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# Preliminary results on the graph matching of structural and functional brain networks

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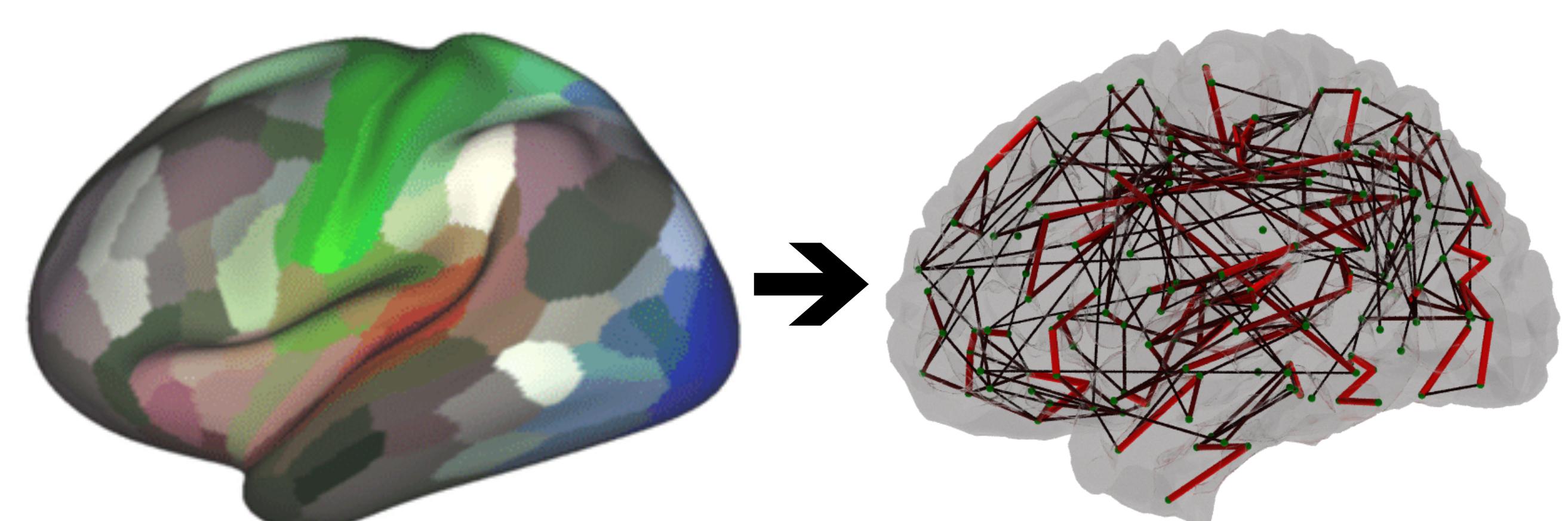
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## CONTEXT

The brain, responsible for human behavior, can be subdivided into "functional" regions following an atlas. The cortical **atlas** proposed by Glasser et al. [1] used in this work contains 180 regions per hemisphere. Different types of connectivities can be defined between regions.

The regions and their relationship can be represented as a **graph**, with regions of the atlas being the nodes and the connectivity being the edges [2]. The strength of the connectivity between two regions is represented by a scalar value. In this work, we consider structural and functional connectivity. Structural connectivity is estimated from **diffusion Magnetic Resonance Imaging** (dMRI), whereas functional connectivity stems from **resting-state functional MRI** (rs-fMRI), that is a derived measure of brain activity.

The edges of the brain graph representing the connectivity can be represented by a square matrix, called **connectome**. Each entry  $(i,j)$  of the matrix is the connectivity between region **labeled i** and **j**.



