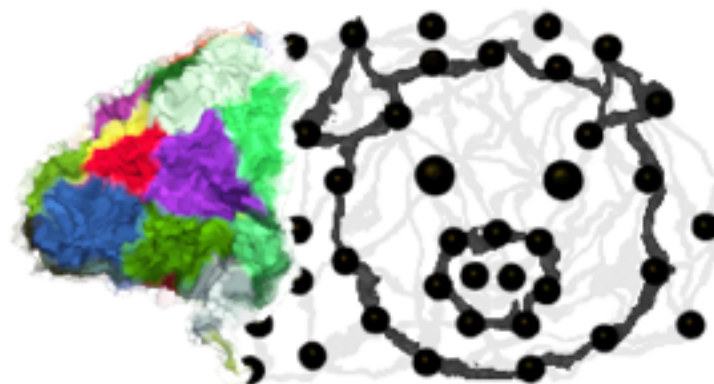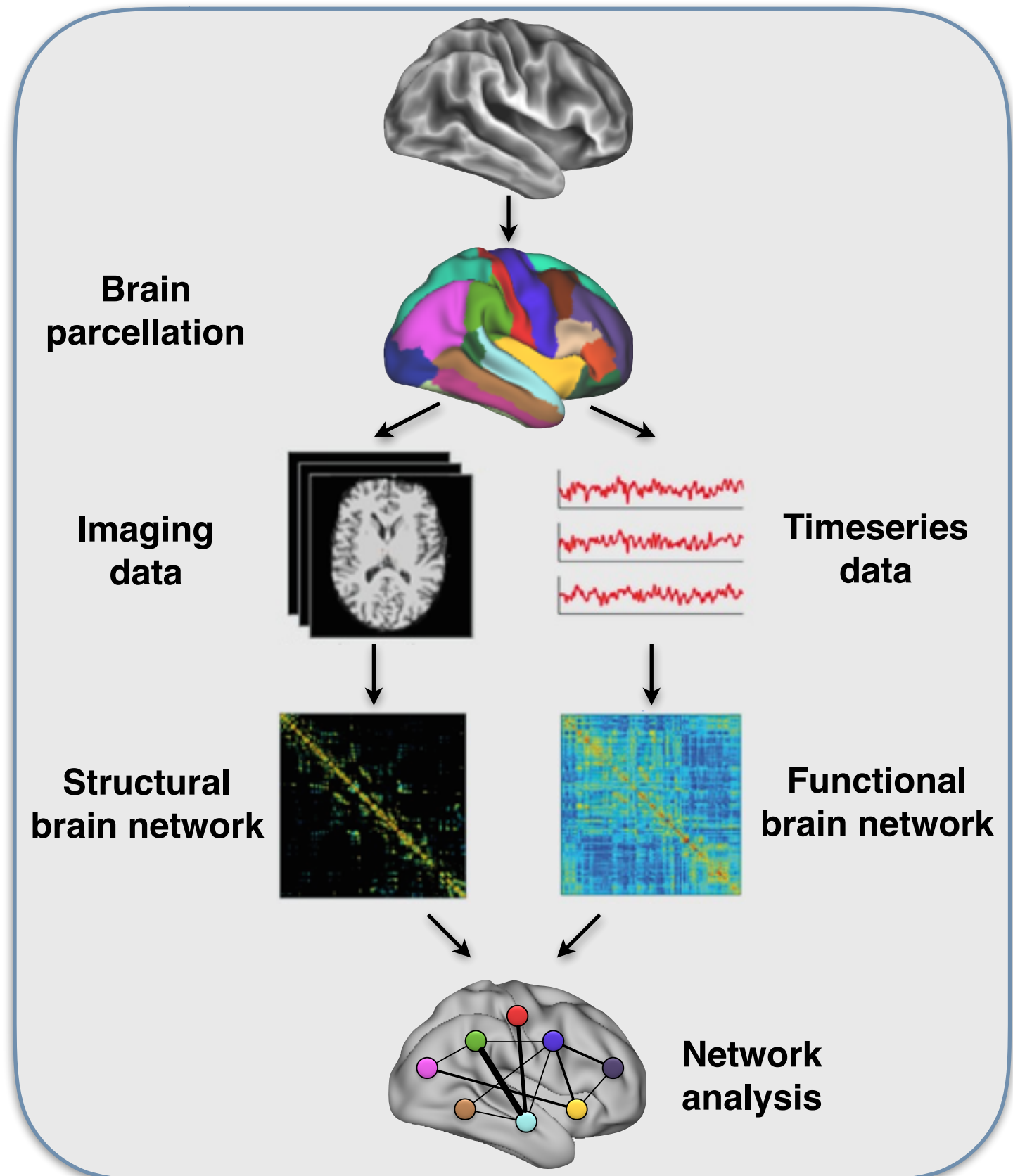# COMPARISON OF BRAIN NETWORKS WITH UNKNOWN CORRESPONDENCES

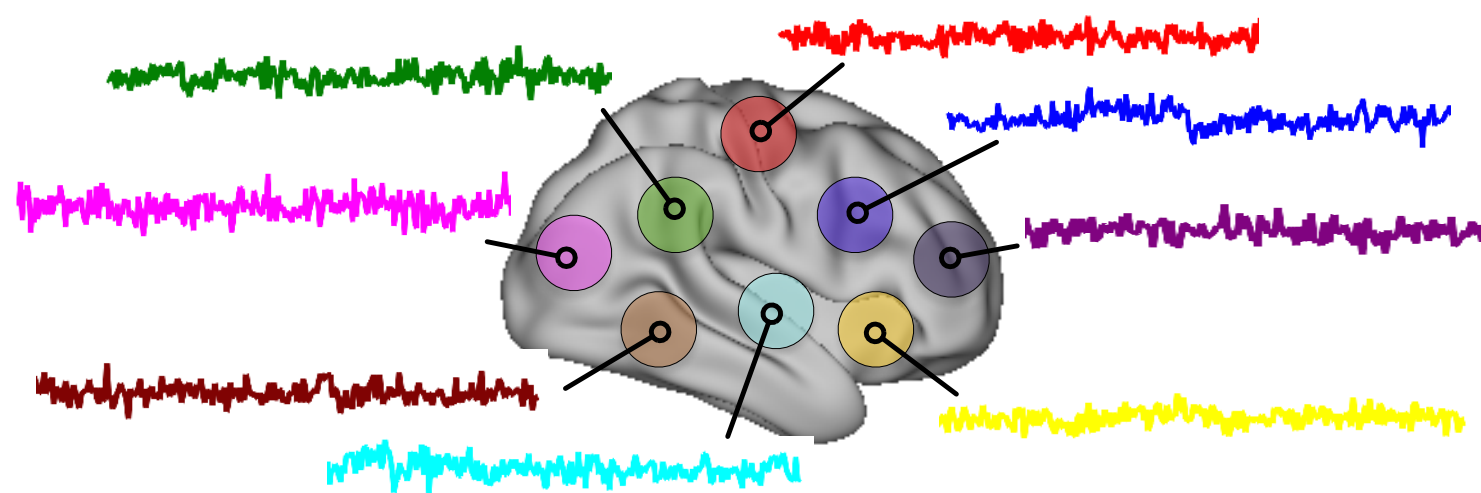SI Ktena, S Parisot, J Passerat-Palmbach and D Rueckert

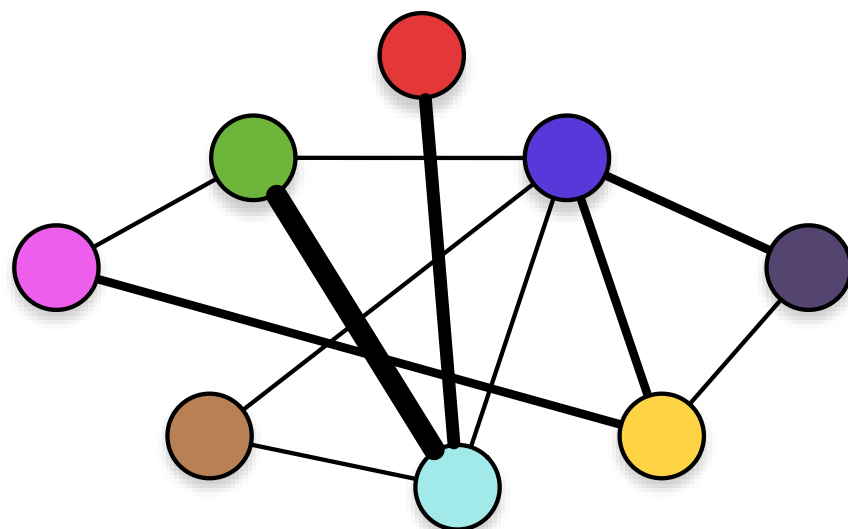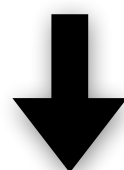# The brain from a network perspective

