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Network alignment and similarity reveal atlas-based topological differences in structural connectomes

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Abstract

Brain atlases are central objects in network neuroscience, where the interactions between different brain regions are modeled as a graph called connectome. In structural connectomes, nodes are parcels from a predefined cortical atlas and edges encode the strength of the axonal connectivity between regions measured via diffusion Magnetic Resonance Imaging (MRI) tractography. Herein, we aim at providing a novel perspective on the evaluation of brain atlases by modeling it as a network alignment problem, with the goal of tackling the following question: given an atlas, how robustly does it capture the network topology across different subjects? To answer such a question, we introduce two novel concepts arising as natural generalizations of previous ones. First, the graph Jaccard index (GJI), a graph similarity measure based on the well-established Jaccard index between sets; the GJI exhibits natural mathematical properties that are not satisfied by previous approaches. Second, we devise WL-align, a new technique for aligning connectomes obtained by adapting the Weisfeiler-Lehman (WL) graph-isomorphism test. We validated the GJI and WL-align on data from the Human Connectome Project database, inferring a strategy for choosing a suitable parcellation for structural connectivity studies. Code and data are publicly available.

1 Introduction

Due to the immense complexity of the brain, it is impossible to gain any insight into its global operation without simplifying assumptions. One such assumption, which has been widely used by neuroscientists, is that the brain, and in particular the cortical surface, can be divided into distinct and homogeneous areas. Of course the definition of homogeneous areas greatly depends on one's point of view, which has led to a plethora of brain parcellations. For example, the cortical surface has been subdivided based on its cytoarchitecture (Brodmann, 1909), gyri (Desikan et al., 2006), functional organization (Schaefer et al., 2017), axonal connectivity (Gallardo et al., 2018b), and combinations of these and other features (Glasser et al., 2016). There is also significant evidence that cortical regions vary in shape, size, number, and location across subjects and even across individual tasks, making the existence of a single canonical atlas unlikely. In addition to studying the characteristics of specific brain regions defined by a parcellation, there has been a growing interest in their relationship and interactions, an emerging field known as connectomics. In this context, the focus is shifted from understanding how information is segregated in the brain to how it is integrated. For example, through diffusion Magnetic Resonance Imaging (MRI) tractography, structural connections between brain areas can be recovered. The result is a network whose nodes correspond to cortical regions and whose edge weights represent the strength of the structural connectivity between pairs of regions. A similar network can also be built from resting state functional MRI yielding a functional, rather than structural, network. These brain networks, which encode the structural and functional connections of the brain, are referred to as connectomes (Sporns et al., 2005; Hagmann, 2005). Given functional or structural connectomes, their features can be compared across subjects and populations to link network changes to pathology or to further increase our understanding of its organization. An underlying assumption is that a correspondence exists between nodes of the network across subjects, a condition which is usually satisfied by using a group parcellation (Parisot et al., 2015; Gallardo et al., 2018b). The drawback of this strategy is that it ignores any subject specific changes in cortical organization and reduces the specificity of the results. An alternative approach is to construct a mapping between the nodes of the network prior to the comparison, therefore allowing the use of subject specific atlases. To our knowledge, this approach has never been investigated in the field of network neuroscience.

The construction of a mapping between network nodes corresponds to what is known in various fields as *network alignment* or *graph matching* (Barak et al., 2019) and has been applied in fields other than neuroscience (Singh et al., 2008; Conte et al., 2004; Ayache and Faverjon, 1987; Korula and Lattanzi, 2014). Graph alignment solutions (called *alignments*) correspond to a permutation of the labels of the nodes of a graph which maximizes its similarity to a second graph. There is no standard way to measure

49 the quality of its solutions (Bayati et al., 2013). This is also reflected in the neuroimaging literature, where
50 various measures of similarity between brain networks are used (Chung et al., 2017; Becker et al., 2018;
51 Osmanlıoğlu et al., 2019; Deslauriers-Gauthier et al., 2020; Villareal-Haro et al., 2020). In the context
52 of connectomics, a graph alignment is a reordering of the labels of the nodes of a brain network that
53 maximizes its similarity with a second one while preserving the topology. Describing the brain network
54 through its connectivity (a.k.a. adjacency) matrix, permutations of the node labels correspond to identical
55 permutations of the rows and columns of the connectivity matrix. This problem is distinct from the brain
56 atlas correspondence and parcel matching problems (Mars et al., 2016; Gallardo et al., 2018a). The main
57 difference is that there the permutation acts only on the rows of the connectivity matrix because they
58 find correspondences between *connectivity fingerprints* that rely on external features. Conversely, graph
59 alignment does not rely on any external information and uses only information contained in the topology
60 of the graphs.

61 The complexity of finding the optimal alignment between two graphs using brute force is exponential
62 in the number of nodes. It is therefore intractable even for the smallest of brain networks, which typically
63 have 50 cortical regions. Spectral methods are a popular approach to the alignment problem (Nassar
64 et al., 2018; Feizi et al., 2019; Hayhoe et al., 2019), despite being subject to limitations (Wilson and
65 Zhu, 2008). Modern machine learning paradigms exploit deep learning techniques for finding an alignment
66 (Liu et al., 2016; Li et al., 2018; Heimann et al., 2018), however they make use of partially available
67 information about the alignment (Liu et al., 2016), or lack explainability and interpretability.

68 We first introduce, in Section 2, the *graph Jaccard index* (GJI), a natural objective function for the
69 network alignment problem. For a given alignment, the GJI rewards correct matches while simultaneously
70 penalizing mismatches, overcoming shortcomings of previous approaches (Feizi et al., 2019).

71 We then propose, in Section 2.3, a new graph alignment heuristic, the *Weisfeiler-Lehman Alignment*
72 (WL-align), based on a weighted variant of the Weisfeiler-Lehman algorithm for graph isomorphism
73 (Weisfeiler and Leman, 1968). WL-align is amenable to concrete interpretability in terms of local network
74 structure around each node (Figure 3) and can be integrated with other heuristics.

75 After reviewing alternative approaches, we compare WL-align against FAQ (Vogelstein et al., 2015),
76 another efficient brain-alignment heuristic which is solely based on network structure.

77 2 Theory

78 A brain network is characterized as an edge-weighted graph $G = (V, E)$, where each of the n nodes
79 represents a brain region and each weight w_{ij} encodes the strength of the connection between regions
80 i and j . The graph G can always be considered as complete, given that if an edge (i, j) is not in G it

81 can be associated to a null weight $w_{ij} = 0$. The matrix that encodes in position (i, j) the weight of
 82 the edge w_{ij} between nodes i and j is called adjacency matrix of G and is denoted as $\text{Adj}(G)$. In the
 83 context of connectomics (Sporns et al., 2005; Hagmann, 2005), the adjacency matrix is also known as
 84 *connectivity* matrix. In this work we consider only networks with non-negative edge weights. For structural
 85 connectomes this does not impose any special preprocessing, since they are usually constructed using
 86 streamline count, length, or weights which are already non-negative. However, functional connectomes
 87 can contain negative entries because they are typically based on the correlation of resting state functional
 88 MRI signals. A practical solution, already used in other studies (Deslauriers-Gauthier et al., 2020), is to
 89 threshold the connectomes, therefore replacing negative entries by zeros.

