Depicting axon fibers on a diffusion phantom by means of hybrid DBF-DT data

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Abstract. Diffusion weighted magnetic resonance imaging is widely used to study the structure of the fiber pathways of brain white matter. We present our automatic reconstruction and tractography methods and the results obtained for the "Fiber Cup 2009" contest phantom. We fit the classic Diffusion Tensor which is a plausible model for voxels containing a single axon bundle and also the Diffusion Basis Function model which is capable to detect bundle crossings. Our tractography stage uses information of both reconstruction methods in order to improve the results.

1 Introduction

The most widely-used approach for studying water diffusion in the human brain is Diffusion Tensor imaging (DTI) [1], where the diffusion tensor's (DT) main eigenvector corresponds to the axis of maximum diffusion. In white matter, the main eigenvector is aligned with the local average orientation of the fibers, making it possible to study brain connectivity patterns *in-vivo*. The chief limitation of DTI is that the DT is constrained to represent only one maximum diffusion orientation and thus it is inadequate in voxels where two or more fiber bundles cross, split or "kiss" [2]. This limitation represents a significant problem for diffusion tractography, where we must rely on local fiber–orientation estimates for reconstructing fiber pathways. According to recent studies, as many as one third of white-matter voxels contain more than one fiber bundle orientation. A more plausible model for solving intra-voxel fiber orientations is the Gaussian Mixture Model (GMM) or multi–DT [3] by assuming no exchange between fibers, i.e. each bundle signal is independently added.

In this work we present our fiber tracking results for the diffusion phantom proposed in [4]. We fitted DT and multi-DT models and then we use their directional information in our tractography stage, as is explained in the following section.

2 Methods

Volume selection and image preprocessing. We selected the volume with $b = 1500$ value which allows to depict fiber crossings and also presents a higher SNR w.r.t. higher b values. We also selected the $3{\times}3{\times}3$ mm voxel size volume in which the partial volume problem is lower w.r.t. the $6{\times}6{\times}6$ one. We visually inspected the volumes and we did not notice a significant eddy-current effect. Thus, in this case we decide not to apply a co–registration process to the raw images, avoiding in this way an unnecessary smoothing effect which could destroy anatomical information. Our results are presented within a binary activity mask computed by thresholding all voxels with B0 value bigger than 100.

Diffusion Tensor Fitting. We fitted the DT model to the raw data over the averaged B0 and 64 Diffusion Weighted (DW) orientations. We used home–made software running on Matlab$^{\text{TM}}$which solves the linearized DT observation model [1]. Not additional constraints were enforced (e.g., about the positive–definite tensor feature). Expectral decomposition was applied in order to compute the DT's Principal Diffusion Direction (PDD).

DBF Fitting. In [3] the authors proposed a Diffusion Basis Functions (DBF) observation model that is capable to resolve bundle crossings and bifurcations. They simplified the fitting of GMM by using a fixed tensor basis $\bar{\mathbf{T}}_k$, ($k = 1,\ldots,M$, with M large). Thus, the j–th DBF is pre–computed as the DW–MRI signal due to a single fiber (modeled by the fixed basis tensor $\bar{\mathbf{T}}_j$), thus the unknowns are the mixture contribution of each signal. This model is fitted by solving a linear system of equations and it is stable for recovering more than two fiber orientations per voxel. The recovered orientations are discrete, so that, an small angular error is present. We fitted the DBF model to the raw data over the averaged B0+64DW orientations by using the fast Matlab$^{\text{TM}}$NNLS routine. We only took into account at most the two biggest tensors per voxel.

Tractography. Our tractography method is defined as follows:

1. Our depicted tracks $\{p_0,\ldots,p_N\}$ (with spatial positions $p_i = [x_i, y_i, z_i]$) follow the PDD of the DT or the multi-PDD obtained by means of DBF method.
2. Given a seed position p_0, we started a track for the negative and positive direction (unit vectors d_0 and $-d_0$) of the PDD of the multi tensor recovered at p_0 with the biggest contribution, i.e. with the biggest size compartment.
3. All the displacements inside a voxel were directed by the selected direction d_i, i.e. no data interpolation on neighboring voxels was performed.
4. We constrained all positions p_i along the track to be inside the binary activity mask (described above): the tracking was stopped when a walk reached a position outside this mask. We also forced all our tracks to be inside the available slices: positions which reached an slice above or below the three available slices (that is to say $z_i < 1$ or $z_i > 3$) were sent them back to the slice of the previous position $z_i = z_{i-1}$.

