Paper E

Two-tensor Fiber Tractography

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TWO-TENSOR FIBER TRACTOGRAPHY

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ABSTRACT

Estimating white matter fiber pathways from a diffusion tensor MRI dataset has many important applications in medical research. However, the standard approach of performing tracking on single-tensor estimates per voxel is confounded by regions of multiple pathways in different directions. Building on previous work for estimating multiple tensors from MR value partitioning, we present here a *two-tensor fiber tractography* method that estimates two tensors from the acquired MR values, interpolated at each step of the path, and follows the tensor most aligned with the current direction. The method is verified on a synthetic dataset and applied to two locations of fiber crossing in an in vivo diffusion MRI.

Index Terms— Diffusion tensors, fiber tractography, multiple-tensor estimation, fiber crossing

1. INTRODUCTION

Two of the major applications of Diffusion Tensor Magnetic Resonance Imaging (DTI) in the central nervous system are in fiber tractography and quantitative white matter analysis. In white matter tractography, the shape of the anisotropic diffusion tensor is used to delineate fiber tract direction, and trace brain connections. The DTI technique has raised hopes in the neuroscience community for a better understanding of the fiber tract anatomy of the human brain.

Upon inspection of histology, however, much of the white matter in primates is composed of multiple interdigitating fiber bundles. DTI fits the average diffusion in the voxel but on the spatial scale of MRI, many voxels will contain more than one main fiber direction. Fitting diffusion data from heterogeneous white matter voxels to a single tensor can lead to errors in both the assessment of white matter tract disruption and the computed tract direction.

One approach to resolving crossing tracts is to fit two tensors to the diffusion data. Tuch et al. [1] was able, with some constraints, to solve for two diffusion tensors in an multitensor extension of the Stejskal-Tanner equations (presented in equation (2)) by applying a conjugate gradient algorithm to high-angular resolution acquisitions (HARDI). This model is also examined in [2, 3] to analyze partial voluming effects. Peled et al. [4] solves the same set of equations more efficiently by examining the disc-shape of a single-tensor fit. Using the plane of this disc as well as an assumption of cylindrically symmetric diffusion, the number of unknowns can be greatly reduced and the equations solved using a non-linear least-squares minimization algorithm. In Refs. [5, 6] diffusion spectrum and q-ball imaging is examined. This approach can be considered model free in the sense that the 3D Fourier transform of the samples are estimated directly on the sphere yielding a orientation distribution function (ODF) describing the diffusion.

Various methods have been proposed to use DTI data to visualize the anatomy of fiber pathways and derive connectivity between different parts of the brain in vivo [7]. A simple and effective method for tracking nerve fibers using DTI is to follow the direction of the maximum diffusion in each voxel, equivalent to the direction of the main eigenvector in each tensor. This method is usually referred to as tracking using the Principal Diffusion Direction (PDD).

Alternatives to PDD tracking methods have been explored. Among them are "front propagation" methods (also commonly referred to as "fast marching" techniques) which are designed to be less sensitive to local noise [8, 9].

In Ref. [10] tracking is performed by extracting a PDD as the direction of the maximum of the ODF. This tracking algorithm is thus very similar to traditional single-tensor PDD tracking although termination criteria are not discussed. Behrens et al. [11] pioneered a method where the probability density function of the local fiber orientation is derived in a Bayesian framework, later extended by Friman et al. [12]. Ref. [13] relates this probabilistic diffusion tractography to the case of multiple fiber orientations. In Ref. [10] an ODF is approximated voxelwise by the q-ball [6], and this ODF is reduced to a set of tensors capturing multiple crossing fiber-bundles.

Another approach to resolve multiple orientations is to explicitly model multiple tensors. Ref. [14] describes a tractography algorithm that uses mixtures of two Gaussian densities in regions where the single Gaussian model is inadequate. Ref. [15] also uses a multi-tensor approach for analysis and tracking of complex fiber configurations using one isotropic and two anisotropic tensors to model the data.

In this work we present a tractography method based on our multiple-tensor estimation method presented in [16]. One advantage of the multiple tensor approach is that it allows

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a more meaningful termination criterion based on fractional anisotropy (FA) calculated for each direction independently. In the single tensor case, FA will be artificially low because of model mismatch.

2. METHODS

2.1. Multi-tensor estimation

The Stejskal-Tanner equation (1) describes the relationship between one diffusion tensor X and the measured MRI signals S_i

$$S_i = S_0 \exp(-br_i^T X r_i) \tag{1}$$

at a given position. However, sometimes the measured *S*-values are not well modeled by a single diffusion tensor due to the presence of multiple fiber bundle orientations.

To cope with this situation, the relationship between k tensors X_j and the measured S_i values is

$$S_{i} = S_{0} \sum_{j=1}^{k} f_{j} \exp(-br_{i}^{T} X_{j} r_{i})$$
(2)

where f_j are non-negative weights which sum to 1 for $j = 1, \dots, k$ and $i = 1, \dots, n$. This model can be solved using any method for multiple tensor estimation. Here we used the one in Ref. [16].

The multi-tensor estimation procedure in [16] is a weighted linear least-squares method. The k diffusion tensors are found by solving

$$\min_{x_j} \|W_j(Rx_j - d)\|_2^2 \tag{3}$$

when $j = 1, 2, \dots, k$ and where W_j is a diagonal 0-1 matrix so that $\sum_{j=1}^{k} W_j$ equals the identity matrix. In the two-tensor case the weights prescribe a partitioning of the samples into two distinct sets from each of which one tensor is estimated.

2.2. Two-tensor interpolation

Diffusion weighted images S are effectively discretized at a scanner specific resolution - the diffusion tensors are usually calculated at these discretized positions. Single tensor trilinear interpolation can then be done at a given position p by evaluating a weighted sum of neighboring tensors where the weights depend on the normalized distance from p to the neighboring voxels.

