Comparing connectivity-based groupwise parcellations generated from resting-state fMRI and DTI data: Preliminary results

Salim Arslan, Sarah Parisot, Daniel Rueckert
Imperial College London

BioMedIA
Imperial College London

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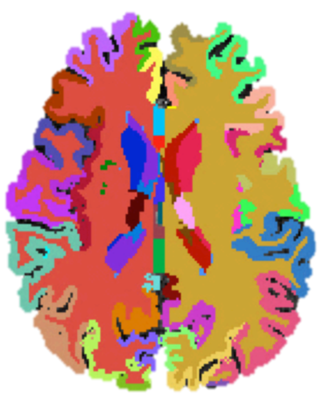
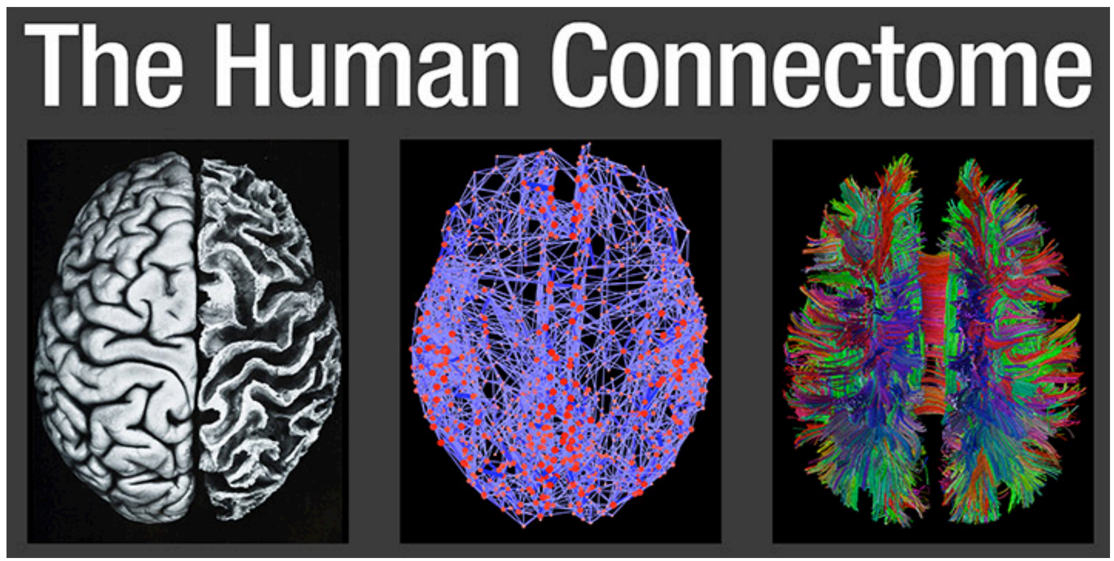
Introduction

Identification of functional/structural connections within the brain has potential to reveal the brain's neural organisation in health and disease





http://scimaps.org/images/maps/865W/IT_06_02_Connectome.jpg

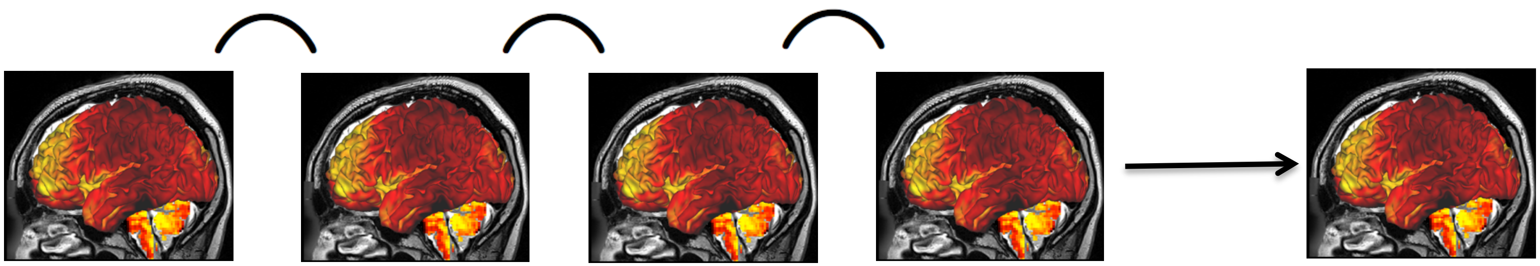
A critical stage in connectome analysis is the parcellation of the cerebral cortex into a set of subregions that can be used as the network nodes

Motivation

- Traditional anatomical atlases are being replaced by functional/structural parcellations for network analysis
- Relationship between functional and structural connectivity is a hot topic, but direct comparison of parcellations is rare
- Compare parcellations derived from different data sources, but via the same parcellation framework
- Aim: Locate cortical subregions that have been consistently assigned to the same parcels across different parcellations/modalities
- Assess the performance of the parcellations in order to judge their potential for further analyses

Data acquisition and preprocessing

- Rs-fMRI and dMRI datasets of 50 unrelated subjects from the **Human Connectome Project (HCP)** [1]
- Preprocessed, de-noised, and ready to analyze [2]
- **Rs-fMRI**: Time-series normalized to unit-variance and zero-mean, and concatenated across different scans