90 2.1 Brain alignment

91 In order to compare two networks it is of fundamental importance to establish a correspondence between
 92 the nodes of the two graphs. Given two networks $G_1 = (V_1, E_1)$ and $G_2 = (V_2, E_2)$ respectively of n_1 and
 93 n_2 nodes, it is possible to define an injective map¹ $m : V_1 \rightarrow V_2$ that is called *graph matching* or *network*
 94 *alignment*. An edge $(u, v) \in E_1$ is correctly *matched* by m if $(m(u), m(v)) \in E_2$ and both edges have the
 95 same weight. Notice that a graph matching that matches all edges corresponds to an injective graph
 96 homomorphism. In the context of connectomics we will refer to m also as a *brain alignment*. A simple
 97 representation of this function is that of a matching matrix P_m of dimension $n_2 \times n_1$ (with $n_2 \geq n_1$)
 98 defined as

$$(P_m)_{ij} = \begin{cases} 1 & \text{if } m(j) = i, \\ 0 & \text{otherwise.} \end{cases} \quad (1)$$

99 Notice that if $n_1 = n_2$ then P_m is a permutation matrix. If m is an isomorphism between G_1 and G_2 ,
 100 then the transformation between the adjacency matrices of the two graphs is fully characterized by the
 101 matching matrix and is given by

$$\text{Adj}(G_1) = P_m^T \text{Adj}(G_2) P_m. \quad (2)$$

102 2.2 Quality of brain alignments

103 Once a brain alignment is identified, its quality can be assessed by evaluating the (dis)similarity of the
 104 resulting two networks. On a lexical note, we remark how the concept of *similarity between networks*
 105 used throughout this work fits well the standard concept of *matrix similarity* in the particular case where
 106 the change of basis matrix is a permutation matrix. In the following, the similarity measures are defined

¹The existence of the map m is granted whenever $|V_1| \leq |V_2|$.

107 for equal-sized networks, as typically encountered in connectomics. Classical metrics for this task are
 108 based on the comparison of the adjacency matrices of the two graphs by means of Pearson’s correlation
 109 coefficient, ℓ_p distance, or Frobenius distance (Vogelstein et al., 2015). The norm-based distances estimate
 110 the dissimilarity between two graphs G_1 and G_2 by computing the distance between their adjacency
 111 matrices as follows

$$d_t(G_1, G_2) = \|\text{Adj}(G_1) - \text{Adj}(G_2)\|_t \quad (3)$$

112 where t indicates the type of norm (p for ℓ^p norms and F for Frobenius norm). Note that higher distance
 113 corresponds to lower similarity. Another similarity measure that has been widely adopted in neuroimaging
 114 and brain connectivity is correlation; among the many definitions of correlation, we consider

$$C(G_1, G_2) = \frac{\langle \text{Adj}(\vec{G}_1), \text{Adj}(\vec{G}_2) \rangle}{\|\text{Adj}(\vec{G}_1)\|_2 \cdot \|\text{Adj}(\vec{G}_2)\|_2} \quad (4)$$

115 where the numerator is the scalar product between the vectorizations of the adjacency matrices of the
 116 two graphs and the denominator is the product of their norms. This similarity measure is also known as
 117 *cosine similarity*, since it corresponds to the cosine of the angle between the two vectors. More recently,
 118 distances based on geometrical (Venkatesh et al., 2020) and homological (Chung et al., 2017) properties
 119 of the networks have been introduced. All such measures capture some aspects of the similarity between
 120 two graphs, but none of them satisfies the following requirements:

- 121 • arising as a natural generalization of other similarity measures for less structured data, e.g., for sets
 122 of values without a network structure;
- 123 • being applicable to the algorithmic graph isomorphism and induced subgraph isomorphism problems,
 124 as fundamental special cases of the problem of measuring the similarity between two graphs;
- 125 • being simple enough so that its value can be easily interpreted;
- 126 • giving a straightforward notion of metric in the considered space.

127 We therefore propose a new measure obtained by generalizing the Jaccard similarity index, a similarity
 128 metric widely adopted in data mining, so that algorithmic problems such as induced subgraph isomorphism
 129 can be retrieved as special cases. Moreover, while our proposed measure assigns a clear meaning to the
 130 correspondence between two edges of two given graphs, it also crucially depends on the global network
 131 structure.

132 **2.2.1 Weighted graph Jaccard similarity index**

133 The *Jaccard similarity index* was originally proposed in the context of set theory to measure the similarity
 134 between two sets S and T . It is computed as the ratio between the size of their intersection and the size
 135 of their union, that is

$$J(S, T) = \frac{|S \cap T|}{|S \cup T|}. \quad (5)$$

136 An example of what is measured by the Jaccard index on sets is given in Figure 1. Notice that $J(S, T)$
 137 is defined in the $[0, 1]$ range and the extreme values are attained either when the intersection of the two sets
 138 is empty (i.e., $S \cap T = \emptyset \implies J(S, T) = 0$) or when the two sets are equal (i.e., $S = T \implies J(S, T) = 1$).

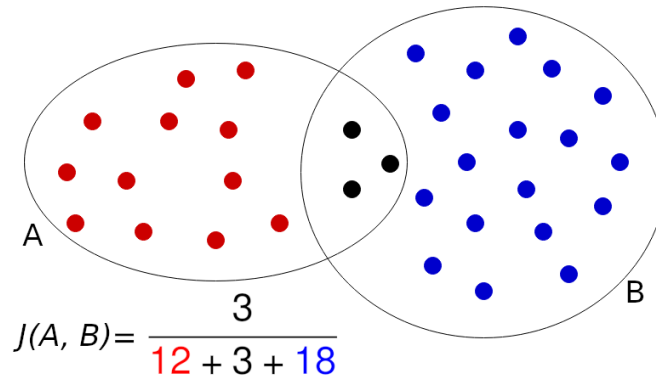


Figure 1: The two sets contoured by the circles have a non-empty intersection marked by the black dots. The Jaccard similarity index between the two sets is the result of the ratio between the number of elements in the intersection and the number of elements in the union of the two sets. The resulting Jaccard index is equal to $J = 3/33 \approx 0.09$.

139 The Jaccard similarity index has also been generalized to non-negative real vectors and, in this more
 140 general setting, is also known as Ruzicka similarity. In detail, given two vectors $x, y \in \mathbb{R}^d$ such that
 141 $x_i \geq 0$ and $y_i \geq 0$, their *weighted Jaccard similarity index* can be computed as $J(x, y) = \frac{\sum_{i=1}^d \min(x_i, y_i)}{\sum_{i=1}^d \max(x_i, y_i)}$.
 142 Note that Jaccard similarity index between two sets is a special case whenever the vectors x, y are binary
 143 and their dimension d is equal to the size of the union of the two sets. Noticeably, the weighted Jaccard
 144 similarity index induces a metric (Charikar, 2002).

145 Our adaptation of the concept of Jaccard similarity index to weighted graphs is based on the
 146 identification of the nodes of the two graphs. Given two brain networks G_1 and G_2 with adjacency
 147 matrices $\text{Adj}(G_1) = A$ and $\text{Adj}(G_2) = B$, the *weighted graph Jaccard similarity index* of G_1 and G_2 is

$$J(G_1, G_2) = \frac{\sum_{(i,j) \in \mathcal{E}} \min(A_{i,j}, B_{i,j})}{\sum_{(i,j) \in \mathcal{E}} \max(A_{i,j}, B_{i,j})} \quad (6)$$

148 where \mathcal{E} is the set of all possible pairs of nodes. For the sake of the present work, we remark that we can

149 think of B as having been previously aligned to A via Equation 2. Alternatively, the weighted graph
 150 Jaccard similarity index is defined as the weighted Jaccard index of the vectorizations of the graphs'
 151 adjacency matrices. Notice that $J(G_1, G_2)$ is not well defined when both G_1 and G_2 are empty (i.e.,
 152 $E_1 = E_2 = \emptyset$). Whenever $\text{Adj}(G_1) = \text{Adj}(G_2)$, the min and the max in Equation (6) coincide and
 153 $J(G_1, G_2) = 1$. On the contrary, if G_1 and G_2 do not have any edge in common (i.e., $E_1 \cap E_2 = \emptyset$), the
 154 numerator of Equation (6) will be equal to zero and $J(G_1, G_2) = 0$. An example of how the GJI acts on
 155 two graphs is given in Figure 2.

