# MDT Based Fiber Tracking in Complex Crossing Regions by Using a Spatial Point Process

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## INTRODUCTION

Fiber tractography based on diffusion weighted MRT is a powerful method to extract the anatomical connectivity in white matter *in vivo*. Usually, fitting a model to the diffusion weighted signal and the reconstruction of the fiber trajectory is done in separate steps. Using too simple models to describe the diffusion distribution, essential information might get lost especially in regions of fiber crossing. When more complex models such as the **M**ulti **D**iffusion **T**ensor (MDT) model is used, the result suffers often from numerical instability. In this paper we introduce a method for simultaneous fiber reconstruction and model fitting of the diffusion weighted signal. Thereby, fibers are approximated by tubes. Their volume fraction to the surrounding voxel is used to simulate the diffusion weighted signal in respect to the MDT model. The method is based on a spatial point process with a **R**eversal **J**ump **M**onte **C**arlo **M**arcov **C**hain (RJMCMC) dynamic. Using an appropriate annealing schedule, the global error term is minimized. The performance of this approach is shown in an example, where the projection fibers and association fibers are reconstructed in the area of the primary motor cortex. Medial-lateral, superior-inferior, and posterior-anterior directed fibers are crossing in this area.

## METHODS

The *in vivo* DTI-measurements were done on a Siemens 3T TIM Trio using a DW SE EPI sequence with automatic distortion correction [1], voxel size of 2x2x2mm$^3$, 61 diffusion-encoding directions, and an effective b-value of 1000 s/mm$^2$. Additional a 3D T1 MPRAGE dataset with a resolution of 1 mm$^3$ cubic was acquired.

The T1 weighted dataset was segmented in CSF, white matter, and gray matter and normalized to the MNI template by SPM5 [2]. The primary motor cortex M1 (Brodmann area 4) was extracted from an anatomical atlas using WFU PickAtlas Tool [3] and resliced to the coordinate system of the DTI-dataset. This mask was grown by 4mm in each direction and used as ROI M1 (red area in Fig 2) for fiber selection. Additionally, the cortical spinal tract near the third ventricle (CST in blue), the corpus callosum (CC in green), area of the frontal occipital fibers more ventral (FOV in magenta), and more dorsal (FOD in cyan) were marked by hand (Fig 2).

The method used for fiber tractography is related to the road tracking algorithm introduced in [4]. There, the roads are modeled by an interacting point process, the so called Candy Model. Line segments (marked points), which can be created, deleted, or moved in the images by random until they fit the road network. The different operations are done by a RJMCMC. Using an annealing procedure to sharpen the probability distribution a configuration with high probability is extracted.

The Candy Model was adapted to the problem of fiber tractography. Here, the basic elements were tubes with a fixed radius of 0.3mm. Around the endpoints of the tubes the **C**onnection **A**rea (CA) and a bigger **A**ttraction **A**rea (AA) were defined (see Fig 1 **A**). Additionally, single endpoints were predefined automatically at the transition between white and gray matter. The tubes can be in different states (see Fig1 **B**): If an endpoint of a tube is inside the CA of an other tube, they are *connected*. A connected endpoint is *ill connected* if the angle of two connected tubes is too sharp (> 60°) or if a third tube is involved. The following proposal kernels were implemented as RJMCMC dynamics: Birth, death, and move of a single or respectively a connected tube, connect of two non-connected endpoints inside the AA, and break of two connected tubes. For each voxel $x$ the volume fraction $f_{x,k}$ of the tube $k$ was calculated. The error between the model and the data was determined by the MDT according to [5]. Thereby, for each tube the diffusion weighted signal was simulated with a given diffusion distribution. The mean error between the measured signal and the simulated signal of the MDT was summed over all voxel and used as error function *err*. The total unnormalized probability of the model was defined according to the Gibbs process [4]:

$$P(\theta) \sim \beta^{n(\theta)} \left[\exp\left(-err(\theta, X) - w_f n_f(\theta) - w_s n_s(\theta) - w_v n_v(\theta)\right)\right]^{1/T}$$

