Multi-Subject Comparison of Whole-Brain Connectivity-Based Hierarchical Parcellations

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Introduction

Diffusion MRI (dMRI) and probabilistic tractography [Behrens, 2003] allows in-vivo cortex parcellation based on the brain connectivity structure. Existing methods are typically restricted to finding a predefined number of clusters in smaller regions of grey matter [e.g., Anwander et al., 2007]. Furthermore, all the available methods rely on finding one optimal number of clusters, but in a whole-brain approach, this might be unrealistic.

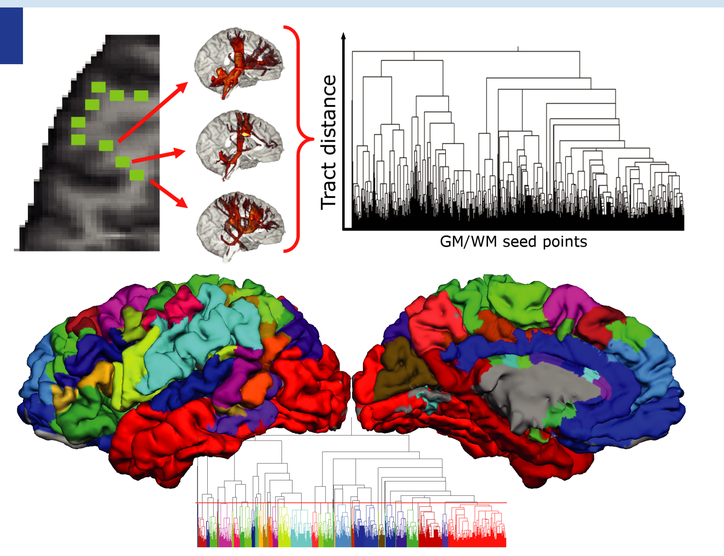
In our previous work, a hierarchical clustering approach was introduced, encoding the connectivity structure at all granularity levels in a hierarchical tree, and the possibility for tree comparison was suggested [Moreno-Dominguez et al., 2012].

In this work we extend on the method analyzing the qualitative comparison of whole connectivity structure across subjects or acquisitions. We also present a new algorithm for selecting partitions of a desired granularity that additionally enables the search of relevant granularities within a single subject.

Methods

- dMRI images were acquired on a Siemens TimTrio (1.5 mm iso, 60 dir, b=1000 s/mm^2, GRAPPA/3, AV=3).
- 4 healthy participants (A,B,C and D) were scanned. One participant (D) was scanned twice and low SNR datasets were generated by using AV=1.
- All voxels at the cortex/white matter boundary (FA<0.15) were selected as seed points for probabilistic tractography [Anwander et al., 2007]. Tractogram similarity was computed as the normalized inner product between pairs of tracts. A bottom-up agglomerative hierarchical tree was generated for each hemisphere [Moreno-Dominguez et al., 2012] (see Fig. 1).
- As a new initial processing step, individual seed points were combined into a set of 5000 meta-leaves. For each dataset comparison, these meta-leaves are matched between trees based on their mean tractograms [Moreno-Dominguez et al., 2012], and cophenetic correlation [Farris et al. 1969] and triples methods [Critchlow et al. 1996] are used to assess dendrogram similarity. To estimate the global matching quality the average tractogram similarity between all matched meta-leaves was computed.
- In order to search for relevant partitions within the tree of a single subject, a top-down partition search algorithm was coupled to a Spread vs. Separation (*SS*) partition quality coefficient. This measure tests for average within-cluster spread against inter-cluster distance. As a result, an optimal partition is obtained for each granularity level.

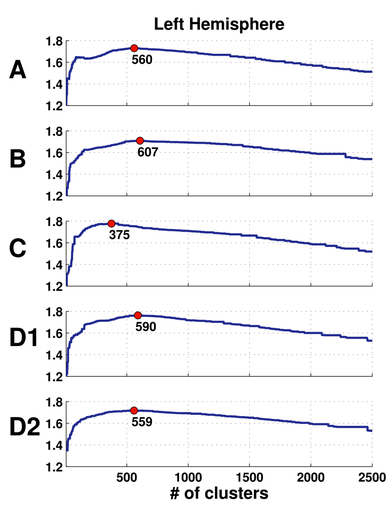
1



Schematic of the hierarchical clustering process.

