Effects of the gradient number to resolve two crossing fiber tracts in HARDI

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Introduction Conventional diffusion tensor imaging (DTI), based on a single tensor model, is unable to correctly estimate the multiple fiber orientations within a voxel. High angular resolution diffusion imaging (HARDI) is one of the novel methods for estimating the distributions of intravoxel multiple fiber orientations [1]. Spherical harmonic decomposition (SHD) [2] is used to quantitatively characterize the 3D apparent diffusion profile (D_{app}) in the HARDI approach and the fiber orientation distribution function (ODF) in q-ball imaging. While a number of the satisfactory results using HARDI have been described in the literature, the performance of the SHD in HARDI in terms of gradient resolution, crossing angle of multiple fibers and noise has not fully understood yet. The aim of this study is to analyze the ability to separate crossing fibers in simulations and human brain data in terms of the number of diffusion gradients, fiber crossing angle and noise.

Methods Simulations and actual HARDI experiments were performed to demonstrate the validity of the SHD approach. For *in vivo* performance analysis, brain diffusion acquisitions was performed on a normal volunteer on an Philips 1.5T scanner (Philips Intera, Philips Medical System, Best, The Netherlands) with 45 and 128 gradient directions. To simulate crossing fibers, diffusion profile (D_{app}) with multiple fibers was generated assuming a crossed prolate tensor ($\lambda_1>\lambda_2=\lambda_3$) model with each relative anisotropy (RA) and a crossing angle [3]. Regular SHD between the simulated ADC profile $D_{app}(\theta,\varphi)$ and the spherical harmonic kernel functions $Y_l^m(\theta,\varphi)$ can be represented by $r_{lm}=\int_0^{2\pi}\int_0^{\pi} D_{app}(\theta,\varphi)Y_l^m(\theta,\varphi)\sin(\theta)d\theta d\varphi$. Even values of l were calculated due to the assumption of the antipodal symmetry of the data. As single and crossing fiber correspond to l=2 and l=4 components from SHD respectively, the coefficients to describe the crossing of two fibers were determined by fractional multifiber index (FMI) [1], defined as $L_4/L_2=\sum_{m=-l}^{l}|r_{lm}|^2\Big|_{l=4}\Big/\sum_{m=-l}^{l}|r_{lm}|^2\Big|_{l=2}$. SHD performance was estimated for the simulated model in terms of (1) RA of an individual fiber in crossing, (2) the crossing angle between two fibers and (3) SNR corresponding to Gaussian noise. Then sampled diffusion profiles from diffusion gradients with 15, 32, 45, 64, 96 and 128 directions were constructed to 4000 vertices using Laplacian interpolation for the SHD evaluation [4]. RMS error for FMI between the simulated model and the reconstructed profiles was calculated for the different gradient directions.

Results Fig. 1 shows the simulation results measured by FMI for several crossing type of fibers. FMI larger than 1 indicates the correct decomposition of the crossed diffusion profiles using SHD. The ability to separate crossing fibers was dependent mainly on the crossing angle and RA of two individual fibers for about RA ≥ 0.5 and crossing angle ≥ 70° in Fig. 1(A). The mean square error between the simulated model and the reconstructed D_{app} decreased as the increased number of gradients in Fig. 1(D). Diffusion profiles with more than 96 directions appeared to converge to the reliable value. Fig. 2 shows the experimental results from a volunteer within a coronal region of interest containing intersecting tracts. While single tensor model could not resolve the fiber crossing in Fig. 2(B), diffusion profiles from high angular acquisitions represented the crossing more accurately: even the low SNR, D_{app} from 128 directions better represented the ability to separate crossing fibers with FMI ≈ 1.

Discussion In general, a large number of data samples, which are difficult to achieve in clinical settings, are needed to fill the space spanned by the diffusion profiles or q-vectors in HARDI and q-ball imaging. Although the SHD is known to fit the ODF data much better than the D_{app} profiles especially for the l≥4 harmonic components, this study may be used to improve fiber tractography in crossing white matter structures using diffusion profiles from HARDI with the limited gradient directions.

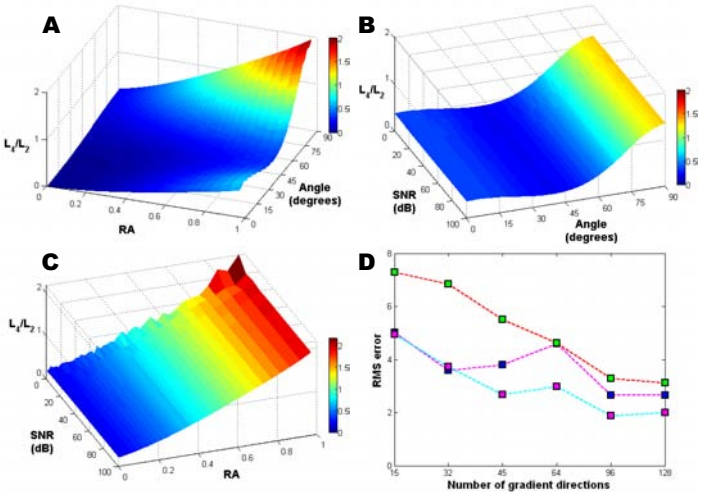

Fig. 1. Numerical simulations showing SHD performance in terms of: (A) RA and the crossing angle, (B) SNR and the crossing angle with RA=0.7, and (C) RA and SNR with crossing angle at 90°. (D) RMS error from the reconstructed diffusion profiles with different gradients. Red, green, and blue box represent RMS error of FMI in terms of SNR-crossing angle, RA-crossing angle and RA-SNR respectively.

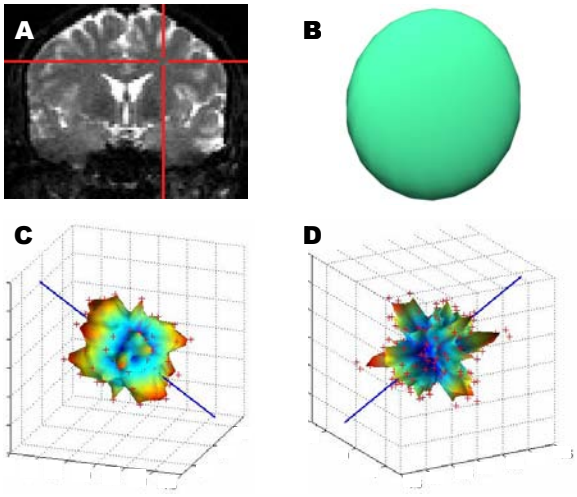

Fig. 2. (A) Single voxel ROI near the centrum semiovale assuming fiber crossing. (B) diffusion ellipsoid from single tensor model with FA=0.2. Diffusion profiles from (C) 45 gradient directions with FMI=0.7809 (D) 128 directions with FMI = 0.9536. Blue line represents the direction of major eigenvector.

References

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