- cognition is a network phenomenon [Sporns, *Dial. Clin. Neurosc.* (2013)]

- no physical trace of certain diseases, only changes in the physical wiring and strength of connections

- given two brain graphs representing connectivity, how similar are they? (*within/between subjects, between modalities etc.*)

Brain parcellation

Imaging data

Timeseries data

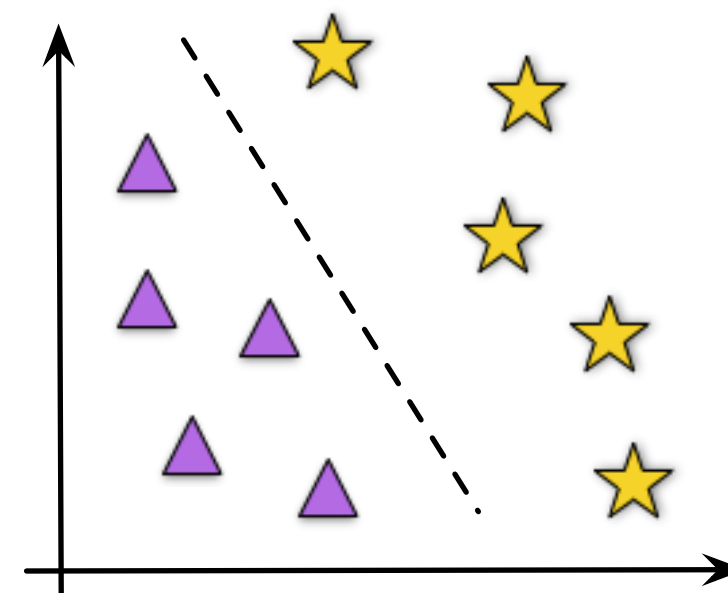**Structural brain network**

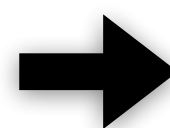**Functional brain network**

Network analysis
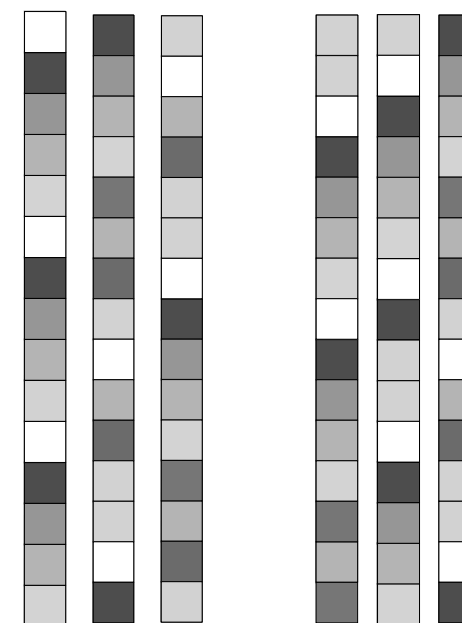
Inference: Naive approach

Graph construction

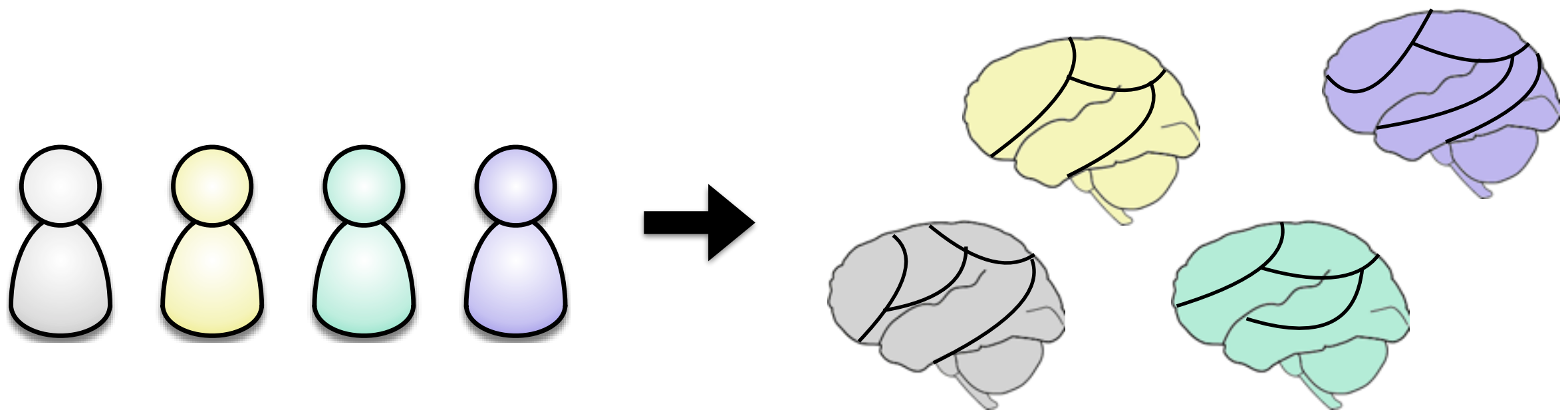Graph embedding

Model training and inference

class △

class ⭐

Richiardi et al., *IEEE Signal Processing Magazine* (2013)
Varoquaux and Craddock, *Neuroimage* (2013)

Why individual parcellations?

- Standard anatomical atlases subdivide the brain based on cytoarchitecture (e.g. Brodmann) or anatomical landmarks (e.g. Desikan-Killiany)

- Individual variability in terms of anatomy or function due to maturation or brain injury are not accounted for [Timofiyeva, *PLoS One* (2014)]

