A novel robust network community identification method for structural connectome analysis

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Introduction

In complex networks, the communities of a graph are clusters divided by the connectivity attributes of nodes. The community structure can be described as the sets of nodes with dense intra-set connectivity and scattered inter-set connections. Our case study is the brain structural connectomes derived from DW-MRI tractography [Hagmann et al.2007]. The communities represent local neighborhoods in the topological connectivity of the brain network. Detecting the regions of the brain that interact between each other have applications for brain development and functional organization analysis [Bullmore and Sporns, 2009]. Although the communities have been widely studied [Bullmore and Sporns, 2009], little has been done to study its estimation reproducibility. Here we propose a subject-specific robust method to capture structural connectome communities. It works despite the noise introduced by the acquisition noise, processing pipeline of the images, modeling, tractography parameters and graph construction parameters.

Methods

Data. We used six 2mm isotropic resolution DW-MRI datasets with 64 diffusion measurements with b-value 1000s/mm^2, two b-value=0s/mm^2 images (including one reversed phase-encoded), see Chamberland (2019). A 1mm^3 voxel resolution T1-weighted MPRAGE image was also acquired for each dataset. The datasets are from two subjects (S1, S2) and two acquisitions per-subject (A1, A2). The DW-MRI images were corrected for EPI distortions using FSL/TOPUP [Andersson et al.2003]. The connectomes were computed from the cortical regions of the *Lausanne2008* parcellation (463 regions) [Daducci et al., 2012]. We used Mrtrix3 [Tournier et al., 2012] iFOD2 tractography to generate two tractograms replicas using 10 million streamlines each (R1, R2). The communities are computed using the Louvain algorithm [Blondel et al.2008].

To compare the similarity of two different connectomes we use the *JIG* metric [Villarreal et.al. 2019] that compare communities. Given the partitions P1 and P2 from two connectomes respectively, the JIG is defined as:

$$JIG(P_1, P_2, V) = \sqrt{\sum_{A_i \in P_1} \sum_{B_j \in P_2} JI(A_i, B_j) \times \frac{|A_i \cap B_j|}{|V|}} .$$

Averaged Community Matrix (ACoMi). We propose to build a novel matrix denoted as *ACoMi* to characterize the node's probability to couple to different communities and use it to measure the topological differences between connectomes. The methods are described in Figure 2.1

Results and Discussion

The connectome's communities allows to characterize the connectivity properties and differentiate among subjects, see Figure 1a). In Figure 1b), distances between connectomes are computed using the JIG metric. The difference between different subjects and acquisitions are, on average, of 0.15, for the intra-subject, and 0.18 for the inter-subject (ratio intra to inter of 0.86). Ideally, this ratio should toward zero. In Figure 2.1, we introduce the ACoMi method that replaces the community organization with a robust representation capturing the communities variability. Figure 2.2a) shows the novel ACoMi matrices and in Figure 2.2b) the L2 distance among them is reported. The ratio of intra to inter is now 0.45 (average intra-subject distance of 7.65 and inter-subject of 16.98).

Conclusions

We present a new method to study community organization in structural connectomes robust to the sources of pernicious variability in the construction of connectomes This study provides a tool to improve the brain's community structure estimation. We show that this method improves the reproducibility in the estimations, then it allows to capture subject-specific features. In the future work, the ACoMi analysis can be applied to estimate structure at different brain parcellation scales (number of cortical regions). Moreover, the ACoMi matrix can be generalized to study structural networks derived from other means than streamlines count with more-informative connectivity weights, such as from COMMIT [Daducci et.al.2014].