In the case of 2-tensor estimation this approach introduces a correspondence problem since the ordering of the pre-computed two diffusion tensors at each voxel may be arbitrary. For example, if at location p there are 8 neighboring voxels, then there are $2^8 = 256$ possible combinations for choosing which one of the two tensors at each voxel should be included in the 8 element weighted sum.

Because of this problem we have chosen to componentwise interpolate the diffusion weighted images S themselves. This gives n interpolated values \hat{S}_i at any location p to which the multi-tensor estimation procedure of the previous section can be applied.

2.3. Two-tensor fiber-tracking

The fiber-tracking is started from a given position p_0 . The *S*-values are interpolated at position p_0 and two diffusion tensors $X_1(p_0)$ and $X_2(p_0)$ are computed. The major eigenvectors $e_1(X_1)$ and $e_1(X_2)$ are estimated. Since p_0 is generally not a fiber endpoint, the initial tracking step must proceed along both the positive and negative of these directions to obtain the whole fibers.

An updated position p_1 is found for each of the directions by integrating the principal eigenvector using some numerical procedure. Now, considering only one of the updated positions, the S-values are again element-wise interpolated at position p_1 and two new tensors are calculated. The tracking will now proceed along the principal diffusion direction $\pm e_1(X_j(p_1))$ where the sign and $j \in \{1, 2\}$ is chosen so that the angular difference between the previous and current principal eigenvector is minimal. The output of the 2-tensor tracking algorithm consists of two paths, one for each of the two tensors estimated at the initial position p_0 .

2.4. Tract seeding and termination criteria

The seeding and termination criteria are usually defined in terms of the single-tensor estimate X. This causes problems for the tractography methods which work by solving equation (2). When the diffusion is described as a sum of multiple tensors X_1, X_2, \cdots examining tensor invariants (such as FA) of each individual tensor X_j may not be fruitful. In our implementation tracking proceeds along each of the original directions until a termination criterion based on each individual tensor anisotropy is met.

2.5. In-vivo imaging

MRI scanning was performed on a 3T GE system with an 8 channel coil. DTI data was acquired using a double-echo echo planar parallel imaging sequence with ASSET factor 2. 51 directions were acquired with b = 700, 8 baseline scans with b = 0. Other scan parameters were: TR 17000ms, TE 78ms, FOV 24cm, matrix 144 × 144, 1.7mm slice thickness. 81 axial-oblique slices parallel to the AC-PC line were acquired, covering the whole brain, with a total scan time of 17 minutes.

3. RESULTS

3.1. Synthetic data

Figure 1 shows an example of tensor estimation and tracking in a synthetic dataset. The dataset consists of a set of diffusion weighted images S generated from equation (2) where the diffusion tensors X_j are known and given by a torus model. The torus model defines two diffusion tensors per voxel, one



Fig. 1. Results on the synthetic torus dataset.



Fig. 2. Results near corpus callosum and corona radiata around coronal slice of in vivo DWI.

with its main diffusion direction parallel to the tube, along the larger radius, and the other goes around the tube, tangential to the circular cross section.

A cutting plane samples the field in figure 1(a) on which glyphs indicate the single-tensor fit. That the diffusion is disc-shaped indicating the expected crossing fiber trajectories. Also note that there is no well defined principal direction of diffusion, so standard tractography would fail to reveal the underlying anisotropic structure. Figure 1(b) displays the two tensors estimated per voxel using our multi-tensor estimation procedure outlined in section 2.1, as visualized on the same slice through the same data as in figure 1(a). The figure shows that the estimated diffusion tensors seem to correspond well with the two orthogonal principal diffusion directions in the original data. Finally, figure 1(c) show the results of our multi-tensor tracking procedure. Since the synthetic model is defined with uniform FA for all voxels, the tracts in this example terminate after a fixed number of integration steps.

All tensor samples in figures 1,2 and 3 are visualized with super-quadratic tensor glyphs [17].

3.2. MRI data

Figure 2 shows results centered around the corpus callosum and the ascending fibers of the internal capsule and corona radiata. The glyphs in figure 2(a) indicate a region of high and consistently oriented planar anisotropy, suggesting fiber crossing. Indeed, single-tensor fiber tractography results seeded in the area (figure 2(b)) fail to pass through the area, due to the single tensor fit dropping below the FA=0.15 threshold. The two-tensor fiber tracking shown in figure 2(c) uses the same FA=0.15 threshold, with tracts passing through the region of single-tensor planar anisotropy. As expected from prior knowledge of anatomy, some of the fibers from the internal capsule successfully extend upwards into the corona radiata.

Figure 3 shows results in a portion of the superior longitudinal fasciculus, an area where the dominant anterior-posterior fibers (left-right in figure) are crossed by medial-lateral projections (up-down in figure) [13], resulting in the planar anisotropy visible in the glyphs of figure 3(a). While the single-tensor fiber tracks (figure 3(b)) follow the anterior-posterior orientation, the two-tensor fiber tracks (figure 3(c)) have better coverage of the same region, and additionally indicate some of



(a) Single tensor estimation.

(b) Single-tensor tractography seeded in region.

(c) 2-tensor tractography with same seed-points.

Fig. 3. Results in superior longitudinal fasciculus.

the crossing fibers.

4. DISCUSSION

In this work we have investigated alternatives to single tensor fiber-tracking. Our results show that multi-tensor fibertracking can alleviate some of the problems associated with single-tensor based methods, particularly when crossing fibers or fiber-bundles are involved. The presented tracking algorithm provides a straightforward generalization of its singletensor equivalent, and because of this similarity it should be possible to incorporate it into already existing fiber-tracking software with a minimal number of changes.

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