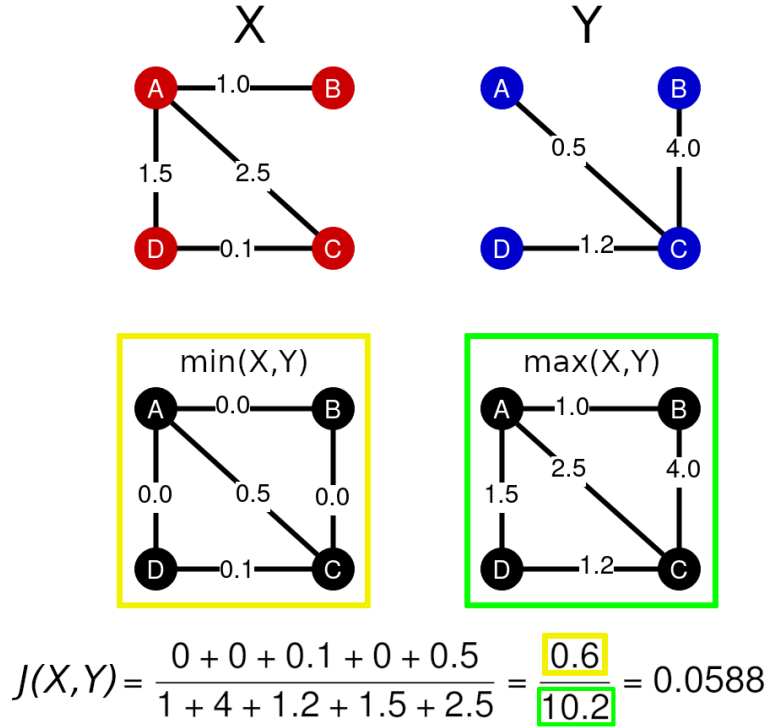


Figure 2: This figure shows an example of how to compute the GJI between two compatible graphs X and Y . For each pair of nodes $i, j \in \{A, B, C, D\}$, one computes the minimum and maximum between $X_{i,j}$ and $Y_{i,j}$. These two quantities will be used to define the numerator and the denominator of the GJI defined in Equation (6). As shown in the min (yellow) and max (green) graphs, edges that are not in a graph are associated to a null weight. The GJI is then computed as the ratio between the sum of the minimal weights and the sum of the maximal weights.

156 We have so far formally established the notion of network alignment (Equation (1)), and presented
 157 the Jaccard index as a principled way to measure the quality of an alignment (Equation (6)). We are
 158 thus ready, in the next section, to describe our variant of the Weisfeiler-Lehman heuristic and to show
 159 how to employ it to construct a network alignment.

2.3 Weisfeiler-Lehman network alignment

In this work we propose a brain alignment technique that allows to define the graph matching m between two brain networks G_1 and G_2 with a three-step procedure:

1. For each node u in both graphs, define a vector H_u that we call its *signature*.
2. Define a *complete bipartite graph* where on one side there are the nodes of the first graph and on the other side there are the nodes of the second graph; the euclidean distance between two signatures becomes the weight of each edge of the bipartite graph.
3. The graph matching is given by the solution of the *minimum weight bipartite matching problem*, also known as *assignment problem*, on the bipartite graph previously defined.

The novelty element of this brain alignment algorithm is given by the definition of the node signature, defined by an algorithm inspired by the Weisfeiler-Lehman method for graph isomorphism testing (Weisfeiler and Leman, 1968). For this reason, WL-align seems to be a reasonable name for our proposed brain alignment algorithm.

Node signature The signature that we associate to each node of the two graphs describes the local connectivity pattern of the node. It relies on the concept of *volume* of a node, which is defined as the sum of the weights of the edges outgoing from the node itself, namely

$$\text{vol}(v) = \sum_{u \in V} w_{uv} \quad (7)$$

where v is the node of which we compute the volume $\text{vol}(v)$, V is the set of nodes in the graph, and w_{uv} is the weight of the edge connecting nodes u and v . The algorithm that defines the signature of node u considers the subnetwork H induced by the nodes that are reachable from u in at most ℓ hops. At each of these hops, H retains only the k nodes which are connected by the edges with the highest weights. This subnetwork is a complete k -ary tree of depth ℓ which can be obtained from a breadth-first search (BFS) starting from u , and has a total of $d = \sum_{i=0}^{\ell} k^i$ nodes. For this reason the parameters k and ℓ are respectively called *width* and *depth*. The entries of the signature $H_u \in \mathbb{R}^d$ are then computed starting from u and following the BFS by recursively estimating the contribution of each edge to the volume of the considered node. A graphical intuition of how H_u is defined is illustrated in Figure 3 and a rigorous presentation of the whole WL-align algorithm is provided in the Supplementary Materials.

Bipartite graph Once a signature is computed for each node of the two graphs, we define a weighted complete bipartite graph where the nodes on the left represent the nodes of the first graph, while the

