Fast-marching Tractography for Connection matrix (Fast-TraC)

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Introduction

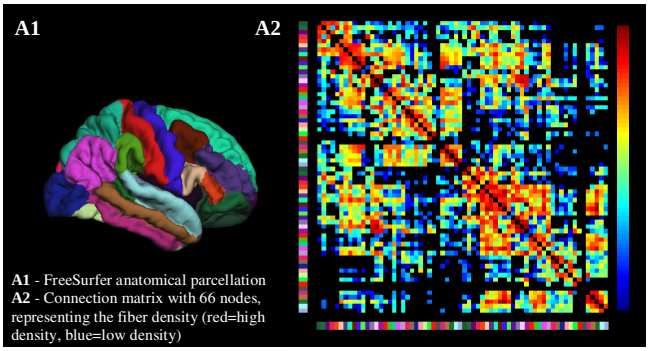
Although high angular resolution diffusion MRI techniques are able to solve multiple intra-voxel fiber orientations, the usual streamline Diffusion Spectrum Imaging (DSI) tractography algorithms present some limitations in their ability to map complex fiber-crossings in the brain white matter because they select locally only the most linear trajectories. Fast marching (FM) methods [1,2] have shown several advantages, such as the computation of a connectivity measure or their potential in resolving fiber branching. However, these techniques are currently limited to DTI, and thus have trouble solving fiber crossings. Moreover, like many probabilistic approaches they suffer from discretization. Furthermore, DSI [3] has shown its capacity to image multiple intra-voxel fiber directions. In this work, we present a fast marching tractography algorithm for DSI, called Fast-TraC, which 1) is able to efficiently address this issue, 2) creates fiber trajectories between 1000 small cortical ROIs covering the entire brain and 3) builds a whole brain connection matrix. We also see selected tracts that are accurately reconstructed.

Material and Methods

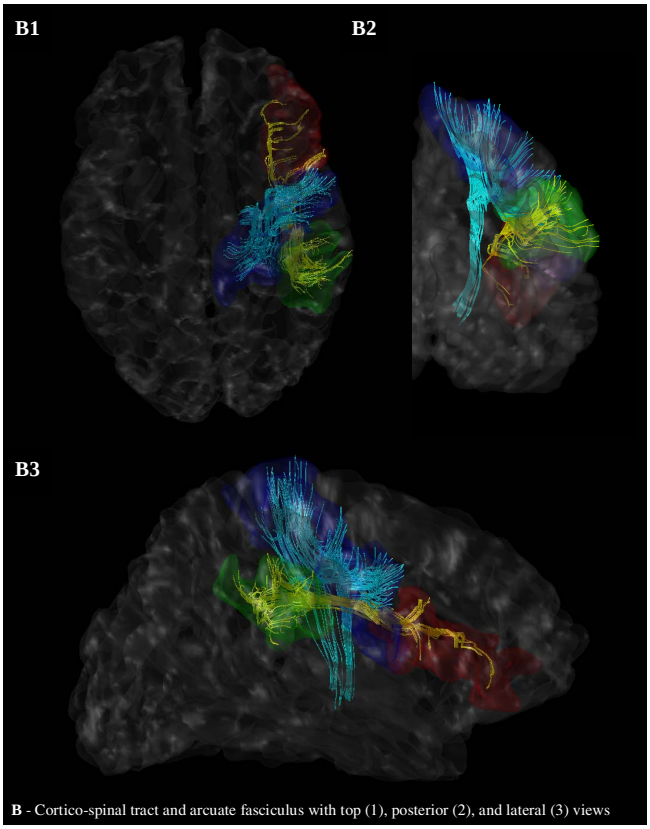
The MR diffusion images of a human brain are obtained on a healthy volunteer with an Achieva 3T Philips scanner, with a standard DSI scheme [4] using 257 encoding gradients (acquisition time 18 minutes). A diffusion weighted single shot EPI sequence is used with $TR/TE/\Delta/\delta$ = 3000/89/47.6/35 ms and b-max = 9000 mm^2/s. The acquisition block is made of 32 slices of a 128 x 128 matrix with a spatial resolution of 2 x 2 x 3 mm^3. In every brain voxel, the obtained 3D diffusion pdf is converted into an orientation distribution function, which is reduced into a set of unitary direction vectors corresponding to the local maxima of the diffusion pdf. Moreover, a high resolution T1w acquisition is used to define a mask of WM and the WM-GM interface. The WM-GM interface is partitioned into N=1000 ROIs with a unique number and Brodmann area identifier, using the technique described in [5]. Then, for every ROI fast marching tractography is performed as follows: (1) Starting from a given ROI and considering each voxel in the brain as a node of a graph, the Dijkstra algorithm [6] is used to compute the time of arrival T(**r**) at every position, as defined by Equ. 1, with **r** and **r'** the destination, respectively the origin voxel. F(**r**) is the propagation speed, defined by Equ.3, where $\mathbf{e_1}(\mathbf{r})$ is the direction vector (i.e. one of the local maxima of the diffusion pdf) the most collinear to **n**(**r**) in the voxel **r**. (2) From every voxel belonging to the WM-GM interface a fiber expands with a fixed step size in the direction $-\mathbf{e_1}(\mathbf{r})$, until it reaches the origin ROI. The connectivity metric is defined as the minimum propagation speed along the fiber. A threshold is then applied on this connectivity metric to keep only the most probable connections. Finally, we create a connection matrix, representing the network of structural connectivity.