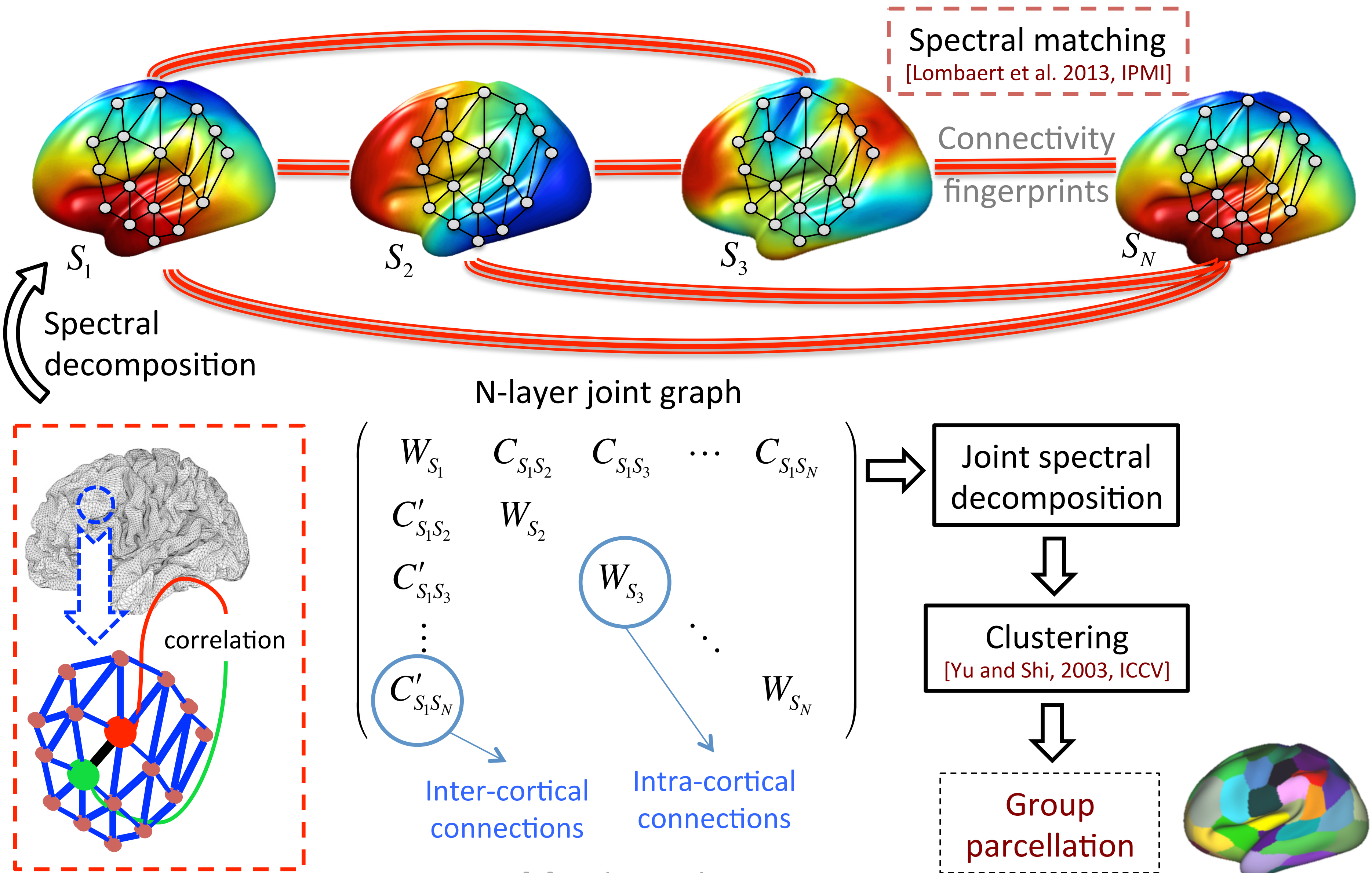


- **dMRI**: Tractography matrix obtained on the native mesh via probabilistic tractography (see details in [3])

HUMAN Connectome PROJECT

[1] Van Essen et al. 2013, NeuroImage
[2] Glasser et al. 2013, NeuroImage
[3] Parisot et al. 2015, IPMI

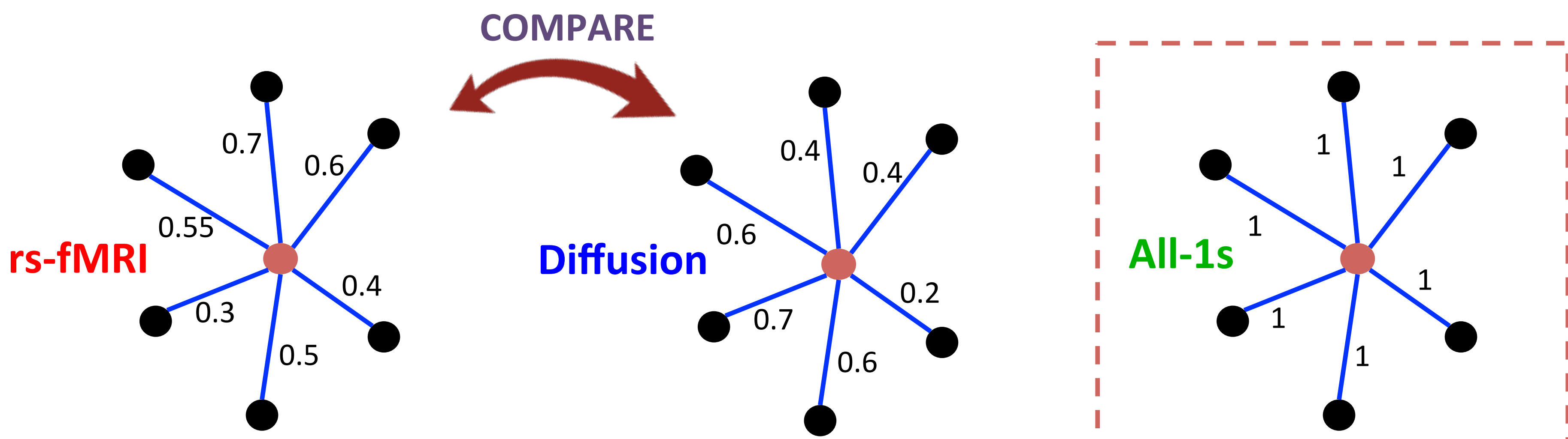
Joint spectral decomposition[1]



[1] Arslan et al. 2015, IPMI

Parcellation setting

- Each subject is registered to the same standard cortical model
- Adjacency matrices and inter-cortical connections are weighted by different modalities



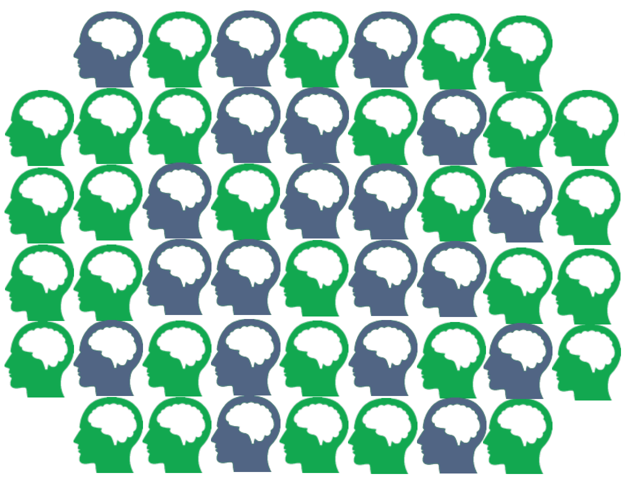
Weight edges with resting-state fMRI correlations

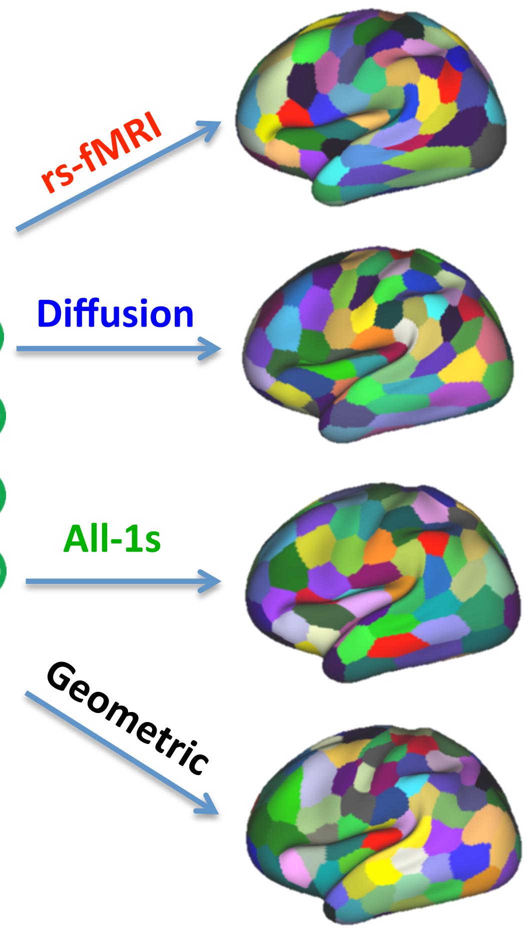
Weight edges with log-transformed tractography correlations

Weight edges with ones. No functional/structural information encoded.

Experimental setting

Randomly pick 20 subjects from a set of 50





K = 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200 per hemisphere

repeat the process

×100

Clustering spatial coordinates of cortical vertices with k-means. No connectivity involved.