Brain atlas extracted from [3]

**Due to inter-subject structural and functional variability, the atlas may not fit all subjects perfectly [4,5]. In this work, we correct the inter-subject structural and functional variability using concepts of graph alignment.**

## MATERIALS AND METHODS

### Connectome generation pipeline

1050 subjects preprocessed dataset of the Human Connectome Project (HCP) [6] including:

- Diffusion MRI data
- Resting-state functional MRI data

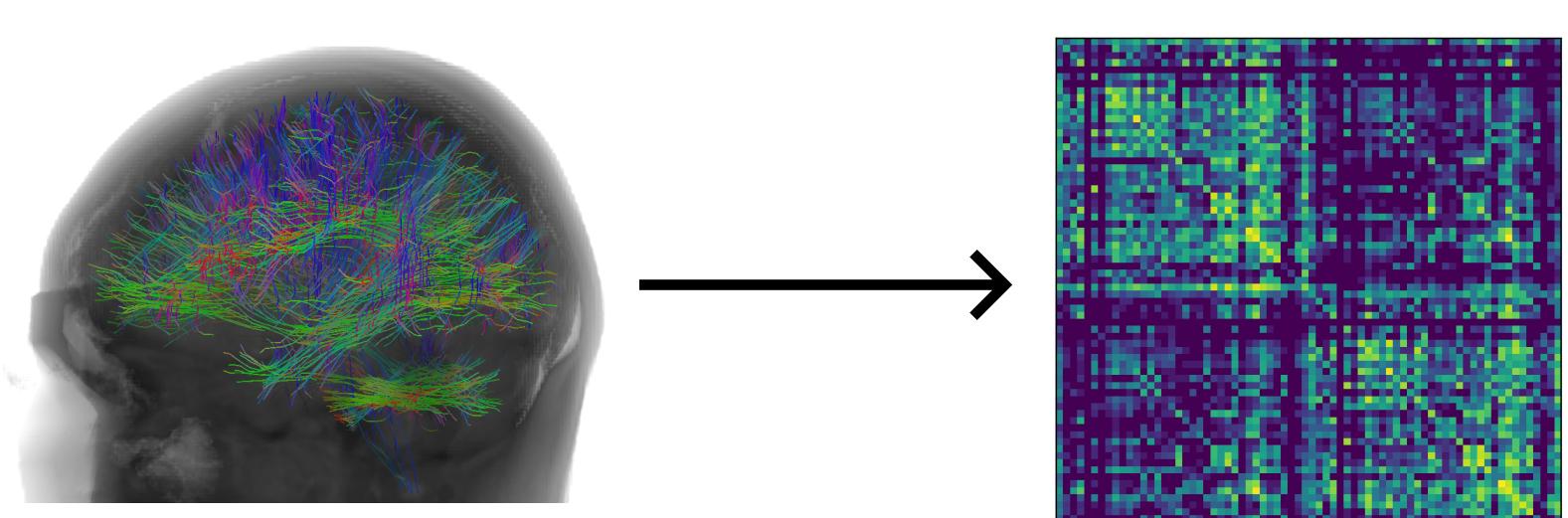
#### Diffusion MRI

We used the Tractoflow pipeline [7] to construct a tractogram [8] of ~ 2 millions of streamlines from the dMRI data of the HCP.

A streamline is a sequence of connected points supposed to follow a fiber bundle.

From the collection of streamlines, we construct the structural connectome by performing a local search to find the closest cortical region to the endpoints of the streamline [9].