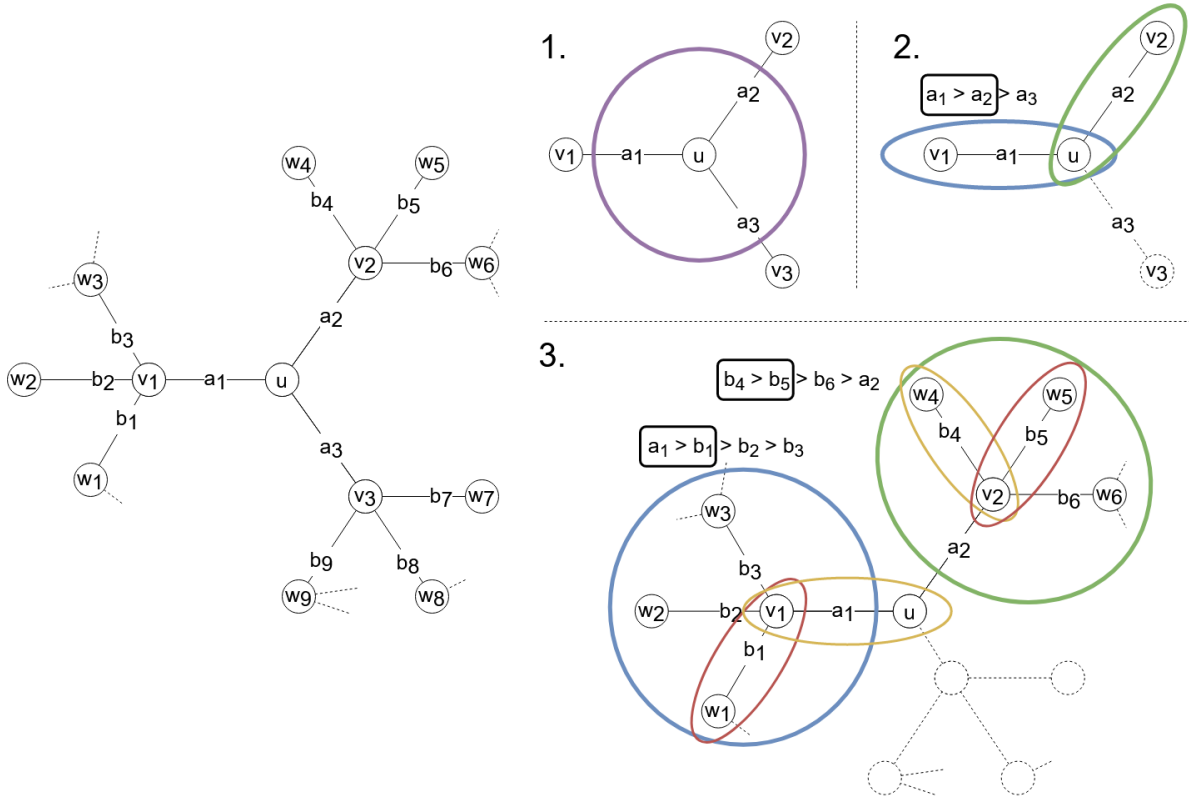


Figure 3: The graph on the left is the one that serves as an example for explaining the algorithm for computing the signature H_u of node u with $k = 2$ and $\ell = 2$. The first entry of H_u is $H_u[1] = \text{vol}(u)$, which is obtained by considering all the edges touching node u contoured by the purple circle in panel 1. The focus moves then to the two edges with highest weights (a_1 and a_2) which are marked by the blue and green circles in panel 2. They are considered in decreasing order and the corresponding entries in H_u are computed from Equation (1) of the Supplementary Material. For instance, the second entry of H_u is equal to $H_u[2] = H_u[1] \cdot a_1 / \text{vol}(u)$. The third entry is computed in an analogous way as $H_u[3] = H_u[1] \cdot a_2 / \text{vol}(u)$. This concludes the definition of the first $1 + k$ entries of H_u . The next entries are defined by considering first the blue and then the green subnetworks in panel 3. These are defined by rescaling the previous entries of H_u w.r.t. the weights of the nodes that are visited next. The fourth entry is equal to $H_u[4] = H_u[2] \cdot a_1 / \text{vol}(v_1)$ and the fifth is $H_u[5] = H_u[2] \cdot b_1 / \text{vol}(v_1)$. Analogously, the sixth and the last entry will be $H_u[6] = H_u[3] \cdot b_4 / \text{vol}(v_2)$ and $H_u[7] = H_u[3] \cdot b_5 / \text{vol}(v_2)$.

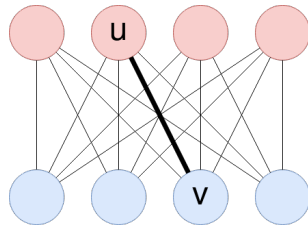


Figure 4: The red and blue nodes in the two rows represent the two graphs $G_1 = (V_1, E_1)$ $G_2 = (V_2, E_2)$ being aligned. The displayed complete bipartite graph is the one constructed in the second step of the WL-align algorithm. Each edge has weight equal to the euclidean distance between the signatures of the nodes that it connects. For instance, the weight associated to the edge connecting nodes $u \in V_1$ and $v \in V_2$ is $\|H(u) - H(v)\|_2$, where $H(\cdot)$ is the node signature defined in the first step of the WL-align algorithm.

188 nodes on the right represent the nodes of the second graph. The edge-weights encode the distance between
189 the signatures of pairs of nodes belonging to different graphs. Figure 4 shows a simple example of the
190 defined bipartite graph.

191 **Assignment problem** The final step towards finding the wanted matching is the resolution of the
192 assignment problem corresponding to the bipartite graph defined in the previous paragraph. The matching
193 can be found by selecting a minimum-weight graph matching, namely a subset of edges of the bipartite
194 graph such that every node has degree 1 and the sum of the weights of all edges of the subset is minimal.
195 This assignment problem is efficiently solved by the Hungarian algorithm (Jacobi, 1890; Kuhn, 1955).

196 3 Methods

197 We processed the data of 100 unrelated subjects from the HCP database and obtained the structural
198 brain networks via dMRI-based tractography as described in Section 3.1. For each of the 100 subject we
199 considered 23 parcellations (Desikan, Glasser, Gallardo at 11 different resolutions, Schaefer at 10 different
200 resolutions) described in Section 3.1.1, obtaining a total of 2300 weighted graphs. For each parcellation,
201 we retrieved a network alignment between each of the 5050 pairs of subjects using WL-align, which is
202 the novel technique introduced in this work, and the state-of-the-art competitor FAQ, as described in
203 Section 3.2, for a total of 232300 alignments. The quality of the obtained alignments was then assessed
204 using four network similarity measures described in Section 3.3.

205 3.1 Data and preprocessing

206 To build the structural brain networks, we considered the preprocessed data of the Human Connectome
207 Project (HCP) database (U100 subject group) (Van Essen et al., 2012; WU-Minn Human Connectome
208 Project consortium, 2017; Glasser et al., 2013). For each subject, a five-tissue-type image (Smith et al.,
209 2012) was obtained using the Freesurfer pipeline (Fischl, 2012) invoked through Mrtrix3 (Tournier et al.,
210 2019). A response function was estimated for the white matter, gray matter, and cerebrospinal fluid
211 using a maximal spherical harmonic order of 8 for all tissues (Jeurissen et al., 2014). The fiber orientation
212 distribution functions (fODFs) were then computed using the multi-shell multi-tissue constrained spherical
213 deconvolution algorithm (Jeurissen et al., 2014). Finally, the fODFs were used as input for probabilistic
214 anatomically-constrained tractography performed with the iFOD2 algorithm (Smith et al., 2012) seeding
215 from the gray matter - white matter interface and obtaining a total of five million streamlines per subject.

216 3.1.1 Parcellations

217 The four parcellations considered in this work subdivide the cerebral cortex following different character-
218 istics of the brain. The Desikan (Desikan et al., 2006) parcellation is based on the manual segmentation
219 of a template of the brain cortex that takes into account the morphological consistencies of healthy
220 human brains. For each subject, it was obtained directly from the Human Connectome Project database
221 (*aparc+aseg.nii.gz*) together with the cortical surface in fsLR32k space. The Glasser parcellation Glasser
222 et al. (2016) follows a multi-modal approach that considers cortical architecture, function, connectiv-
223 ity, and topography. Its projection onto the fsLR32k space was obtained from the BALSAs repository
224 (of Medicine, 2020). The Gallardo parcellation Gallardo et al. (2018b) is based on the segmentation
225 of the structural connectivity profiles associated to each point of the cortical surface and the Schaefer
226 parcellation Schaefer et al. (2017) is based on the analysis of the co-activation patterns of the brain by
227 means of the analysis of resting-state functional connectivity. The Gallardo and the Schaefer parcellations
228 were computed with a granularity of 100, 200, 300, 400, 500, 600, 700, 800, 900, and 1000 parcels. The
229 Gallardo parcellation was computed also with a granularity of 50 parcels. We extracted the 11 Gallardo
230 atlases from the extrinsic connectivity parcellation of Gallardo et al. (Gallardo et al., 2018b). The used
231 Schaefer atlas Schaefer et al. (2017) was downloaded from the repository of the CBIG laboratory (Yeo,
232 2020) for the *seven-networks* parcellation (Yeo et al., 2011). The use of multi-resolution parcellations
233 reflects the multi-scale nature of the brain network and allows to inspect how the atlas resolution affects
234 the similarity and the alignment of brain networks.

235 3.1.2 Connectomes

236 For each subject and parcellation an in-house software was used for counting the number of streamlines
237 connecting each pair of regions. The obtained quantity was encoded as the weight of the edge connecting
238 the two parcels in the brain network. All the edge weights were then divided by the sum of all the weights
239 in the graph. A total of 23 connectomes of different sizes was obtained for each subject. Given the
240 limitations of dMRI-based tractography, self-connections were excluded from the connectomes, i.e., the
241 diagonal of the adjacency matrix is set to zero. Because of the high resolution of some parcellations, some
242 regions turned out to be isolated (i.e., not connected to any other region). In order to have a connected
243 graph, which is a requirement of the WL-align algorithm, we artificially connected these isolated (i.e.,
244 zero-volume) nodes to the others by adding small-weighted edges connecting each of these nodes to all
245 the other nodes in the graph. This weight was set to 1 (before normalization), which from the point of
246 view of tractography is equivalent to the existence of one single streamline connecting the region to the
247 others. The obtained graphs are undirected and weighted.

248 3.2 Network alignments

249 In order to assess the ability of WL-align to retrieve the wanted brain alignment map, we prepared the
250 dataset in a way that allows to test the quality of the alignment against a known ground truth. In
251 practice, for each parcellation p , we randomly permuted the brains of all subjects and kept track of the
252 permutation maps. By using the permutation maps, we computed the ground truth matching m^* for
253 each pair of brains of each parcellation.