Evaluation

Quantitative assessment

- A probabilistic model of the task-fMRI signal [1]

$$\mathbf{y} = \boxed{\mu}\mathbf{1} + \mathbf{X}\boxed{\boldsymbol{\beta}} + \boxed{\boldsymbol{\varepsilon}}$$

- **Goodness of fit**: Log-likelihood and Bayesian information criterion (BIC)
- **Reproducibility**: Dice index (requires pre-matching), adjusted rand index (invariant to permutation of labels)

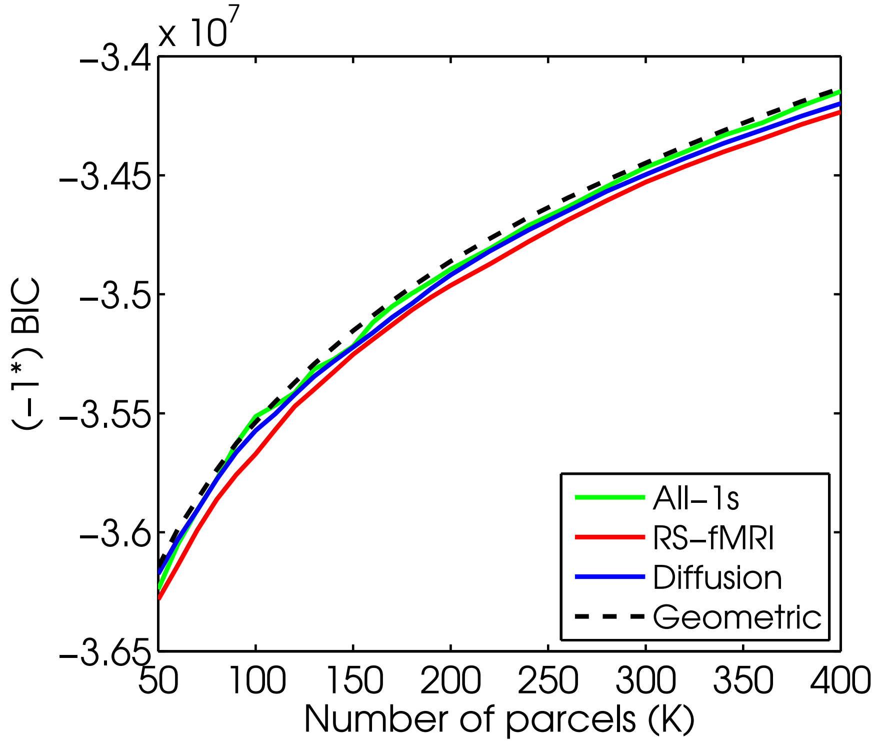
Qualitative (visual) inspection

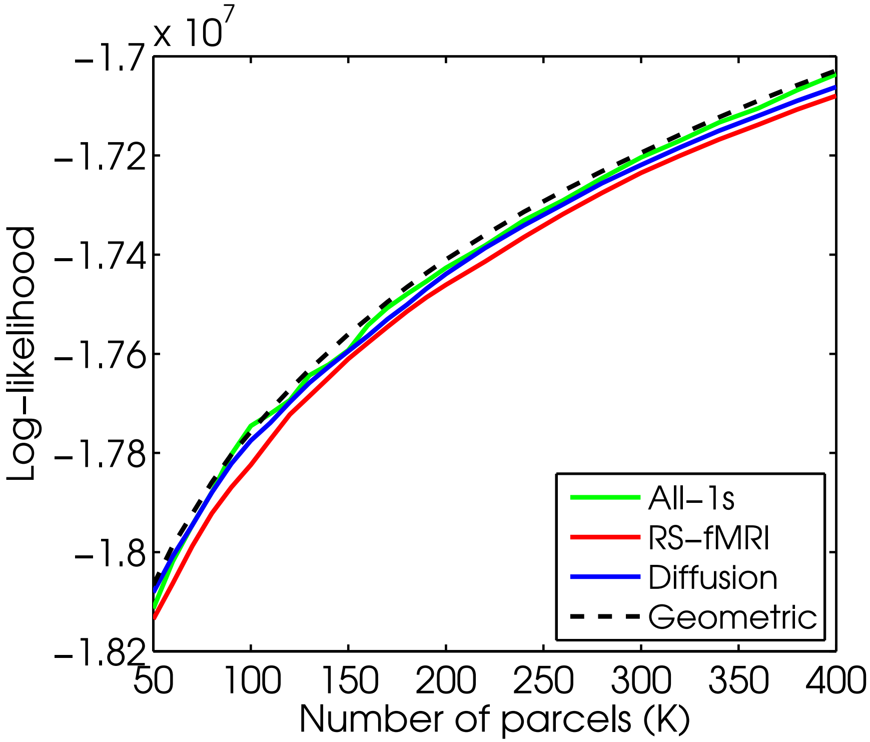
- Locate cortical areas that have been consistently assigned to the same parcels across different parcellations

[1] Thirion et al. 2014, Frontiers

ⓘ github.com/bthirion/frontiers_2014

Goodness of fit

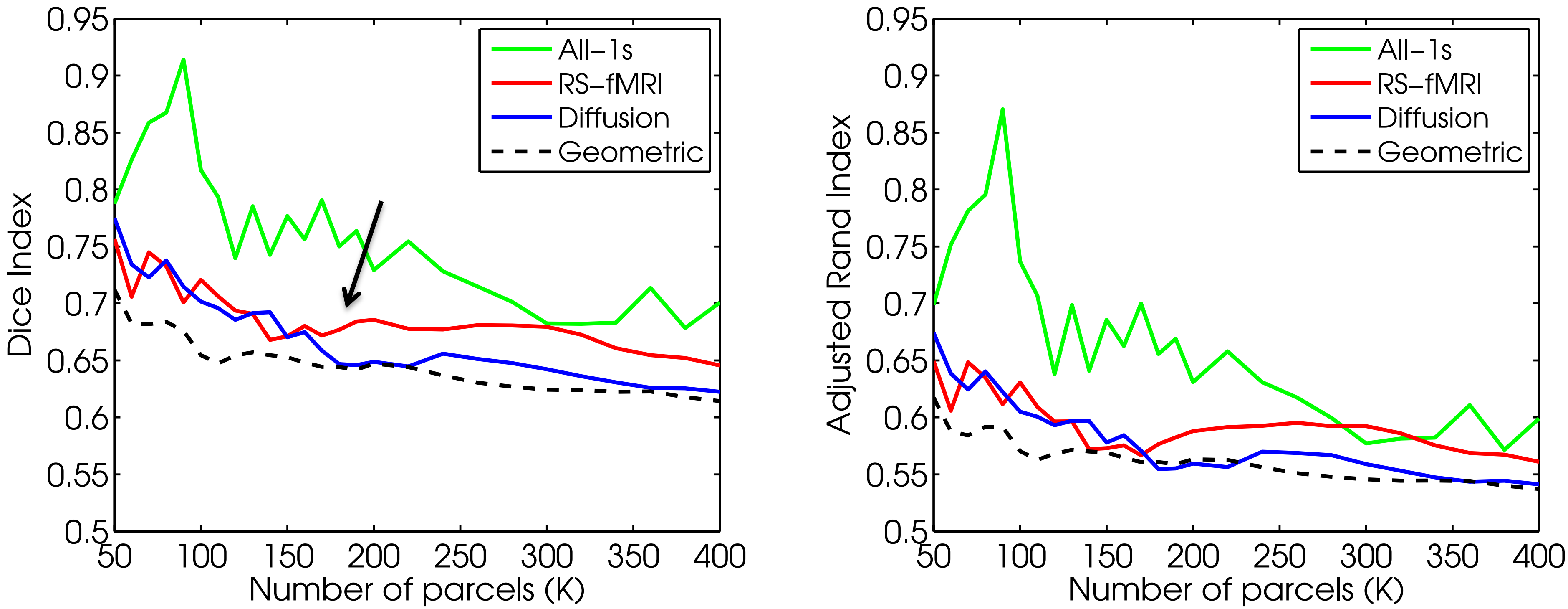




Geometric and All-1s achieve the best fit, which is attributed to their tendency to generate more equally-sized parcels compared to the others.

Among the connectivity-driven parcellations, Diffusion consistently performs better than RS-fMRI for all parcellation resolutions.

