Statistical Fiber Tracking on DT-MRI data as a Potential Tool for Morphological Brain Studies

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Introduction:
The main potential of diffusion weighted MR imaging resides certainly in its capability to give information about nerve fiber tract orientation in the brain [1].
In order to isolate fiber tracts on a 3D tensor field, a specific algorithm is necessary. Deterministic as well as probabilistic approaches are possible. Modeling a nerve fiber tract as a smooth curve following the main directions of diffusion would be an example in the first case [2], whereas in the second case a stochastic process [3] is justified by the fact that the macroscopic description of water diffusion is done in probabilistic terms and the diffusion measured in a voxel is an average of many different sub-compartments. Here a combination of both approaches is implemented and is used to tackle a morphological question.
By means of a statistical study we explore the divergence of the nerve fiber tracts radiating from different positions on the sagital midline of the corpus callosum into the hemispheres.

Material and Methods:
The brain imaging was performed on a 1.5 Tesla Siemens Magnetom Symphony system with a standard 30mT/m field gradient. The images were acquired with a diffusion-weighted single-shot EPI sequence using the Siemens Diffusion Tensor Imaging Works-in-Progress Package. Imaging parameters were: TR=7200 s, TE=120 s, b=1000 s/mm^2, 10 time averaging, field of view 21 cm, acquisition matrix of 128x128x34 points with a resolution of 1.64x1.64x3.3 mm^3. Six linearly independent diffusion weighted gradient and one standard T2 acquisitions were used to build the tensor field according to the literature [4].
The algorithm of fiber tracking is based on a virtual particle random walk model. The particles are launched from a given position in the brain and travel according to a random experiment where the displacement probability function for each step is shaped in order to model the medium constraint that is the water diffusion information we get from the diffusion tensor MRI acquisition and the nerve fiber geometry constraint based on the hypothesis that nerve fiber-tracts follow smooth curves.
A way to implement these parameters is to try to find an optimal solution of the following fitness function [5]:

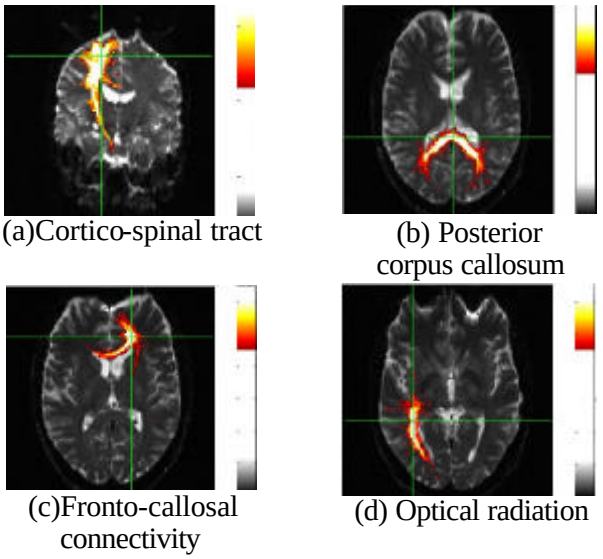
$$F\left(\mathbf{C}(q) \to \mathbf{C}(q')\right) = P_d\left(\mathbf{C}(q) \to \mathbf{C}(q')\right) \cdot P_k\left(\mathbf{C}(q) \to \mathbf{C}(q')\right).$$

$\mathbf{C}(q)$ is the parametric equation of the curve modeling the fiber tract, $P_d\left(\mathbf{C}(q) \to \mathbf{C}(q')\right)$ the probability that the particle diffuses from $\mathbf{C}(q)$ to $\mathbf{C}(q')$ and $P_k\left(\mathbf{C}(q) \to \mathbf{C}(q')\right)$ the tract curvature function meant to regularize its global shape.
In order to visualize these probabilistic data in a clinically sensible way, the connectivity maps are superimposed on anatomical slices. The color-coding varies from deep brown to white, passing by red and yellow. The brighter the color the higher the probability of the hit voxel to be connected with the seed point. Two orthogonal lines indicate the seed point.
In order to obtain a measure of the divergence of the fibers passing by a chosen point in the corpus callosum and spreading in both hemispheres, a parameterized plane of finite dimension is placed orthogonal to the particle main stream and at a distance defined as the mean distance the particles have traveled when passing through the center of the distribution. The particles that pass through the surface define a 2D probability density function (pdf) from which we can infer statistical information about the spreading of fiber-tracts. We can estimate the covariance matrix and imposing that the mean distance from the seed point to the plane is

the same and assuming the distribution to be Gaussian, we can compare two distributions and apply significance testing.