- Data-driven single subject parcellations capture this variability

Inexact graph matching

• Evaluate <u>how much</u> two graphs share
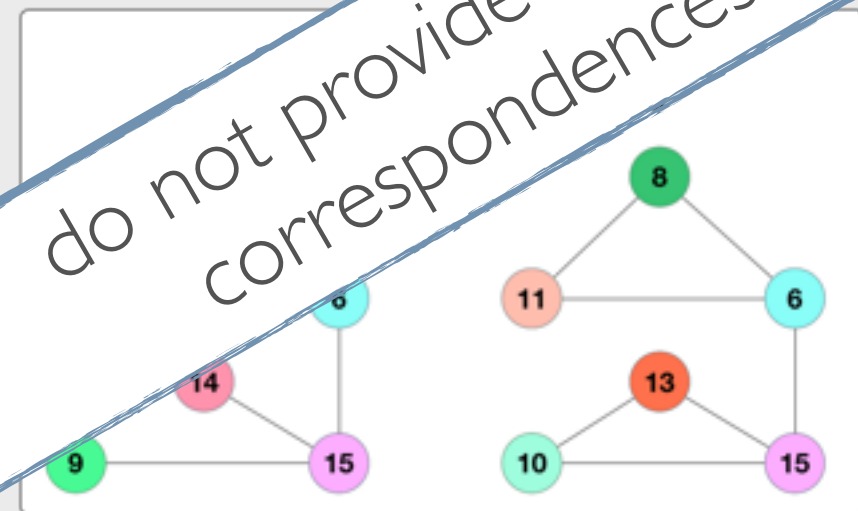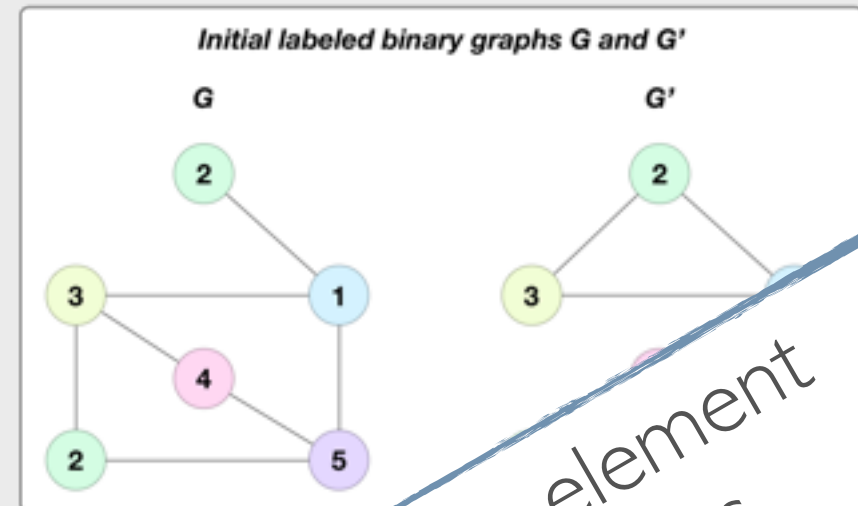
Graph embedding
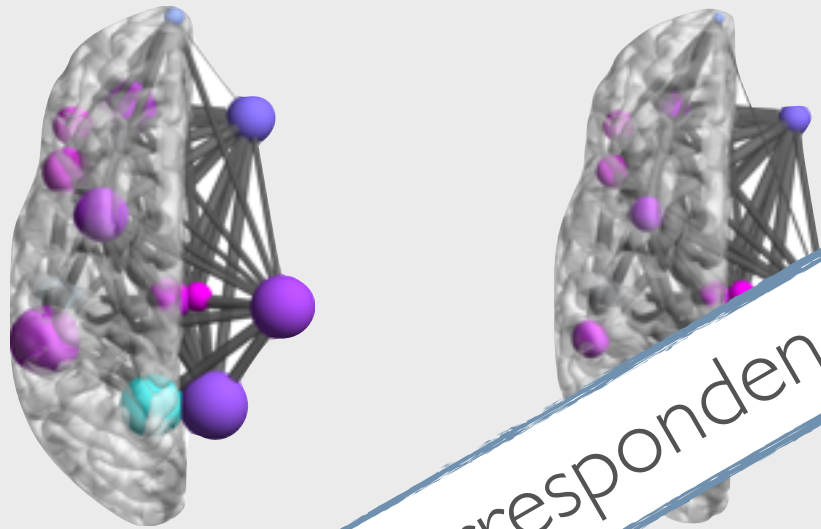
requires node correspondences

Craddock et al., *Nature Methods* (2013)

Graph kernels

Initial labeled binary graphs G and G'

do not provide element correspondences
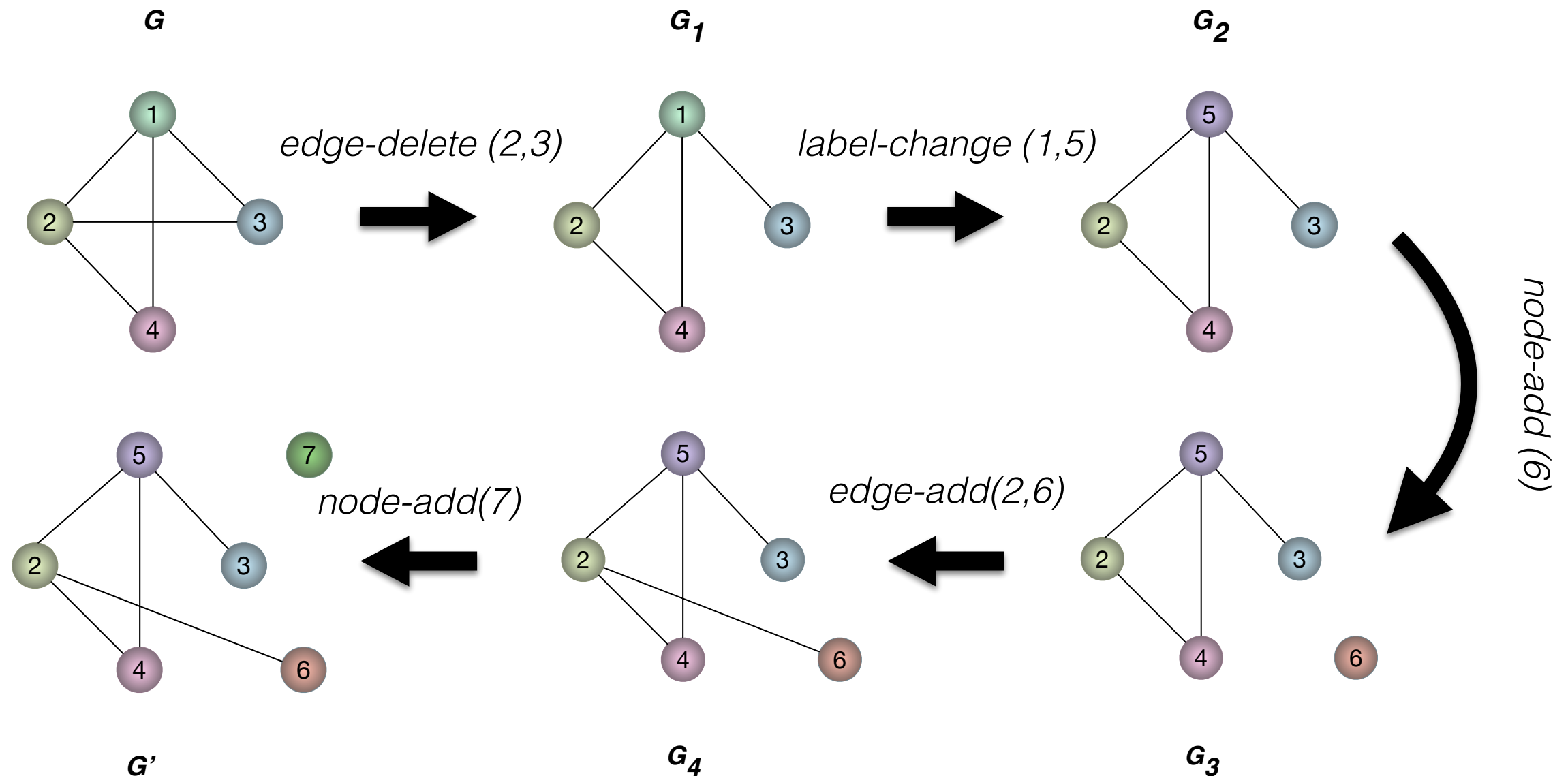
Feature vector representations of G and G'

$$\phi_{WL}(G) = (1, 2, 1, 1, 1, 1, 1, 0, 1, 0, 0, 1, 0, 1, 1)$$
$$\phi_{WL}(G') = (1, 2, 1, 1, 1, 1, 0, 1, 0, 1, 1, 0, 1, 0, 1)$$
$$k_{WL}(G, G') = < \phi_{WL}(G), \phi_{WL}(G') > = 8$$

Jie et al. *Human Brain Mapping* (2014)

Graph edit distance

- Measure of dissimilarity between graphs, defined directly in their domain $\mathcal{G}$ as a nonnegative function $d : \mathcal{G} \times \mathcal{G} \to \mathbb{R}^+$. Able to model structural variation in a very intuitive and illustrative way.

GED computation

- The Hungarian algorithm provides a fast approximate solution to the GED computation [Riesen & Bunke, *Img & Vis. Comp.*, (2009)]

