Free-Spin Tracking: A Novel Global Tractography Algorithm

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Introduction

Diffusion MRI [1] and fiber tractography have become a reference to study the neural structure of the brain white matter. Standard tractography algorithms behave generally locally, i.e., a single fiber is initiated at a seed point and is constructed iteratively, thus making fibers subject to cumulative errors. On the contrary, in global approaches the entire white matter is tracked at once: in case of an ambiguity within a voxel, several fiber contributions coming from the entire volume can help choose the correct neural pathway. Global approaches have been proposed recently, such as the Gibbs tracking [2], which is an analogy to polymer creation in chemistry: pieces of fibers arrange themselves to minimize the resemblance between the simulated and real diffusion-weighted images (DWI). Although such approach is a very promising alternative to the standard techniques, it appears to be computationally expensive and uses the raw DWI instead of a diffusion model like the tensor [1]. Raw DWI are subject to MR noise, and model fitting can help remove this noise [3] and yields a good compression of the signal, which is important to speed up computation. Another global approach was proposed by Cointepas et al. [4], where fibers are obtained by optimizing a spin field. A spin represents a piece of fiber of unit length which tends to align along the more probable fiber direction (e.g., the main tensor eigenvector), while associating with other spins such that the curvature of the fiber joining them is minimal. Such approach is appealing because: 1. it relies on the only prior that brain fibers have a low curvature, and 2. each fiber can be optimized independently from the others making the parallelization of the algorithm straightforward. However, the proposed model has severe limitations: only one spin per voxel was placed, which assumes only one fiber contribution per voxel (which is not true inside crossings), and spin position was fixed which may lead to a non-optimal sampling of the fibers. In this work, we propose to liberate the spins so that they are free to move, and that their number within a region (like a voxel) is driven by the data by allowing the creation, or birth, of new spins. We show that even diffusion tensors can be used to successfully reconstruct fiber crossings and kissings at a reasonable computational cost.

Methods

An initial spin field is randomly generated. Given a spin, its orientation separates the space into two spin sets: those which are backward, or behind it, and those which are forward, or in front of it. The key idea of the algorithm is to associate to each spin a unique forward and backward spin, such that the curvature of the fiber joining them is minimal. If no forward or backward candidate is found, or candidates lead to a too high curvature, no association is made. This first step produces a set of fiber branches possibly ending within the white matter (Fig. 1 a b). The second step consists in optimizing every spin of each branch, such that: 1. curvature between backward and forward spins is kept minimal, and 2. spin orientation fits the diffusion data (e.g., in case of diffusion tensors, spins tend to align with the main tensor eigenvector). Thus, there is a competition between a data attachment term (fidelity to the diffusion data), and an alignment term (minimization of the fiber curvature). This last energy acts as a regularization term: within a branch, each spin will receive a contribution from its direct neighbors, themselves receiving contributions from their neighbors, etc. Doing so, we implicitly model fibers as Markov chains. In other words, all spins have influence on all spins in a branch, which make the overall algorithm robust to noise by essence. Note that as spins are allowed to move, they are able to perfectly align themselves (Fig. 1 a versus c). Third, spin association is performed again to merge the fiber branches which end inside the white matter (branches that go outside the white matter are detected as such and will not be further associated: fibers are thus ensured to start and end at the interface of the grey-white matter). If no candidate branch is found, we allow the birth of new spins. This process permits to generate spins when missing in regions where many fibers can be found, such as crossings. The whole process is iterated until convergence (no more spin/branch association, and no fiber ending inside the white matter) (Fig. 1 e f). This method can also be described as follows: each fiber branch optimizes itself and grows independently of the others until it merges with another branch or it reaches the grey-white matter interface. The contribution of several pieces of fibers in crossing regions helps reconstruct the correct neural pathway.

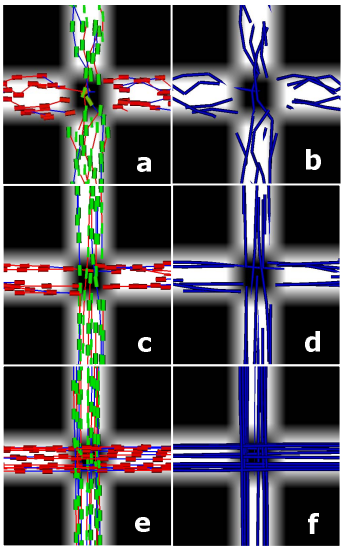

Fig 1. Experiments on a synthetic fiber crossing. Spins are represented by small cylinders. **a - b)** 1st iteration. **c-d)** 2nd iteration: the fiber branches have aligned themselves, but some of them are interrupted. **e-f)** Final result. The fiber crossing was properly reconstructed.

Results and Discussion

Experiments were done on two phantoms representing respectively a 90° crossing and a kissing. Phantoms were elaborated with hydrophobic fibers strongly tightened with a medium and immersed in a solution of water doped with gadolinium [5]. Acquisitions were done on a Signa excite II 1.5T MRI scanner (GE Healthcare, Milwaukee) equipped with a 40mT/m gradient coil and an 8 channel head coil (compensation for Eddy currents to the first order was done). For the 90° crossing, a b-value of 2000s.mm^{-2} and 4000 directions were used. Image size is 32x32x1 and resolution is 10x10x14mm. Results are presented in Fig. 2 a b c (70 iterations were required for a computational time of 1 hour on a 2GHz PC). For the kissing phantom, a b-value of 1500s.mm^{-2} and 200 directions were used. Image size is: 128x128x20 and resolution: 1.8x1.8x3mm. Results are shown in Fig 2 d e f (70 iterations, computational time of 12 hours). Our method was successful to reconstruct both crossing and kissing using diffusion tensors only. It shows that a proper tractography algorithm can push away the limits of a simple model like the tensor. However, one cannot correctly recover crossing fibers with low angular differences (45° or less) using tensors. For this reason, we are currently updating the algorithm to use the fiber ODF model, which was proved to have a much better angular resolution [6]. In the mean time, experiments on real datasets are underway, and a parallelized version of the algorithm running on a PC cluster is being developed, to make it compatible with clinical constraints.

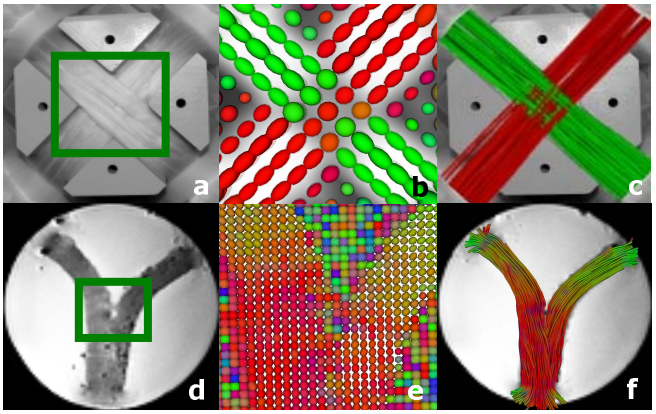

Fig 2. Evaluation of the algorithm on phantoms. **a)** The crossing phantom. **b)** Close-up of the diffusion tensor field inside the green square in a. **c)** Final result (70 iterations, ~1 hour on a regular PC). **e)** The kissing phantom (T2 image). **f)** Tensor field contained in the green square in e. **f)** Final result (70 iterations, 12 hours).

References

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