

Understanding brain function: a complex multi scale problem

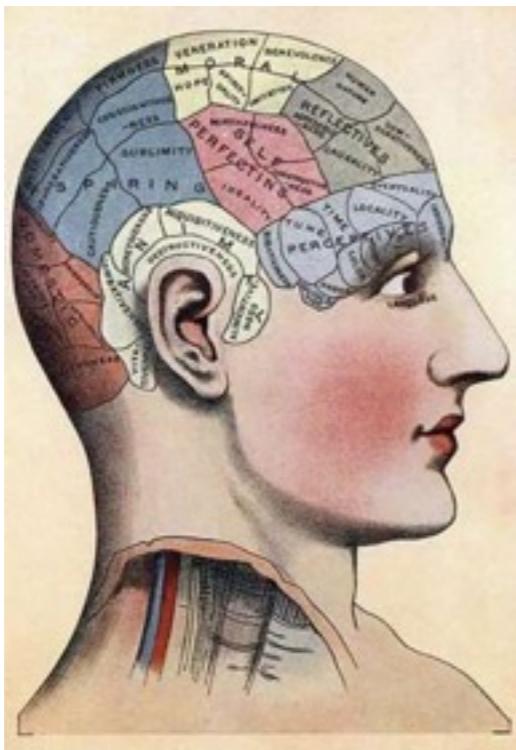


Semiology of catatonia: https://www.youtube.com/watch?v=i9zEJM_OWzE

Lord *et al.*, NeuroImage (2011); Neuroimage Clin(2012).
Turkheimer *et al.*, Neuroscience and Biobehavioral Reviews (2015).

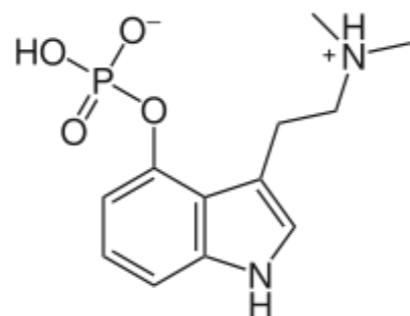
Networks/simplicial complexes

Fundamental paradigm change: from phrenology to an integrated system.



From studying activation variance to covariance.
The importance of this representation cannot be overstated.

Altered states of consciousness: psychedelics

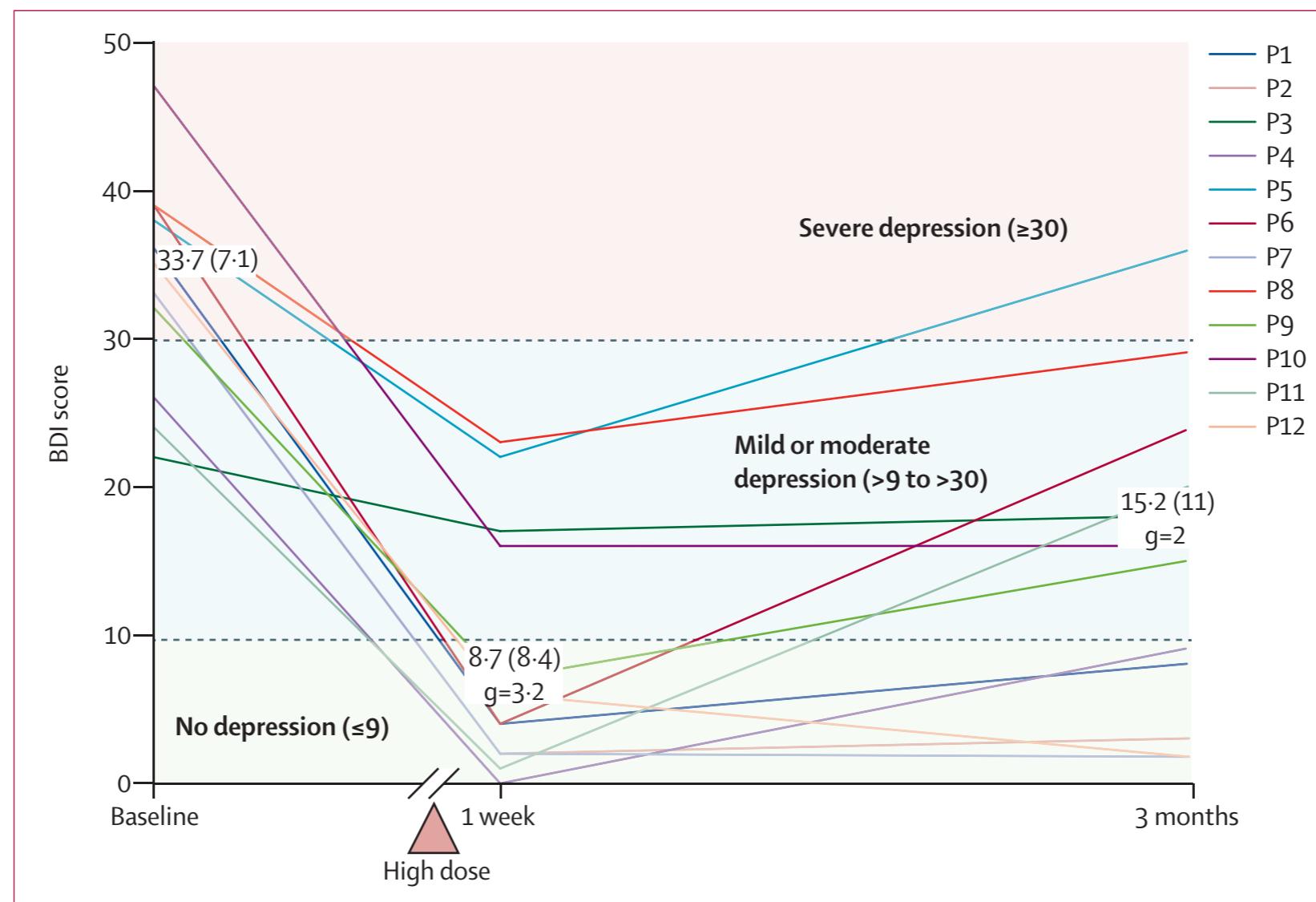


Magic mushrooms: psilocybin

THE CENTRE FOR
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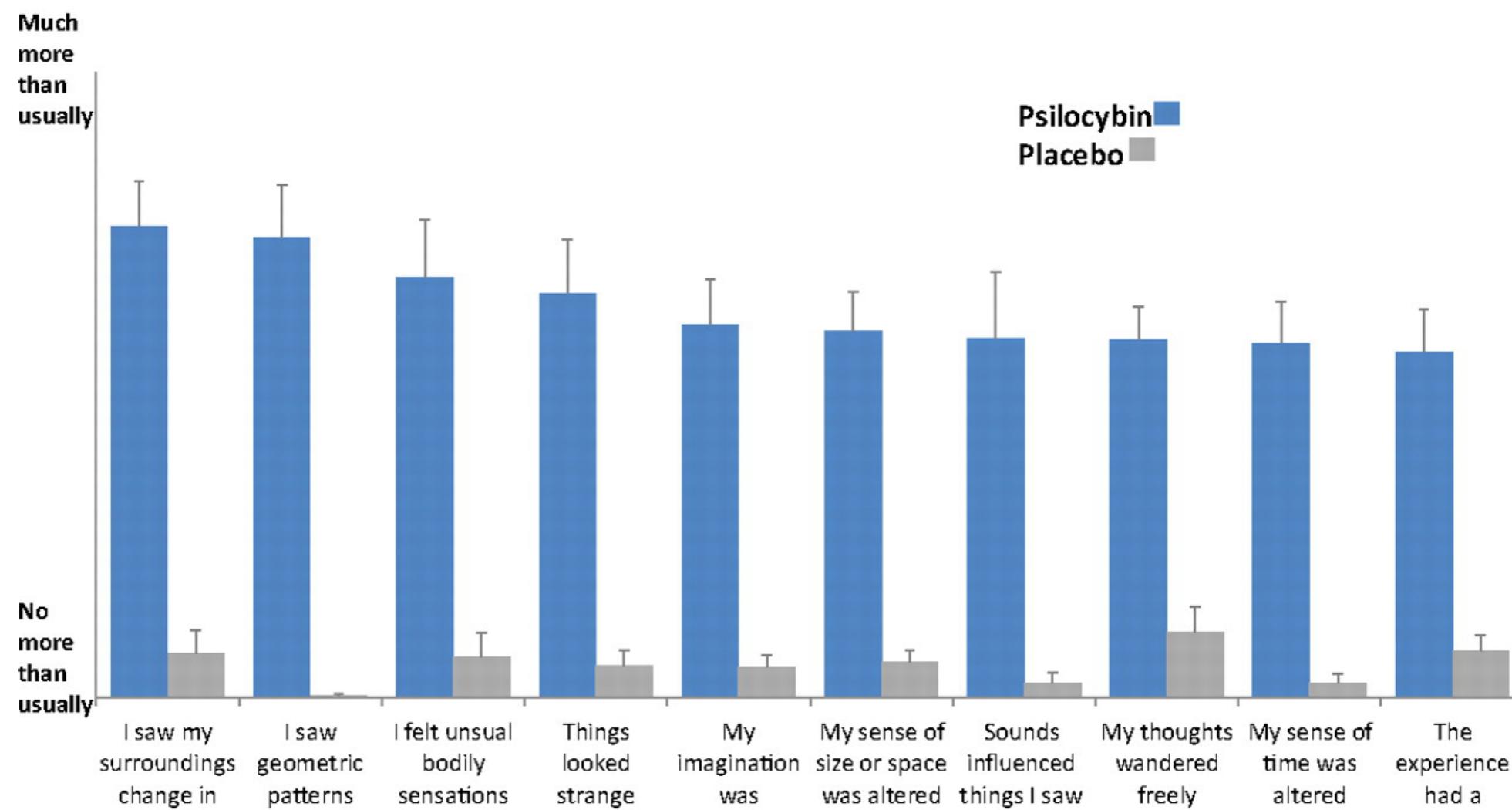
Altered states of consciousness: psychedelics



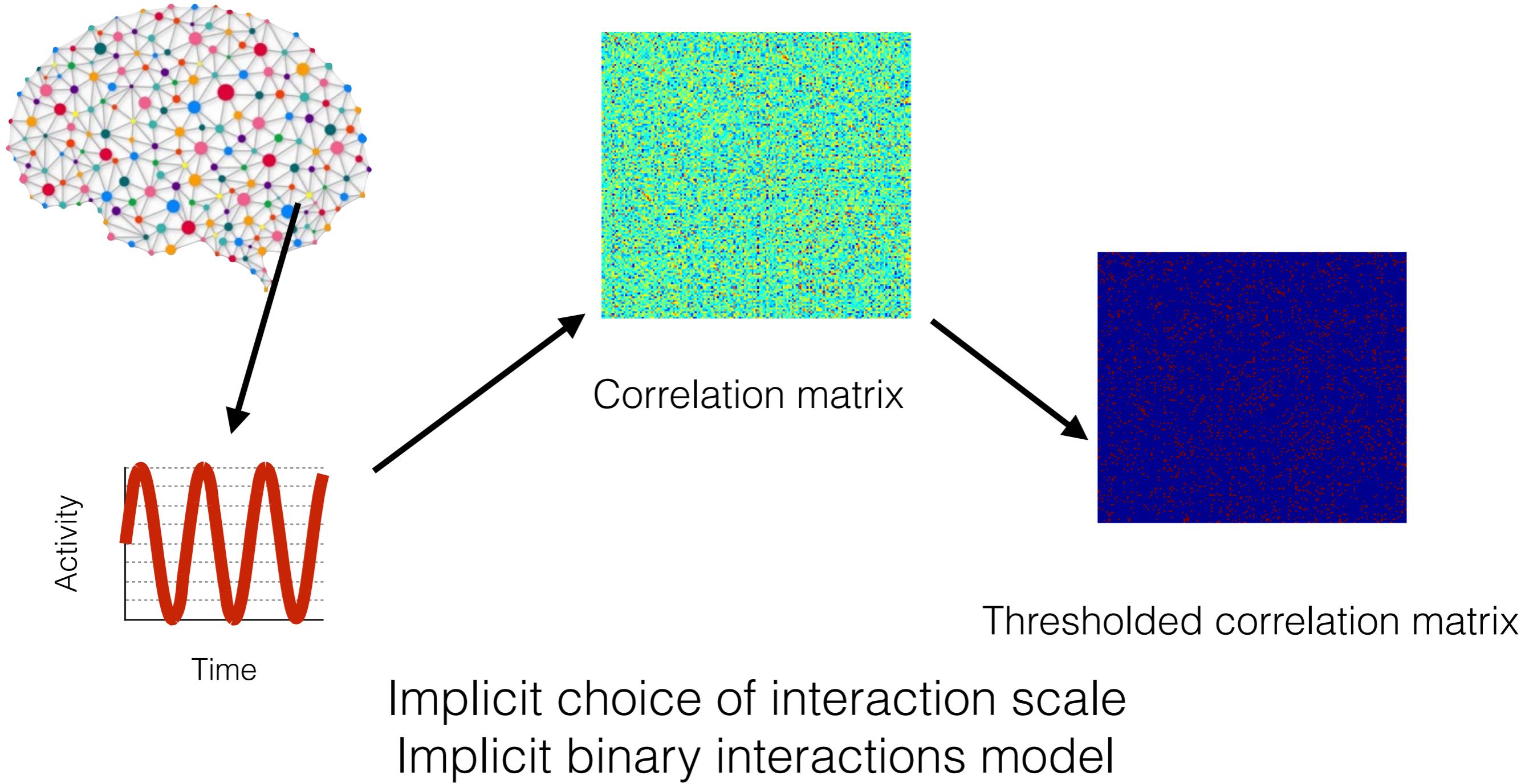
THE CENTRE FOR
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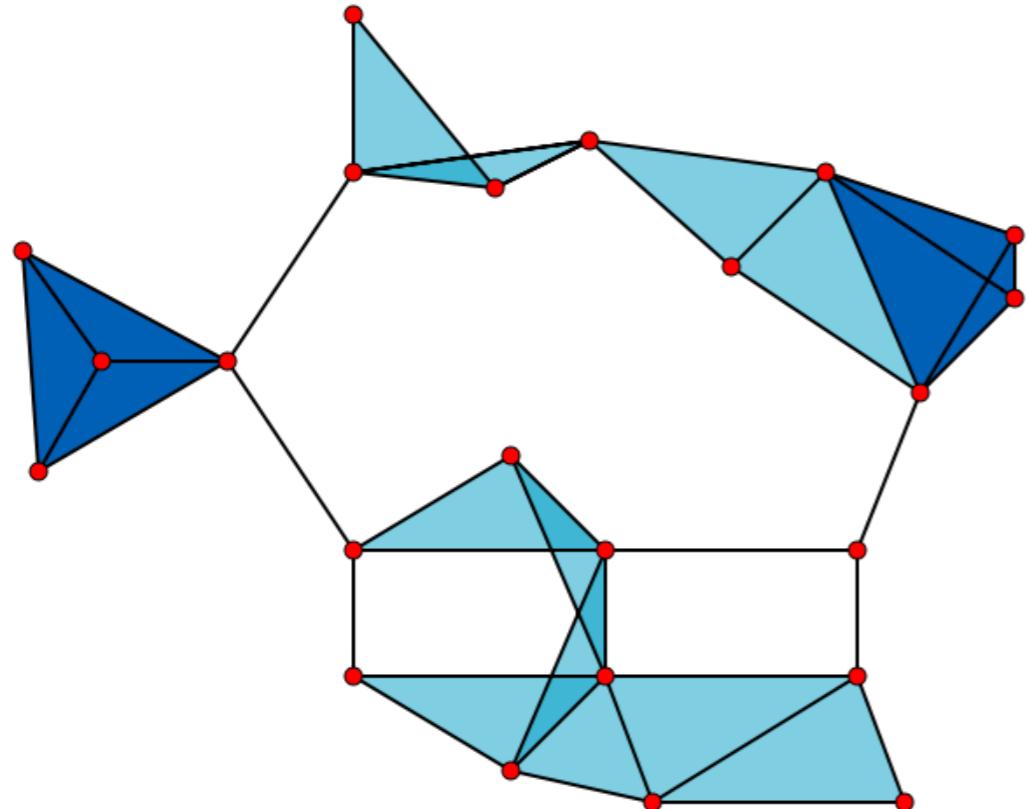
Altered states of consciousness