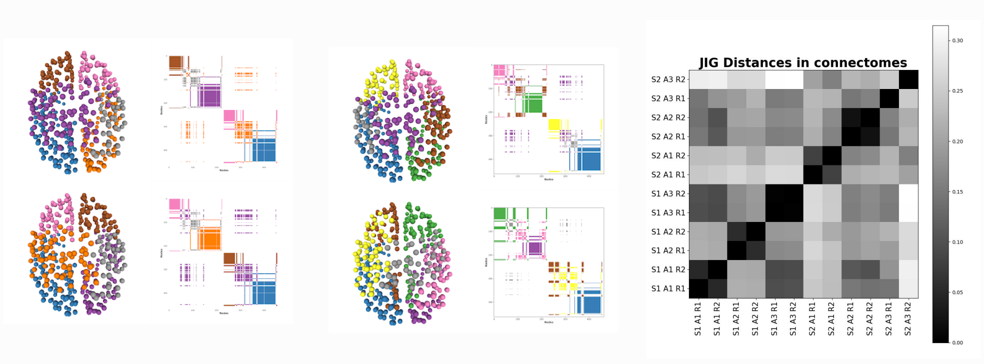

Figure 1. a) For every DW-MRI dataset, we display the network nodes representing the regions of the brain. The colors group the community organization of the respective network. Next to each brain, we plot the Community Matrix (CoMi), where the entry [n1,n2] of the matrix has a value of 1 if the nodes n1 and n2 belong to the same community; otherwise, zero. Here, white represents a value of zero, and any other color represents a value of one. b) The computed distance between datasets using community attributes the JIG. The inter-subject distance and the intra-subject distance have similar values, this analysis is not subject specific. The comparison S2 A3 R1 and S2 A3 R2 is an example in which running tractography makes communities not reproducible; the distance between these two subjects is 0.26, bigger than the average inter distance of 0.18.

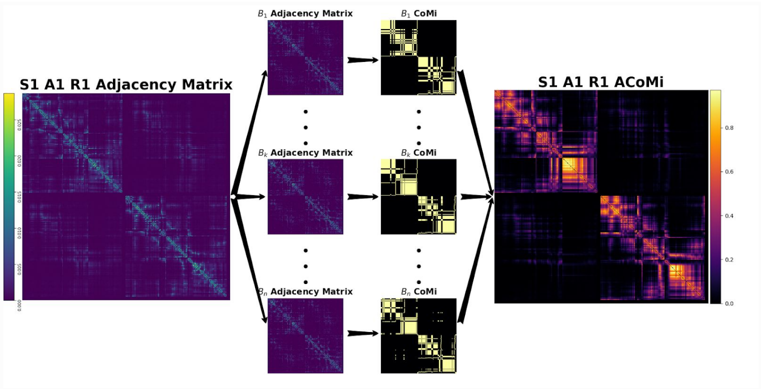

Figure 2.1 a) Structural connectome of subject S1-A1-R1. b) We bootstrap **n** connectomes (**B_1 , ... B_n)** sampling with repetition streamlines from the original connectome. c) For every connectome **B_i**, its Community matrix (CoMi). d) Finally, we average entrywise the CoMi matrices to obtain the *Averaged Community(ACoMi) Matrix.* This ACoMi displays the sensitivity of the nodes to couple to different communities by slightly varying the edge weights in a connectome.

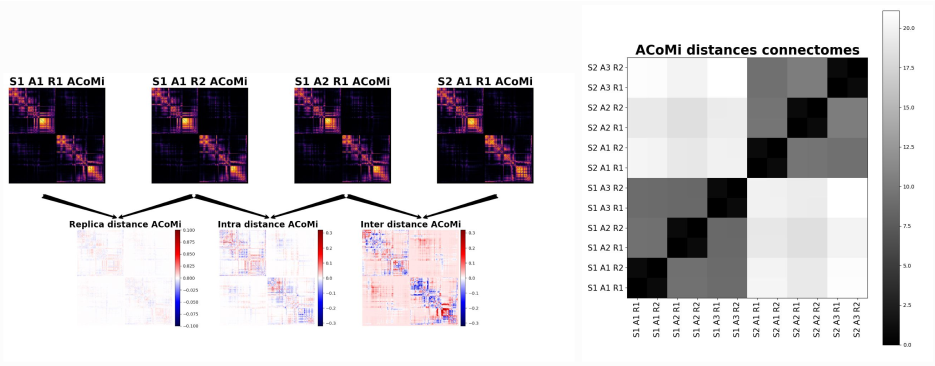

Figure 2.2. In a) we show all the ACoMi matrices for S1 A1 R1,R2 , S1 A2 R1, and S2 A1 R1. Those regions of the brain with intermediate intensity are the ones more susceptible in the community organization. b)The subtraction of ACoMi of two replicas shows negligible values due to sampling noise in the bootstrapping. c) The subtraction of S1 A1 R1 and S1 A2 R1 shows the nodes and the communities displaced by the registration process or other artifacts. d) The L2 matrix distance between Connectomes using their ACoMi matrix. Here is shown that the replica distances are minimized thanks to the bootstrapping procedure. Compared to **Figure 1b)**, The improvement in the subject specificity is notable. Here the replica distances are minimized to almost zero. The intra subject distances are greater than the replica ones, but stable, here, the average intra-subject distance is 7.65. Finally, the average inter-subject is similar for all cases, and its value is 16.98.