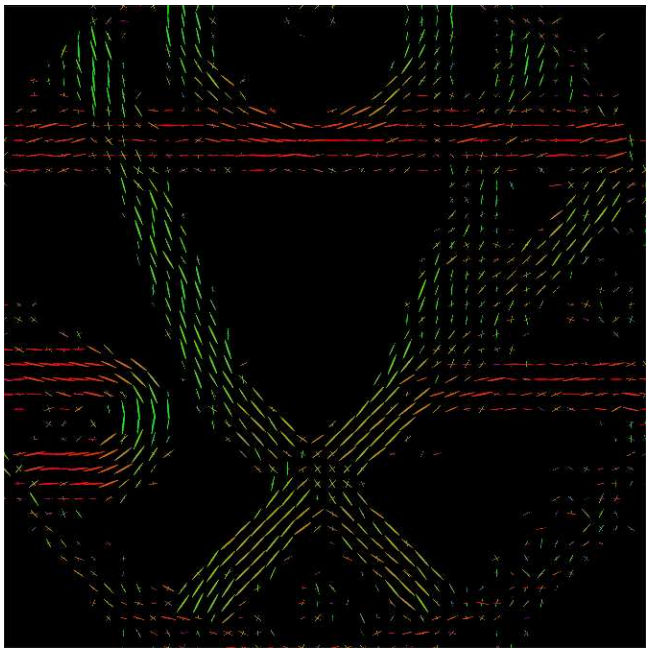

Fig. 1. Recovered multi-DT field for slice # 1 (bottom) on the DTITK viewer.

5. Bends in trajectories were constrained to be smaller than 78^o, otherwise the tracking was stopped.
6. Given a track position p_i, the next PDD to follow was selected in a deterministic way. When the multi–DT solution presented evidence of a voxel containing a single DT (when the size compartment of the biggest multi-DT was bigger than twice of the size compartment of the second one, or, when the Multi-DT solution is composed of a single DT) we dropped off the multi-DT solution and we used instead the DT one. The strategy above was applied in order to improve the orientation estimation (it is well known that, for the single bundle case, the DT orientation is more reliable). For the multi-DT case, we selected the next direction as the PDD with biggest dot product with previous direction (the closest direction).
7. The next position was computed as $p_{i+1} = p_i + \delta\hat{d}_{i+1}$ where $\hat{d}_{i+1} = \alpha\hat{d}_i + (1-\alpha)d_i$ and $\hat{d}_0 = d_0$, which promotes smooth trajectories by weighting the new direction and the past one. For all tracks we used step size $\delta = 1$ and $\alpha = 0.028$, which certainly indicates that, for this case, almost only the new direction was took into account.

3 Results and Conclusions

Figure 1 shows our multi-DT field, we notice how the presumed regions containing crossings present more than a single tensor. Figure 2 shows our recovered

bundle trajectories. As one can see, the DBF solution recovered multi-DT solutions at places where it is likely to find crossings and bifurcations. With respect to the computed tractography, we recovered some plausible long tracks with crossings and bifurcations, but the performance is not good for tracks started on the boundaries of structures.

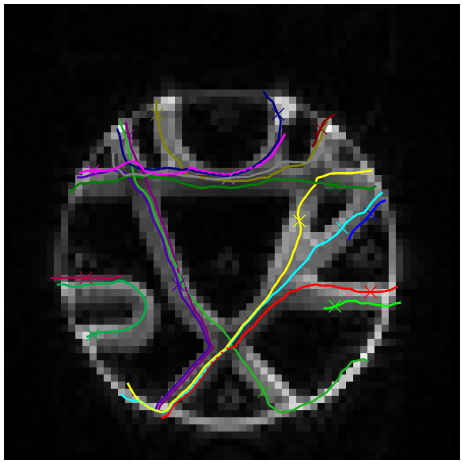

Fig. 2. Fully automatic recovered bundle trajectories overlapped on B0 image, the × marks indicate the starting positions. REMARK: All trajectories were recovered with the same set of parameters.

References

1. Basser, P.J., Pierpaoli, C.: Microstructural and physiological features of tissues elucidated by quantitative-diffusion-tensor MRI. J. Magn. Reson. B **111** (1996) 209–219
2. Alexander, D.C.: An introduction to computational diffusion MRI: the diffusion tensor and beyond. In Weickert, J., Hagen, H., eds.: Visualization and Image Processing of Tensor Fields. Springer, Berlin (2005)
3. Ramirez-Manzanares, A., Rivera, M., Vemuri, B.C., Carney, P., Mareci, T.: Diffusion basis functions decomposition for estimating white matter intravoxel fiber geometry. IEEE Trans. Med. Imag. **26**(8) (2007) 1091–1102
4. Poupon, C., Rieul, B., Kezele, I., Perrin, M., Poupon, F., Mangin, J.F.: New diffusion phantoms dedicated to the study and validation of high-angular-resolution diffusion imaging (hardi) models. Magn. Reson. Med. **60**(6) (Dec 2008) 1276–83