- Given two labeled graphs G_1, G_2 with $|\mathcal{V}(G_1)| = n$ and $|\mathcal{V}(G_2)| = m$ a square cost matrix $\mathbf{C}$ of order $n + m$ is defined, which encodes all the possible edit operation costs

$$
\mathbf{C} = \begin{bmatrix}
c_{1,1} & \cdots & c_{1,m} & c_{1,\varepsilon} & \cdots & \infty \\
\vdots & \text{substitutions} & \vdots & \vdots & \text{deletions} & \vdots \\
c_{n,1} & \cdots & c_{n,m} & \infty & \cdots & c_{n,\varepsilon} \\
c_{\varepsilon,1} & \cdots & \infty & 0 & \cdots & 0 \\
\vdots & \text{insertions} & \vdots & \vdots & \ddots & \vdots \\
\infty & \cdots & c_{\varepsilon,m} & 0 & \cdots & 0
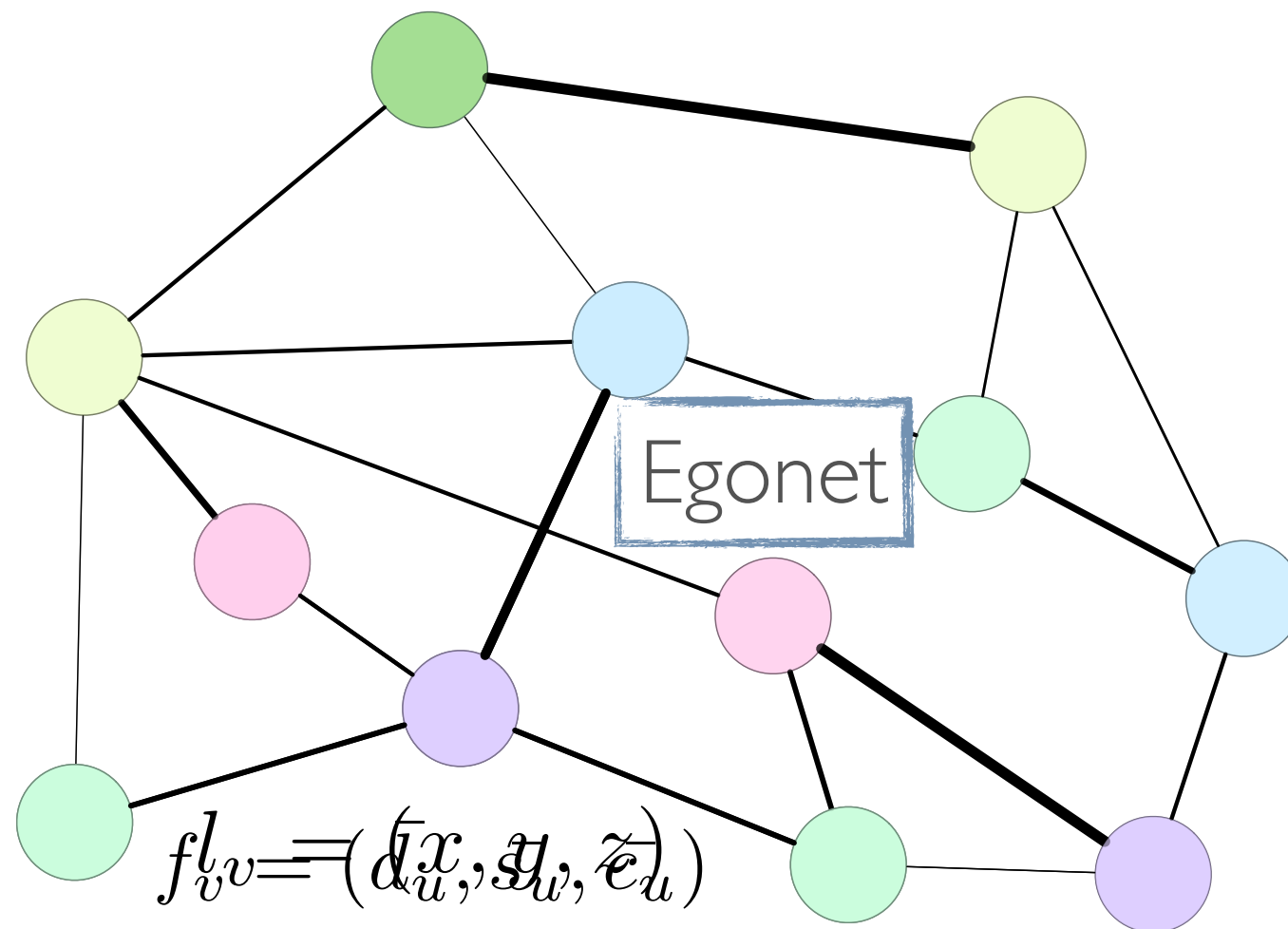\end{bmatrix}
$$

Node features

- Spatial information (coordinates in standard brain space)

- Feature information (network measures, egonet based)
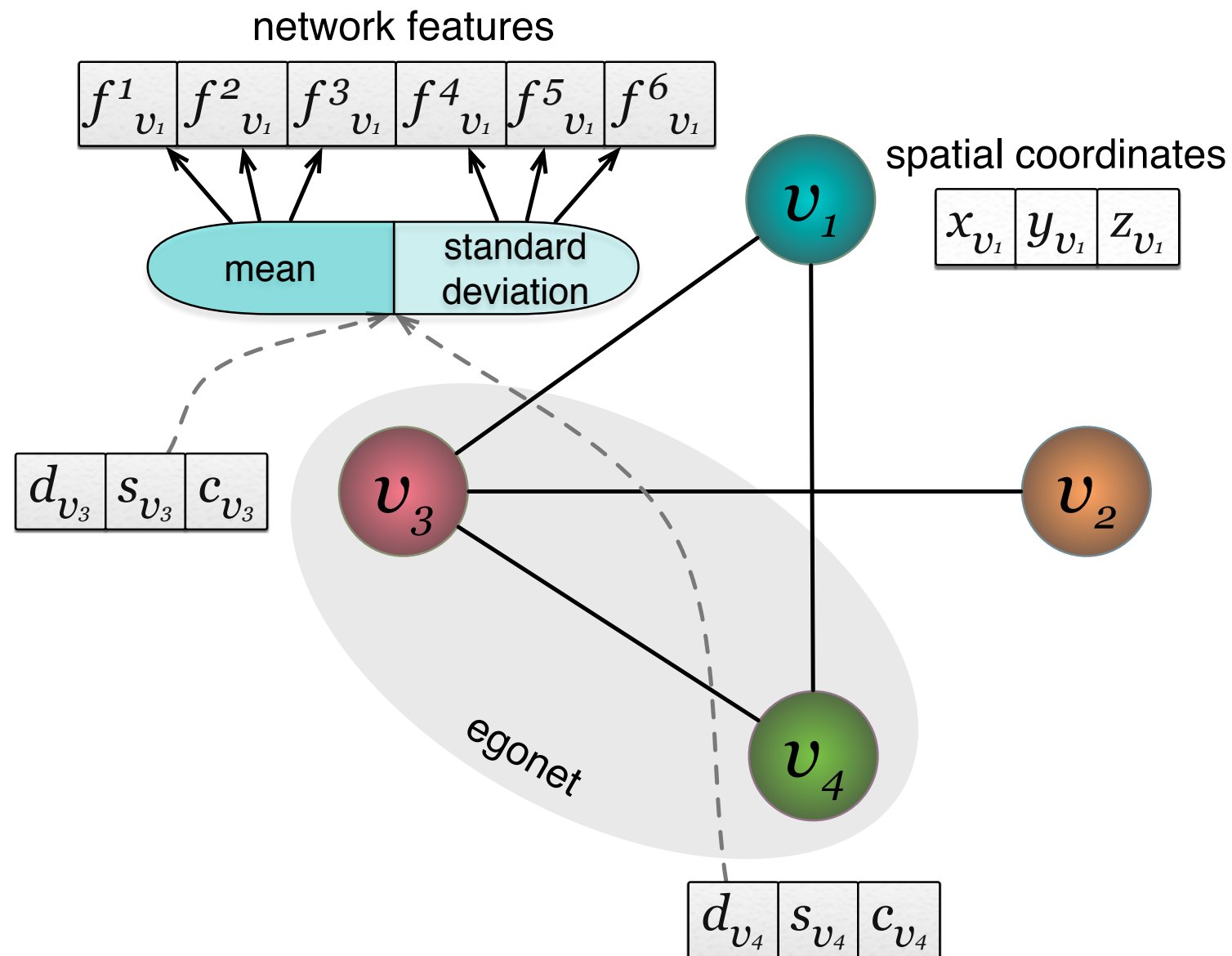
Node distance

- Spatial distance

- Feature distance

Egonet

$$f_v = (x_u, y_u, z_u)$$

$$d_l = d(v_1, v_2) = d_{eucl}(v_1, v_2) + d_{canb}(v_1, v_2) = \sum_{i=1}^{d} \frac{|f_{v_1 i} - f_{v_2 i}|}{|f_{v_1 i}| + |f_{v_2 i}|}$$

Tailoring GED for brain graphs

- In order to achieve better approximation of the true edit distance, edge operations need to be involved.

