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Graph Matching improves the Similarity of Structural Brain Networks

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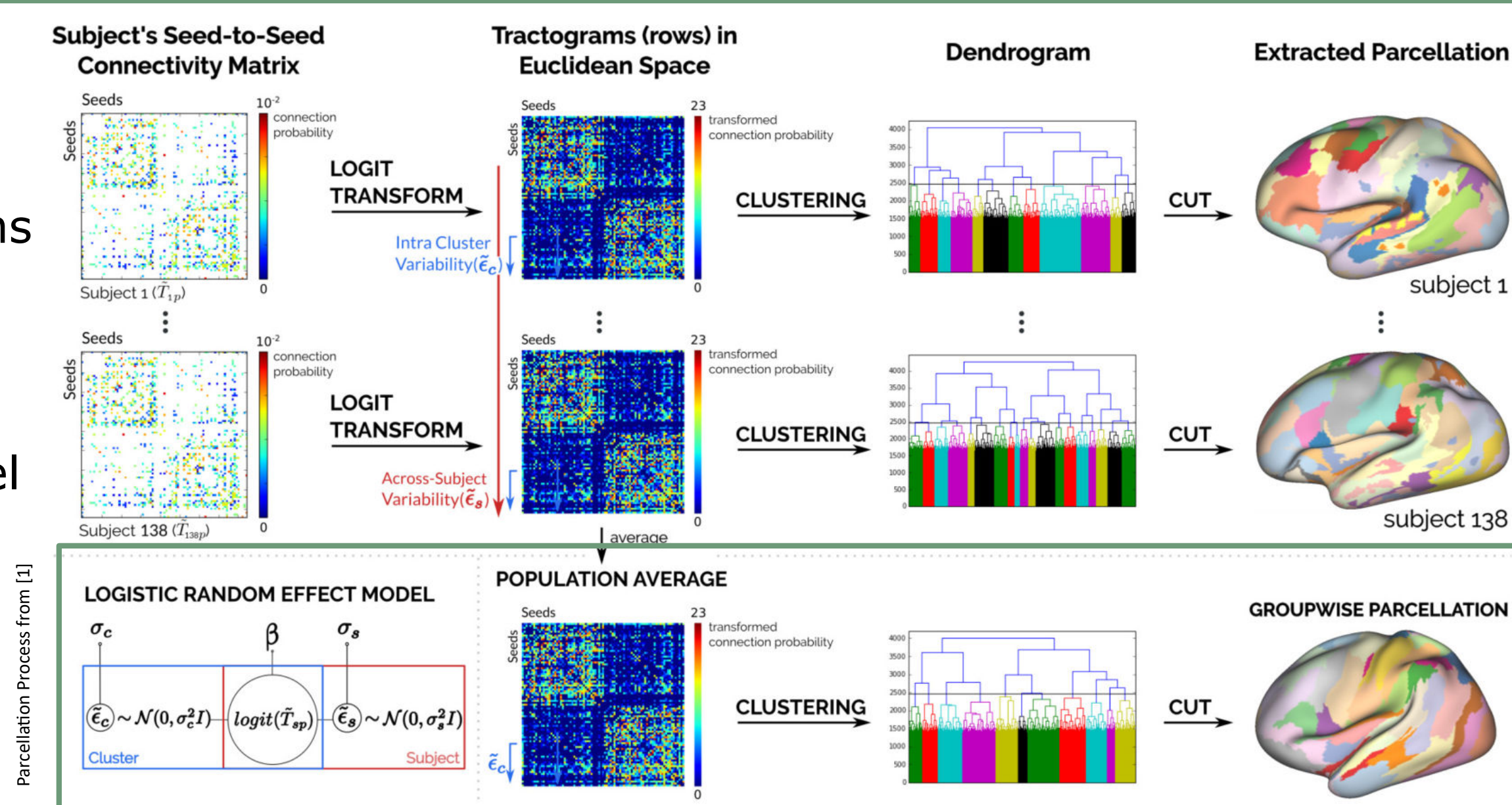
ABSTRACT

Structural parcellations are often built under the assumption of parcels' correspondences across patients. In the current work, we test the robustness of this hypothesis using graph matching strategies. Given the structural parcellation built in [1], we analyse a set of patients at different parcellation granularity (from 50 up to 1000 parcels). The aim of the analysis is to test via graph matching if the graphs obtained with a given parcellation should be considered as labelled or unlabelled. The results show a node correspondence for low resolution and the requirement of an unlabelled embedding for higher number of parcels. We showcase the graph matching results for the different parcellations as well as the importance of a correct geometrical embedding for unlabelled graphs to compute graph-valued statistics.