Functional brain network analysis: limitation



Clique complex



Cliques are set of ROIs that are all pairwise correlated above a given threshold, simplification in subunits.

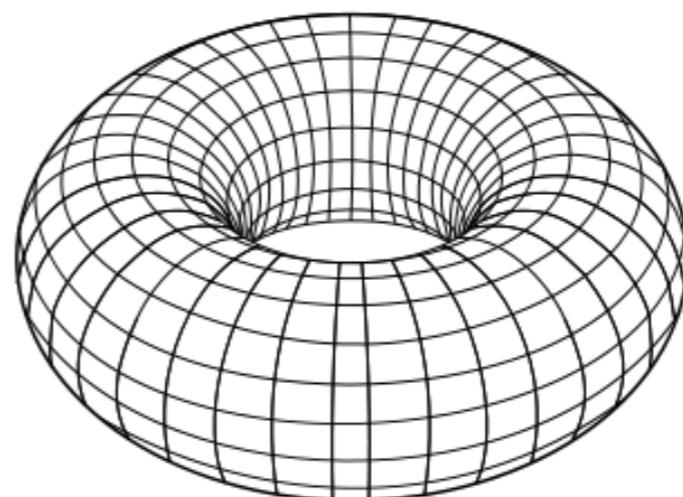
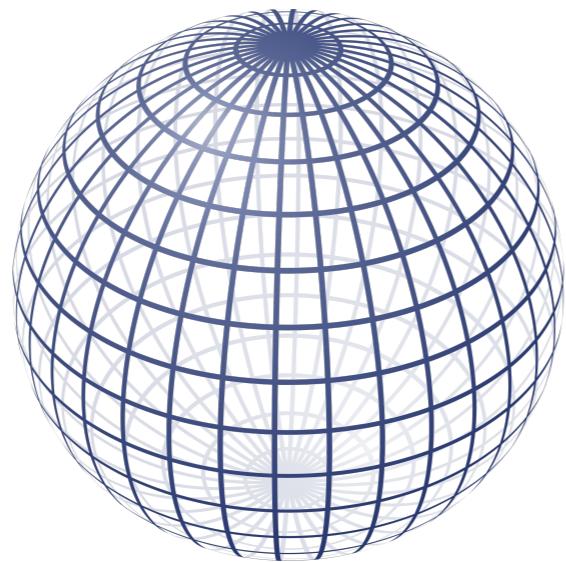
New types of mesoscopic structures appear: holes.

To any undirected graph G can be associated a clique complex $X(G)$.
A clique of size k is represented by a simplex of dimension $k-1$.

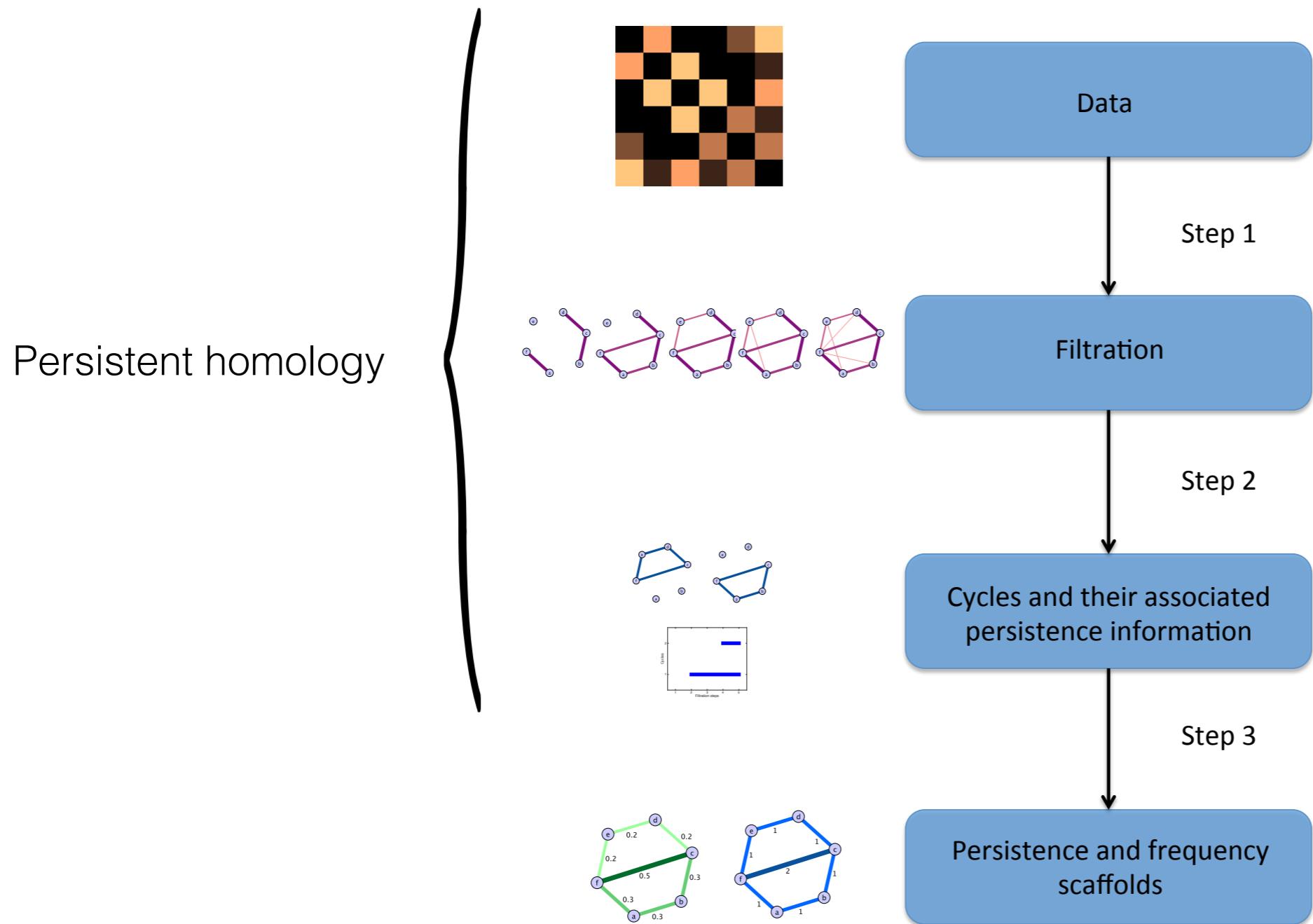
Characterisation of brain function with topological invariants

Holes can be used to characterise topological spaces.
We can derive such spaces for different brain states.

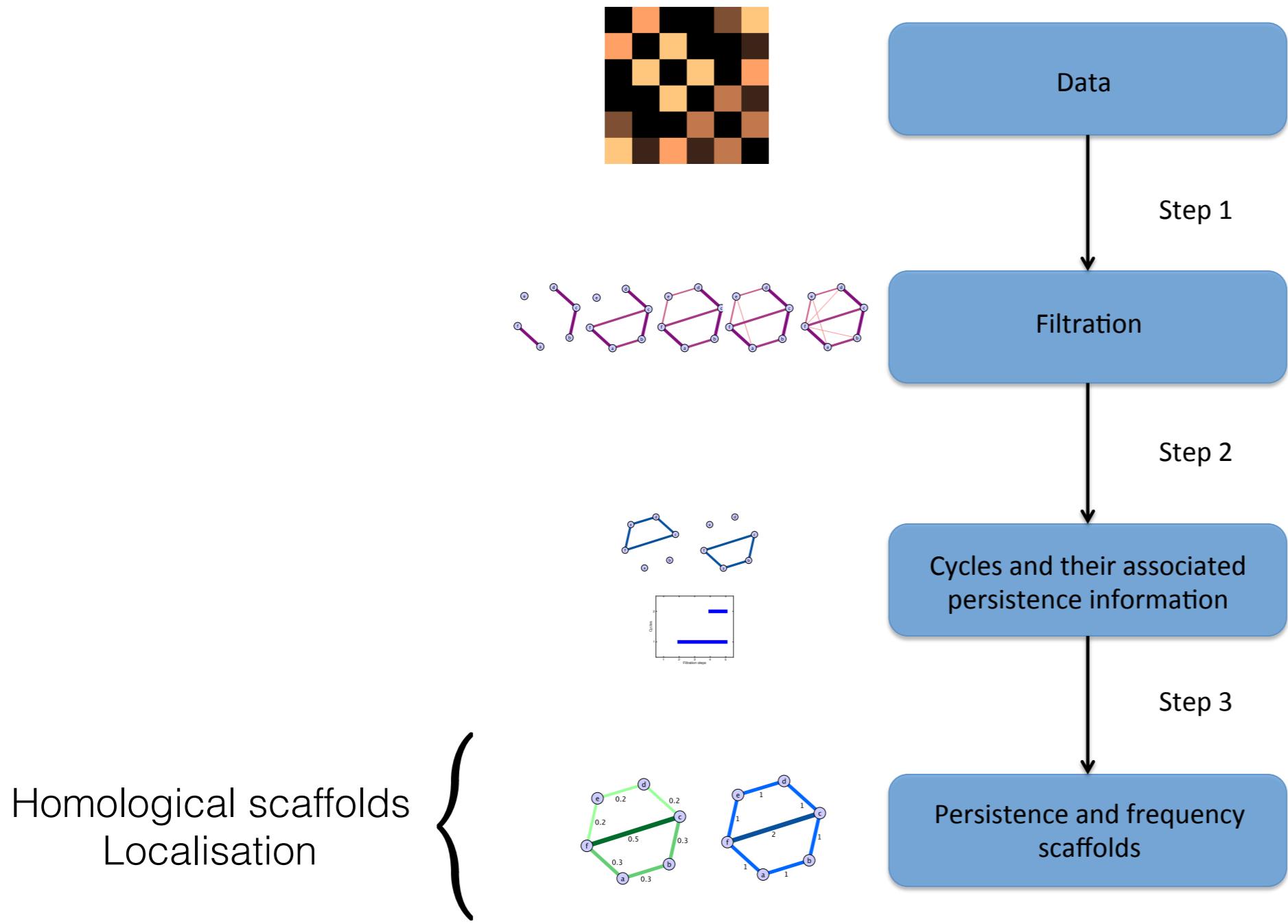
The problem of scales still remains.