- Constrain substitutions to the nearest *N* nodes - set cost to *Inf* for the rest of the substitutions

if $u_j \in neigh(v_i)$ **then**
$$c_{i,j} = \alpha * d_{euclidean}(v_i, u_j) + (1 - \alpha) * d_{canberra}(v_i, u_j) + d_{edge}(v_i, u_j)$$
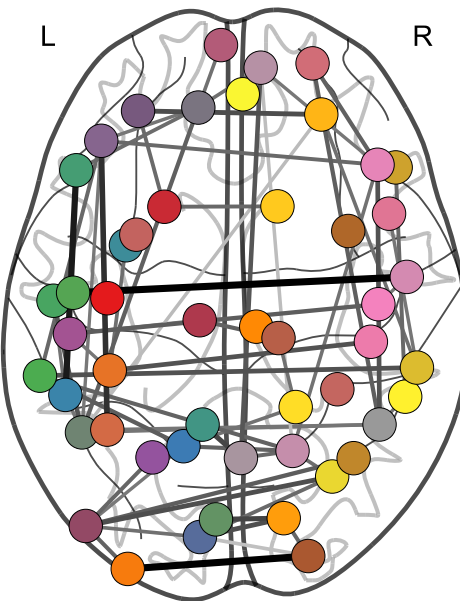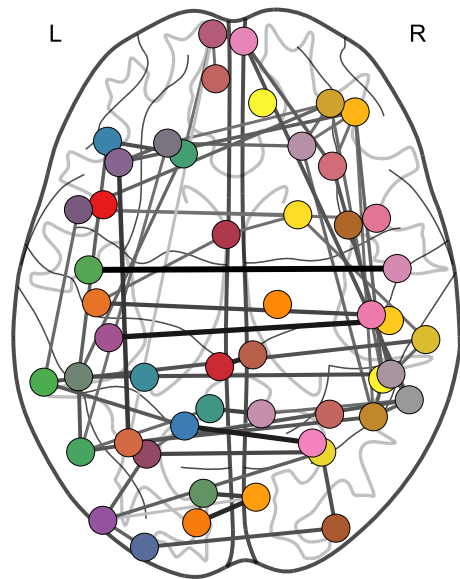**else**
$$c_{i,j} = \infty$$

- Take into account node betweenness centrality *g* for the cost of node insertion/deletion
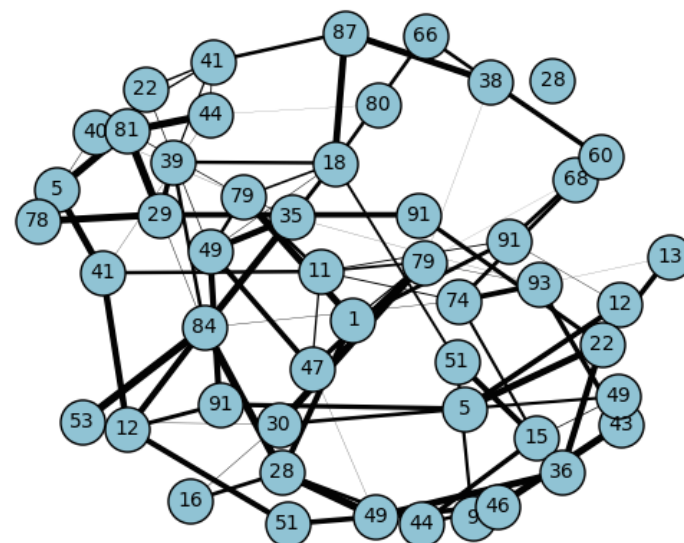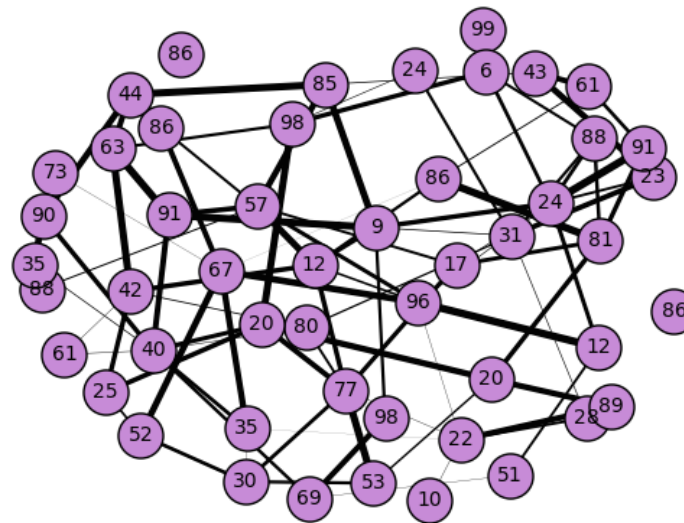
$$c_{\epsilon,j} = \alpha + (1 - \alpha) * g(u_j) \qquad c_{i,\epsilon} = \alpha + (1 - \alpha) * g(v_i)$$
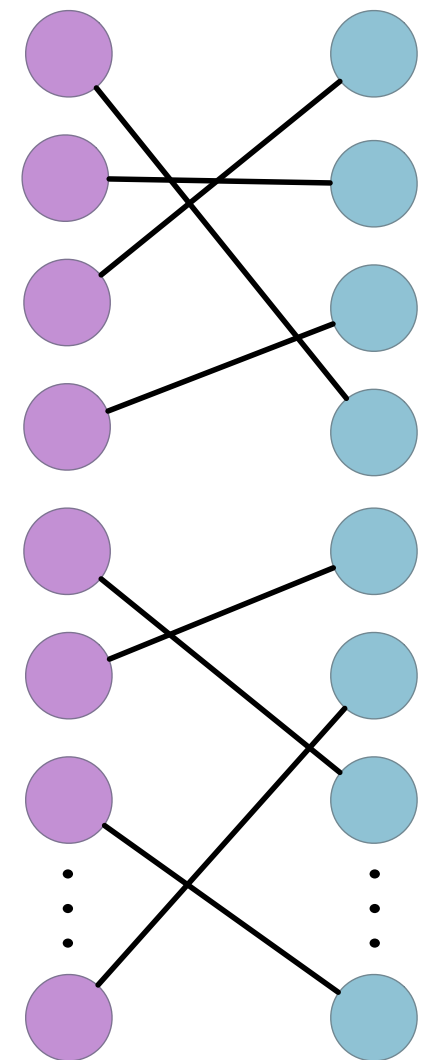
Summary

Evaluation

- Diffusion and functional MRI data from the Human Connectome Project

- 30 healthy unrelated subjects as well as 20 monozygotic and 20 dizygotic female twin pairs (MZ twins share 100% of genetic information, while DZ share only 50%)

- Connectivity driven **single-subject** parcellations [Parisot et al., *MICCAI*, (2016)]

