Dual tensor for tract-based analysis: towards application to routine clinical diffusion images

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Introduction

FA values obtained from single tensor model fail to represent white matter integrity at the locations where white matter tracts cross. These values are usually underestimated with single tensor model used in conventional DTI. Currently a significant amount of diffusion imaging protocols used for fitting single tensor include acquisitions of diffusion weighted images (DWIs) of more than 10 orientations and b values at least 1000s/mm^2. Tract-based analysis, in contrast to voxelwise analysis, has the advantage of delineating the integrity of white matter at the tract level rather than voxel level and has obtained recent attention [e.g. 1,2]. However, in tract-based analysis, bias of the FA of target tracts still exists when they go through the crossing fiber area. In this abstract, we proposed an improved tract-based approach, DTTA (**D**ual **T**ensor for **T**ract based **A**nalysis) to restore the FA values of the targeted tract along its path while removing the influence of crossed fibers. It integrates spherical harmonics (SH) to identify the crossing fiber location and Levenberg-Marquardt estimation algorithm to fit dual tensors. First, we designed a digital phantom to assess the effects to the estimated two FA values caused by the angles between primary eigenvectors of dual tensors, volume fractions and the signal-to-noise ratio (SNR). This DTTA approach was then applied to routine clinical DWI data from 5 normal human subjects. Cortico-spinal tract (CST) was used as a tract example. Results from both conventional single tensor approach and DTTA were presented. DTTA shows significant improvement at the regions with crossing fiber of CST and corpus callosum (CC). It suggests DTTA has great potential to restore true FA values of a tract along its path even with the routine clinical diffusion data.

Methods

Dual tensor model: A simplified Gaussian mixture model, $S_i = f_1 e^{-b_i \vec{G_i}^T \overline{D_1} \vec{G_i}} + f_2 e^{-b_i \vec{G_i}^T \overline{D_2} \vec{G_i}}$, (1) was used, where f_1 and f_2 are the volume fractions of the first and second fiber bundles, b_i is the applied b value, $\vec{G_i}$ is the ith gradient vector, i is the direction of the acquisition, $\overline{D_1}$ and $\overline{D_2}$ are the two tensors representing the first and second fiber bundles. $\overline{D_1}$ and $\overline{D_2}$ are formulated from their eigenvalues E_1=diag[λ_{11}, λ_{12}, λ_{13}], E_2=diag[λ_{21}, λ_{22}, λ_{23}] and rotations R_1, R_2 around X, Y and Z-axes by $\overline{D_j} = \vec{R_j}^T E_j \vec{R_j}$. Rotation around the axes is given by $\vec{R_j} = \vec{R}_{x(\alpha_1)} \vec{R}_{y(\alpha_2)} \vec{R}_{z(\alpha_3 \pm \alpha_4)}$, j = 1,2 for $\overline{D_1}$ and $\overline{D_2}$ respectively, where α_k, k=1,2,3, represent the orientation of the plane in which the principal eigenvectors of the two tensors reside and $2\alpha_4$ is the angle between two primary eigenvectors of $\overline{D_1}$ and $\overline{D_2}$. The 12 degrees of freedom in equation (1) were reduced to 8 degrees of freedom by assuming the same axial diffusivity for the two tensors, same radial diffusivity for each individual tensor [3], and summation of f_1 and f_2 always being 1. *Phantom design:* The four variables we used for our phantom design and their detailed values are as follows: $2\alpha_4$=10, 20,• • •90, f_1=0.1, 0.2,• • •1, FA_1=0.1, 0.2,• • •0.9; FA_2=0.1, 0.2, ,• • •0.9, where FA_1 and FA_2 are the fractional anisotropy of the two tensors. To also understand the noise influence, Gaussian noise with zero mean and different standard deviations was added to this signal to obtain a SNR of 15dB to 105dB in steps of 10dB. For a fixed SNR, different seed numbers were used to generate different Gaussian noises with the same standard deviations. To match our *in vivo* human data, Jones 30 gradient scheme [4] was used to generate 31 diffusion weighted images (DWIs) and one b0 image. b-value was 1000 sec/mm^2 . *Fitting Algorithm:* Levenberg-Marquardt estimation algorithm was used for the designed digital phantom of dual tensors described above. The eigenvalues generated by fitting a single tensor was used to initialize the fitting algorithm. α_1, α_2 and α_3 were initialized to 45^o and f1 was initialized to 0.6. *Diffusion imaging of in vivo human brain:* 5 young healthy volunteers were scanned with a 3T Philips Achieva MR system. DTI data was acquired using a single-shot EPI sequence with SENSE parallel imaging scheme (reduction factor =2.3). DWI parameters were: in plane imaging matrix = 128× 128 reconstructed to 256x256, axial slices thickness = 2.2 mm without gap, Jones 30 gradient scheme [4] with b-value = 1000 sec/mm^2, TE=97ms, TR=7.6s. With two repetitions, the acquisition time was 9 minutes. *Identify crossing fiber regions with spherical harmonics:* We used cortico-spinal tract (CST) in the real in vivo human brain data to test the feasibility of DTTA method. SH decomposition was applied to the diffusion coefficient profile, with the traced CST as a mask (see Fig. 2c). Voxels with SH order 4 were identified as the ones with crossing fibers [5]. The computation time of both SH decomposition and dual-tensor fitting with a 2GB Dell Precision 690 is less than 10 minutes. *Profile of FA along CST:* Selection of FA1 or FA2 at SH order 4 voxels in CST mask was determined by higher alignment of the primary eigenvector with those of surrounding voxels. The FA values in CST within an axial plane were averaged. For inter-subject averaging, the CST length was linearly adjusted to a template CST path using anatomical landmarks along its course.