Results

2



Plot of *SS* partition quality index at each granularity level from the left hemisphere of the 5 datasets, showing their maximum values (left). Partitions corresponding to the maximum points in Fig. 2-left (right): the top subpanels show the whole brain parcellation, the bottom subpanels zoom into the superior temporal gyrus area and the precentral gyrus. (only A-B-C and D1-D2 are color-matched).

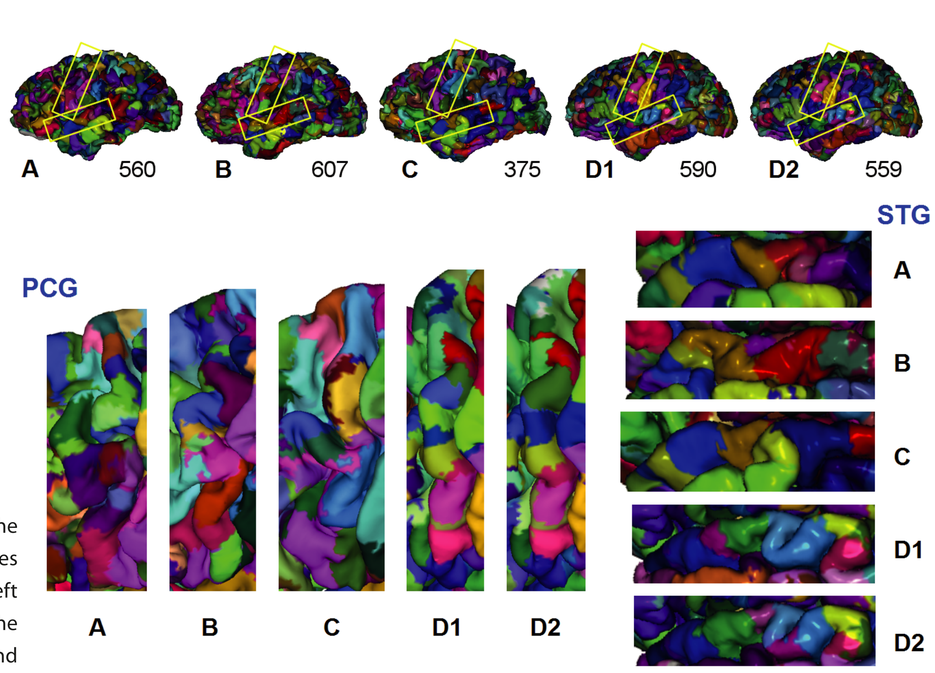
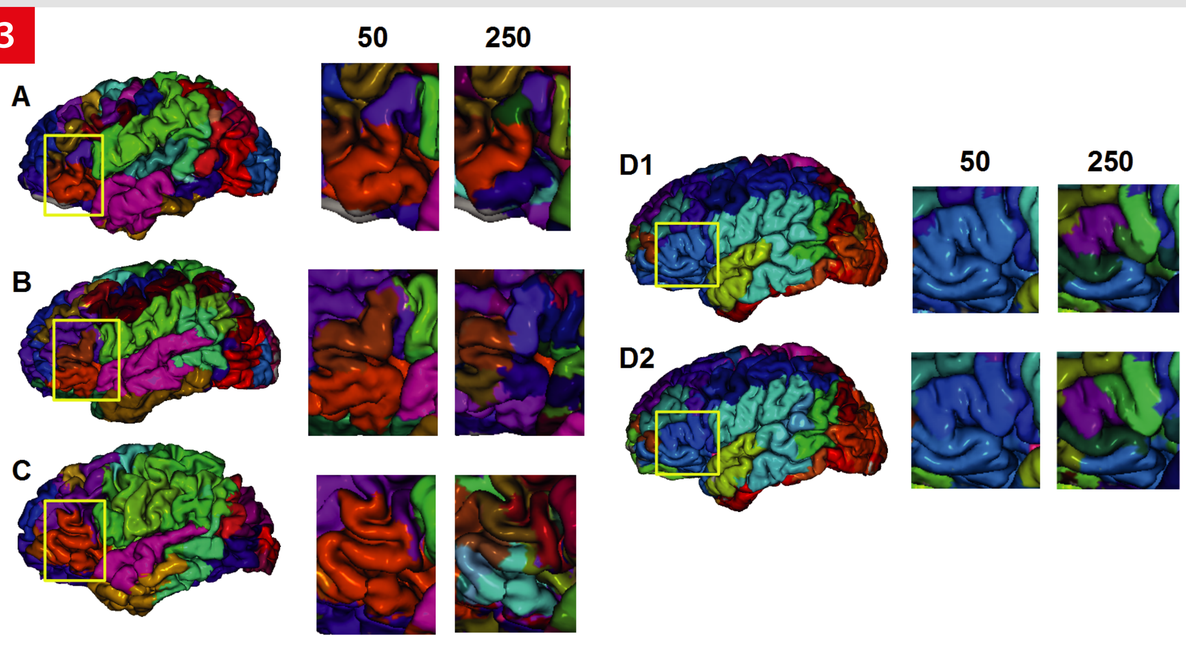