Reproducibility

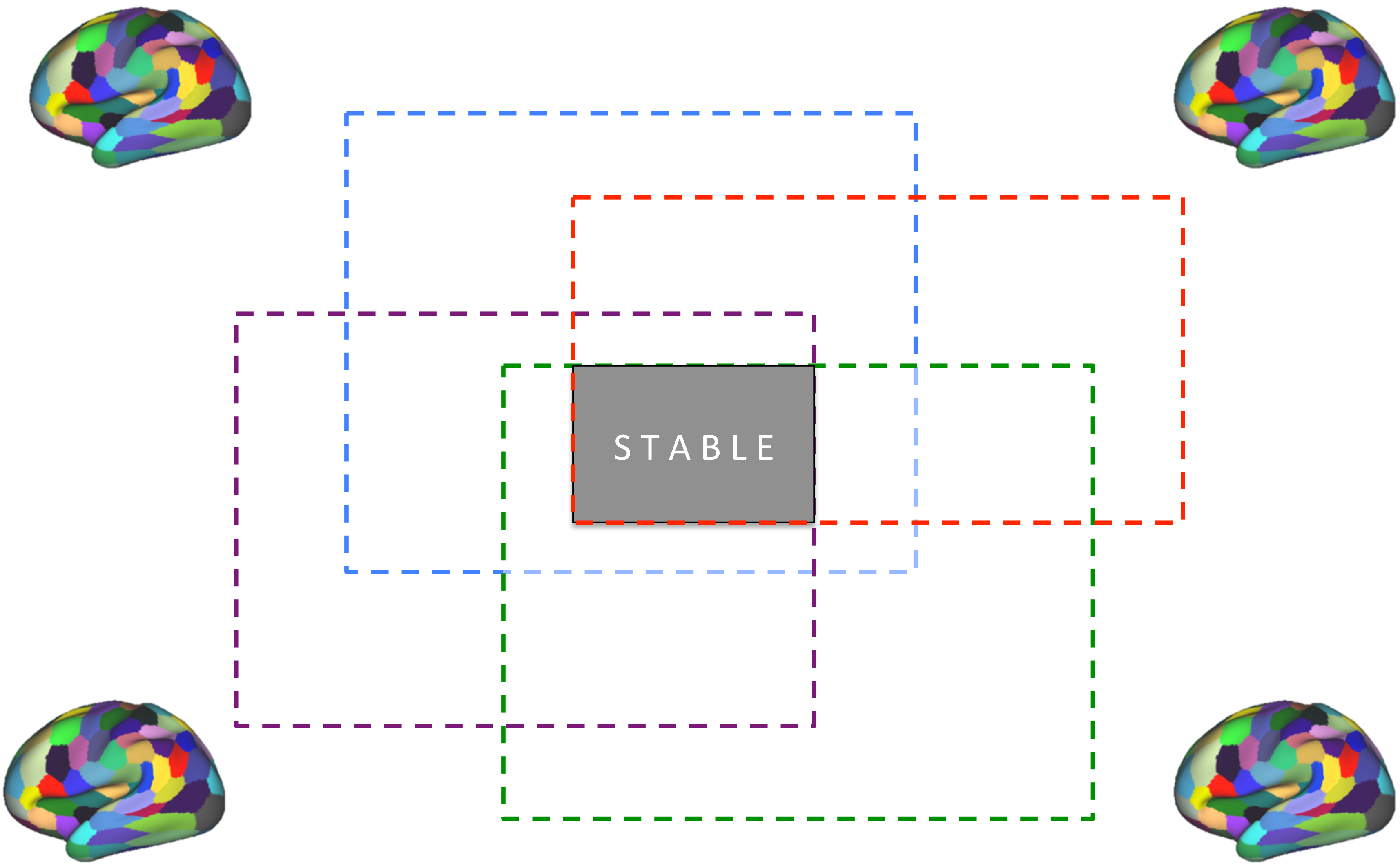


Expectedly, All-1s is able to obtain the most similar parcellations, since the underlying model is almost identical for all groups.

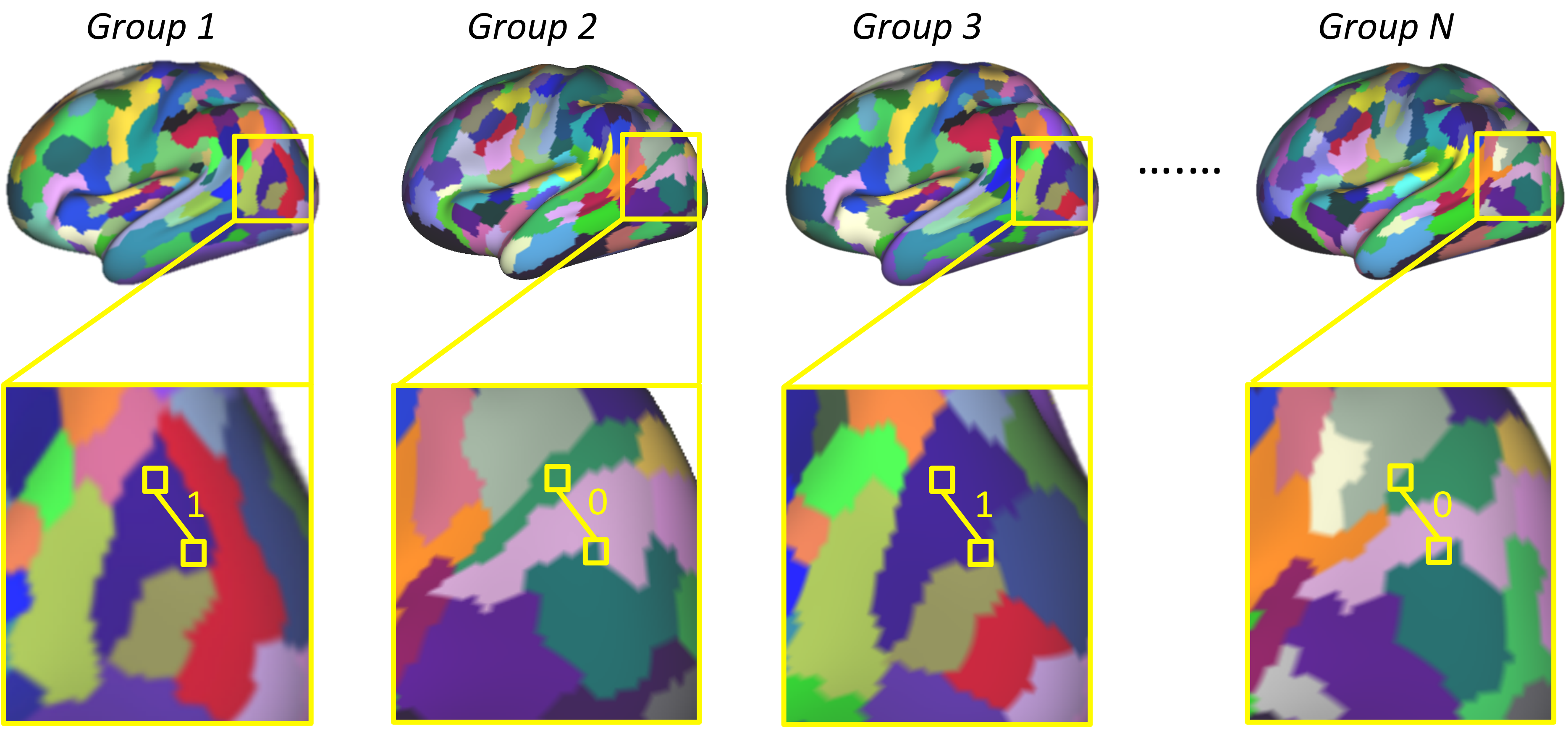
Among the connectivity-driven parcellations, RS-fMRI is more reproducible than Diffusion, for $K > 160$.

Due to anatomical variability across subjects, **Geometric** obtains the least similar parcellations.