MODEL

1 Parcellation

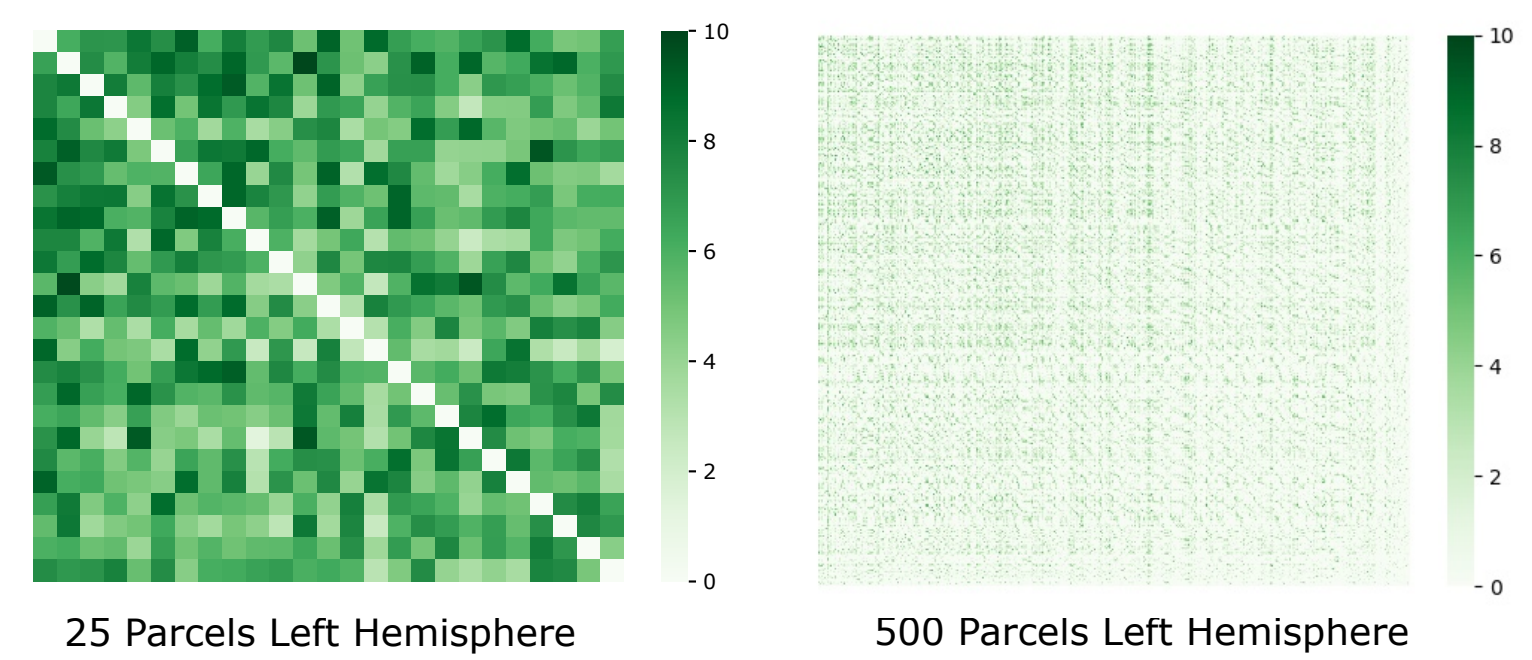
Gallardo Parcellations [1] is built based on 138 tractograms surfaces from Human Connectome Project. Each tractogram is transformed with a logit model the parcels are obtained with Hierarchical Clustering.



HP. Node Correspondence

2 Structural Brain Data

Data: 100 healthy patients from HCP
Parcels: 25 to 500 nodes per hemisphere
Graphs: 100 Structural Brain Connectivity



3 Graph Space

Every hemisphere and p parcels \rightarrow Log Weighted Adjacency Matrices $A_i \in \mathbb{R}^{p \times p}$

Graph Space [2] $G = A/P$ a quotient space obtained by applying the node permutation P action to an adjacency matrix: $[A] = \{P^T A P : P \in \mathcal{P}\}$. The space of A can be equipped with the Frobenius norm $d_A(A_i, A_j) = \text{trace}(A_i A_j^T)$, which induces the following distance on the quotient:

$$d_G([A_i], [A_j]) = \min_{P \in \mathcal{P}} d_F(A_i, P^T A_j P) \quad (1)$$

IS PATIENT i ALIGNED with PATIENT j ?

