Assembling the large-scale human connectome: How do we partition the brain?

Etay Ziv[1], Olga Tymofiyeva[1], Christopher P Hess[1], Donna M Ferriero[2], A James Barkovich[1], and Duan Xu[1]

[1]*Department of Radiology & Biomedical Imaging, UCSF, San Francisco, CA, United States,* [2]*Department of Pediatrics, UCSF, San Francisco, CA, United States*

Introduction. Structural connectivity networks derived from diffusion MRI [1] vary with choice of brain parcellation. In adults, parcellation and subsequent assembly of the large-scale human connectome relies heavily on brain atlases. However, in the context of the rapidly developing pediatric brain, such approaches introduce problematic biases. Here we present a network-driven brain parcellation that does not rely on brain atlases and propose a method to define the optimal number and size of nodes.

Methods. Diffusion MRI was performed on 10 term-born babies at the age of six months who had transient encephalopathy at birth, but no evidence of brain injury and good neurological outcome. The babies were scanned on a 3T GE EXCITE MR scanner using SE EPI with a FOV=24 cm, 128x128 matrix, min TE, 30 directions, b-value=700 s/mm^2. To construct structural networks, the following steps were performed.

- Tensor-based reconstruction and deterministic whole-brain streamline fiber tractography was undertaken using standard techniques (Diffusion Toolkit [2]).
- The subcortical surface was extracted and all fiber tract connections that go through this surface were recorded, resulting in an all-to-all voxel-wise adjacency matrix ("dense connectome").
- The subcortical surface was partitioned into a broad range of nodes (N = 10, 40, 100, 500, 1000, 2000, 3000, 4000, 5000, 6000, 7000, 8000, 9000, 10000 and 20000) based on Recursive Zonal Equal Area Sphere Partitioning [3]. This approach differs from template-based techniques and can better address variable anatomy (e.g. developing brain). Corresponding adjacency matrices were calculated by adding and recombining the dense connectome entries.
- For each parcellation, all of the connected components were enumerated by identifying a spanning tree of each component using a depth-first search algorithm. The *giant component* was defined as the largest connected component for a given network at a given parcellation [4].

Results. Fig. 1 illustrates giant components at different parcellations (N=40, 100, 1000 and 3000) mapped onto the brain surface for a typical subject. Fig. 2 shows a representative example of the dependence of the size of the giant component on the parcellation size. Assuming all cortical areas of the brain are connected and no part of the brain is structurally isolated, the optimal parcellation can be defined as the finest parcellation that still represents the whole brain. That is, the point where the size of the giant component starts to deviate from the number of total nodes. In our cohort of 6-month old babies and with given acquisition and tractography parameters, the optimal number of nodes was 100 and consistent across the entire cohort.

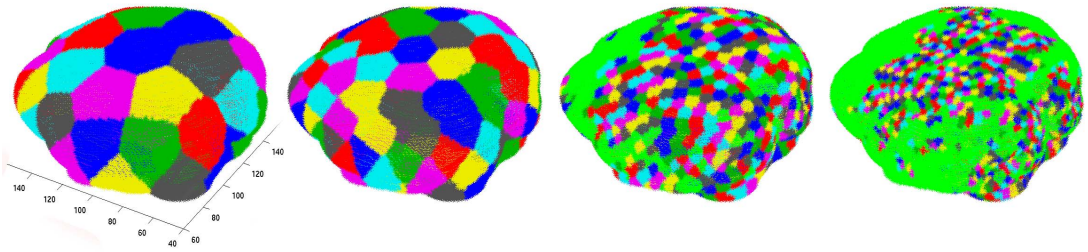

Fig. 1

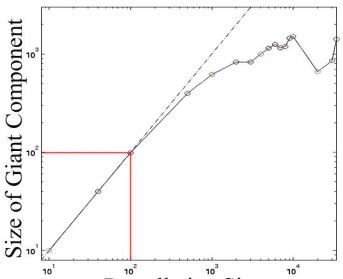

Fig. 2

Fig.1 Giant component mapped on the brain (N=40, 100, 1000, 3000). Fig.2 Dependence of the giant component on the parcellation.

Discussion. The proposed network-driven brain parcellation defines an unbiased, optimal number and size of nodes for a given population and set of acquisition and tractography parameters. The method does not presume any prior anatomic map; it begins with equal area sphere partitioning and then ultimately leads to an optimum directly derived from the data. The only inherent assumption made is that no regions of the brain are structurally isolated from the rest of the brain. The methodology is particularly useful in the context of developing brains where anatomical maps are both unknown and evolving. More broadly the approach should allow for a network-driven choice of node size and number for any cohort and thus facilitate a standardized analysis of brain networks.

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