Stable regions across parcellations

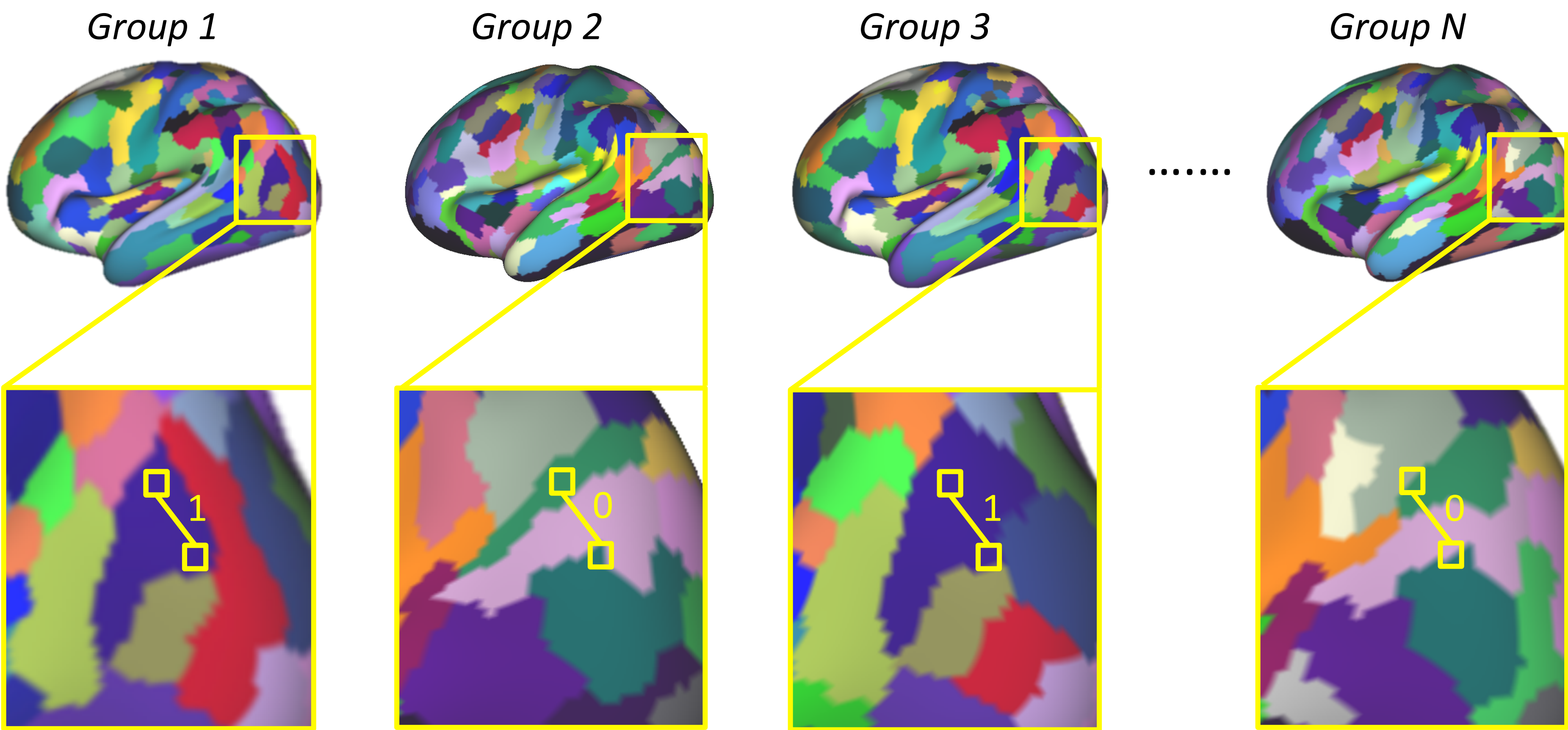


We compute a graphical model of the parcel stability across the parcellations (N = 100).



An edge between two vertices is weighted by the number of times they appear in the same parcel across parcellations.

We compute a graphical model of the parcel stability across the parcellations (*N = 100*).



$$w = \frac{\quad + \quad + \quad + \cdots + \quad}{N}$$

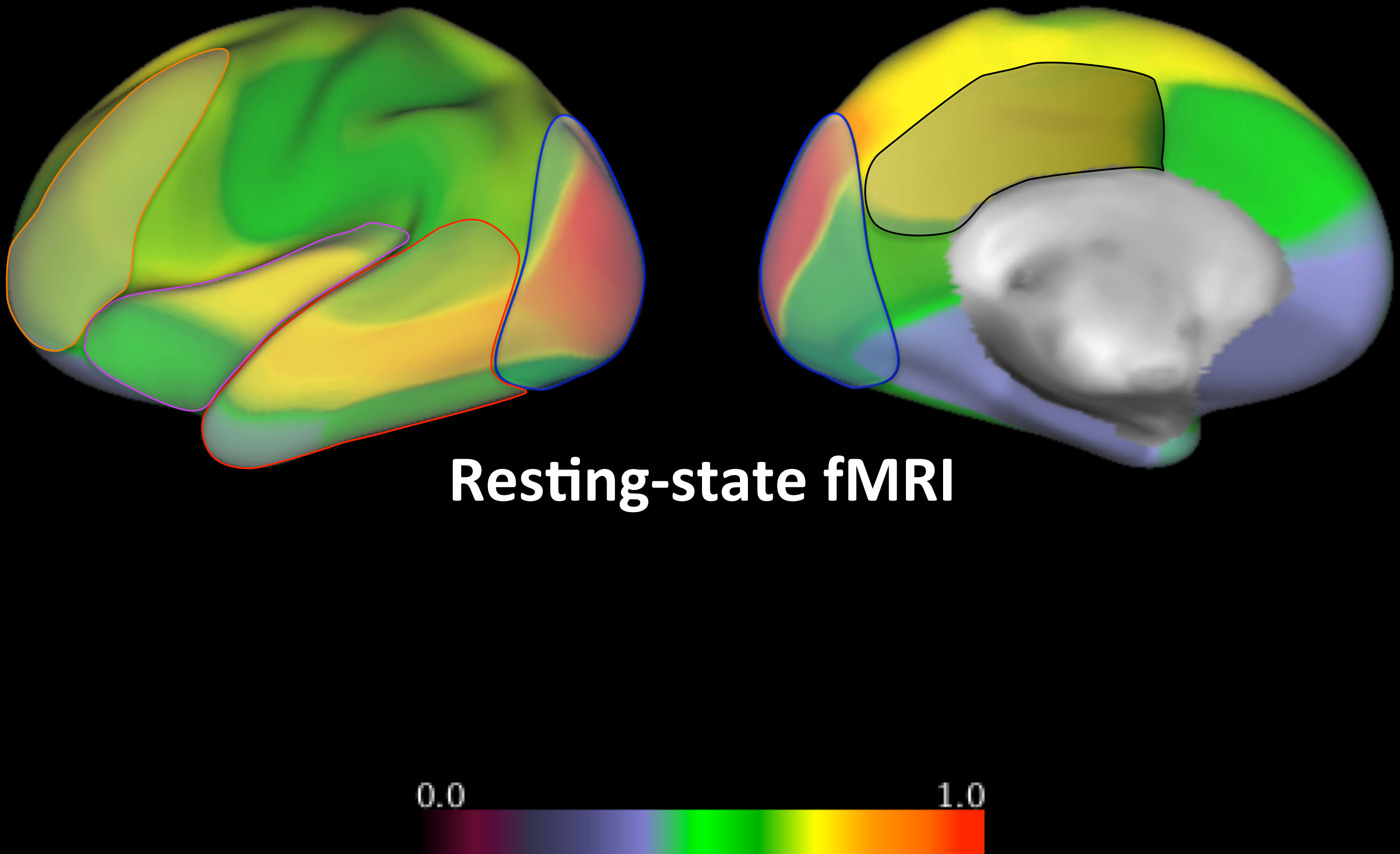
Stability graphs → cortical surface

- Transform stability graphs into degree (centrality) vectors and assign each vertex a stability score