- Structural networks derived with probabilistic tractography

- Functional networks estimated using partial correlation

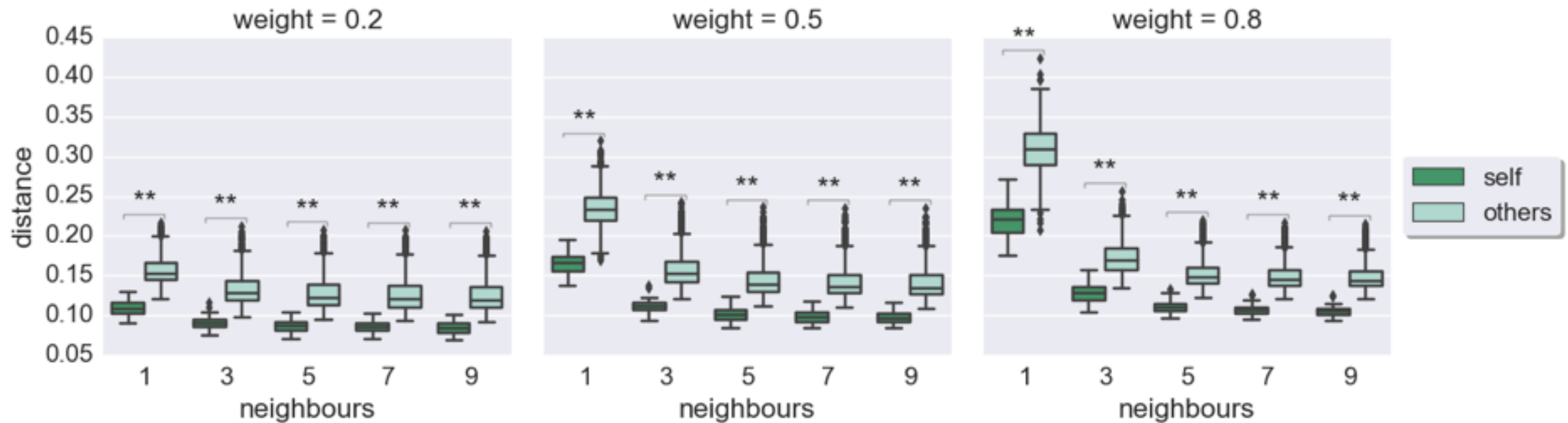# Single-subject parcellations
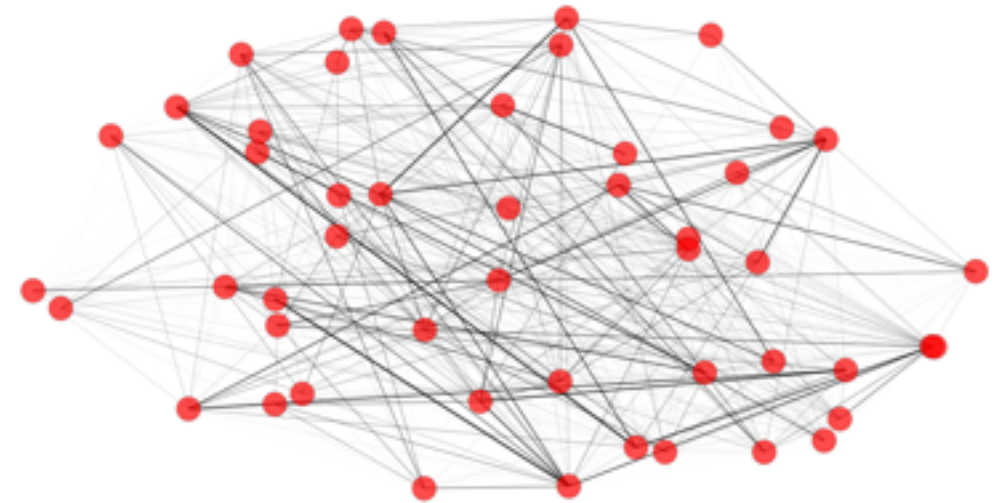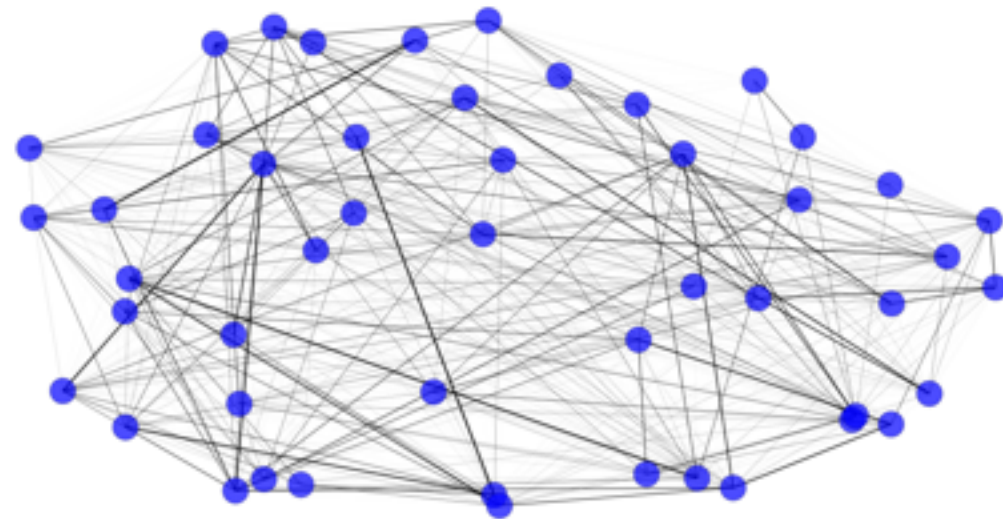
same subject

different subjects
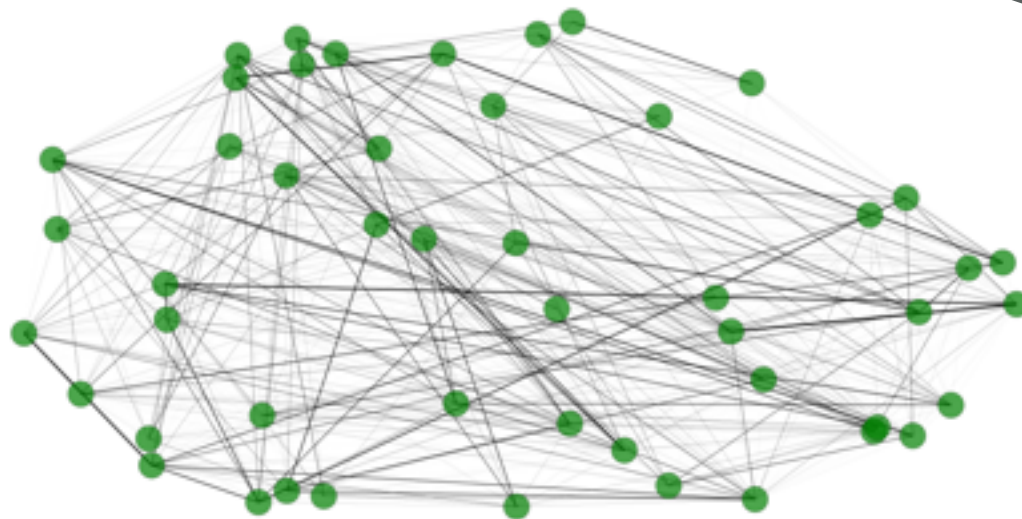
GED(same subject) < GED(different subjects)

Structural networks

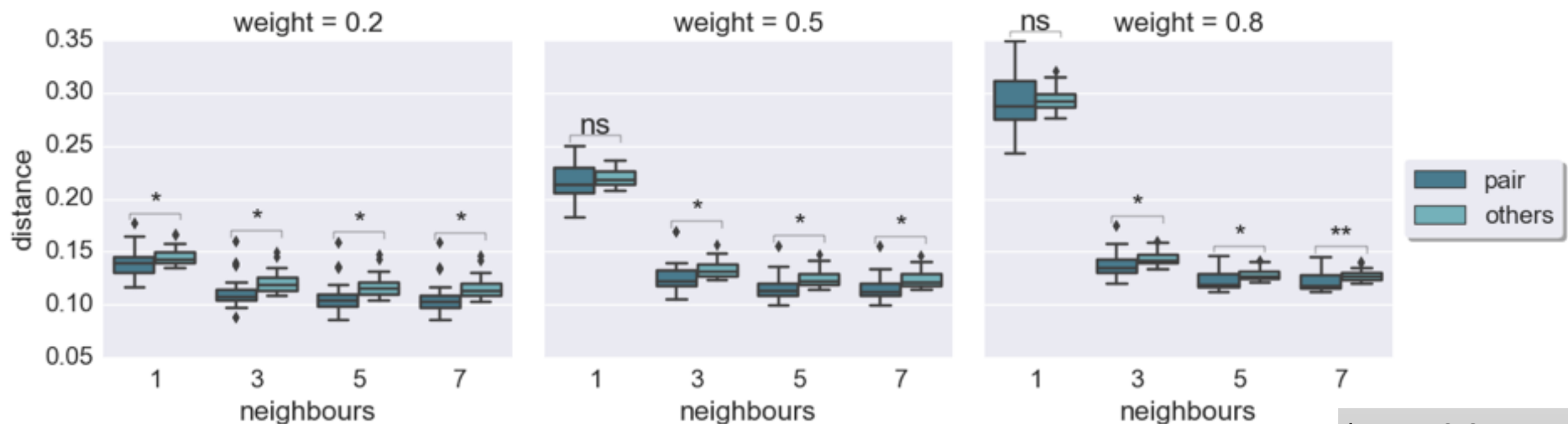

Single subject structural networks (50 nodes)