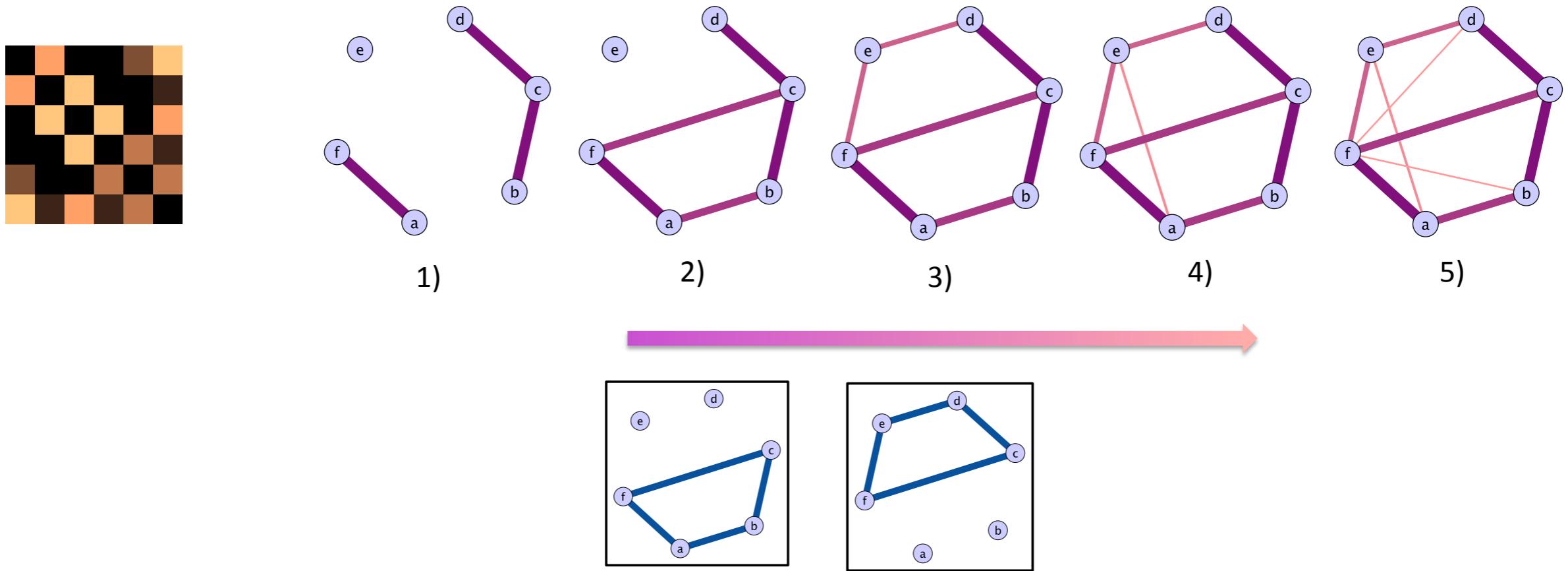
Persistent homology



Localisation

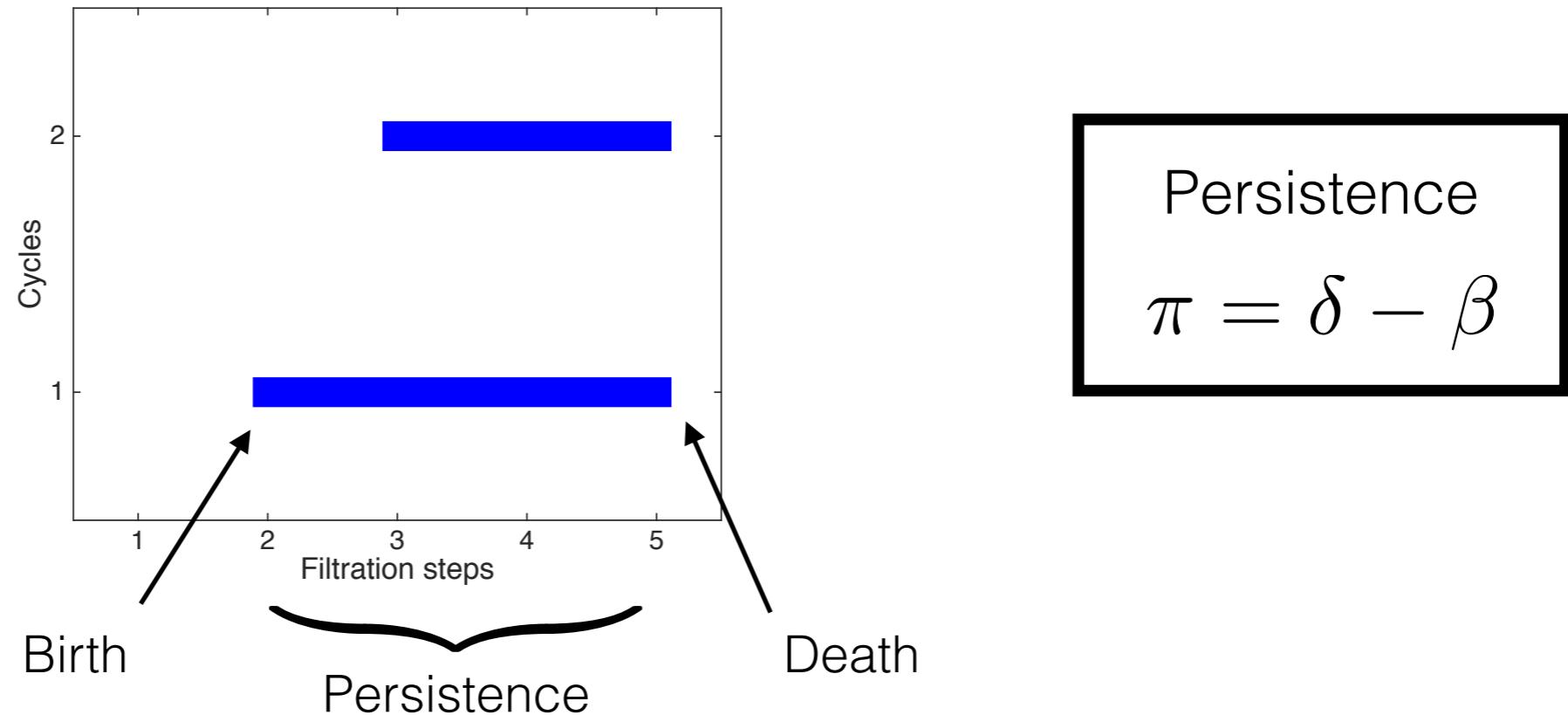
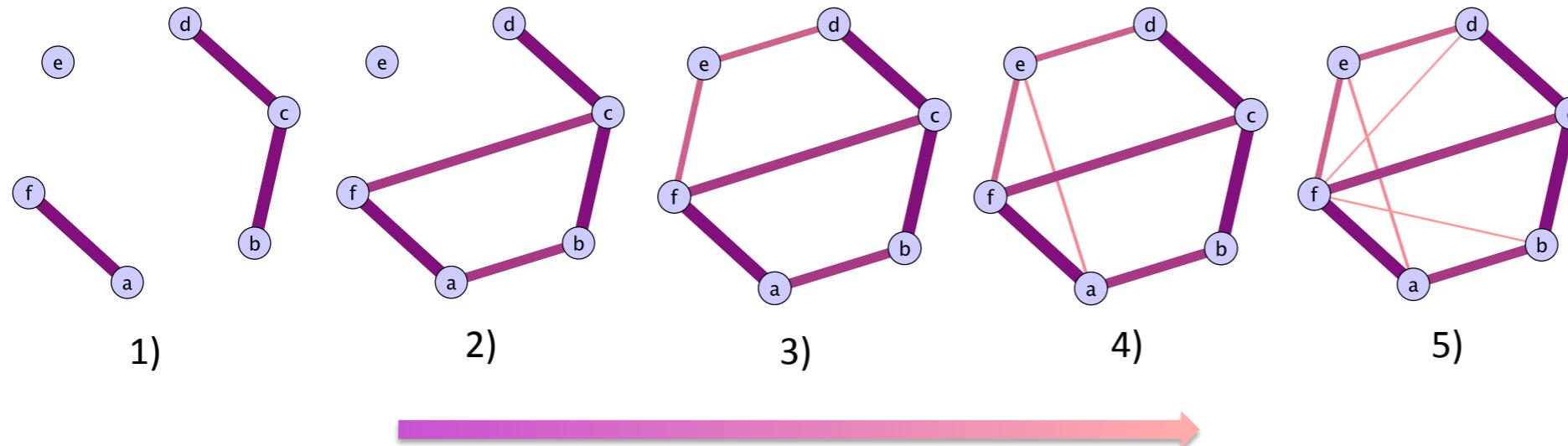


Weight Clique Rank Filtration

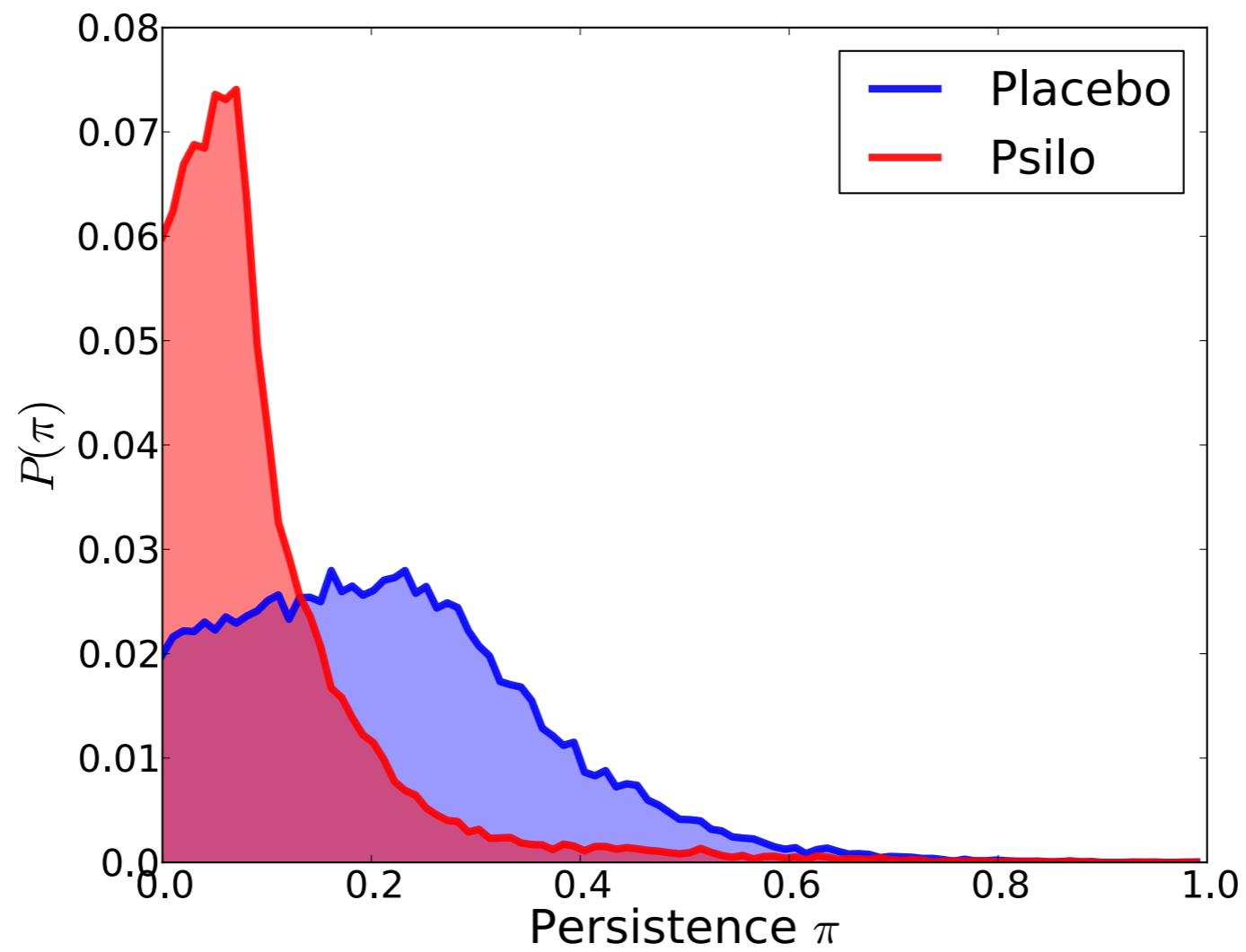


- Start with an empty network of ROIs.
- Add an edge from the correlation matrix in decreasing order of weight.
- At each step, generate the associated clique complex and compute its 1st homology group