Results and Discussion:

The algorithm has been tested on several well-known anatomical structures, such as the cortico-spinal tract, the posterior corpus callosum, the fronto-callosal connections and the optical radiation. The random walk was chosen to be between 50 and 100 steps long according to the expected length of the tract. A good idea of the shape of the tract can already be obtained with a launch of 500 particles taking for a Matlab® routine a couple of minutes whereas for getting better defined tracts between one and two thousand particle launches are necessary. In the present study, where large tracts have been chosen, the algorithm showed a good match with known anatomy (Figure 1).



(a)Cortico-spinal tract (b) Posterior corpus callosum

(c)Fronto-callosal connectivity (d) Optical radiation

Figure 1.

In order to explore the spreading of the axon bundles in the corpus callosum, we made three experiments, choosing the most rostral, the mid and the most caudal part of the corpus callosum as seed points. In each case 2000 virtual particles were launched under the same constraints. The three corresponding parameterized planes were all placed at a same distance, as explained above, so that the particles that passed through the mean of the distribution travel an average of 15 steps.

In each case a covariance matrix of the distribution was estimated. It showed strong variation of spreading according to the location of the experiment. Rostral and caudal distributions where narrower and rotationally more symmetric than the one placed in the mid corpus callosum which fanned out antero-posteriorily (Figure 2).

Seed point	Variance along main axis (first eigenvalue of the covariance matrix)	Variance along second axis (second eigenvalue of the covariance matrix)
Rostral corpus callosum	21.0511	9.3993
Mid corpus callosum	33.8076	4.6223
Caudal corpus callosum	26.2553	12.4802

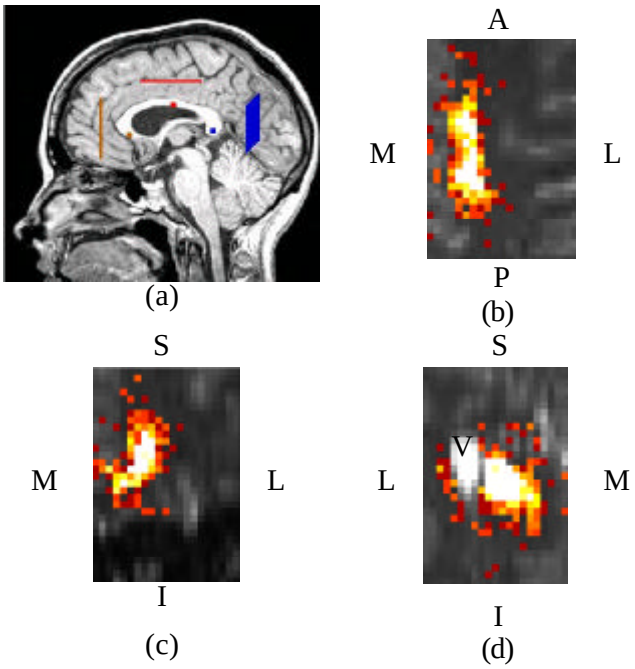


Figure 2: (a) The three small boxes are the seed points and the lines show the location of the corresponding planes and for each the bi-dimensional pdf is shown: (b) for the mid, (c) for the rostral and (d) for the caudal corpus callosum. The pdfs are color-coded and display the number of particles that passed the plane at a certain position. M=medial, L=lateral, P=posterior, A=anterior, S=superior, I=inferior, V=ventricle.

A test of homogeneity of covariance (Box's M test) was also performed. The M value had to be tested against the 5% critical value 7.8 provided by the χ^2_3 distribution. Since the M-values of the mid against the rostral (M=210) and of the mid against the caudal (M value = 251) corpus callosum are highly significant we conclude that the respective covariance matrices are not equal.

Conclusion:

Statistical reasoning is an attractive approach to an ill-defined problem such as fiber tracking in a discrete, noise-contaminated tensor field. Here it shows not only its capacity to segment large nerve fiber tracts but also opens a way for investigating clinical questions that in vivo techniques have not solved yet.

In our example of application, the probability density functions suggest that fibers passing by the mid corpus callosum fan out antero-posteriorly whereas the projections in the rostral and caudal corpus callosum form rather dense bundles. These differences in axon trajectories are most likely related to local differences in corpus callosum topography (e. g [6])

Reference:

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