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My Thesis Title

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Abstract

Your abstract here. A brief summary of the research, including the purpose, methods, results, and conclusions.

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0.1 Dataset Preprocessing

Several connectomic datasets have been proliferated such as the Human Connectome Project (HCP) [18], the Baby Connectome Project (BCP) [19] and the Connectome Related to Human Disease (CRHD) [20]. In these datasets, connectivity matrices were estimated using different tools. For instance, functional connectivity matrices were generated using CONN toolbox or groupwise whole-brain parcellation approaches [21], [22]. On the other hand, structural and morphological connectivity matrices were measured using FSL toolbox and Desikan-Killiany atlas via FreeSurfer software [23], [24], respectively [BMR22]

The pre-processing of the resting state fMRI data was performed using both FSL (https://fsl.fmrib.ox.ac.uk/fsl/ fslwiki)and AFNI (Automated Functional Neuroimaging) (http://afni.nimh.nih.gov/afni) toolbox. In brief, the pre-processing steps were as follows: ... [Zha+22a].

Functional networks are rendered as temporal correlation matrices, and anatomical networks were converted into structural correlation matrices. The transformation applied to SC networks is fundamental for this analysis and in general for those analysis aimed at comparing SC and FC topological organization. If we had preserved SC networks in the form of a sparse positive matrix with weights possibly much higher than 1 (i.e., maximum weight reachable in FC networks), the community detection process would have been biased: depending it on the weights of the matrices, it would have found modules reflecting almost exclusively the anatomical modular organization. Moreover, this transformation allowed us to use the same mathematical instruments (i.e., the same spatial null model in the optimization) on both matrices. [Pux+22].

0.2 Structural and Functional Connectivity Matrices

Structural connectivity (SC) matrices represent the anatomical connections between different brain regions. Functional connectivity (FC) matrices represent the temporal correlations between brain regions during resting state.

Functional brain graphs. Conventionally, a functional graph is constructed from functional MRI (fMRI), more specifically from the blood-oxygen level-dependent (BOLD) signal which shows the changes in blood oxygenation over time linked to neural activity [11] in a particular region in the brain. First, the reported signal is averaged within each brain ROI. Next, a measure of correlation such as Pearson's correlation coefficient is computed between pairwise regions which results in the functional connectivity depicting the communication between pairs of brain regions. In functional brain graphs, nodes do not have features and edges are generally undirected and weighted [BMR22]

Most existing studies focus more on structural brain networks and functional brain networks, where both brain networks are undirected attributed graphs with undirected edge eij between vi and vj (i.e., eij ¼ eji). The difference between structural networks and functional networks is that the e 2 E in structural networks

are positive values, while they can be negative in functional networks. Since the functional networks are constructed based on the BOLD signal correlation among different brain nodes, the positive and negative edges represent synchronous activation and asynchronous activation among brain regions, respectively. [Tan+23].

The blood oxygenated level-dependent (BOLD) signal of functional MRI (fMRI) reveals the spatial and temporal brain activity across diferent brain regions [Zha+22b].

We first constructed the connectome of functional connectivity (FC) and structural connectivity (SC) for each participant, using the a priori Schaefer cortical parcellation atlas of 400 regions43.

Particularly, based on the resting-state fMRI data, FC was defined as the Pearson correlation coefficients between each pair of regional time series, resulting in a 400×400 symmetrical FC matrix for each participant. The matrix consisted of 79,800 unique elements, with each element denoted as an "edge" connecting two cortical regions. Fisher r-to-z was applied to improve the normality of FC edge strength.

Meanwhile, using the diffusion MRI data, we reconstructed the whole-brain white matter tracts of individual participants via probabilistic fiber tractography with multi-shell, multi-tissue constrained spherical deconvolution (CSD)44. Anatomically constrained tractography (ACT)45 and spherical deconvolution informed filtering of tractograms (SIFT)46 were applied to improve the biological accuracy of fiber reconstruction. For each participant, we quantified the number of streamlines connecting every pair of cortical regions from the Schaefer atlas to construct a structural connectome of streamline counts. The edge weights of the SC matrix were log-transformed. [Che+24]

We construct the fMRI brain networks by computing the edge weights as Pearson correlations between each pair of regional time series. The nodes in the networks are accordant with brain regions defined in the chosen brain atlas. [Zha+22a]

0.3 Dataset Description

The dataset used in this study comprises structural connectivity (SC) and functional connectivity (FC) matrices obtained from MRI and fMRI scans, respectively. The data is categorized into three age groups: young (10 years old), adult (30 years old), and old (70 years old). Each age group contains data from 5 different subjects. Both SC and FC matrices have dimensions of $200 \times 200 \times 5$ (nodes × nodes × subjects).

Nodes are already aligned across subjects and modalities based on a common parcellation scheme, so no graph matching is needed? [Pux+22]

For a given participant, the edge weights of graph matrix in functional and structural networks fall in the same range and their number of nodes are identical. The node definition follows the organization of brain atlas used in this study [Zha+22a]