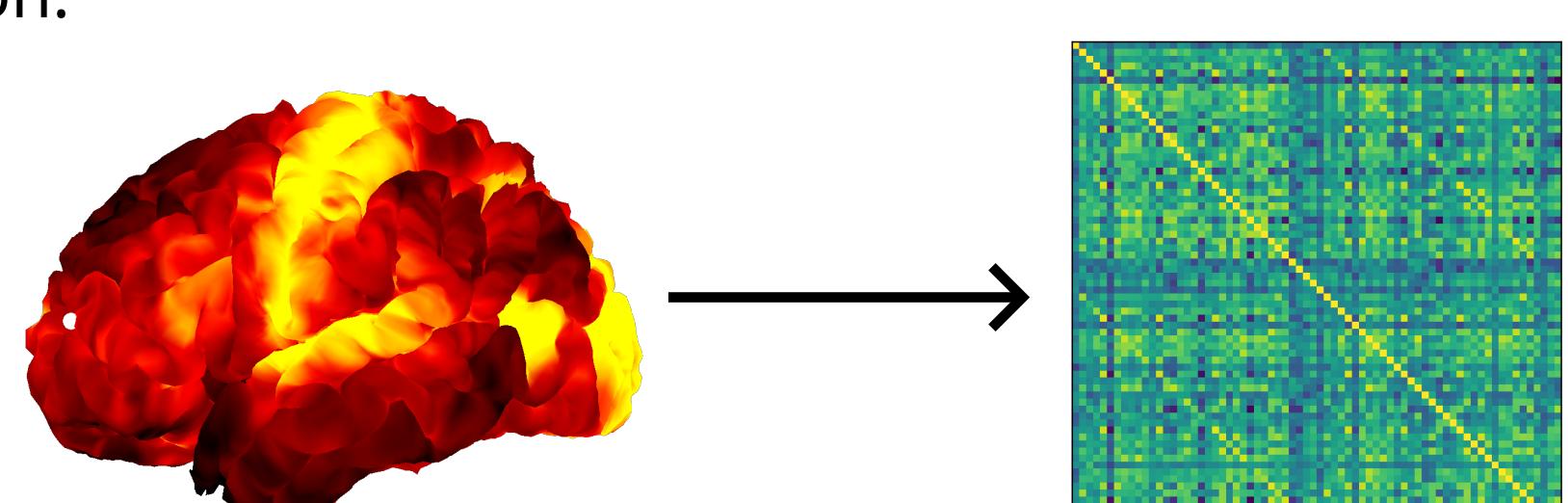
Each entry  $(i,j)$  in the connectome contains the number of streamlines that connects the regions labeled **i** and **j**.



#### Resting-state functional MRI

A Butterworth bandpass filter is used to keep only meaningful signal from HCP data.

The Pearson's coefficient is computed between every fMRI signal that is averaged over all the voxels of the region.



### Graph alignment, FAQ algorithm

The Fast Approximate Quadratic (FAQ) algorithm [10] solves the optimization problem:

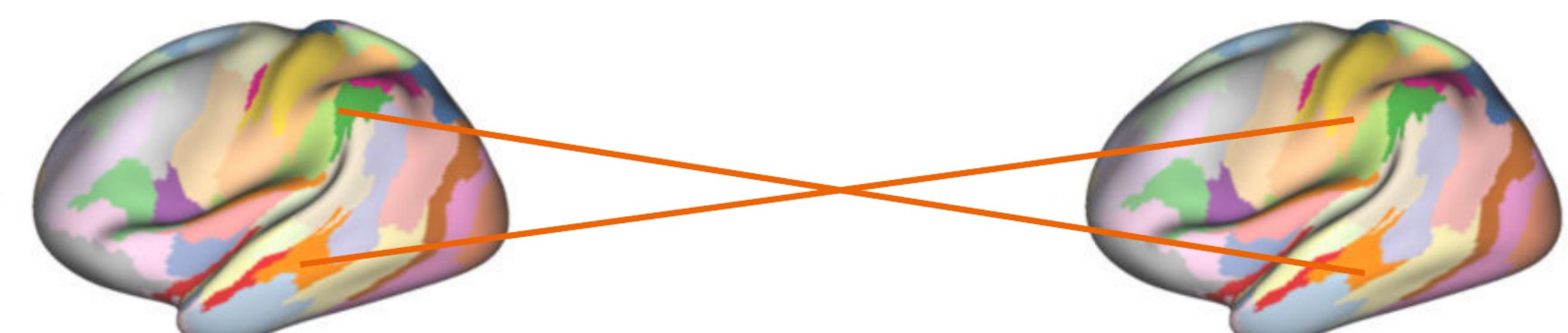
$$\underset{P}{\text{minimize}} \quad \|PC_S P^T - C_S^{\text{ref}}\|_F^2$$

It yields a permutation matrix  $P$  that permutes the labels of the structural connectome  $C_S$  in order to maximize the similarity with the connectome of reference  $C_S^{\text{ref}}$ .