4 Fast Quadratic Assignment Matching (FAQ)

FAQ [3] Given two adjacency matrices $A_i, A_j \in \mathbb{R}^{p \times p}$

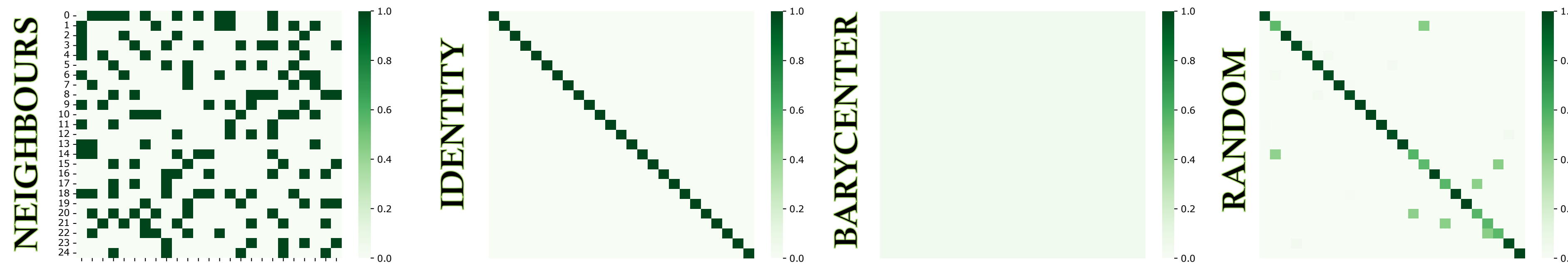
$$\min_P f(P) = \text{trace}(A_i P A_j^T P^T)$$

$$\text{s.t. } P \in \mathcal{D} = \{P \in \mathbb{R}^{p \times p} : P^T 1 = 1, P 1 = 1, P \geq 0\}$$

Given $P_0 \in \mathcal{D}$, FAQ is using Gradient descent in \mathcal{D} . The solution $\hat{D} \in \mathcal{D}$ is projected giving $\hat{P} \in \mathcal{P}$.

SIMULATIONS PARAMETERS

Initialization: four different initial values are compared



EVALUATION FUNCTION:

$$\frac{f_{faq}}{f_{id}}$$

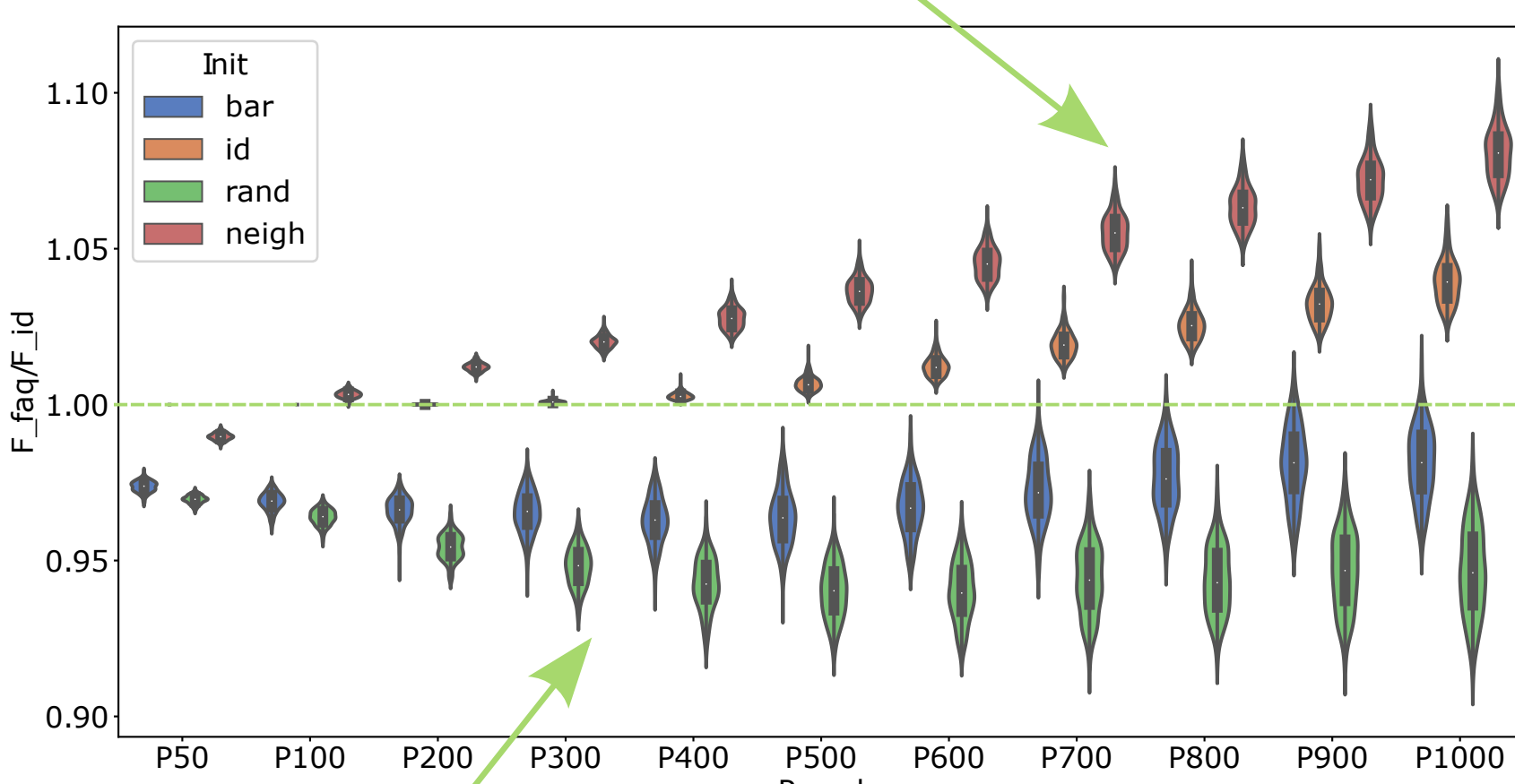
Objective function obtained with FAQ

Objective function obtained without matching

Goal: Comparing the Initializations

Violin Plot comparing the different initializations at different parcels, showing the sample distribution of the ratio between the FAQ and the non-matching.

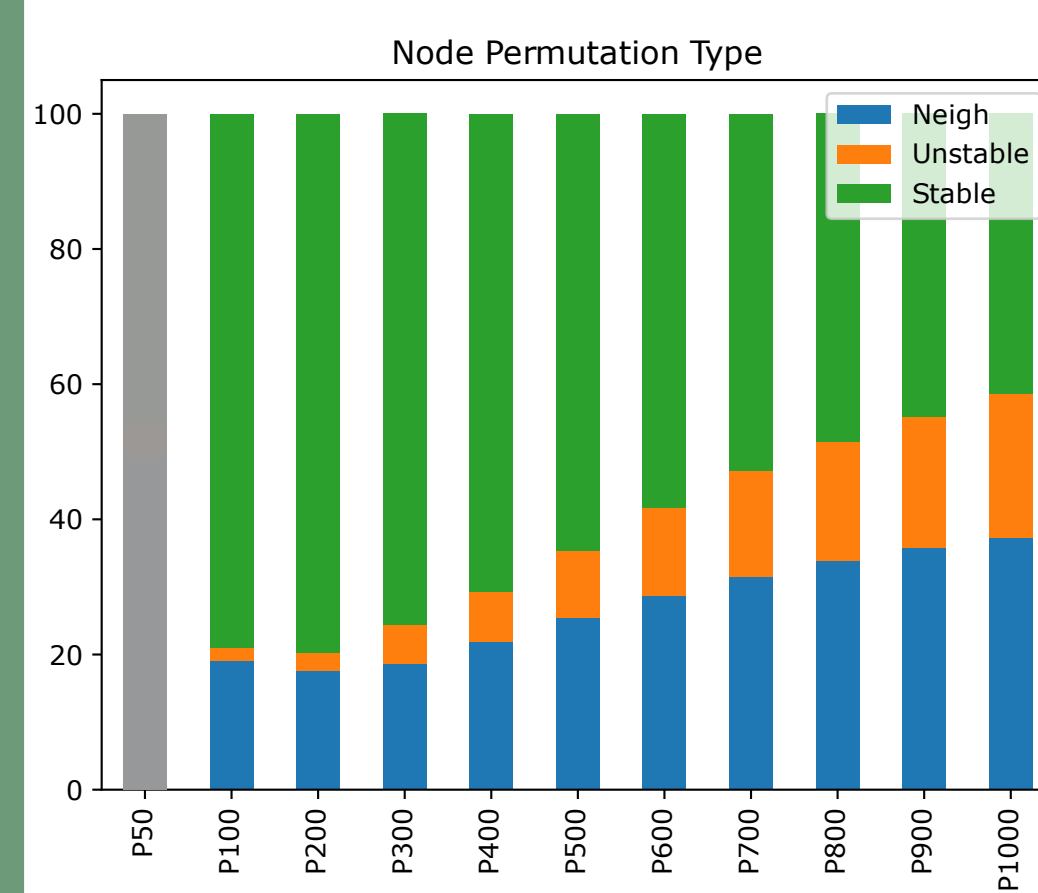
Neighbours and Identity initializations suggest that matching should be performed over 200 parcels.