$$D = \sum_j w_{ij}$$

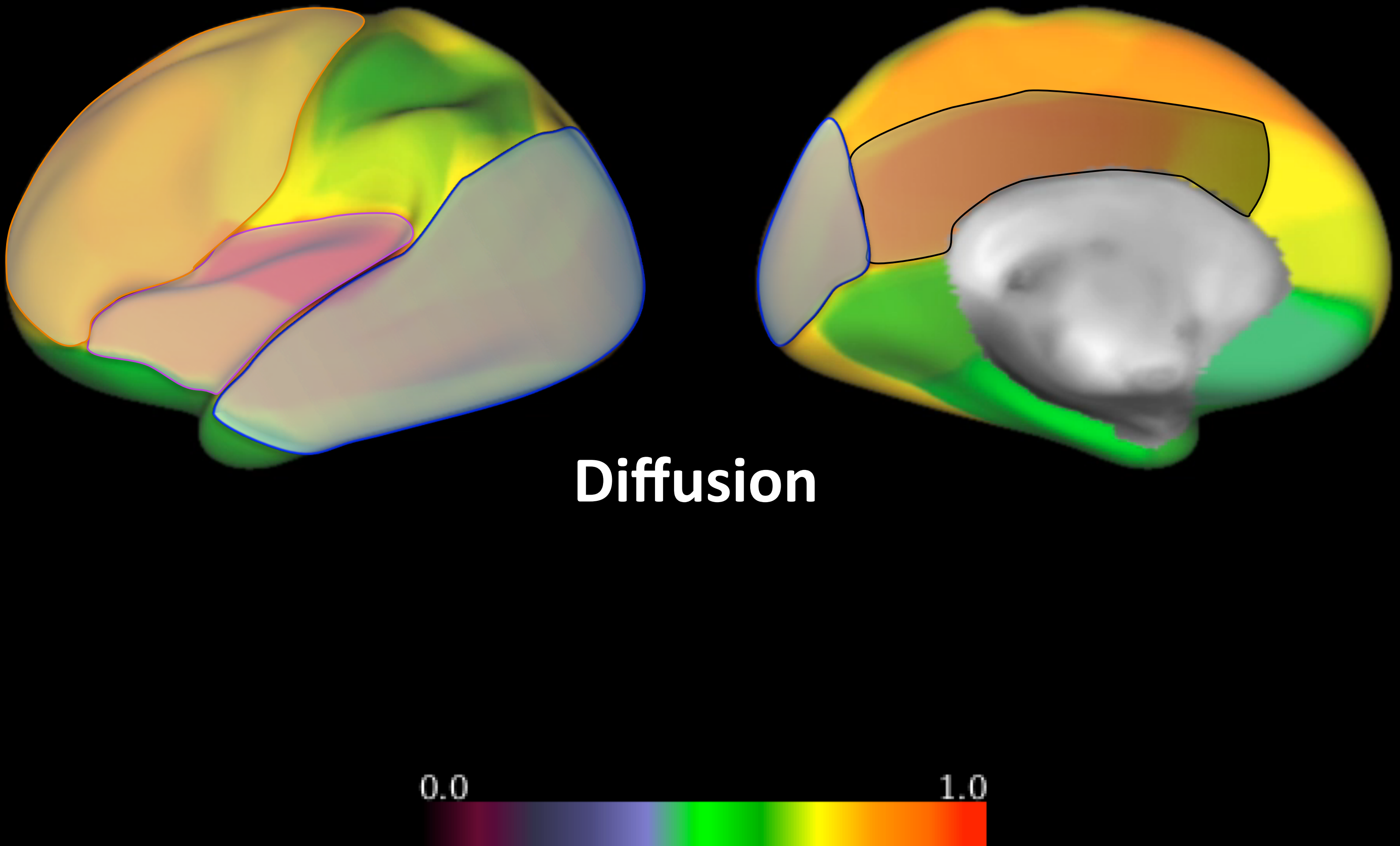
- Scale into the range of [0, 1] for better visualization as well as for a fair comparison across different resolutions and methods

