

Group-representative partitions of human brain structural networks

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Introduction

Diffusion imaging, tractography and graph analysis are emerging as powerful instruments for *in vivo* characterization of the human connectome and of its organizational principles. The human brain network proved to be small-world and organized according to a hierarchical modular architecture, composed by communities of nodes highly interconnected between them, but sparsely connected with other modules [1]. The study of the brain modular topology and decomposability is raising new interest. Particularly, modularity is thought to be a crucial characteristic in terms of brain evolution and development [2], and its study may therefore become one of the investigation keys when approaching for example neurodevelopmental disorders. In order to characterize the communities fingerprint in health and pathology, it is necessary to correctly identify a partition representative of a group of subjects. Here we characterize the modular topology of structural brain networks, we quantify the similarity of communities structure using information theory derived metrics, and we propose the consensus clustering algorithm [3] as a means to estimate a smooth representative group partition for a set of 40 healthy subjects.

Methods

40 healthy subjects aged 25±4 years underwent an MRI imaging session (3T Siemens TrioTim, 32-channel coil), composed of a diffusion spectrum imaging (DSI) sequence (257 volumes, maximum b-value 8000 mm²/s), and a high resolution MPRAGE morphological acquisition as anatomical reference. Whole brain structural connectivity was determined by tissues segmentation and streamline tractography as described in [4], and using the Connectome Mapping Toolkit (www.cmtk.org). This processing yielded 40 weighted structural networks, each one composed of 448 nodes (each node being a cortical region, according to the parcellation described in [5]), and with edges representing the connectivity density between regions. For each network, the optimal decomposition into modules was determined using the Brain Connectivity Toolbox (<https://sites.google.com/site/bctnet/>) by selecting the highest modularity partition from 100 runs of the Louvain algorithm [6]. In order to determine a representative partition for the group of healthy subjects, we run the *consensus clustering* algorithm ('Cons.Clust.') with tau=0.3 (threshold value on the consensus matrix) and 100 iterations. For comparison, we computed two well-known representative partitions already proposed in the literature: the Louvain optimal partition from the average network over the 40 subjects (*average partition* or simply 'Avg.Part.') similarly to [8], and the partition of the most central subject in terms of mutual information (*central partition* or simply 'Cent.Part.') similarly to [2]. To quantify the inter-subjects variability of the modular decomposition and the distance between each subject's partition and the three representative ones, we used the normalized mutual information (MI) and the normalized variation of information (VI) values, as described in [7].

Results

The 40 brain networks were decomposed on average into 14 modules (min=10, max=16), each comprising on average 32 nodes (min=1, max=76). The average VI and MI values between each pair of subjects were 0.328±0.023 and 0.605±0.029, respectively. The consensus clustering was composed of 8 modules (fig.A), the nodes building each module being spatially contiguous; the average partition was composed of 13 modules; the central partition was composed by 16 modules. Fig.B represents a single subject connectivity matrix (color scale: log-connectivity density), organized according to the consensus clustering partition. The VI of each subject respect to the consensus clustering was 0.266±0.025; respect to average partition was 0.272±0.028; respect to the central partition was 0.304±0.018. The VI respect to the consensus clustering was significantly lower than the inter-subject VI, and than the central partition VI. The average MI of each subject respect to the consensus clustering was 0.643±0.030; respect to the average partition was 0.667±0.035; respect to the central partition was 0.644±0.022. The MI respect to the consensus clustering was significantly higher than the inter-subject VI, and lower than the average partition MI. (fig. C,D)

Discussion

The brain structural modular architecture was characterized for 40 healthy subjects. The relatively high inter-subjects MI and low inter-subjects VI indicated a good degree of consistency between subjects partitions. Group-representative partitions were identified using three different approaches. We can assume that a partition effectively represents a group, if the distance (for example in terms of VI and MI) between each subject of the group and that partition is small. The VI and MI distributions between each subject and the representative partitions, suggest that the consensus clustering and the average partition better represent the modular topology of the group. Moreover, visually inspecting the individual and representative partitions (consensus clustering only is shown in fig.A), and considering the lower number of modules forming the consensus clustering, we hypothesize a smoothing and denoising property inherent to this technique, which conceptually determines an agreement partition from a set. These aspects deserve further investigation.

Conclusion

We were able to decompose brain structural networks into meaningful modules, and quantify the variability of such decompositions. We determined representative partitions for a group of 40 healthy subjects, and evaluated their representativeness by means of information theory-derived measures. To our knowledge this is the first time that consensus clustering is applied on brain networks with this objective. The individuation of effective agreement partitions from sets of subjects is central for the characterization of the brain modular organization, and in view of groups comparison.

References

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