Random and Barycenter initializations underperform, finding suboptimal solutions.

Goal: Neighbouring Initialization

Type of permutations suggested by FAQ



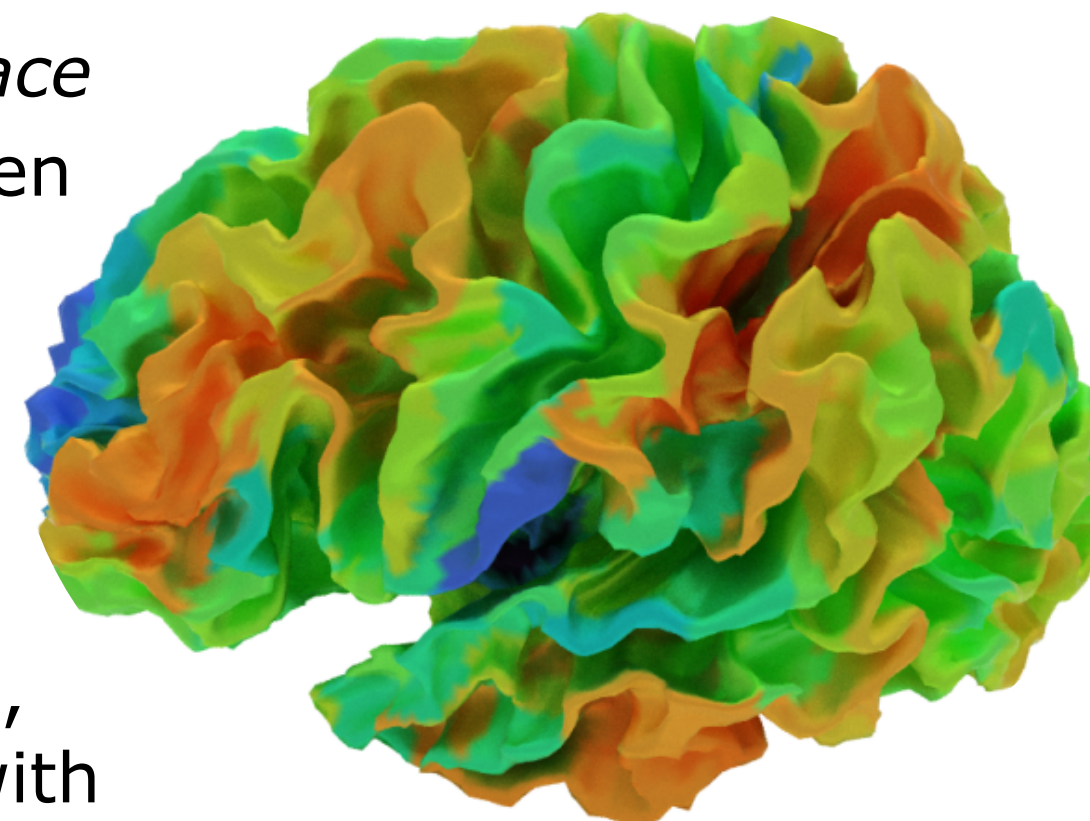
Stable: permuted with itself

Unstable: permuted with other parcels

Neighbours: permuted with neighbouring parcels

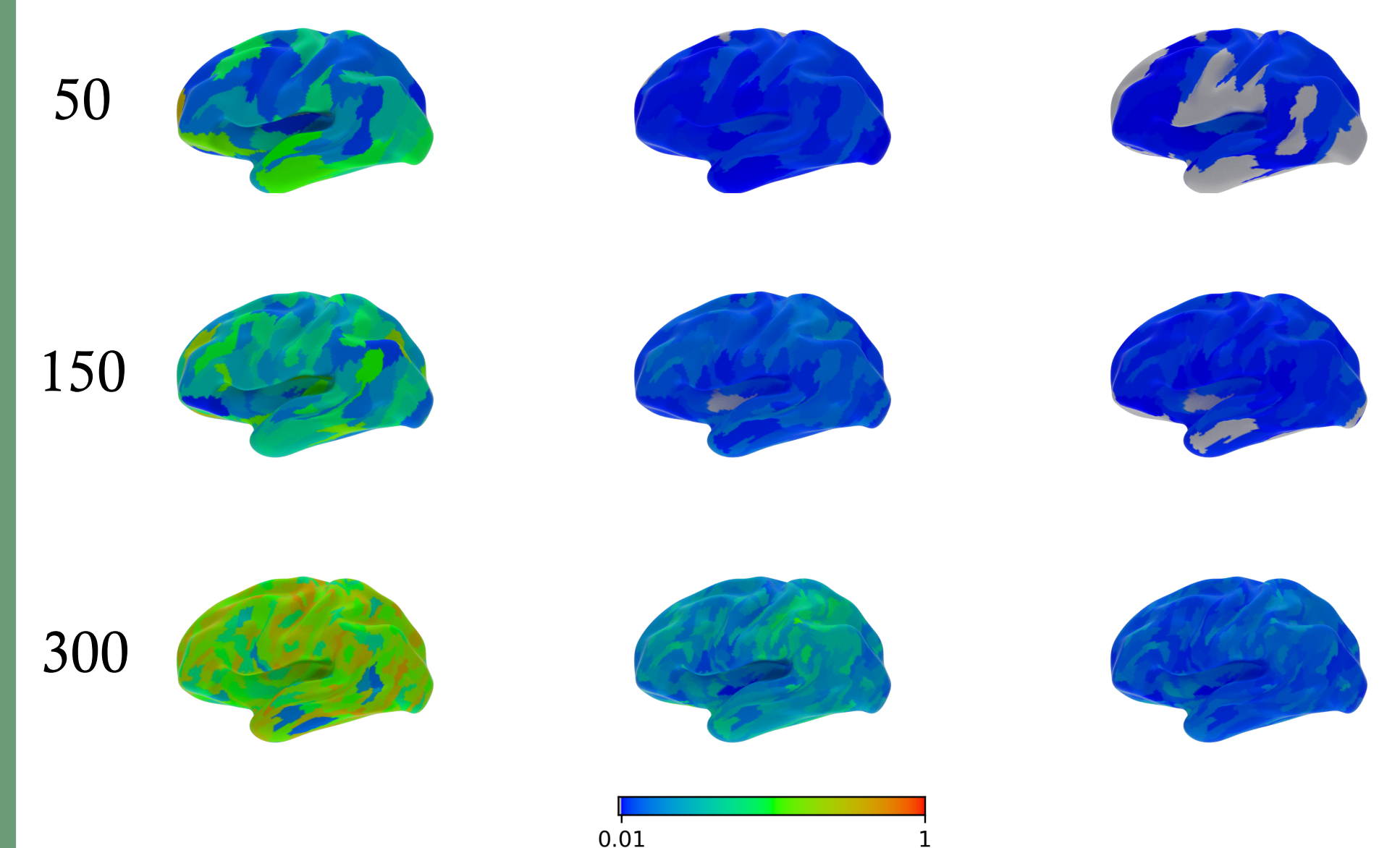
FOCUS: Parcels Surface

Some regions are often permuted (red) while others are more stable (green). A few regions are rarely permuted (blue). In most cases, permutations occur with direct neighbours (not shown).



Focus: Permutation Type on Surface

Any Permutation Permutations with 2nd or higher order Neighbours Permutations with 3rd or higher order Neighbours



For each regions, we considered the rate at which a regions was permuted. Gray indicates a permutation rate below 1%.

CONCLUSION

THE ALIGNMENT DEPENDS ON THE PARCELLATIONS

In this work, we studied the alignment across patients for structural brain connectivity network at different granularity of parcellations. We used the FAQ graph matching strategy as state of the art method to perform alignment. As the dimension of the parcels decreases, the parcels start being mis-aligned. The matching procedure shows how the optimal matching is realized with neighbouring parcels. Analyzing graphs without alignment is a model choice, which should be taken with caution when the dimension of the parcels decreases.

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