Structural networks for MZ twins

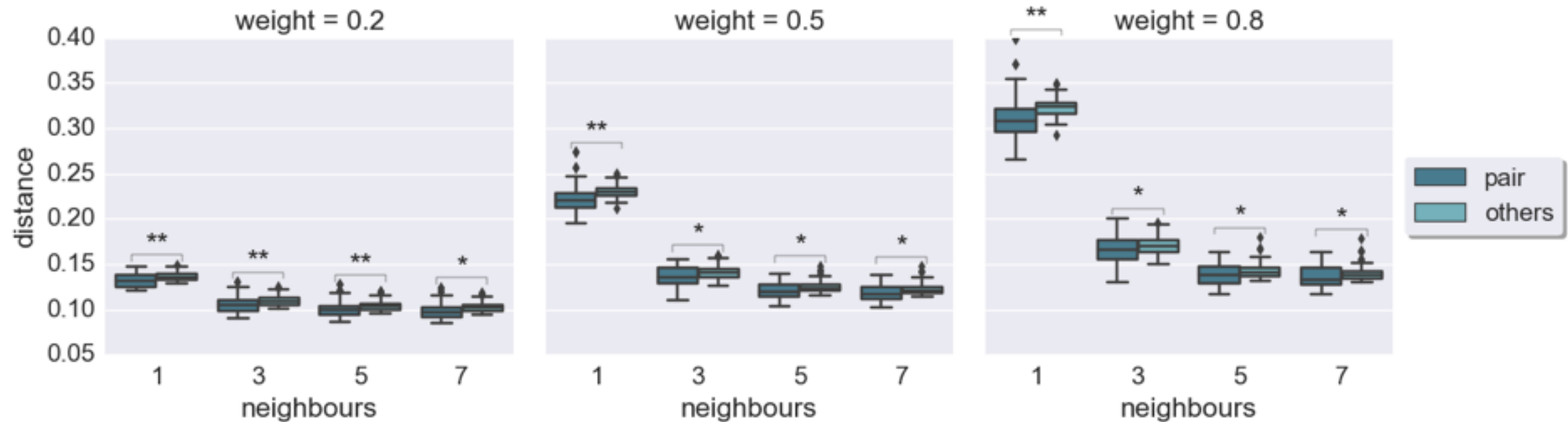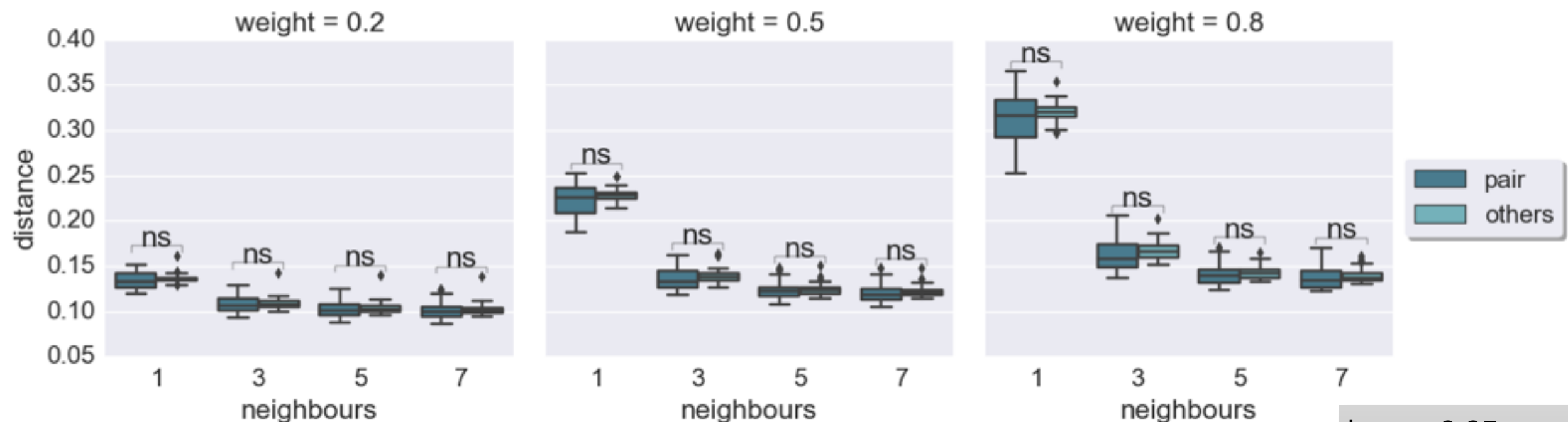*   *p<0.05*
**   *p<0.001*
ns   *non-significant*