254 For the same set of brains, we also computed two graph matchings. The first is m_{WL} , which is
255 computed with the proposed WL-align technique. The width and depth parameters of the WL-align
256 algorithm were fixed to $k = \lfloor \log_2 n \rfloor$, where n is the number of nodes in the considered network (i.e., one
257 hemisphere), and $\ell = 2$.

258 The second is m_{FAQ} , which is computed with the Fast Approximate Quadratic Programming for
259 Graph Matching (FAQ) algorithm (Vogelstein et al., 2015), which is the state-of-the-art technique for
260 network alignment. Given two graphs, FAQ first finds a bi-stochastic matrix which acts as a relaxed
261 permutation matrix that transforms the adjacency matrix of the first graph into one with minimal
262 Frobenius distance from the adjacency matrix of the second graph, then projects the obtained solution
263 onto the proper space of permutation matrices. Notice that optimality with respect to the Frobenius
264 distance might not correspond to absolute optimality. The chosen termination criteria for FAQ are a
265 maximum number of 5000 iterations and an absolute tolerance on the objective function of 10^{-7} . Since
266 an implementation of FAQ was not available, we provide our own implementation that also corrects some
267 errors that we identified in the description provided in the original paper (Vogelstein et al., 2015) (see
268 Supplementary Materials for a description of the error).

269 Both algorithms were run separately on each hemisphere of the brain and the two resulting partial
270 alignments were then combined into a single one.

271 3.3 Quality of alignments

272 Given two networks $G_1 = (V_1, E_1)$ and $G_2 = (V_2, E_2)$ defined on the same parcellation and given a
273 matching m between them, we consider the following metrics to evaluate the quality of the matching m .

- 274 • Node Matching ratio (NMr): the fraction of nodes that have been correctly matched by m with
275 respect to the ground truth matching m^* (known a priori), namely

$$\text{NMr}(m) = \frac{|\{u \in V_1 : m(u) = m^*(u)\}|}{|V_1|}. \quad (8)$$

276 The NMr metric is defined in the $[0, 1]$ range and higher values correspond to better alignments.

277 • Graph Jaccard index J : as defined in Equation (6), namely

$$J(m) = J(m(G_1), G_2) \quad (9)$$

278 where, with an abuse of notation, we write $m(G_1)$ to denote the relabeling of the nodes obtained by
 279 applying the matching m on the nodes of G_1 . Recall that the graph Jaccard index is defined in the
 280 $[0, 1]$ range and higher values correspond to better alignment.

281 • J -ratio (Jr): the ratio between the graph Jaccard index $J(m)$ obtained by m and the graph Jaccard
 282 index J_p^* obtained by the ground truth matching m^* , namely

$$\text{Jr}(m) = \frac{J(m)}{J(m^*)}. \quad (10)$$

283 When the ground truth matching m^* is also an optimal matching, the denominator $J(m^*)$ acts as a
 284 normalization factor, which takes into account how complex it is to retrieve the matching m^* in
 285 terms of Jaccard similarity; under such assumption of ground-truth optimality, the Jr metric takes
 286 value in the $[0, 1]$ range, where higher values correspond to better alignment.

287 • Frobenius norm (FRO): the Frobenius norm of the difference between the adjacency matrices of
 288 $m(G_1)$ and G_2 , namely

$$\text{FRO}(m) = \|\text{Adj}(m(G_1)) - P_m^\top \text{Adj}(G_2) P_m\|_F \quad (11)$$

289 where, as also done for J , we write $m(G_1)$ to denote the relabeling of the nodes obtained by applying
 290 the matching m on the nodes of G_1 and where P_m is the permutation matrix associated to the
 291 matching m , as defined in Equation (1). The FRO metric is defined in the $[0, 2]$ range (since the
 292 adjacency matrices both have norm 1) and lower values correspond to better alignment.

293 For each considered parcellation p and for each network alignment algorithm of interest x (either
 294 WL-align or FAQ), we report the average quality metric, computed among all pairs of brains in the
 295 parcellation. For example, considering NMr as quality metric, we compute

$$\text{NMr}_p^x = \frac{1}{|\mathcal{P}|} \sum_{(G_1, G_2) \in \mathcal{P}} \text{NMr}(m)$$

296 where \mathcal{P} is the set of all pairs of brains with parcellation p and m is the matching found by algorithm x
 297 for the input pair of graphs G_1, G_2 . Analogously, this is done for all quality metrics.

4 Results

4.1 Experiments

We processed the data of 100 unrelated subjects from the HCP database obtaining the structural brain networks as detailed in Section 3. For each of the 100 subjects we considered 23 parcellations (Desikan, Glasser, Gallardo x 11, Schaefer x 10), obtaining 2300 weighted graphs. For each parcellation, we retrieved a network alignment between each pair of subjects using WL-align and FAQ. The ability of WL-align to retrieve the correct brain-alignment map was quantitatively evaluated by means of four similarity measures. First, a novel measure of similarity between brain networks called graph Jaccard Index was introduced in Section 2 as an adaptation of the concept of Jaccard index between sets. While behaving in a way which is similar to the commonly used correlation index defined in Equation (4), the graph Jaccard index has the property of defining a metric in the space of connectomes. This is a remarkable property in the context of modern data science, as many standard machine learning techniques can be applied only in metric spaces. The second considered similarity measure is the aforementioned correlation index defined in Equation (4), also known as cosine similarity. The third similarity measure is the Frobenius distance defined in Equation (3), which actually is a dissimilarity measure, therefore connectomes showing higher Frobenius distance are less similar and vice-versa. The node matching ratio defined in Equation (8) is the last considered similarity measure.

4.2 Comparison between similarity measures

Each employed similarity metric answers a specific question. The node matching ratio corresponds to what the expression suggests, namely it counts how many nodes were correctly matched and normalizes the result by the number of nodes in the graph. The other similarity measures have less intuitive definitions. For this reason, we measured how much the subjects in the considered datasets are similar to each other with respect to each metric and each parcellation. We recall that the dataset contains only healthy unrelated subjects which do not exhibit any family structure (WU-Minn Human Connectome Project consortium, 2017). This allows to compare how the within-group similarity reacts to the change in resolution and type of the used parcellation.

Figure 5 shows the average similarity between all the subjects in the cohort evaluated with the graph Jaccard index, the Frobenius norm, and the correlation. The used alignment is the one defined by the ground truth, which for our experiments is known a priori. The most noticeable fact is that the graph Jaccard index and the correlation show an inverted trend with respect to the one of the Frobenius norm. A higher number of parcels gives both lower Jaccard/correlation index and lower Frobenius distance,