Characterisation of cycles

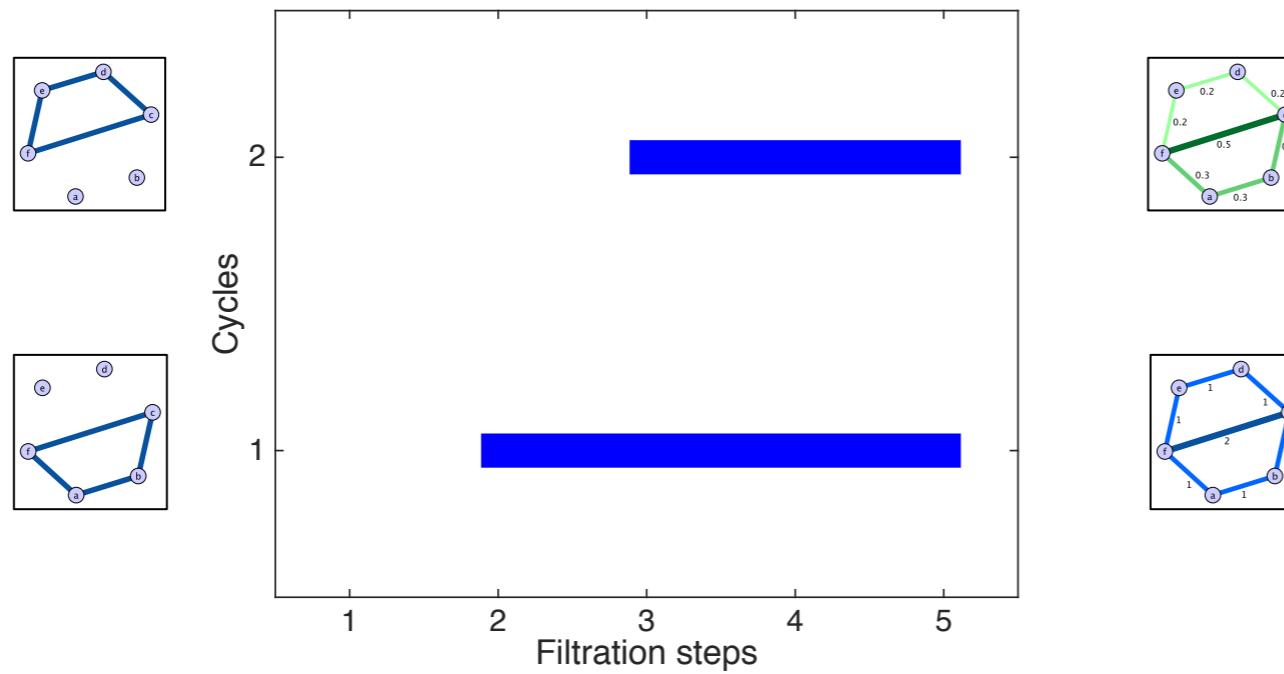
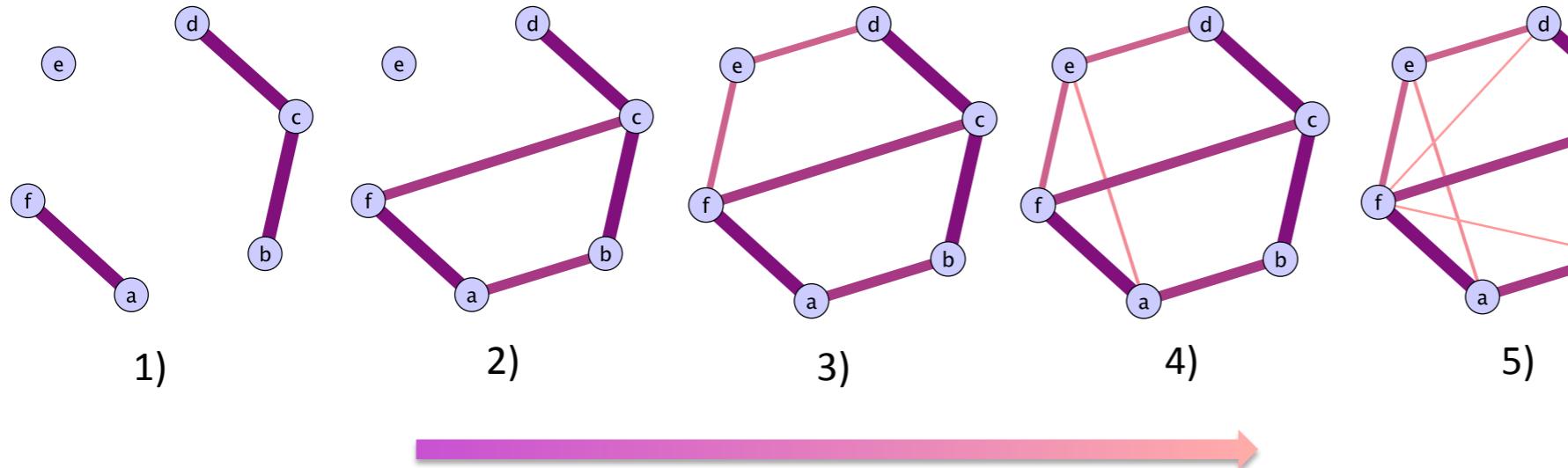


Cycles statistics



What does the average persistence tell us?

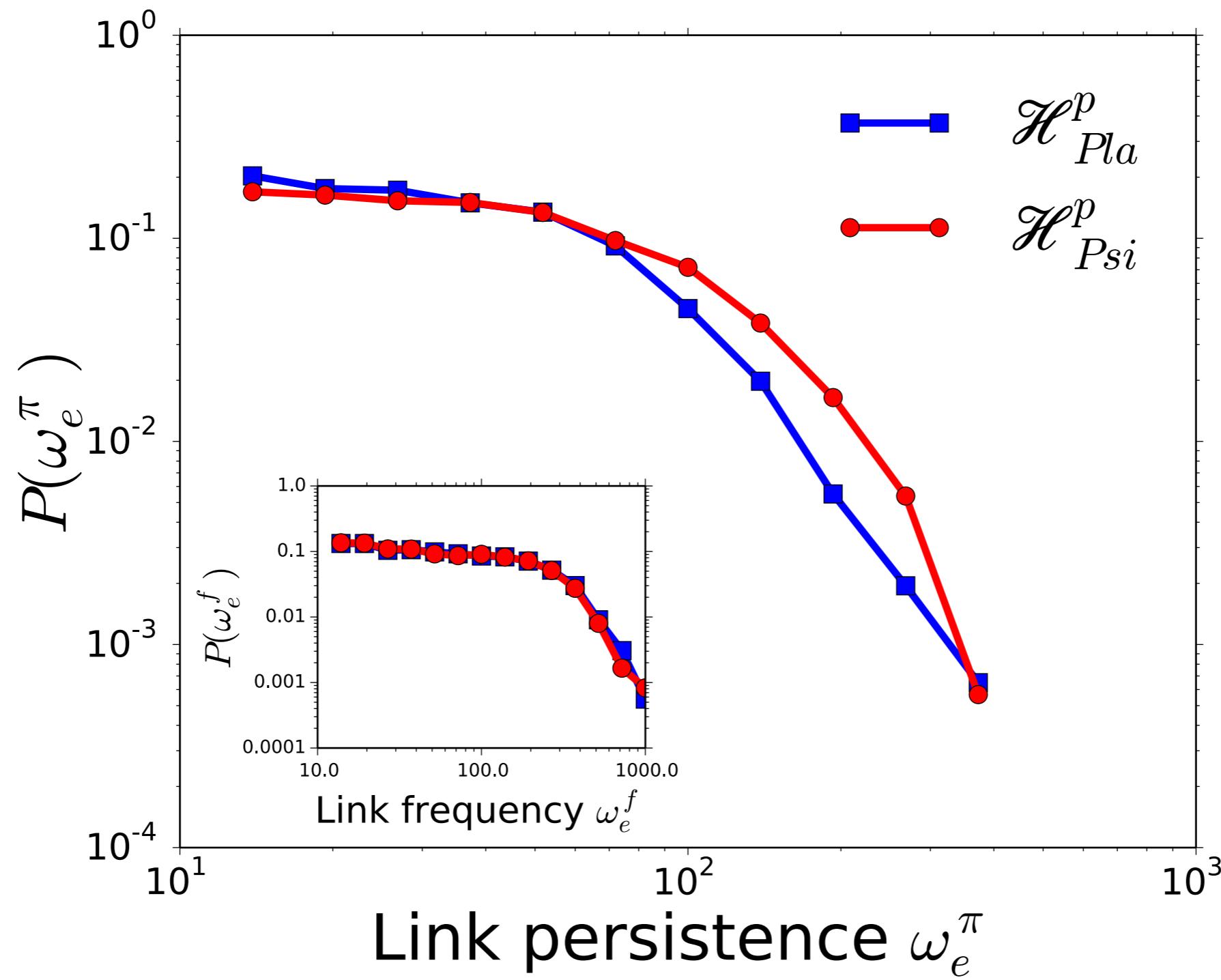
Localisation: Homological scaffolds



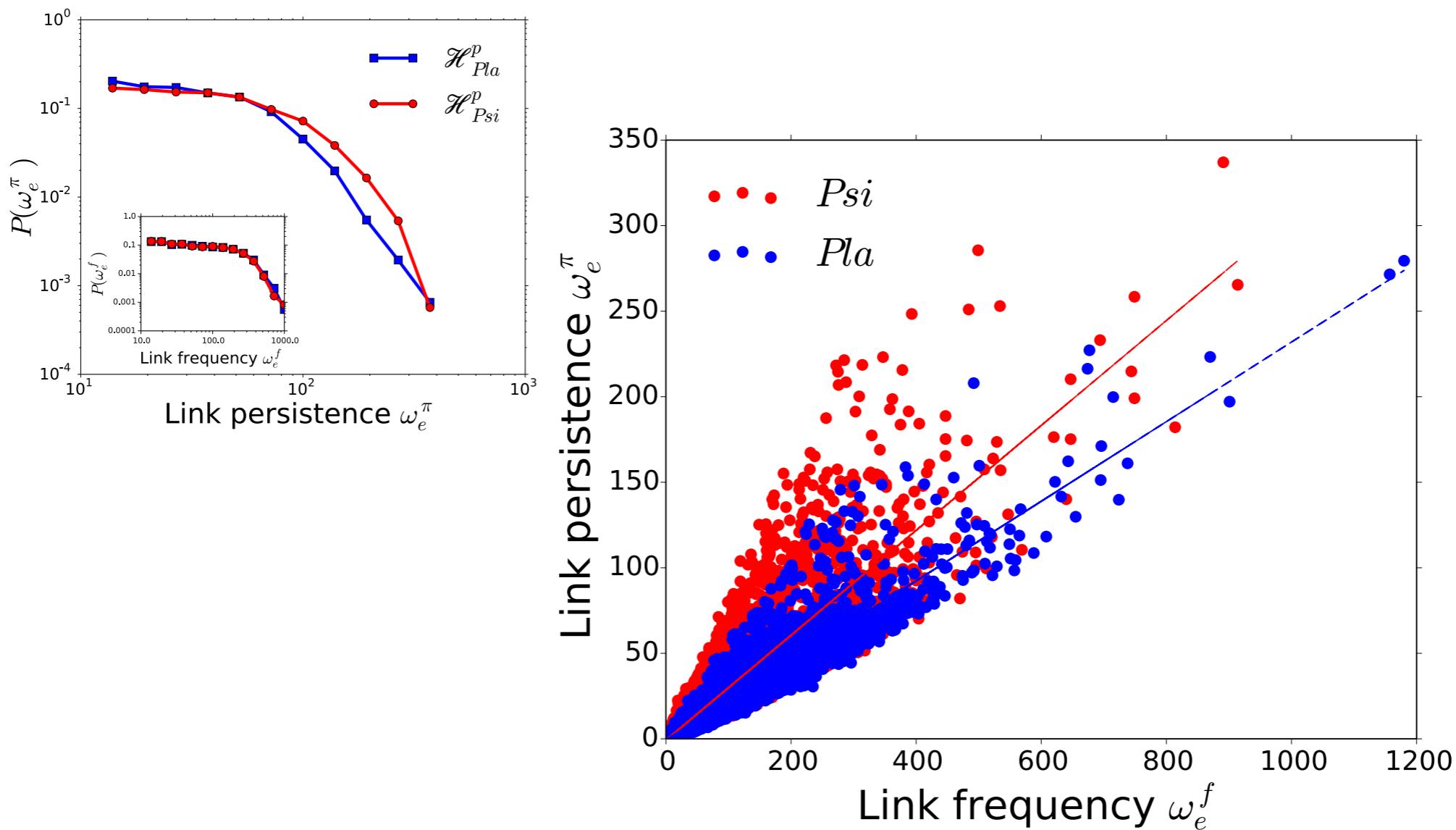
$$\omega_e^\pi = \sum_{g_i | e \in g_i} \pi_{g_i}$$

$$\omega_e^f = \sum_{g_i | e \in g_i} 1_{g_i}$$

Edge weights distributions

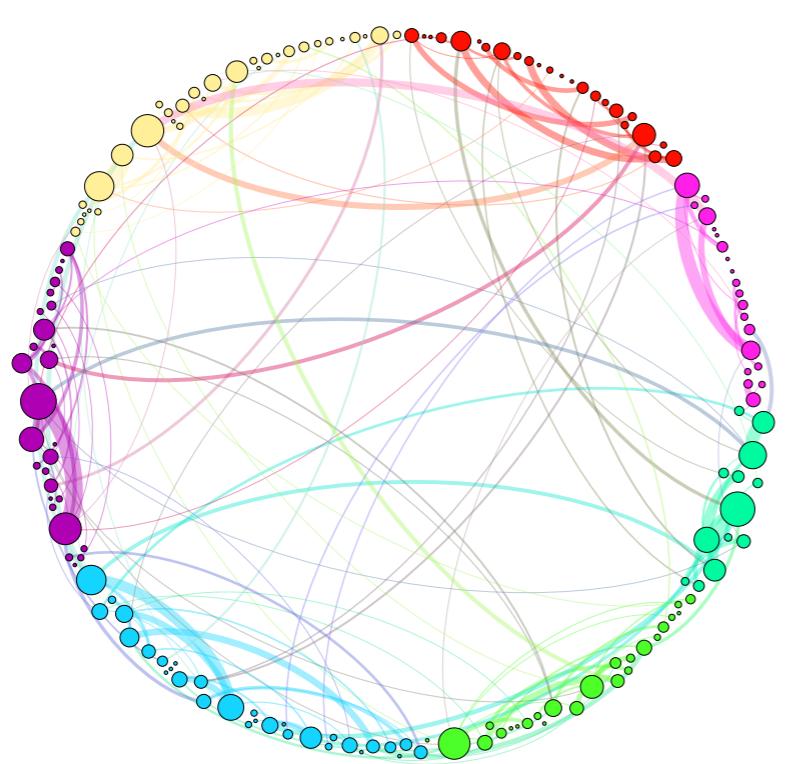


Frequency vs persistence

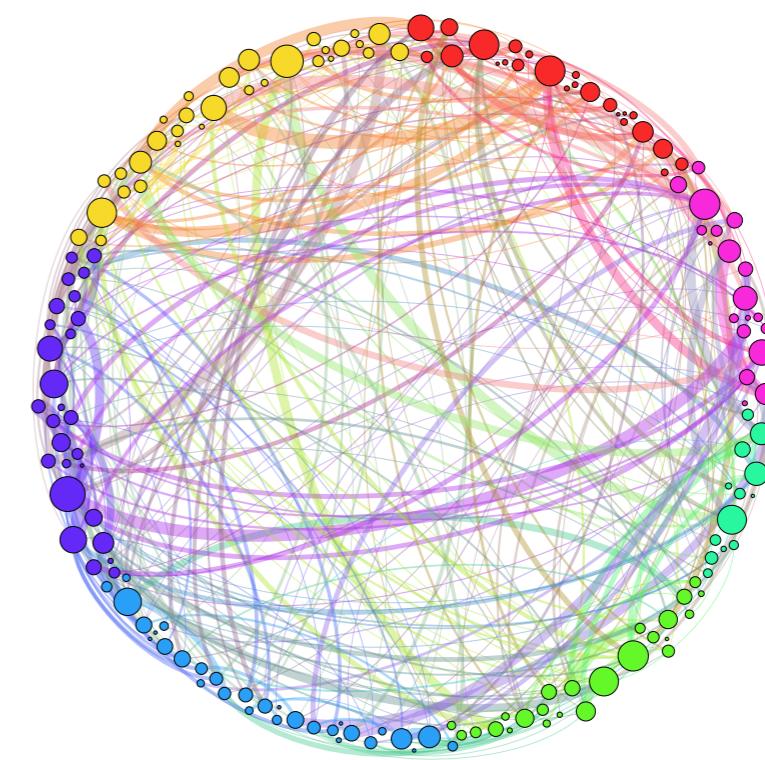


The dependence is much more scattered for the psilocybin group.