|4

Functional networks

Monozygotic vs. unrelated pair

Monozygotic vs. unrelated pair

Conclusions
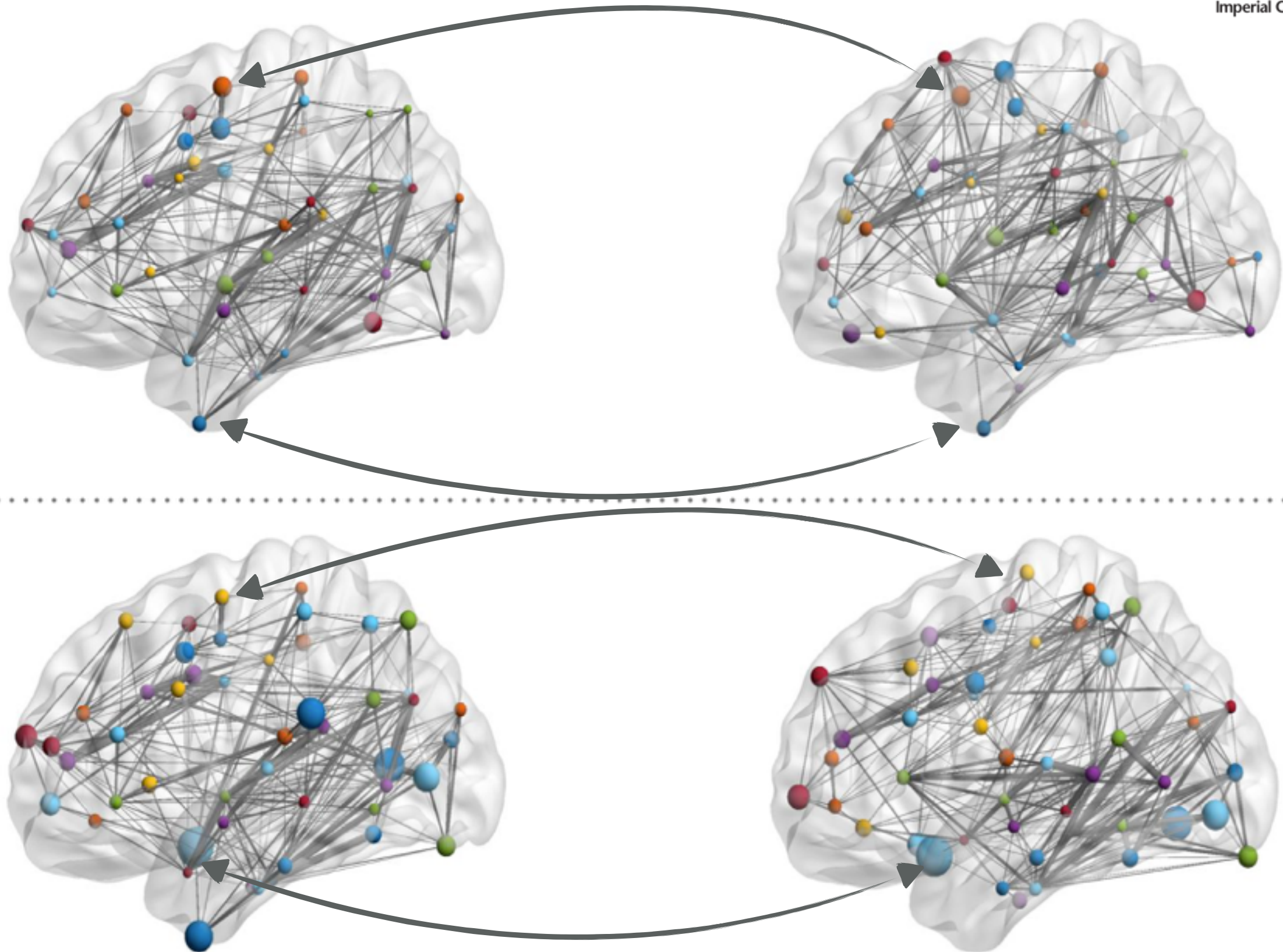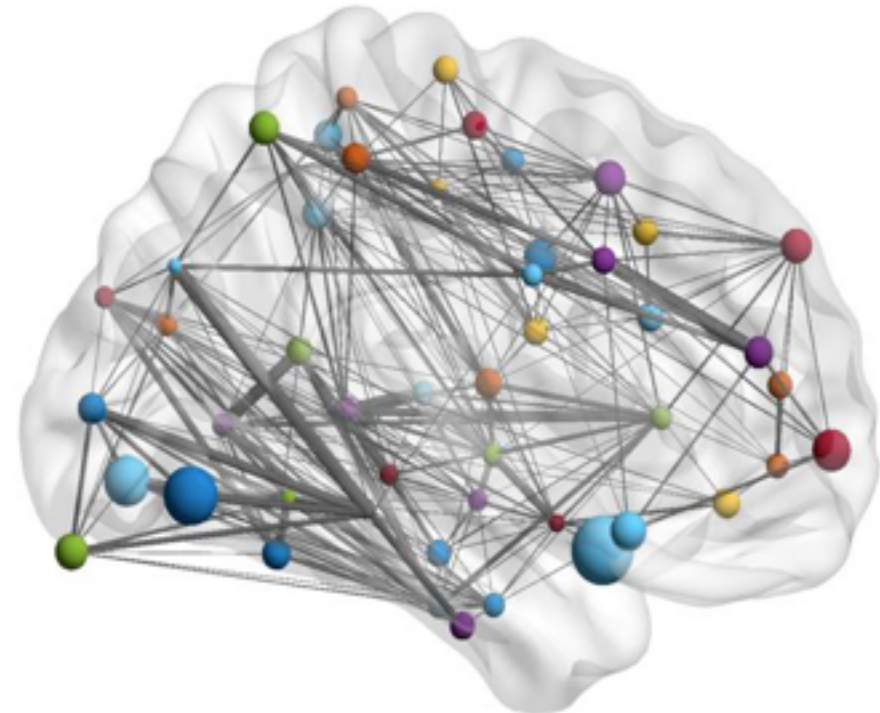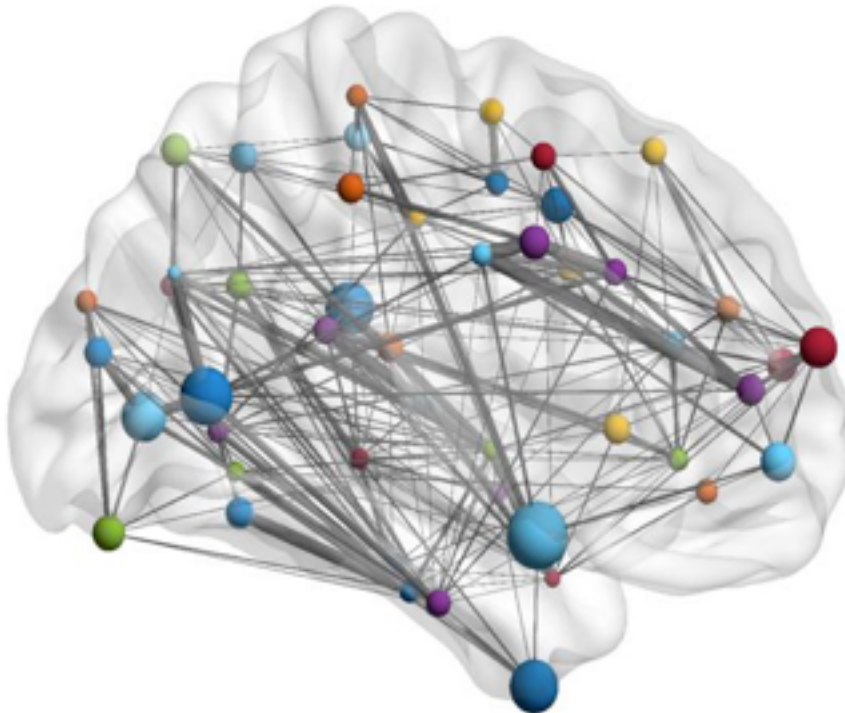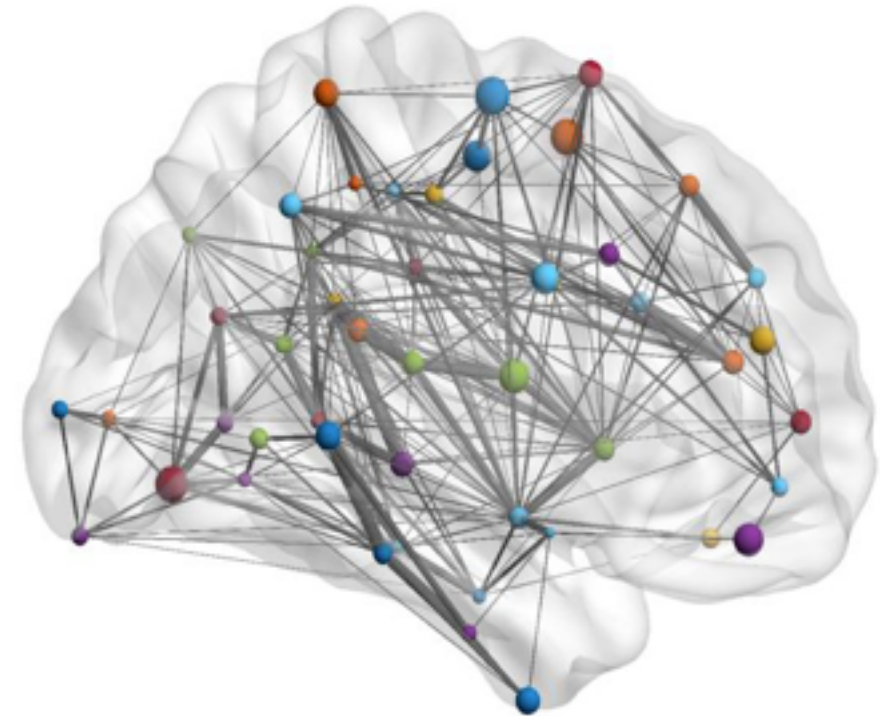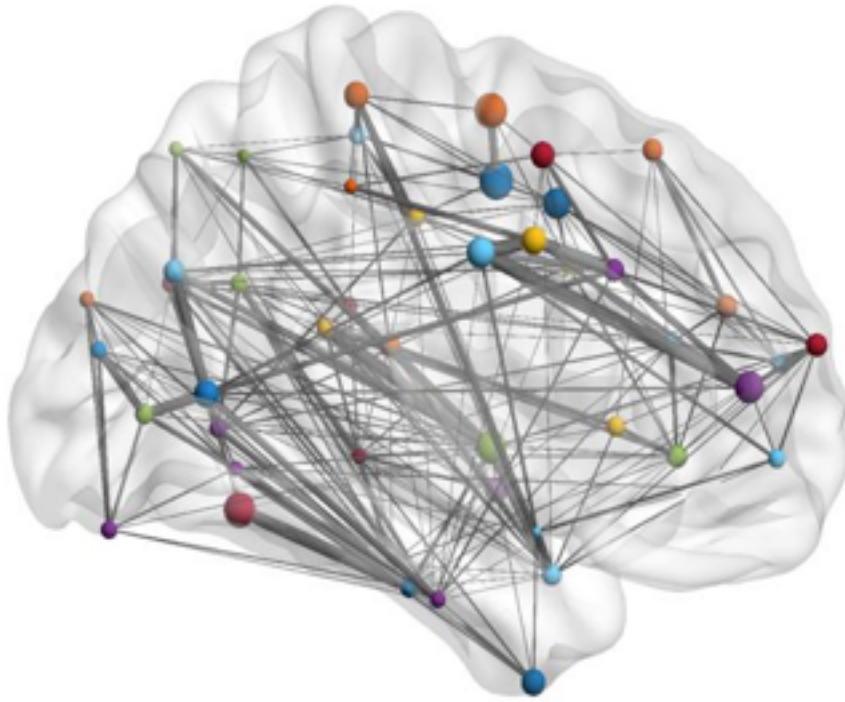
- Novel way of evaluating graph similarity between brain networks based on graph edit distance

- Enforces spatial constraints and incorporates feature information

- Applied on healthy unrelated subjects and twin pairs and was able to reflect similarities between corresponding networks

- Future steps:

  ‣ Predicting phenotype using GED distance matrix

  ‣ Network dynamics (brain development, disease progression, brain plasticity)

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