Imaging the brain neuronal network with diffusion MRI: a way to understand its global architecture

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Introduction

Biological neuronal networks, and in particular the human brain, are remarkable natural systems capable of complicated patterns of behavior. To understand the emergence of higher level brain functions, the individual study of its components clearly seems insufficient. It is necessary to consider global properties of such complex systems. The backbone of complexity in the nervous system is composed by the large scale architectural characteristics of the neuronal network. We propose to study these properties by using DSI tractography. After having proposed a procedure to image the human long-range brain axonal network, we report on its small world and hierarchical architecture.

Material and Methods

We perform a whole brain study of a healthy volunteer on an Achieva 3T Philips scanner. We use a diffusion weighted EPI sequence following the parameters: TE/TI/delta = 3000/100/47.6/65 ms and b-max = 12000 mm^2/s. Q-space is sampled and the data reconstructed according to a standard DSI scheme [1]. The acquisition block was made of 32 slices of a 128x128 matrix with a spatial resolution of 2x2x3 mm^3. DSI tractography is performed as described in [2] by initiating fibers uniformly over the whole brain. As opposed to the classical procedure of tract selection using manually chosen ROIs, in the present experiment we choose the ROIs differently. We place a 3D grid over the brain image. This corresponds to covering the brain with lots of small ROIs of size 8x8x8 mm^3 in study 1 and 4x4x4 mm^3 in study 2. Furthermore we identify the brain Gray Matter (GM) by using a T1w based segmentation algorithm and actually consider as ROIs only the boxes that contain GM. We construct a graph where the vertices represent the set of ROIs defined above. A weighted edge between two vertices is drawn if there is at least one fiber that has its origin and termination in the pair of different ROIs. The edge weight corresponds to the connection density between ROIs: it is the ratio number of fibers / (their average length * cortical surface in the ROI). This graph represents the brain long-range axonal connectivity between small cortical areas, in study 1 made of 748 and in study 2 of 4522 cortex positions. Now, we construct an unweighted version of this graph by setting an arbitrary threshold on the weight of edges, and keeping only the strongest connections, whose weight exceeded this threshold; the resulting graph is denoted by Gbrain. This allows us to apply standard tools to study the large scale properties of the system. First, we test if the graph Gbrain is a small world, which is an important property of many complex networks [3]. The small-world feature of a graph is assessed from two metrics: average path length L and clustering coefficient C. L is the average number of hops between two randomly chosen nodes, and C captures the extent to which the network is clustered. As a reference point we take a random graph Grand with the same coefficient C. L is the average number of hops between two randomly chosen nodes, and C captures the coefficient C which is a unique technique that captures human brain connectivity at large scales and non invasively. Although there is a large resolution discrepancy between the true neuronal world and hierarchical architecture.

Results

By varying the size of ROI we have constructed brain graphs Gbrain of different sizes. In Tab. A, we present the average path length L and the clustering coefficient C obtained for the graphs with 748 and 4522 nodes. For both graph sizes, the average path length Lbrain is comparable with the average path length Lrand of its random graph equivalent, whereas the clustering coefficient is higher for the brain. More importantly, with increasing refinement of the measures (and hence the number of nodes), the ratio Cbrain/Crand increases significantly, enhancing the small world characteristic. The application of the hierarchical clustering algorithm results in a structure that can be nicely summarized by a dendrogram in Fig.B. If we read it from top to bottom, we first notice that there are two main clusters. They are separated by a large linkage distance and clearly correspond to the left and right hemispheres. Considering the right hemisphere first, we notice next that a separation occurs between fronto-temporal and parieto-occipital cortices, which means that, in terms of White Matter (WM) axonal connectivity, fronto-temporal as well as parieto-occipital intra-connectivity is intense as compared to the looser fronto-parietal, fronto-occipital or temporoparieto-occipital links (Fig C). Further decomposition of the lobes occurs into functionally significant areas. Similar decomposition occurs on the left hemisphere. Discussion

The current approach distinguishes itself from the standard tractography as it aims to study the global connective relationships between neuronal components and not the precise trajectories of specific links in 3D Euclidean space. Accordingly we combine conceptual models of neuronal networks with new brain measurement tools. The modeling part uses techniques provided by the fast growing field of complex networks, whereas the brain measurement tools are based on diffusion MRI, which is a unique technique that captures human brain connectivity at large scales and non invasively. Although there is a large resolution discrepancy between the true neuronal world and hierarchical architecture.

References