Results

Digital phantom: Fig. 1 shows the effects of angles of separation (α_4) and SNR with different combination of two tensors in (a), (b) and (c). The 3D visualizations of the two tensors are in the upper left corner of each panel. By comparison with the known ground truth represented by dash line, the green arrows point to the SNR required for estimation error less than 10%. From all panels of Figure 1, small angle of separation causes unstable estimation, especially for two known high FA values in Fig. 1b. It requires much higher SNR to get a stabilized small bias compared to those in the cases of Fig. 1a and Fig.1c. Excluding data with low angles of separation, the minimum SNR for less than 10% estimation error drops to 45dB in Fig. 1b, pointed by orange arrows. *In-vivo data:* As can be seen from Figure 2, at the corona radiata (Fig. 2c), CST goes through a dark region in FA map from single tensor (Fig. 2b), indicated by orange circle. This dark region is caused by underestimation of FA at the crossing areas of CST and CC. It can be clearly appreciated that FA of CST which is FA1 in the phantom of Fig. 1 can be restored close to its real value, demonstrated by the relative flat line of FA from DTTA at the segment of corona radiata in Fig. 2a.

Conclusion and discussion

The proposed DTTA method which includes spherical harmonics decomposition and Levenberg-Marquardt estimation algorithm for dual tensor fitting can effectively restore the FA of the targeted tract at the crossing fiber region. Moreover, with low requirement of DWI data quality (b value, number of orientations, SNR) and relatively short computation time, it has great potential to be applied to routine clinical diffusion images. The phantom study demonstrates that bias for estimating FA1 and FA2 is less than 10% for most cases with SNR greater than 45dB and the separation angles greater than 30 degree. Further studies on automating the processes by incorporating digital white matter tract atlas for tract masks in DTTA are under way.

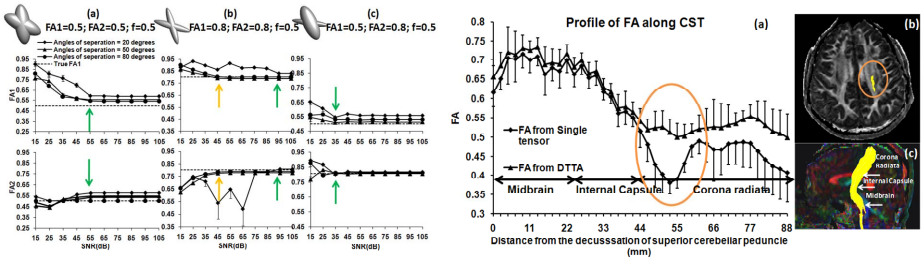

Fig. 1 (left): Estimation of FA1 and FA2 of two crossing fiber components at different SNR and separation angles (20, 50 and 80 degrees). (a), (b) and (c) represent different combination of ground truth FA1, FA2 and volume fraction. Dashed lines indicate true FA values. Fig. 2 (right): Profile of FA along CST with DTTA and single tensor (a), the axial FA map from single tensor fitting at corona radiate (b) and anatomical guidance for separation of CST into segments of midbrain, internal capsule and corona radiata.

References: 1) Pievani et al (2010) HBM (Epub ahead of print). 2) Fan et al (2010) ISMRM 275. 3) Caan et.al (2010) IEEE TMI 29:1504. 4) Jones et al (1999) MRM 32: 515. 5) Alexander et.al (2002) MRM 48: 331. **Acknowledgement:** This study is sponsored by NIH/NIA P30AG12300, NIH RR014982 and NIH EB009545.