Stable regions across parcellations

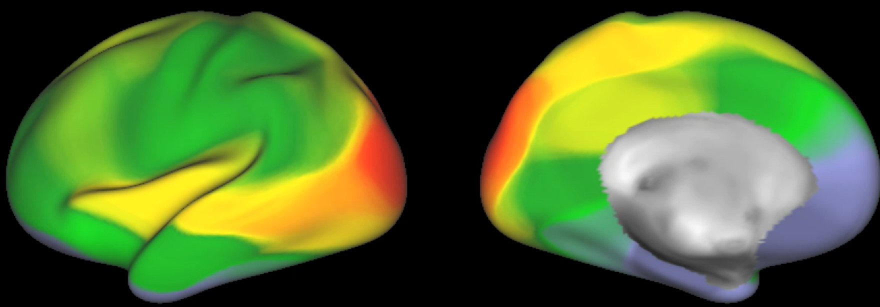


Resting-state fMRI

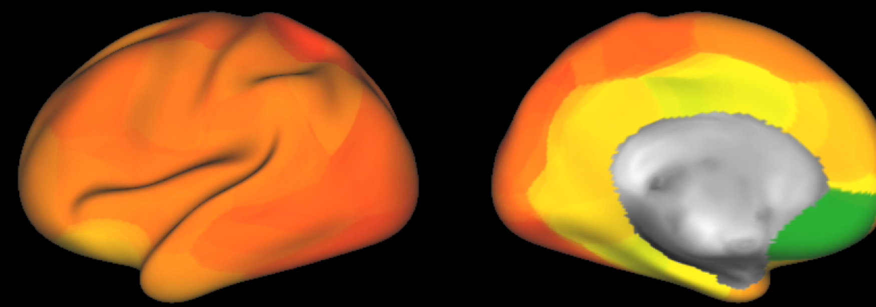
Stable regions across parcellations



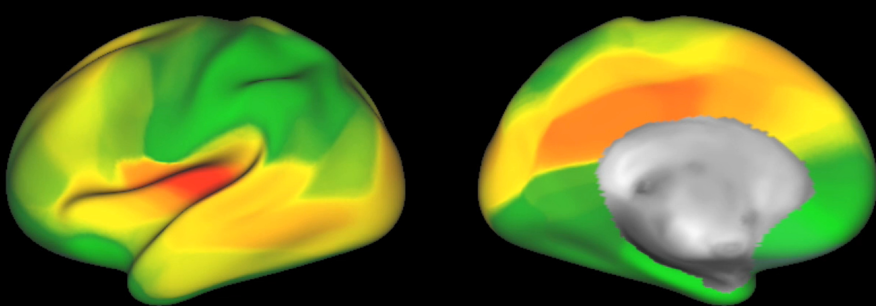
Resting-state fMRI



All-1s



Diffusion MRI

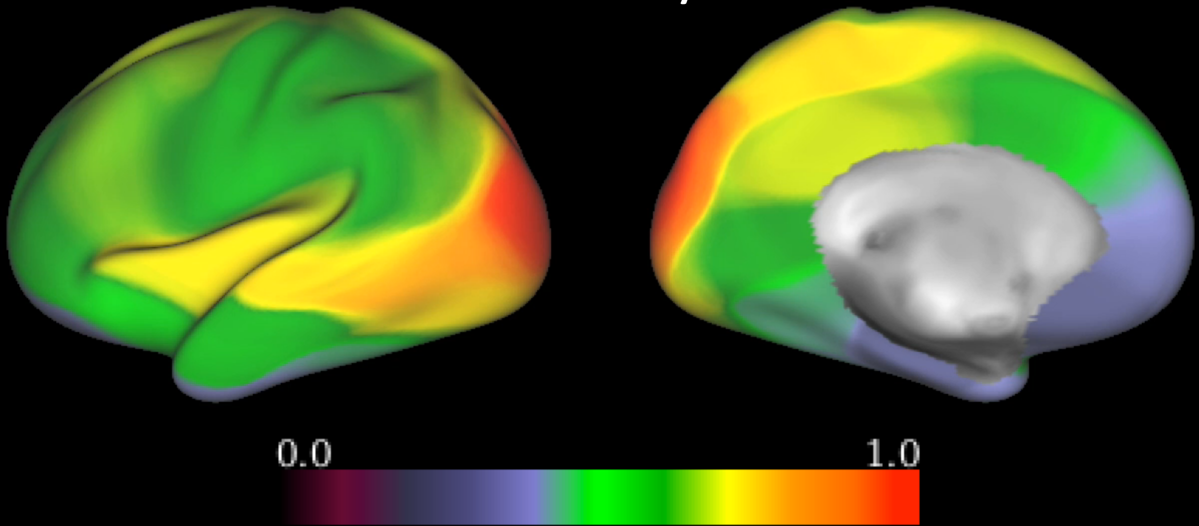


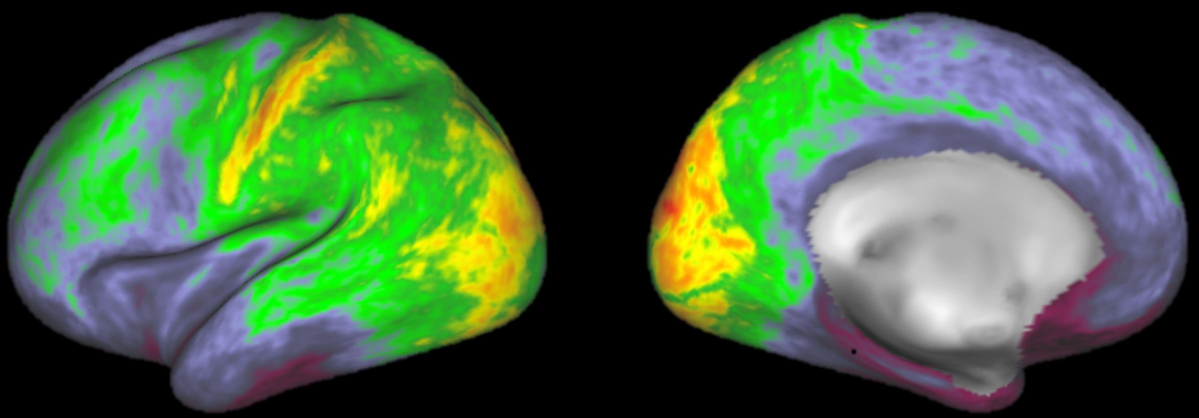
Without any functional/structural information, parcels seem to be randomly distributed across different resolutions.

Overlaps in stability might be due to a link between the structural and functional connectivity.

Resting-state fMRI

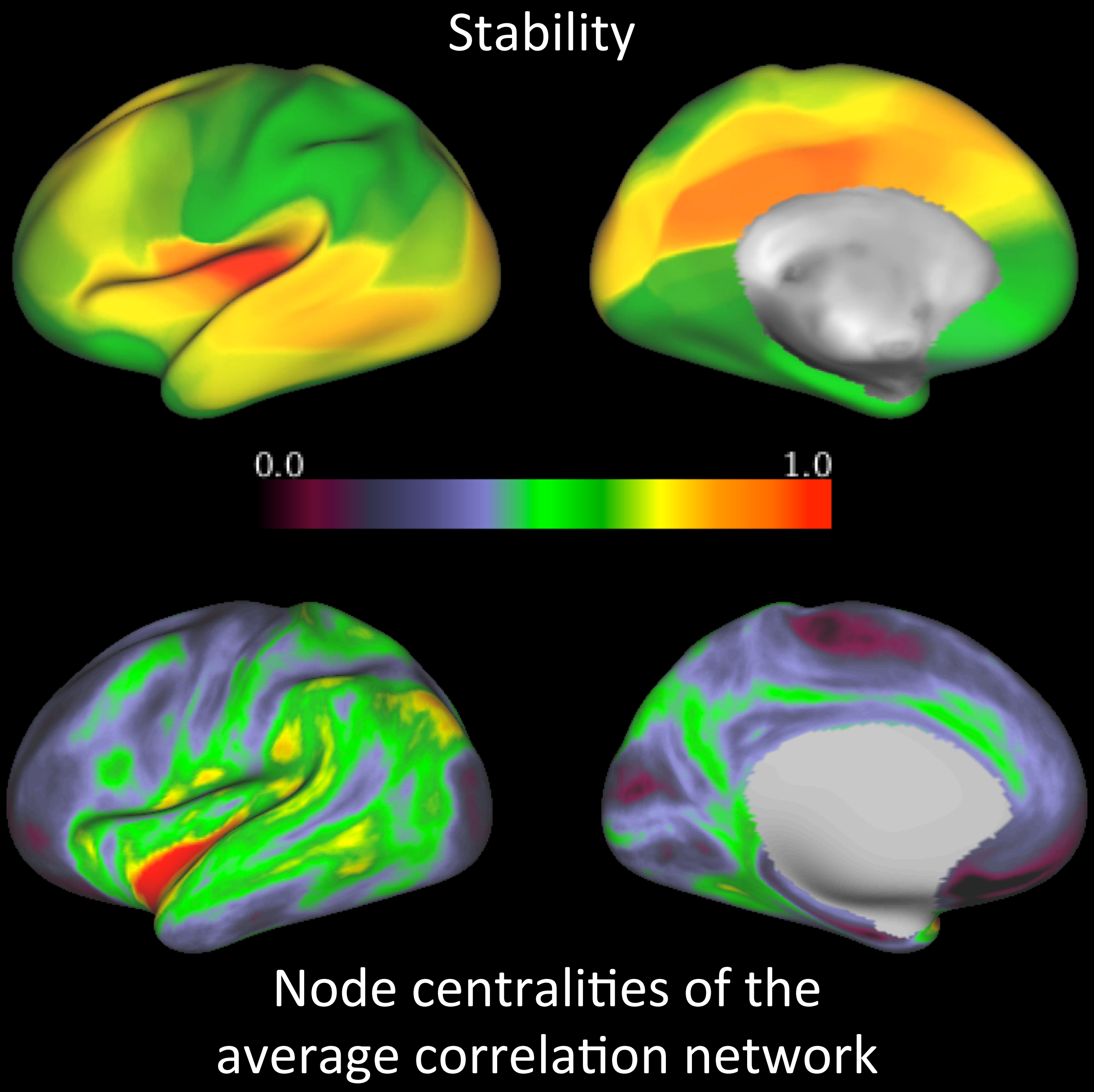
Stability





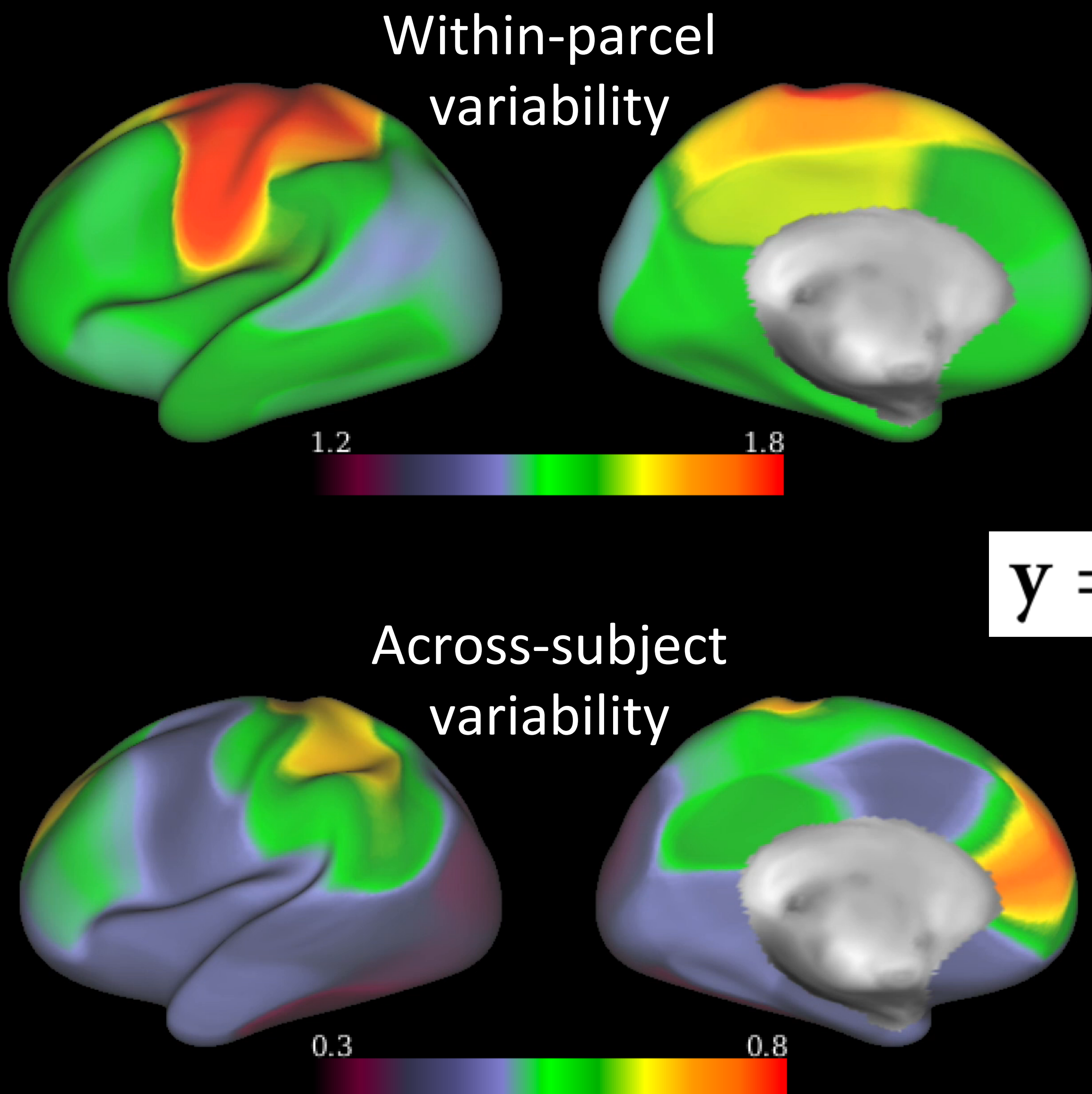
Node centralities of the
average correlation network