Persistence scaffolds



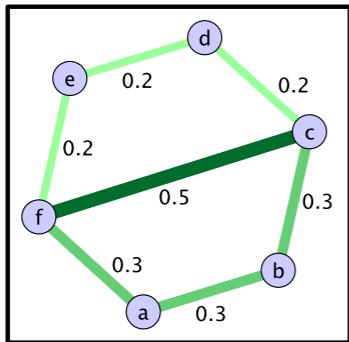
Placebo



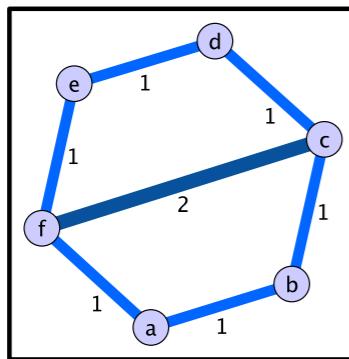
Psilocybin

Different integration patterns.

Scaffolds nodes centrality



$$PSS(i) = \sum_{e \in E(i)} \omega_e^\pi$$



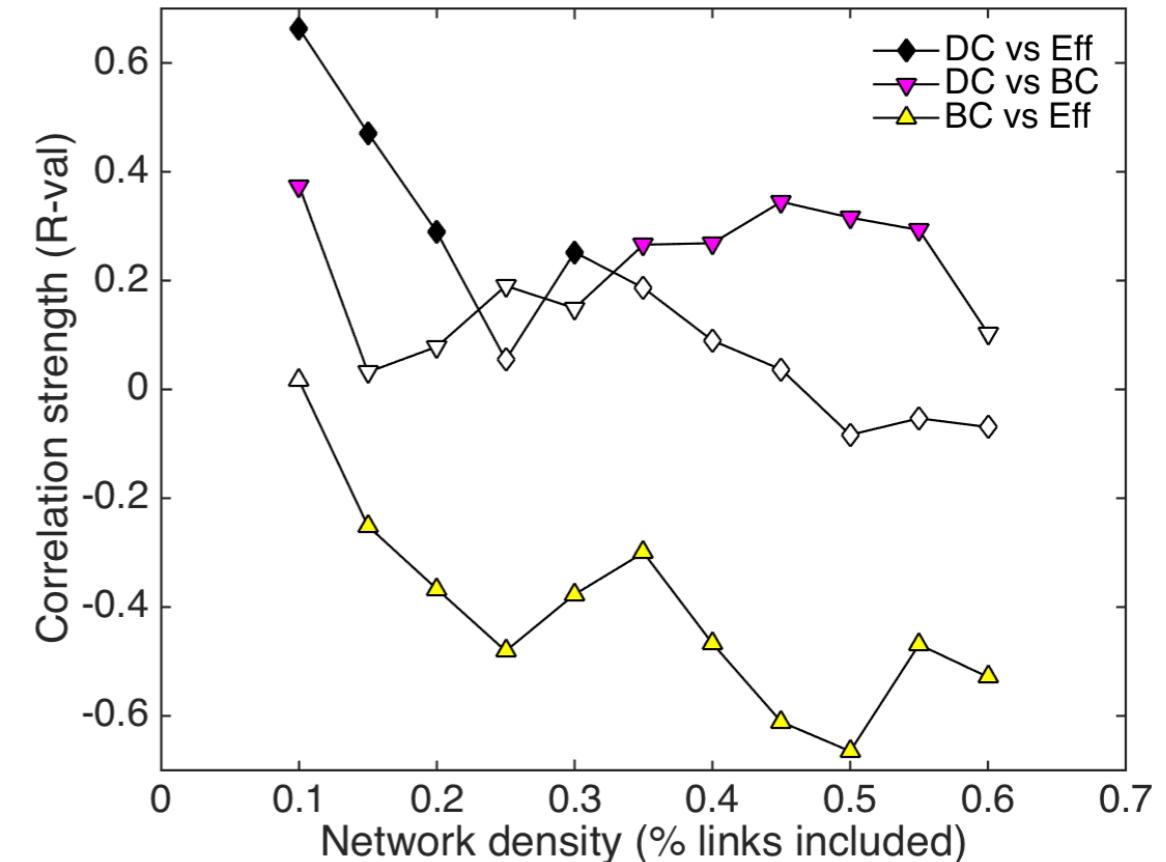
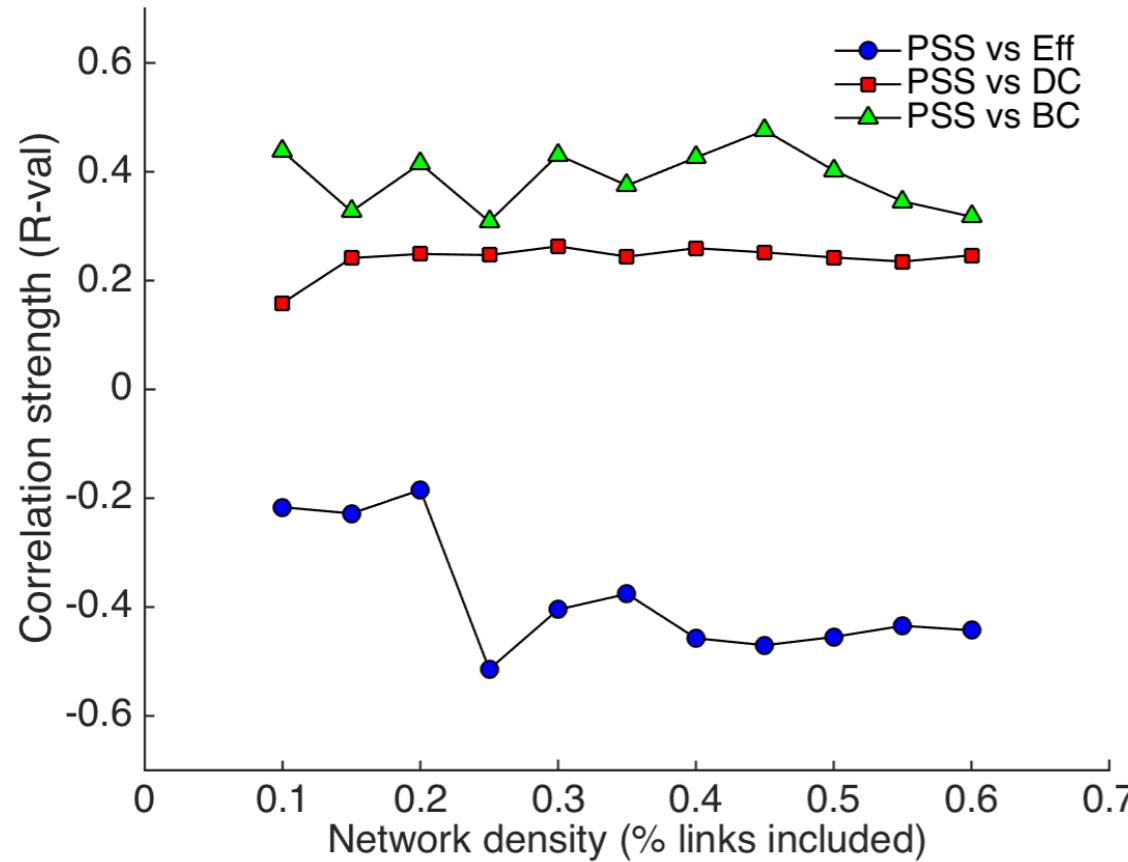
$$FSS(i) = \sum_{e \in E(i)} \omega_e^f$$

Represent centrally extracted from information about the holes structures.

Relation between simplicial and network metrics

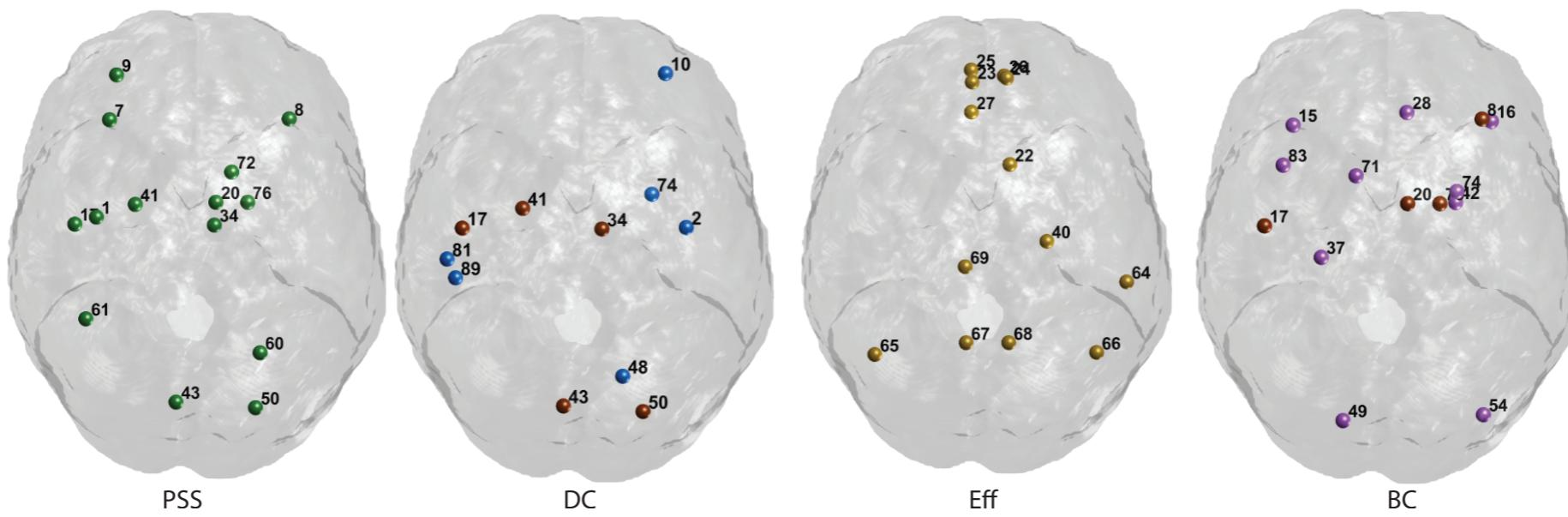
- Data: resting state fMRI time series for 90 ROIs and their associated correlation matrix.
- Persistent homology thread:
Persistent homology with weighted clique rank filtration: homological scaffolds and the associated PSS.
- Network thread:
Thresholding applied for a target density: Degree and betweenness centrality and efficiency computed.

Relation between simplicial and network metrics



PSS naturally combines different aspects of network organisation,
highlighting a type of integrator nodes.