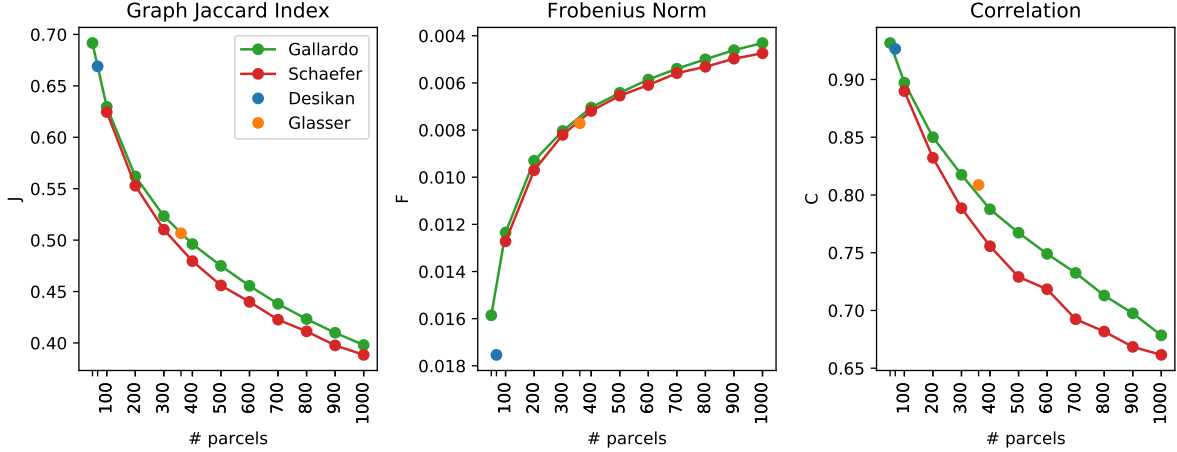


Figure 5: Each point shows the average similarity between every pair of subjects in the considered cohort measured on connectomes obtained with a specific parcellation. The used alignment is the one defined by the ground truth, which in our experiments is known a-priori. All panels show the similarity measure as a function of the number of parcels of the considered atlas. A higher graph Jaccard index and correlation corresponds to higher similarity. On the contrary, a higher Frobenius norm corresponds to lower similarity. In order to keep the intuition that *higher is better*, the y axis of the Frobenius norm is flipped.

329 which a priori is counter-intuitive. This phenomenon is due to the fact that the Frobenius norm is
 330 incapable of capturing the relative difference between edge weights and instead considers only the absolute
 331 difference between them. As a matter of fact, parcellations with a higher number of parcels will create
 332 brain networks with lower edge weights, since the same amount of connectivity (i.e., the same number
 333 of streamlines) is distributed among a number of edges that grows quadratically with the number of
 334 regions. For this reason, the absolute value of the edge weights will be lower, giving also a lower absolute
 335 difference. On the contrary, the graph Jaccard index and the correlation, which are able to capture the
 336 relative difference between edge weights, show lower similarity values between brain networks obtained
 337 with a higher number of parcels compared to brain networks obtained with a lower number of parcels.
 338 This difference suggests that the graph Jaccard index and the correlation mitigate the influence of the
 339 number of parcels in the estimation of the similarity between the compared brain networks. Another
 340 observation can be done on the singular nature of the Desikan and Glasser parcellations. While the
 341 results obtained on the Glasser parcellation are in line with those obtained with the Gallardo and Schaefer
 342 parcellations, connectomes obtained with the Desikan parcellation show a similarity in line with the
 343 Gallardo parcellation only when this is measured with the graph Jaccard index and the correlation.

344 4.3 Computing brain alignments with WL-align

345 In this work, the concept of *similarity between networks* was used as a proxy for the quality of a brain
 346 alignment, since a good graph matching is expected to correspond to a higher similarity between the

347 aligned graph and the ground truth. A separate analysis was performed for each of the 23 considered
 348 parcellations. First, an alignment was computed between each pair of subjects with the proposed technique
 349 WL-align and the state-of-the-art algorithm FAQ, then the similarity between the aligned network and
 350 the ground truth network was computed with the similarity measures listed in Section 3.3. The node
 351 matching ratio (NMr) tells the proportion of nodes that were correctly matched by the alignment. This
 352 measure does not give any information about the topological differences between the original and the
 353 aligned graph, but it gives an important insight on how many nodes are correctly labeled, which may be
 354 of fundamental importance in connectomic studies where the regions are associated to a specific function
 355 of the brain. The second used metric is the Jaccard similarity index introduced and described in this
 356 paper, while the third employed metric is the Jaccard index ratio. The latter measures how the Jaccard
 357 index performed with respect to the Jaccard index of the ground-truth matching shown in Figure 5, which
 358 is known a priori from the design of the experiment. It differs from the raw Jaccard index in the sense
 359 that it takes into account the complexity of the alignment problem, which we showed in the previous
 360 section to be more difficult when the number of parcels is higher. A final comparison was made using the
 361 Frobenius distance, which is what the FAQ algorithm is designed to minimize. This makes it particularly
 362 interesting since we expect FAQ to give Frobenius distance which is less or equal to the one obtained
 363 with WL-align.

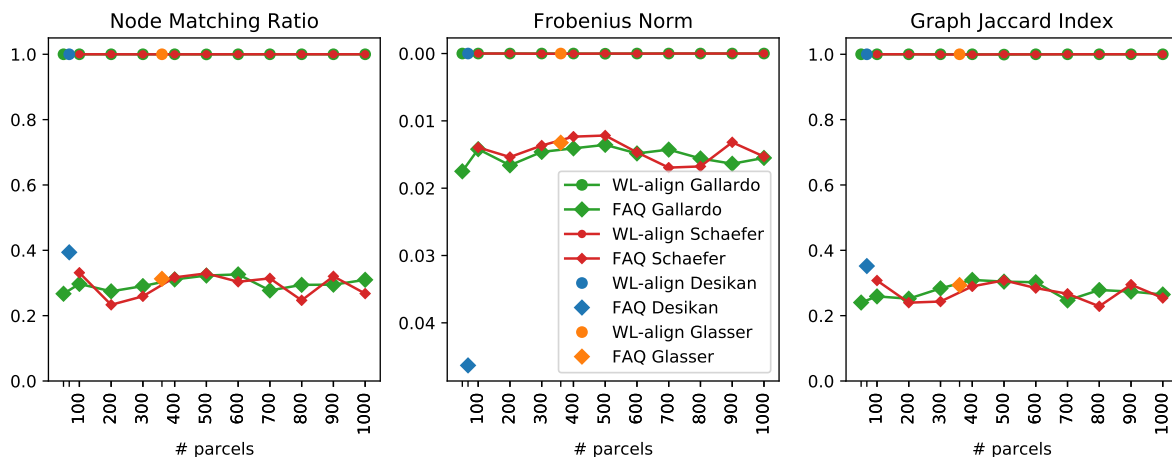


Figure 6: The displayed results concern the alignment between the structural brain network of one subject and its randomly-permuted version. Each panel shows one type of similarity between the aligned networks. Higher values of NMr, Jaccard index and Jaccard index ratio correspond to higher similarity, whereas the Frobenius norm is higher when similarity is lower. In order to keep the intuition that *higher is better*, the y axis of the Frobenius norm is flipped. In each panel, one point corresponds to the average (among subjects) similarity computed between brain networks obtained on a specific parcellation and aligned with one technique among WL-align and FAQ. All the four plots show the similarity as a function of the number of parcels in the considered atlas.

364 **Subject-wise analysis** In the context of this work, the simplest non-trivial alignment to be retrieved
365 is the one between the brain network of a subject and its randomly-permuted version. In this case, a
366 good alignment algorithm is expected to always retrieve the ground truth alignment. In Figure 6 we
367 report the average similarity between the ground truth and the obtained alignment. We notice that
368 WL-align consistently achieves the best possible performance with respect to all the considered metrics.
369 In particular, the naive metric of the node matching ratio always gives similarity equal to 1, meaning
370 that WL-align correctly labels all the nodes whenever a structural brain network is aligned against
371 a randomly-permuted version of itself. These considerations are true for every parcellation. On the
372 contrary, FAQ does not solve the self-alignment problem exactly. All the considered metrics highlight
373 a poor performance of FAQ both in absolute terms and compared to WL-align. As a matter of fact,
374 FAQ on average yields at most 40% of correctly matched nodes, while WL-align consistently gives 100%
375 of correctly matched nodes. Also, different parcellations behave differently when FAQ is employed; for
376 instance, the Desikan parcellation gives lower Frobenius similarity with respect to the other parcellations
377 but shows higher Jaccard index and node matching ratio.