Diffusion MRI



Mixed-effects analysis: **Functional variability**

Task-fMRI image targeting the **motor cortex**



$$\mathbf{y} = \mu\mathbf{1} + \mathbf{X}\boldsymbol{\beta} + \boldsymbol{\varepsilon}$$

Conclusions and future work

- Rs-fMRI and dMRI-based parcellations generated by the same spectral clustering framework have been analyzed
- Connectivity-driven parcellations are more stable with varying *K* compared to the reference model
- Stability is more prominent around the visual, insular and posterior cingulate cortex, and the temporal lobe
- Well-known tracts interconnect commonly found resting-state networks, especially the default mode network [1,2]
- Parcellations might be used in a prediction framework to see if they are functionally similar [3]

[1] van den Heuvel et al., 2009, HBM; [2] Greicius et al., 2008, Cereb Cortex; [3] Deligianni et al., 2013, TMI

Thanks for your attention!

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BioMedIA Imperial College London

Developing Human Connectome Project

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HUMAN Connectome PROJECT

EPSRC Engineering and Physical Sciences Research Council

Questions?

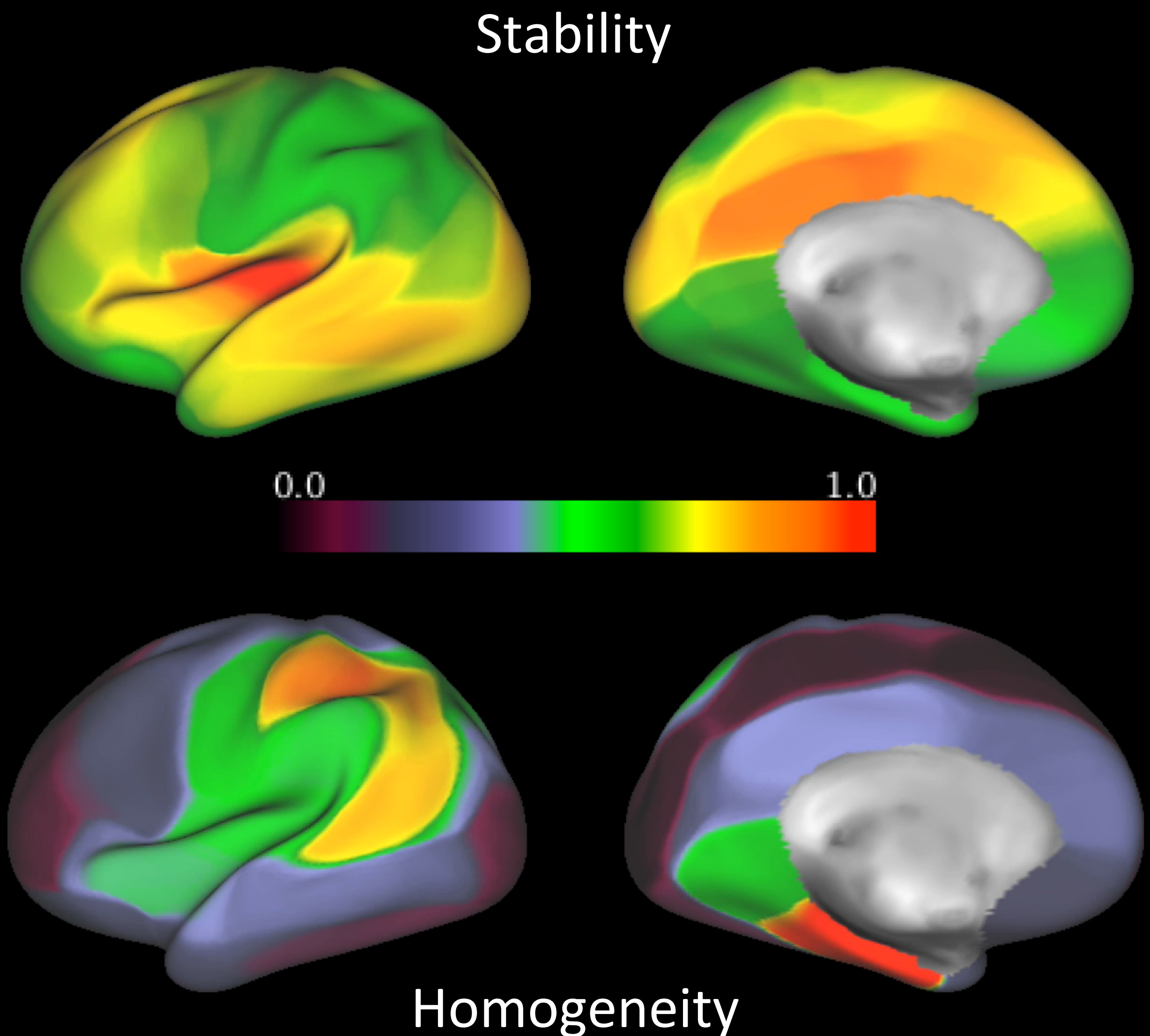
Literature

- Functional and structural organization of the brain network are likely to be linked [Hagmann et al., 2008, PLoS; Honey et al., 2009, PNAS; Bullmore and Sporns, 2009, Nat Rev Neurosci]
- Focus on the default mode network (DMN)
  - Structural connections between posterior cingulate and medial frontal cortex are related to the high functional connectivity [van den Heuvel et al., 2008, J. Neurosci]
  - Other parts of the DMN have been found to be interconnected by structural white matter tracts [Greicius et al., 2008, Cereb Cortex]
- Well-known tracts interconnect commonly found resting-state networks, including primary motor and visual network [van den Heuvel et al., 2009, HBM]

HCP functional contrasts

- *Faces-shape contrast* of the **emotional protocol**
- *Punish-reward contrast* of the **gambling protocol**
- *Math-story contrast* of the **language protocol**
- *Left foot-average contrast* of the **motor protocol**
- *Left hand-average contrast* of the **motor protocol**
- *Match-relation contrast* of the **relational protocol**
- *Theory of mind-random contrast* of the **social protocol**
- *Two back-zero back contrast* of the **working memory** protocol

Diffusion MRI



Resting-state fMRI