$$1)\quad T(\mathbf{r}) = T(\mathbf{r}') + \frac{|\mathbf{r}-\mathbf{r}'|}{F(\mathbf{r})} \qquad 2)\quad \mathbf{n}(\mathbf{r}) = \frac{(\mathbf{r}-\mathbf{r}')}{|\mathbf{r}-\mathbf{r}'|}$$

$$3)\quad F(\mathbf{r}) = \frac{1}{1-\min(|\mathbf{e_1}(\mathbf{r})\cdot\mathbf{n}(\mathbf{r})|, |\mathbf{e_1}(\mathbf{r}')\cdot\mathbf{n}(\mathbf{r})|, |\mathbf{e_1}(\mathbf{r})\cdot\mathbf{e_1}(\mathbf{r}')|)}$$



A1 - FreeSurfer anatomical parcellation
A2 - Connection matrix with 66 nodes, representing the fiber density (red=high density, blue=low density)



B - Cortico-spinal tract and arcuate fasciculus with top (1), posterior (2), and lateral (3) views

Results

In Fig. A2, the connection matrix representing the fiber density has been mapped. To this purpose, the N=1000 ROIs have been organized in 66 regions, according to the standard FreeSurfer anatomical parcellation (Fig. A1). The upper left and lower right blocks of the matrix represent the connections of the right and left hemisphere respectively and the off-diagonal blocks map the inter-hemispheric connections. Fig. B represents examples of connections, namely, the cortico-spinal tract and the arcuate fasciculus, with top (1), posterior (2) and lateral (3) views. The cortico-spinal tract was defined by capturing fibers originating from the precentral gyrus (blue area) and running through the internal capsule. The arcuate fasciculus was selected by mapping the connections linking Broca (red) to Wernicke's (green) areas. We can see that the fibers constituting the cortico-spinal tract are widely distributed throughout the precentral gyrus.

Discussion

Although DSI is able to image multiple intra-voxel fiber directions, classical deterministic algorithms usually fail to accurately map all the paths that intermix in complex crossing areas such as the centrum semi-ovale. This is mainly due to the fact that the standard fiber generation model does not allow direction changes when a crossing area is reached. The Fast-TraC method presented in this work is unaffected by this issue, since the fibers always try to reach the desired ROI, even when an intersection occurs. Note that by using the local maxima of the diffusion pdf instead of the computed gradient to generate fibers, we obtain smoothed trajectories, thus less affected by discretization than with classical FM methods. Moreover, unlike deterministic algorithms, this methodology provides us with a measure of connectivity, that is the connectivity metric defined previously, for each pair of ROIs. We thus have a way to quantify the confidence we can have in the produced trajectories. It also allows us to map the connectivity of the brain to any desired level of complexity, by simply varying the threshold applied on the connectivity metric. The tests on the cortico-spinal tract and the arcuate fasciculus show that the Fast-TraC algorithm can accurately reconstruct the major pathways in the brain WM.

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