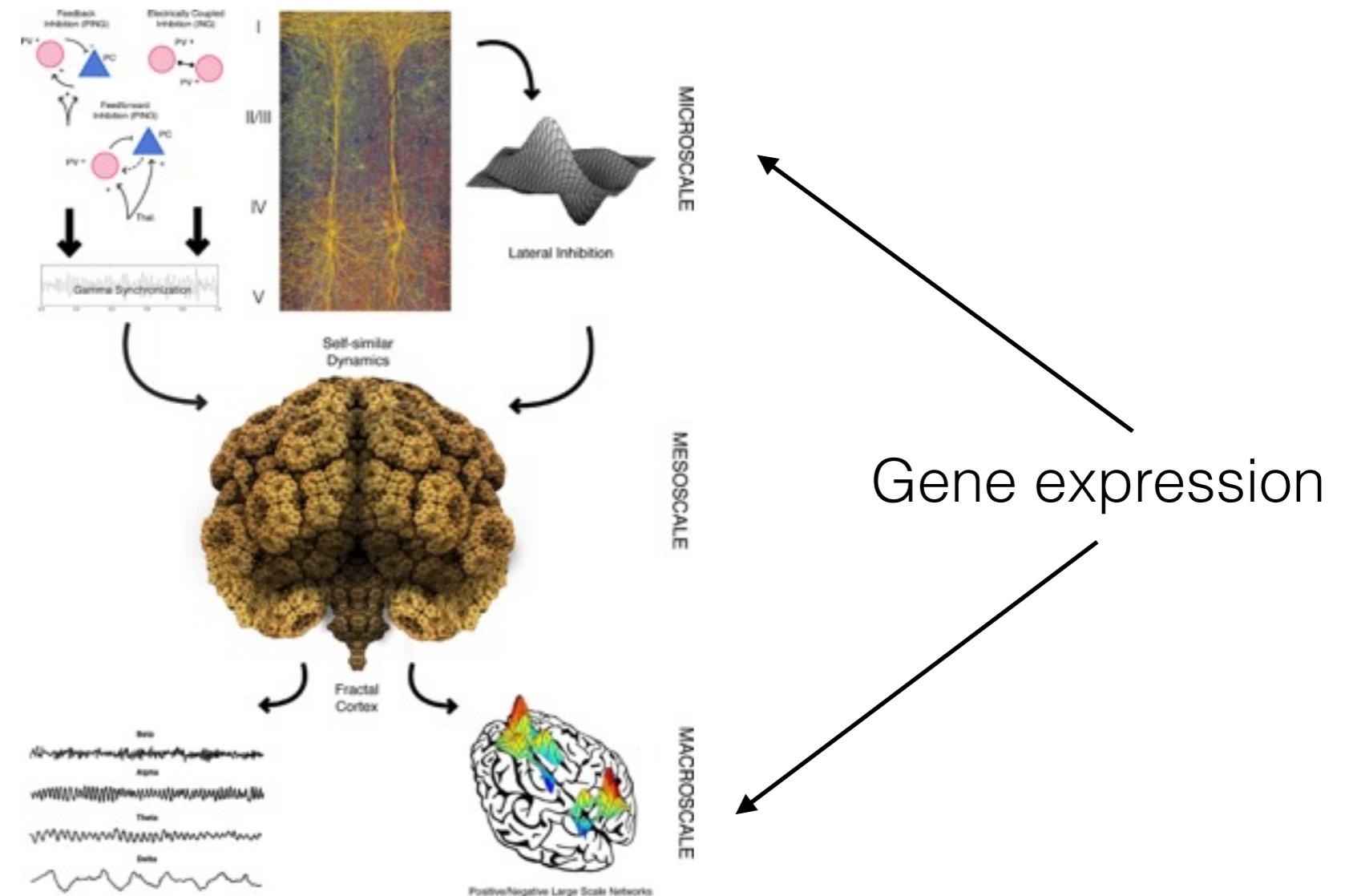
Hubs varieties



Looking at brain function from yet another complementary angle.
How to integrate

Nodes in brown overlap between PSS and network metrics.

The bottom of the barrel

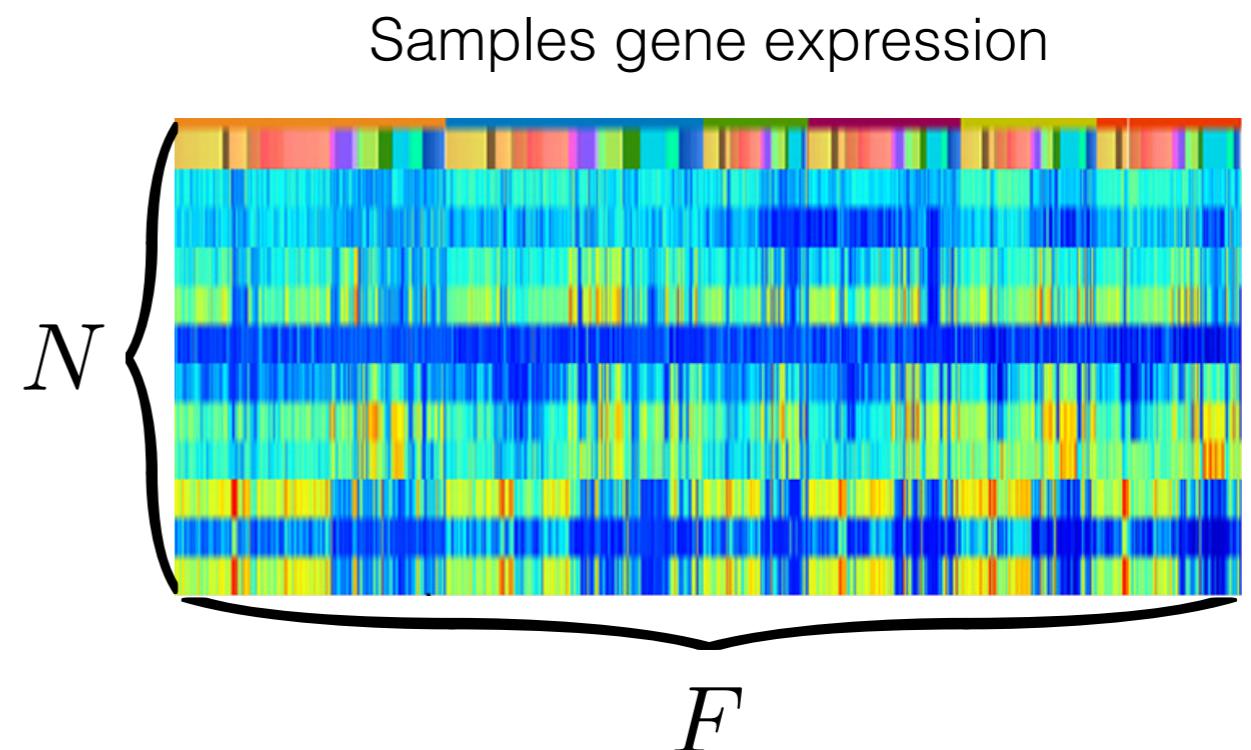


Ultimately, everything is shaped by gene expression.
Altered neurochemistry only uses structure constrained by genes.

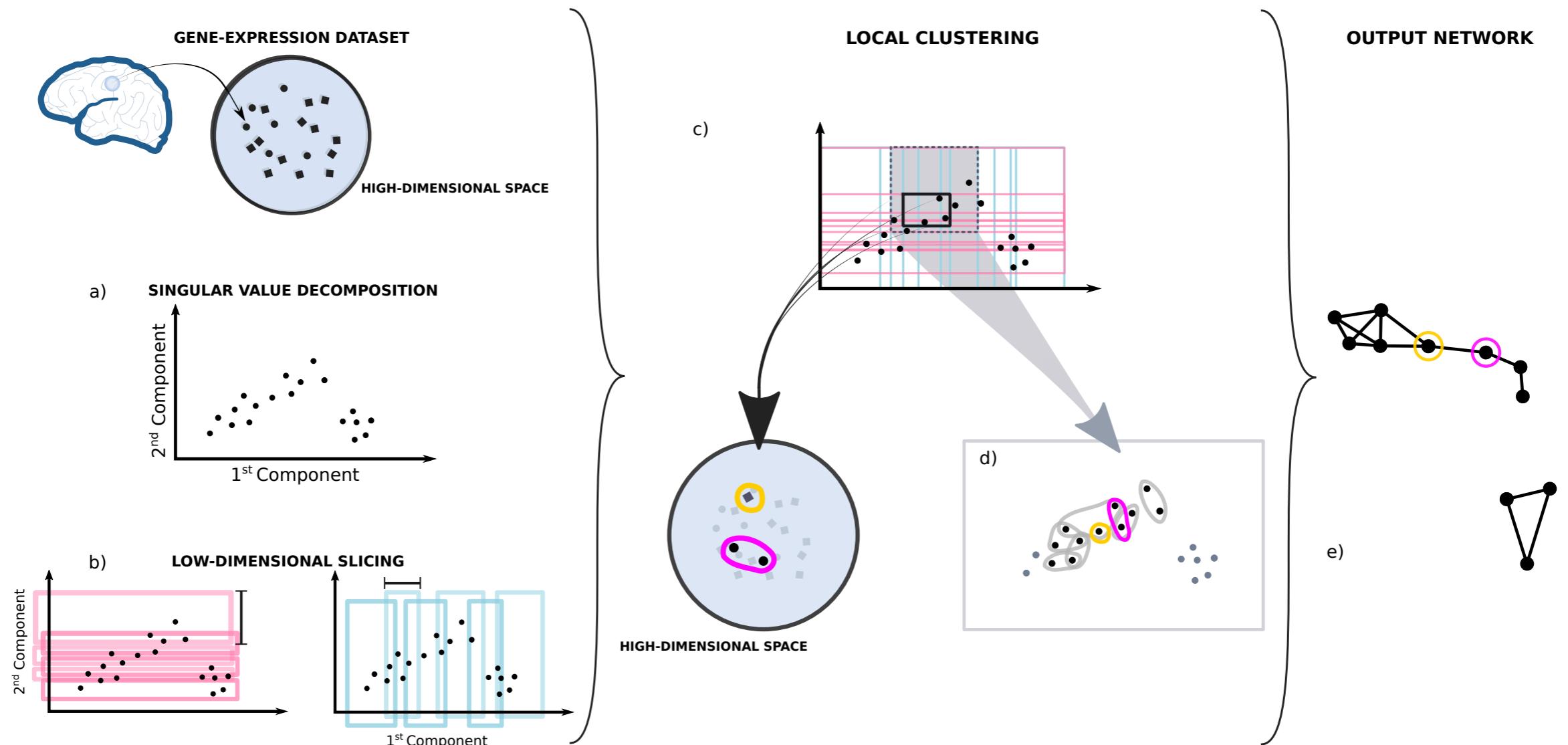
Allen Human Brain Atlas

spatial gene expression patterns

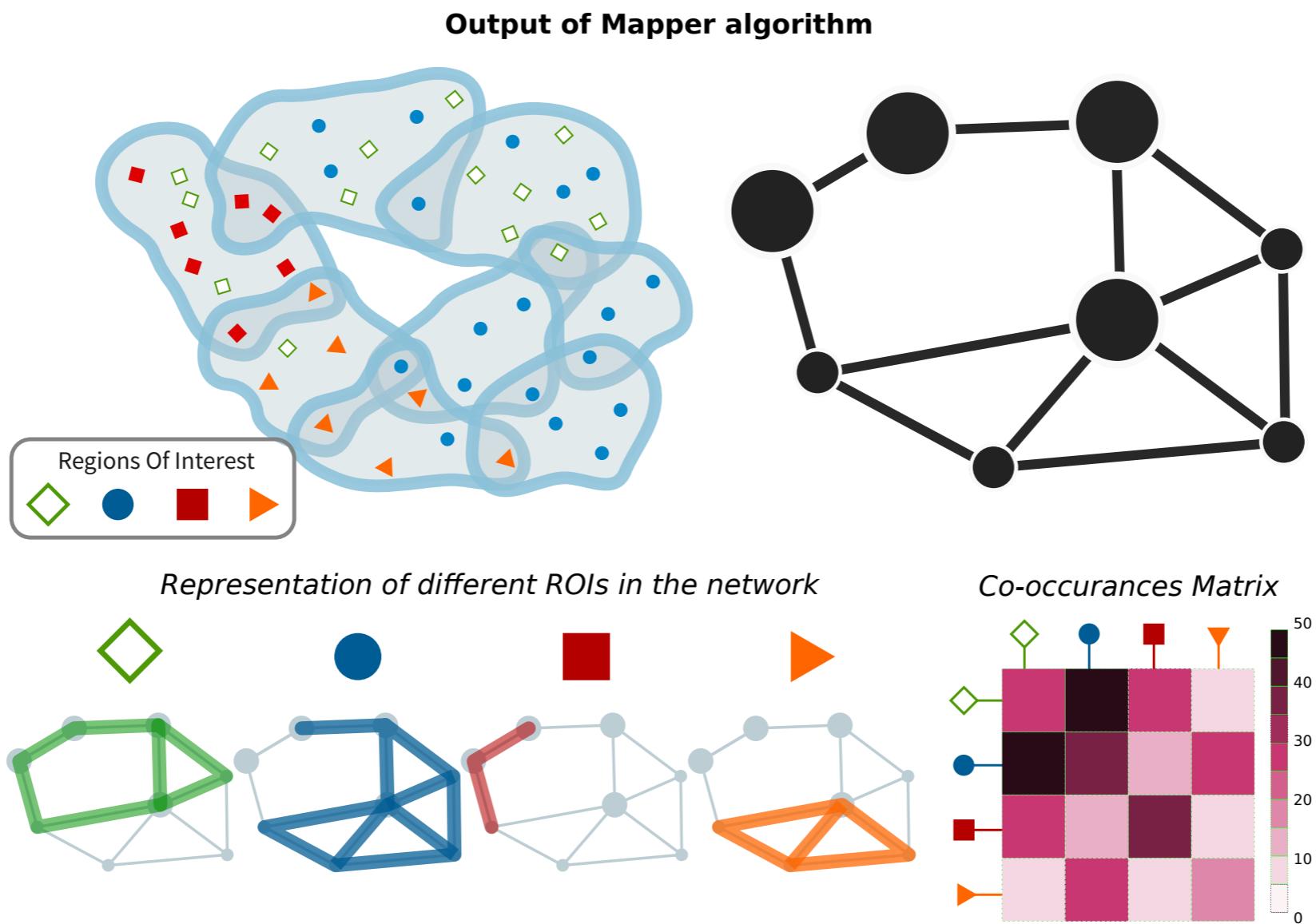
The Allen Institute provides vast amount of freely available data. Including gene expression for samples taken in human brain
<http://portal.brain-map.org>