We modified the FAQ algorithm such that it solves the new optimization problem:

$$\underset{P}{\text{minimize}} \quad \alpha \|PC_S P^T - C_S^{\text{ref}}\|_F^2 + (1 - \alpha) \|PC_F P^T - C_F^{\text{ref}}\|_F^2$$

Now we can align brain regions using the structural connectome  $C_S$  and the functional connectome  $C_F$  with their respective references  $C_S^{\text{ref}}$  and  $C_F^{\text{ref}}$ . The hyperparameter alpha is used to favor one modality over the other, if one is more meaningful or less noisy for instance.



Representation of region permutation as result of graph alignment [5]

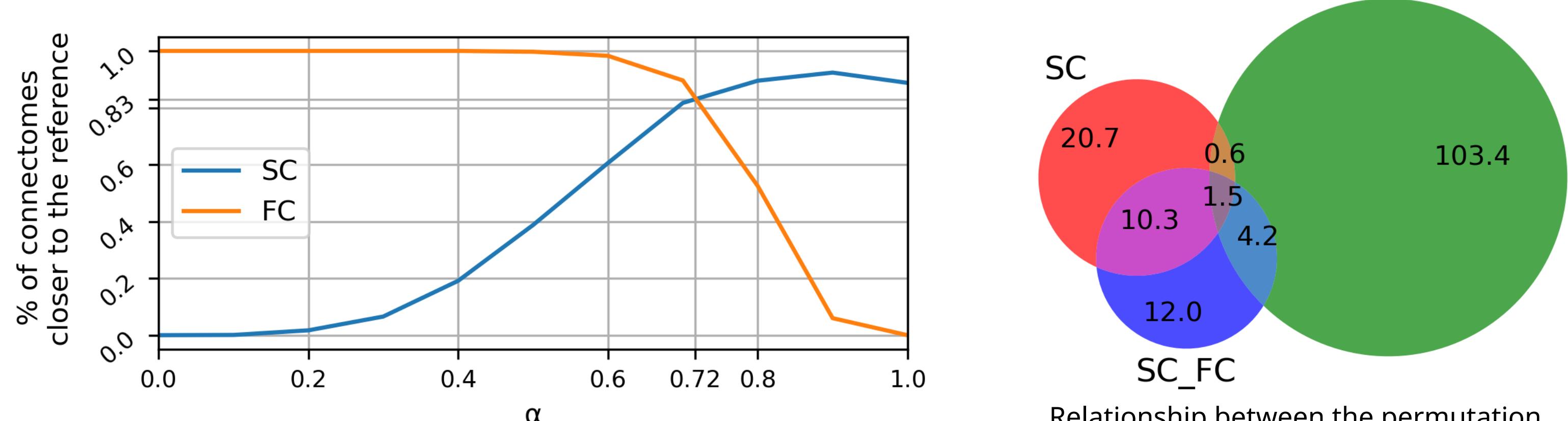
There are two specific cases, the first is when alpha = 0, corresponding to an alignment on structure only. The second is when alpha = 1, corresponding to an alignment on function only.

## RESULTS

The alignment on the structural connectomes only (alpha = 1) does not increase the similarity of the functional connectomes and conversely (alpha = 0). However, at alpha = 0.72, the percentage of connectomes in both modalities in which the connectomes are more similar to the references is over 80%.

Some permutations are common to the 3 cases, alpha = 1 (red circle), alpha = 0 (green circle) and alpha = 0.72 (blue circle).

The functional connectome looks more noisy and suggests more permutations, and many are not consistent with the structural alignment.



## TAKE HOME MESSAGE

The permutations induced by the alignment of structural and functional connectomes independently are distinct and applying the permutations given by one modality does not improve the similarity of the other brain connectivity modality. However some permutations are common and we can find a trade-off which increases the similarity of both connectome modalities. This alignment of brain regions might be a useful step before any group comparison.

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