378 **Full cohort analysis** When all the subject are aligned with the permuted version of each other, the
379 problem is more complicated. Even though we considered healthy subjects whose acquisition followed
380 the same protocol and that have been processed in an identical way, the subject-specific differences and
381 the intrinsic noise of the data yield estimated structural brain networks that are in practice different
382 among each other, despite being substantially coherent. In order to assess the ability of the proposed
383 alignment technique to overcome these differences and yield an alignment as close as possible to the
384 ground truth, we considered all the alignments between each pair of subjects, including the ones between
385 a subject and a randomly-permuted version of itself. The brain alignments obtained with WL-align are
386 compared to the one computed with FAQ and presented in Figure 7, which reports the average similarity
387 between the obtained alignment and the ground truth alignment among all the possible pairs of subjects.
388 In terms of Frobenius norm, the alignments obtained with WL-align and FAQ are very similar, with
389 WL-align systematically showing slightly higher Frobenius similarity. The performance of the Gallardo
390 parcellation is indistinguishable from the one of the Schaefer parcellation. Also, the Desikan and the
391 Glasser parcellations have results in line with the Schaefer and Gallardo parcellation when the alignment
392 is obtained with WL-align. This is not true for the Desikan parcellation when FAQ is employed. Recalling
393 that FAQ is a technique that is inherently based on the Frobenius norm and WL-align is not, we can
394 notice that WL-align gives a brain alignment that does satisfies also the optimality criteria of FAQ,
395 additionally to its own. A second thing that we can notice about the Frobenius norm is that it exhibits
396 the same phenomenon as in Figure 5, where the Frobenius similarity increases with the number of parcels.

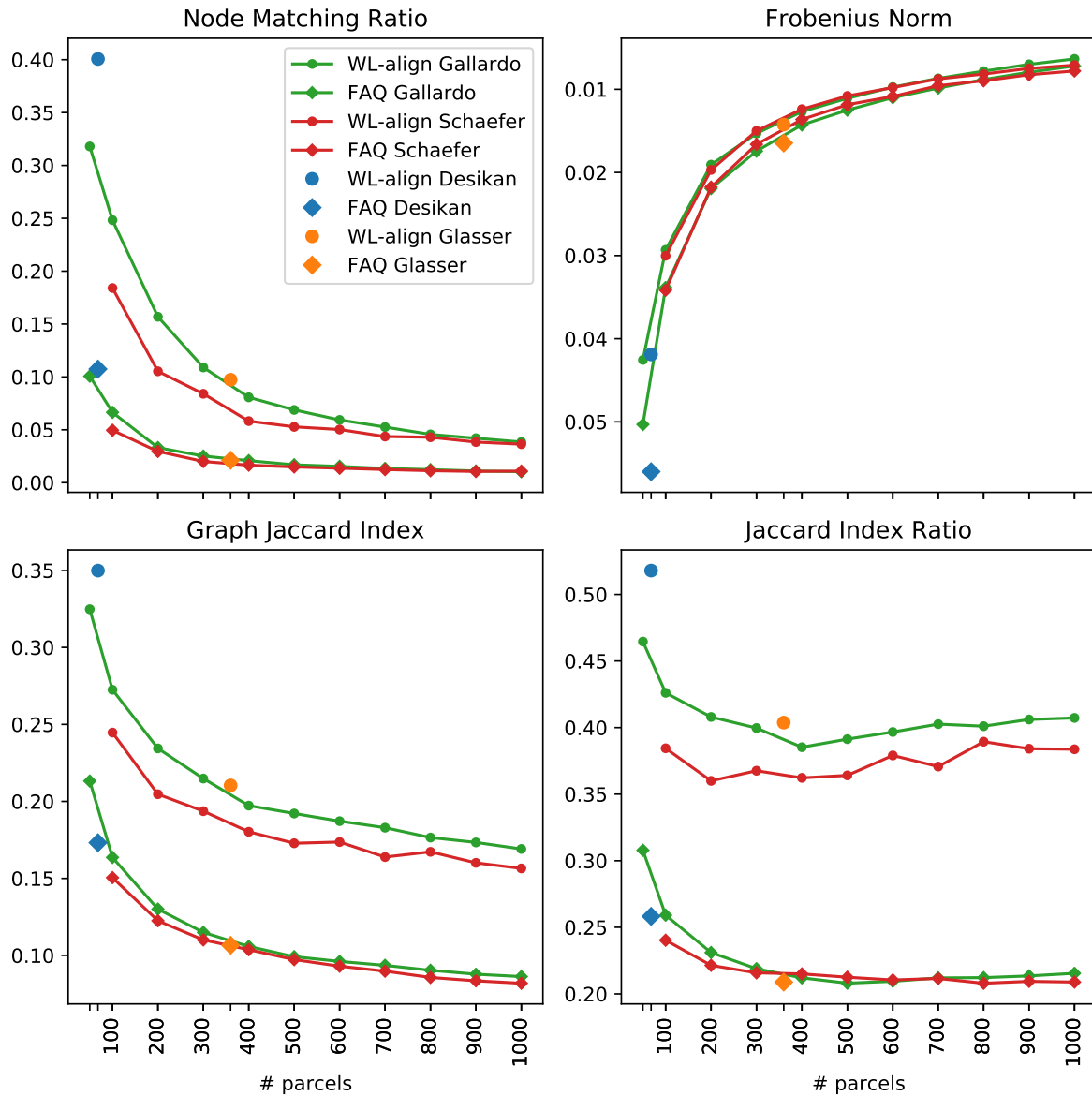


Figure 7: The displayed results concern the alignment between the structural brain networks of each pair of subjects including the self-comparisons. Each panel shows one type of similarity between the aligned brain networks. Higher values of NMr, Jaccard index and Jaccard index ratio correspond to higher similarity, whereas the Frobenius norm is higher when similarity is lower. In order to keep the intuition that *higher is better*, the y axis of the Frobenius norm is flipped. In each panel, one point corresponds to the average (among subjects) similarity computed between brain networks obtained on a specific parcellation and aligned with one technique among WL-align and FAQ. All the four plots show the similarity as a function of the number of parcels in the considered atlas.

397 This phenomenon appears for the same reason as before, namely the Frobenius norm does not capture the
398 relative difference between the edge weights in the compared networks. All the other employed similarity
399 metrics suggest that WL-align has superior performance with respect to FAQ. While FAQ has almost
400 identical performances when applied on the Gallardo and the Schaefer parcellations, WL-align shows
401 relevant and previously unobserved differences between the performances of the two. In particular the
402 Gallardo parcellation allows to retrieve better alignments with respect to the Schaefer parcellation. This
403 may be due to the fact that we are studying structural connectivity, therefore the use of a function-based
404 parcellation like the one of Schaefer may affect the quality of the alignment when compared to the
405 structural connectivity computed on a structure-based parcellation like the one of Gallardo. Looking at
406 the behavior of the Desikan and the Glasser parcellation, we notice two different scenarios. The Glasser
407 parcellation shows Jaccard similarity slightly higher than the one of the Gallardo parcellation, suggesting
408 that the multi-modal nature of the atlas well captures the structural connectivity features that we are
409 looking at. This is true both when we consider WL-align and FAQ. The Desikan parcellation behaves
410 quite differently. Its performance does not follow the pattern of the other parcellations and is not aligned
411 with neither the Gallardo nor the Schaefer parcellation. It has a sensibly superior performance compared
412 to any other parcellation when the WL-align algorithm is considered and this is visible through every
413 employed similarity metric. The same difference does not emerge so clearly when FAQ is employed. We
414 finally notice that atlases with > 400 parcels all behave very similarly, namely they reach a plateau in
415 terms of Jaccard index, Jaccard index ratio and node matching ratio. This is true both when WL-align
416 and FAQ are employed. The performance in this range is lower than the one in the 50 – 400 parcels range.