2D Mapper

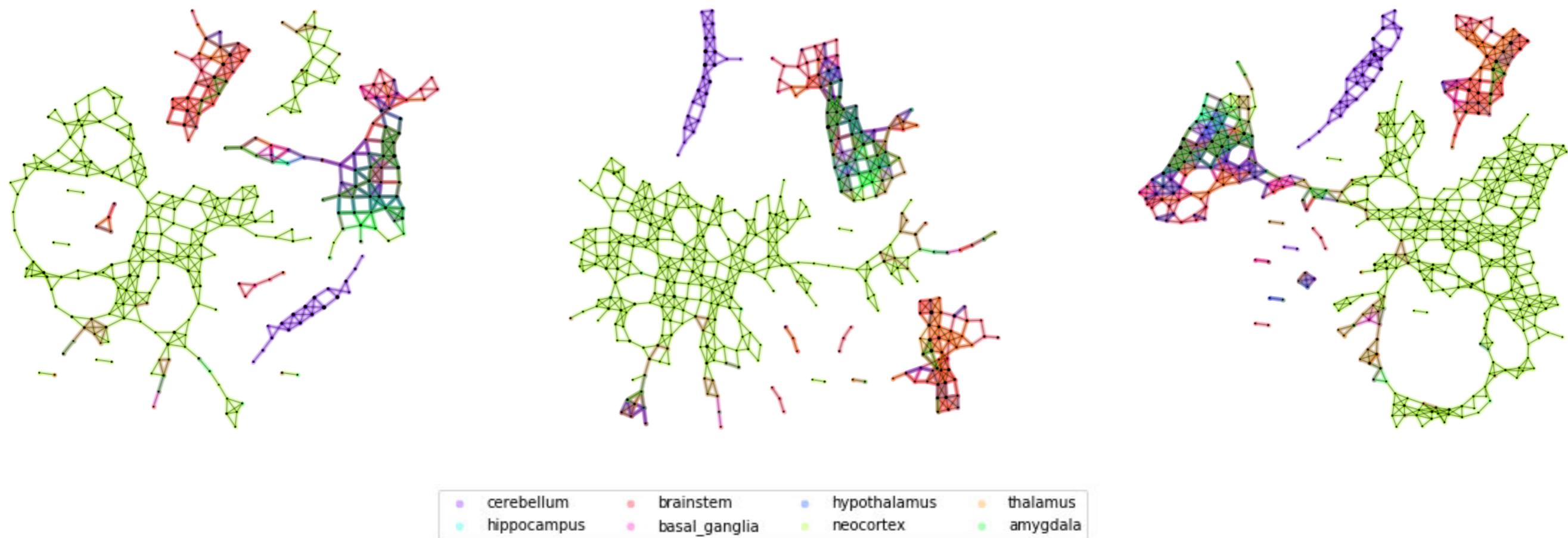


Spatial homogeneity



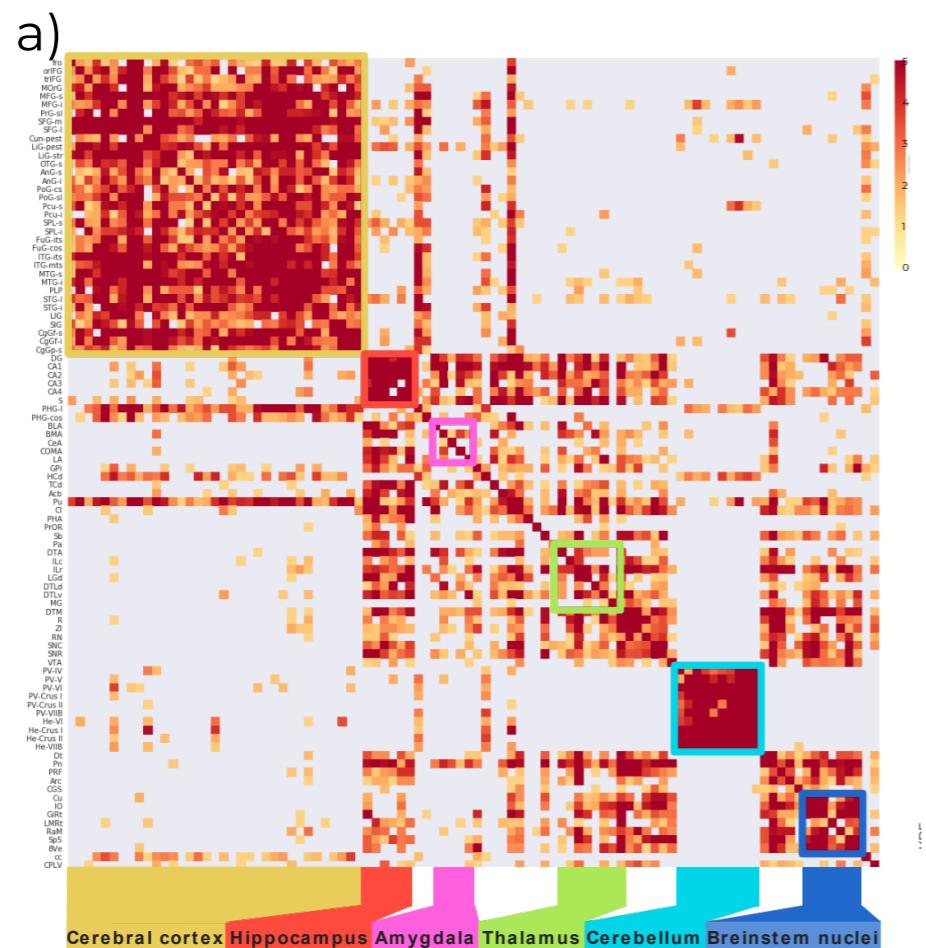
Using gene sample location metadata.

Whole genome Mapper networks

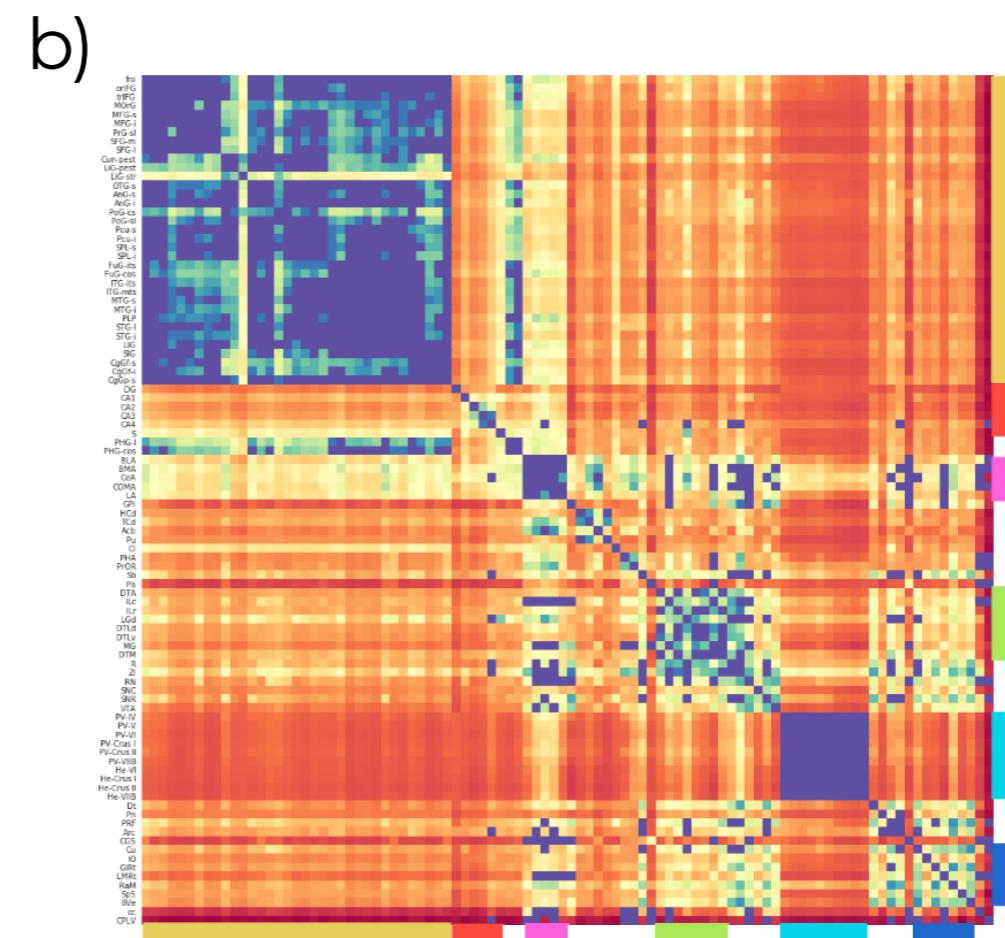


Networks obtained for different overlap values (25, 30, 35%).

Validation

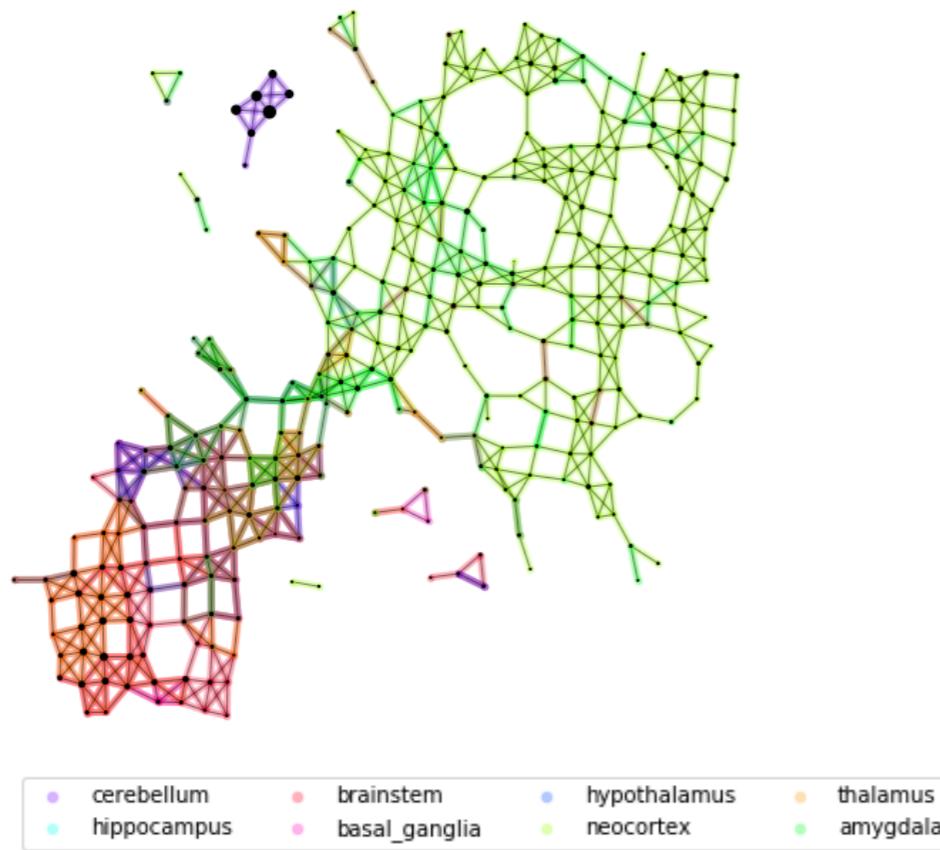


Agreement matrix

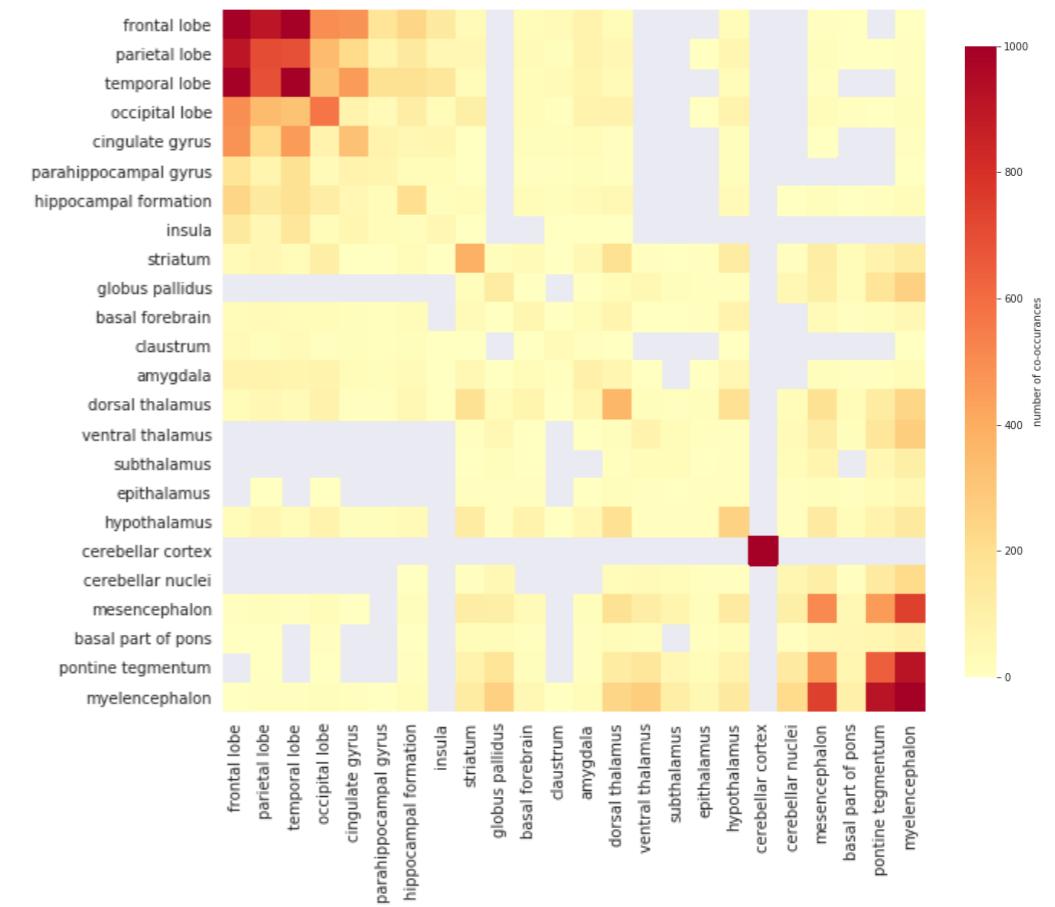


Co-expression matrix

The dopamine system (I)