Figure 2 shows the dependence of partition quality from granularity level (Fig. 2, left), It can be seen that for small numbers of clusters the index rises steeply, meaning that in this range further subdivision usually leads to much better parcellations. At 50-100 clusters the increase turns much more moderate until a maximum value is reached at about 200-600 clusters. The partition with highest quality value for each dataset is shown projected onto the cortical surface (Fig. 2, right).

Figure 3 shows for the left inferior frontal gyrus (IFG), how the local granularity level depends on the global number of clusters in different subjects. It also shows high reproducibility in repeated measurements.

Connectivity similarity values were obtained for the different combinations of the obtained datasets and plotted against their matching quality (Fig. 4). Cophenetic correlation proves more stable against noise than the triples counterpart and within-subject comparisons show much higher similarity values and matching quality.

3

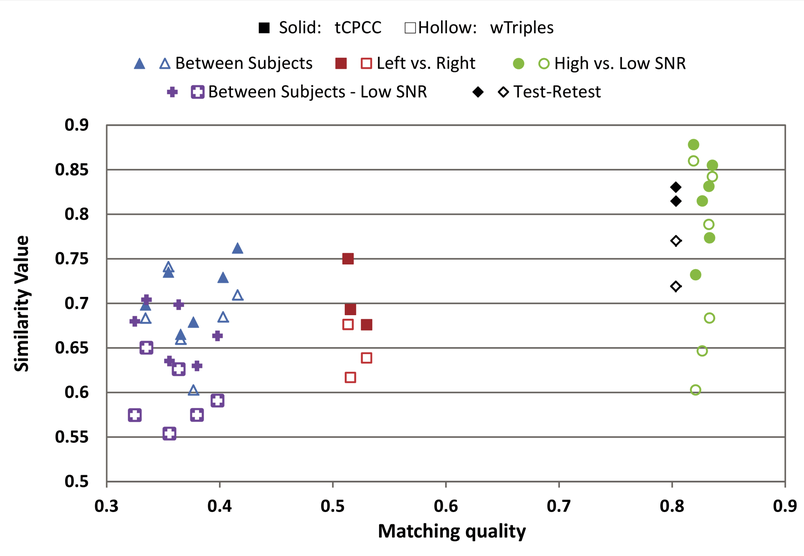


Subdivision of the IFG using the *SS* method at two different levels of granularity, for the left hemispheres of subjects A, B, and C (left), as well as the two acquisitions of subject D (right). (only A-B-C and D1-D2 are color-matched).

4

Tree cophenetic correlation (*tCPCC*) and weighted triples (*wTriples*) similarities between different tree pairs:

- High [resp. low] SNR measurements of the same hemisphere from different subjects (blue triangles [resp. violet crosses]).
- Left vs. right hemispheres of the same subject (red squares).
- Repeated measurements of the same subject and hemisphere (black diamonds).
- High vs. low SNR datasets of the same subject and hemisphere (green circles).



Discussion

We use a previously presented technique for hierarchical parcellation of the cortical surface based on connectivity and expand the method in several important ways. First, we improved the preprocessing so that the resulting trees are much more simple and easy to interpret, without significant loss of information. Second, we offer a way to extract relevant partitions from the tree using a top-down search algorithm and a partition quality measure, which shows a relevant range between 50 and 600 clusters. Third, we present a technique that enables better matching of dendrograms across data sets and comparison of all the similarity information encoded in them. The challenges remain to improve selection of relevant granularities and quality of dendrogram matching.

References

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Acknowledgements

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