Current State of Diffusion Simulation Based Tractography

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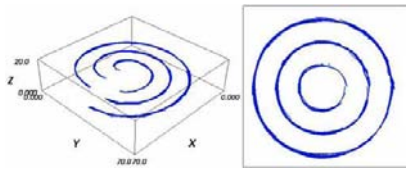
Introduction: Investigating neuronal connectivity in vivo by tracking fiber pathways on diffusion tensor magnetic resonance imaging (DTI) data sets is of interest for neuro-psychology or -surgery. Several fiber tracking methods were proposed for the reconstruction of neuronal fiber pathways [1]. Here we present the method of iterative diffusion simulation based tracking (DST) [2, 3]. This front propagating approach is based on the numerical simulation of the physical diffusion phenomenon, governed by the diffusion tensor obtained from DTI measurements. It is able to reconstruct fiber pathways more robustly in the presence of noise than standard techniques. This method can easily be adapted to more detailed diffusion models (for example higher order tensor descriptions) [3] which promise a more accurate diffusion representation and therefore better tracking results.

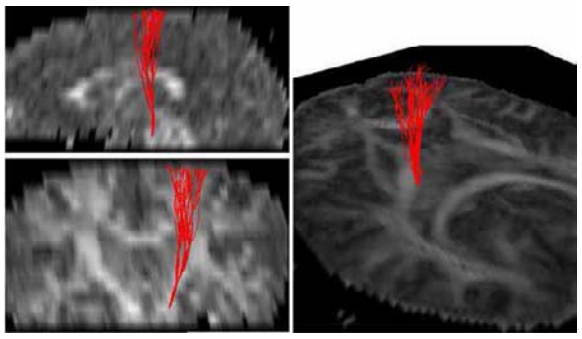
$$\frac{\partial C}{\partial t} = \nabla(D \cdot \nabla C) \qquad (1)$$

Methods: The reconstruction consists of two parts [2], a successive front propagation based on diffusion simulations, and the tract reconstruction. At first all voxels in the selected region of interest (ROI) are stored in a so-called seed queue. For each voxel in this queue, diffusion is simulated over a short period of time, by solving the diffusion equation (1). With D, the diffusion tensor from the DTI measurement, and C, the concentration. The position of the diffusion front at the end of the simulation is computed. For each voxel on the front, it is determined whether it meets all criteria for a valid tract point (smoothness, anisotropy, etc.). For valid voxels, the predecessor (seed of the diffusion simulation on whose front the voxel is situated) is stored and they are appended to the tail of the seed queue to be evaluated later. After all voxels in the queue have been processed the tracts are reconstructed using back propagation, allowing outward branching (seen from the ROI).

The implementation [2] only considered short diffusion times, for which the seed point can be connected to the front points by straight lines. To reduce the number of the computationally demanding diffusion simulations we have proposed the use of spatially more extended diffusion simulations [3]. The limiting case of just one simulation for tracking a fiber does not work in general due to principle limitations in the simulation. For the diffusion simulation results so-called time-of-arrival (TOA) maps are obtained. This is done by locating the diffusion front at the discrete diffusion time steps used in the simulation. The time stamp, when a voxel was flooded is stored in the TOA map. The tract, on the flooded region, is reconstructed by a gradient descend on the TOA map towards the diffusion seed. The end points of these tract pieces are appended to the seed queue. The reconstructed pieces are merged when the queue is emptied.

Results: The algorithm was tested on synthetic and real data. The synthetic data set consists of three single turn helical fiber bundles with radii of 30, 20 and 10mm on a 70x70x20mm grid with 1mm³ voxels. In the anisotropic voxels, on the tract, the principal eigenvalue is 2.5 times larger than the two minor eigenvalues. The anisotropic tensor and an isotropic one, to forge the background, were taken from a real DTI data set. The real data example was acquired on a healthy subject on a Siemens Magnetom Vision 1.5T scanner using a single shot echo planar imaging sequence TR = 15s; TE = 100ms; resolution: 96x128; plane orientation: transversal; Field of View: 240x240mm²; slice thickness: 5mm; number of slices: 16). The diffusion weighing in the 64 directions corresponded to the Stejskal-Tanner gradient scheme (b-factor ~1000s/mm²). Here the fiber pathway of the corticospinal tract was reconstructed from a starting voxel positioned approximately in the left portion of the base of the pons area.





Discussion: The DST approach was tested on synthetic and real DTI data and delivered promising results [2]. In the iterative approach [3] the dependence of tracking errors on the length of the reconstructed pieces in one simulation is currently beeing investigated.

The most time consuming element in both kinds of DST is the simulation step, if preprocessing time is tolerable, the reconstruction can by accelerated by the usage of look-up-tables (LUT). Such a table contains the simulation result for small equally sized sub-blocks of the data set, one for each voxel. To save storage space instead of the complete simulation results, the TOA map [3] or the diffusion front [2] can be stored and the entries corresponding to data points with low fractional anisotropy (here tracking would be terminated anyway) are eliminated. Tracking is than performed on the stored blocks. This is especially useful when more than one fiber population is to be investigated, since all needed simulations are only computed once. In the actual tracking process no diffusion simulation needs to be performed.

References: [1] S. Mori, P.C.M. van Zijl, *Fibertracking: principles and strategies - a technical review,* NMR Biomed **15:**468-480, 2002; [2] N. Kang, J. Zhang, E.S. Carlson, D. Gembris, *White matter fiber tractography via anisotropic diffusion simulation in the human brain,* IEEE Trans Med Imaging 24(9):1127-1137, 2005; [3] S. Mang, D. Gembris, R. Männer, *Tracking white matter fibers using time of arrival maps,* in proceedings ESMRMB, 2005;