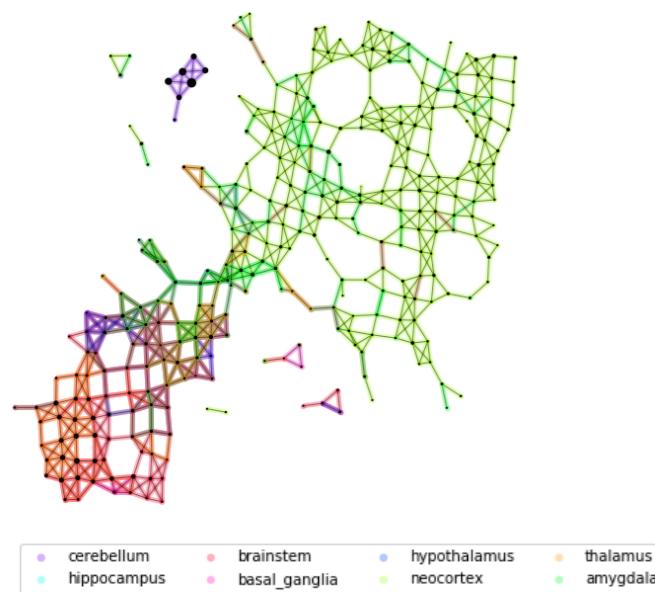


Dopamine Mapper network

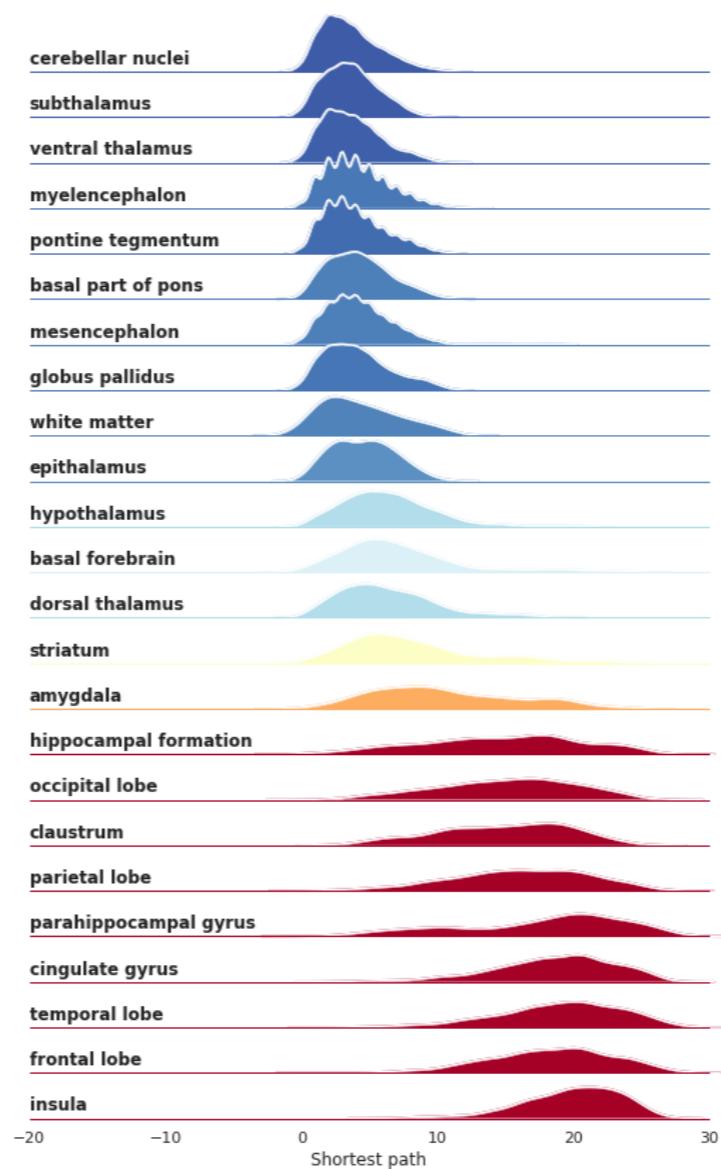


Agreement matrix

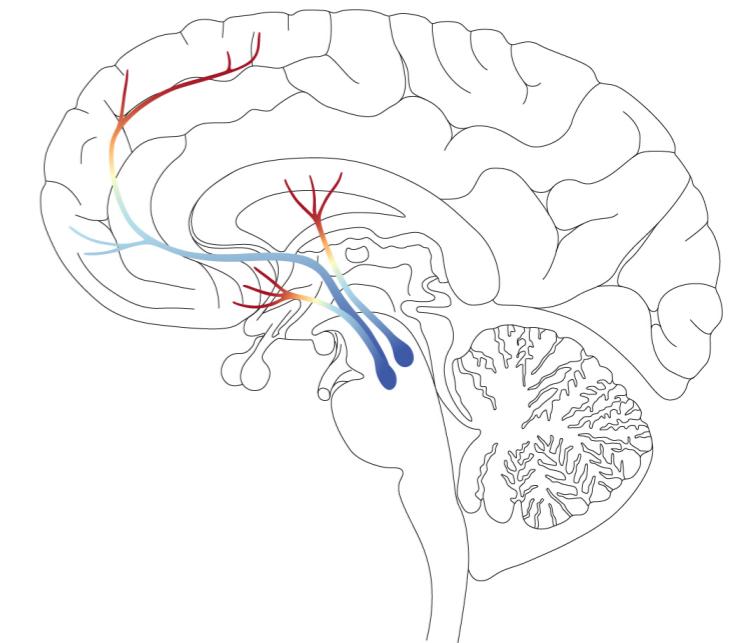
The dopamine system (II)



Dopamine Mapper network

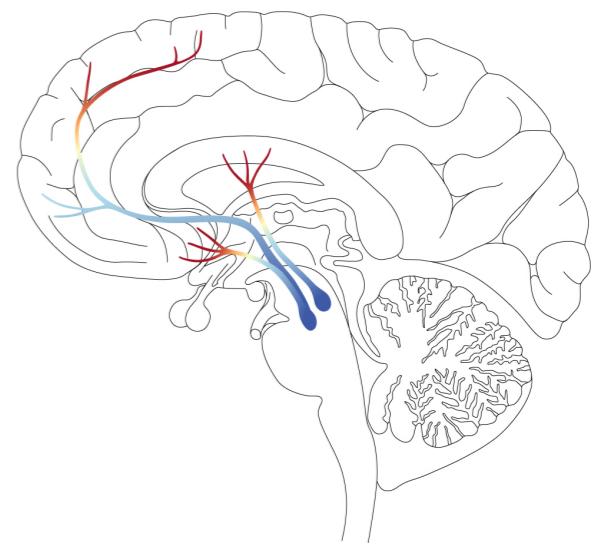
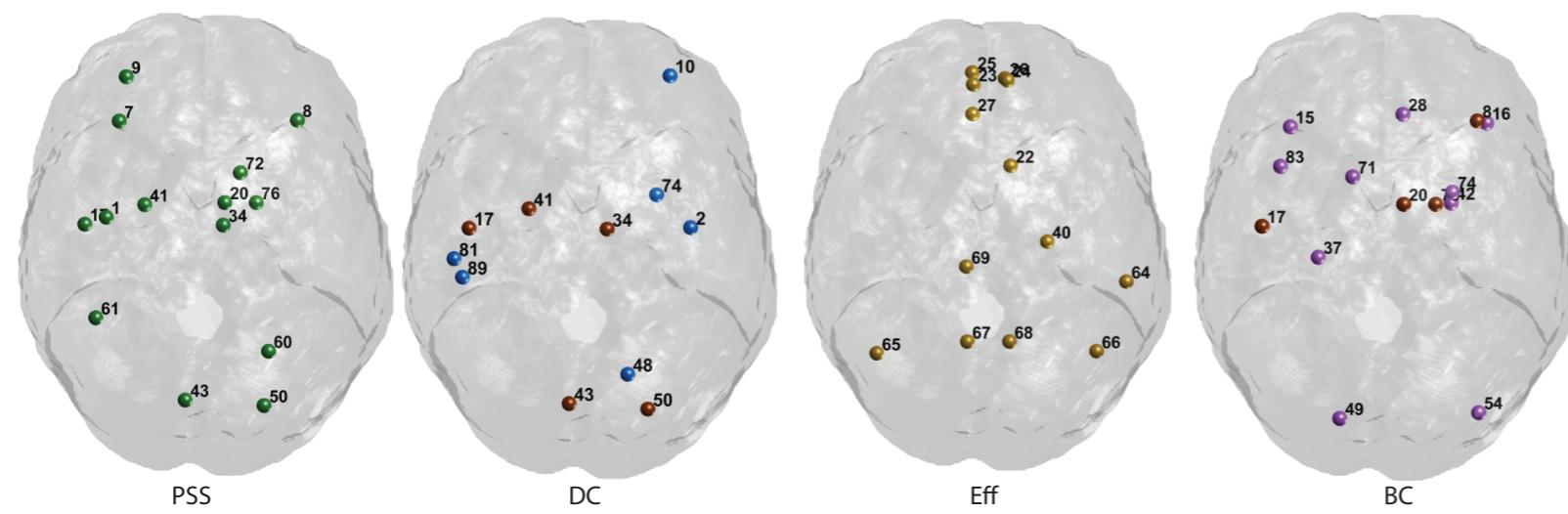
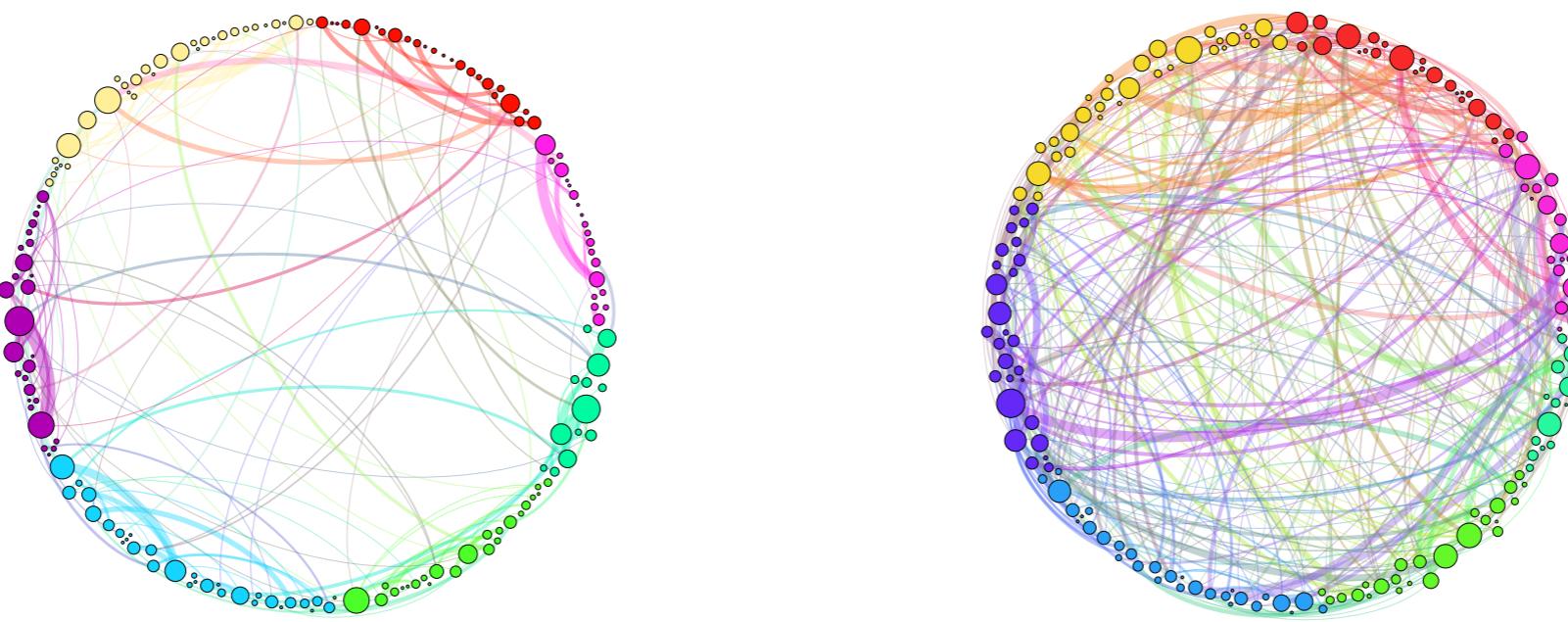


Shortest paths from the substantia nigra



Dopamine pathway

Integration in methods: meta-data, modalities and approach





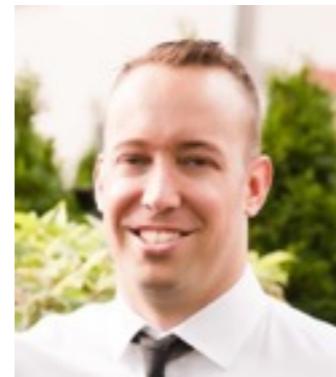
Giovanni Petri, ISI



Alice Patania, IUNI



Federico Turkheimer, KCL



LD Lord, Oxford

Network Neuroscience Focus Features
on Topological Neuroscience



Thank you for listening, questions?