417 **4.4 Self matching rate**

418 Figure 8 illustrates the self matching rate for each region of 9 example atlases, i.e., the fraction of times
419 regions were correctly matched when aligning different brains represented using the same atlas. It is clear
420 that, as the number of parcels is increased, the matching rate is reduced. This can be explained by the
421 increased difficulty of the alignment problem, but also by a decrease in the signal-to-noise ratio of the
422 connectomes driven by the reduction in parcel size. It is also interesting to note that the matching rate
423 does not appear to be symmetric across hemispheres. For example, the right inferior parietal region of
424 the Desikan atlas obtains relatively high matching rate of roughly 0.8, whereas the contralateral region
425 only obtains roughly 0.4.

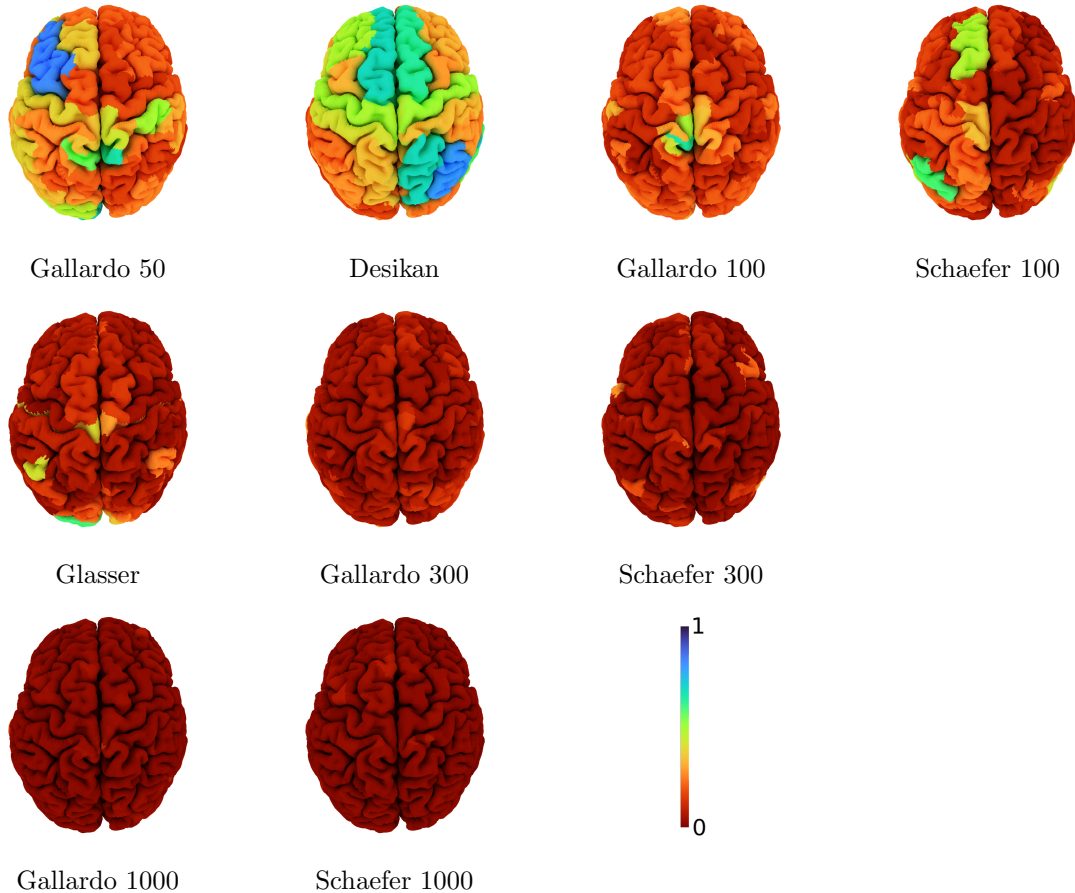


Figure 8: Self matching rate of the labeling per region for different atlases using WL-align. Atlases with 100 regions or less are illustrated in the first row. The second row illustrates atlases with approximately 300 regions and the third row those with 1000 regions.

5 Discussion and conclusions

Among the fundamental problems of network neuroscience at the scale of whole-brain structural connectivity, finding correspondences between brain regions and quantitatively assessing the similarity between brain networks are particularly important when it comes to considering massive heterogeneous datasets and modern data science techniques. In this work we considered these two problems in relation with the unresolved question concerning the choice of the parcellation for structural connectivity studies.

We proposed and analyzed a similarity index between brain networks, inspired by the Jaccard index between sets, that behaves in a way similar to the classical correlation index. Additionally, it enjoys the remarkable property of defining a metric in the space of connectomes, which is interesting both from the theoretical point of view and for data science applications. The proposed graph Jaccard index showed to be less affected by the number of regions in the chosen parcellation than the Frobenius distance, which is one example of (dis)similarity index from the class of norm-based distances.

The second object introduced in this paper is WL-align, a novel algorithm that allows to find the

439 graph alignment between two brain networks. It relies solely on topological features of the brain network,
440 which makes it particularly suitable for being applied also outside the domain of network neuroscience.
441 When WL-align is used in our experiments in order to retrieve the alignment between a network and a
442 permuted version of itself, it gives the exact solution. This does not happen when the main competitor
443 FAQ is employed. The superior performance of WL-align is evident also when brain networks of different
444 subjects are aligned. In this case, the WL-align algorithm was shown to retrieve brain alignments that
445 are closer to the ground truth with respect to the alignments obtained by FAQ. Notice that as it is
446 designed, the WL-align algorithm builds on the construction of a feature vector for each node of the
447 graph, which is then used as an edge weight in an assignment problem on a bipartite graph. This does not
448 include any prior knowledge other than the topological similarity between the two networks to be aligned.
449 The analysis provided in this work was intentionally constrained to the pure topological comparison of
450 networks. Nevertheless, it would be possible to extend the feature vector defined in WL-align with any
451 prior of geometrical, spatial, anatomical or connectomic nature or to add any constraints in the assignment
452 problem on the bipartite graph. Future works will be devoted to the design of these constraints and
453 features.

454 Some remarkable conclusions concerning the parcellations to be used in structural brain connectivity
455 studies can be drawn from the ability of WL-align to find the correct alignment between two brain
456 networks. First, the function-based parcellation of Schaefer is a poorer choice than the structure-based
457 parcellation of Gallardo, the multimodal parcellation of Glasser and the morphological parcellation of
458 Desikan. This was expected as the whole study is centered on measuring *structural* connectivity, hence
459 the choice of a function-based parcellation was never expected to be optimal from any point of view.
460 Allowing to express this concept quantitatively is one of the merits of WL-align. A second remarkable
461 aspect is the performance of the Desikan atlas, which gave much better results in terms of alignability
462 than any other parcellation of any granularity. For this reason, whenever the number of parcels considered
463 in the study is low (less than 200), one should consider using the Desikan atlas as a first choice. Not only
464 it would be a highly reliable choice that has been consistently used throughout time in the community,
465 but with this study we showed that it would also allow to define brain networks with more consistent
466 topological features, in particular those captured by WL-align. As far as brain atlases with a higher
467 number of parcels (more than 200) is concerned, we showed that parcellations with a number of parcels in
468 the > 400 range have lower performance in terms of alignment. For this reason, we suggest to use atlases
469 with a lower number of parcels, if the designed experiment allows it. This difference in performance may
470 be due to the number of streamlines used for defining the structural brain network, which may be lower
471 than what would be necessary for a reliable definition of the brain networks. The lack of a consensus on
472 the number of streamlines to be used in structural connectivity studies leaves this possibility open.

473 As highlighted throughout the paper, this work analyzes the problems of parcellation selection and
474 brain alignment in the context of *structural* connectivity. Any conclusion we made should not be
475 straightforwardly generalized to functional connectivity studies, which would require a separate analysis
476 which was out of the scope of this work.

477 6 Open science

478 The data and code used in this work are all available at open repositories, as indicated in the text. We
479 uploaded the used code and the obtained connectomes and alignments on the Open Science Framework.
480 They can be found at this link: <https://osf.io/depux/>.

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