Thereby $\theta$ is the current configuration of the network. $n$, $n_f$, $n_s$, and $n_v$ are functions calculating the number of total, non-connected, single connected and ill connected tubes. $\beta$ defines the intensity of the underlying Poisson process and was set to 0.19. The weights $w_f$, $w_s$, and $w_v$ influence the different penalty terms and were set to 2.2, 1, and 1.5. $T$ defines the temperature of the system and is used for the annealing procedure ($T_0$= $10^4$ and $T_N$= $10^{-5}$ with a logarithmic schedule). The diffusion distribution was chosen according to the splenium with an FA-index of 0.86. To reduce calculation time, only a section of the dataset was used for the fiber reconstruction (see Fig 2). The temperature schedule of the annealing procedure was chosen to reach the final temperature $T_N$ after 800*10$^6$ iterations (took about 5 days on a standard PC). Projecting fibers going from ROI M1 to CST (see Fig 3 in blue), associating fibers running from ROI M1 to CC (in red), and fibers in occipital frontal direction running from ROI FOF and FOH (in green) were selected.

## RESULTS AND DISCUSSION

The introduced method was able to reconstruct fibers running in three different directions through the crossing region (see Fig 3). There are several additional advantages by using this method: The combined evaluation of fitting the MDT model and reconstruction of the underlying fiber trajectories leads to a higher numerical stability. Additionally, by maximizing the global probability of the model this method is more robust against local artifacts. Further, the used framework is very flexible and allows further non-linear a priori constraints. Compared to classical streamline approaches like the FACT algorithm the number of fibers connecting two areas is related to the degree of connectivity. But still the accuracy and the dependences to the parameters have to be investigated and verified.

For clinical application shorter calculation time is required. However, the underlying method is highly parallelizable and the parameters of the annealing schedule are still not optimized. Therefore, it should be possible to calculate the fibers of the full brain in approximately one day. Even though the method is in the state of an early feasibility study the approach showed the ability to reconstruct fibers in complex crossing regions without extensively searching of proper parameters and without interpolation or strong a priori constraints.

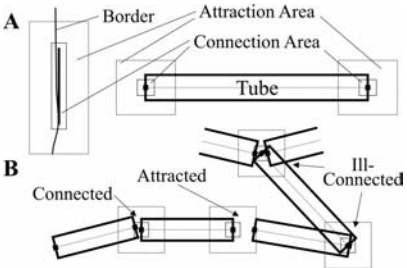


Fig 1: **A** the basic elements of the fibers are shown. The lower image **B** shows the different possible interactions and configurations.

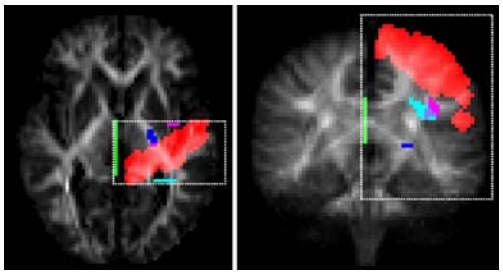

Fig 2: Projected visualization of the ROIs. The rectangle marks the tracked area. The projection of the ROI M1 is colored in red, CST in blue, CC in green, FOV in cyan, and FOD in magenta.

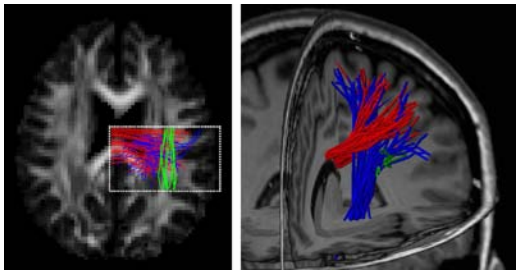

Fig 3: The reconstructed fibers bundles. Projection fibers connecting CST with M1 in blue, association fibers connecting M1 and CC in red, and fibers running in occipital frontal direction in green.

## REFERENCE

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