Optimum Diffusion Encoding Steps for Fiber Tractography

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Abstract

This work investigated the number of diffusion gradient steps in diffusion tensor imaging (DTI) that is optimum for fiber tractography. We quantified the effect of gradient encoding steps on the tractography in terms of a coherence index. The coherence index was a measure of similarity of an individual fiber tract with respect to the gold standard tractography obtained from 75 encoding steps. Tractography of corpus callosum was used to compare among 7, 25, and 43 icosahedrally-oriented gradients under comparable scan time. The coherent indices for 7, 25 and 43 encoding steps were 25.86(8.00), 27.17(8.00) and 27.80(7.83), respectively. The difference between 7 and 25 encoding steps was significant (p=0.02), whereas the difference between 25 and 43 encoding schemes was not significant (p=0.26). Our results indicate that given the same scan time, encoding steps of more than 7 in DTI acquisition produces better fiber tractography. Tractography reconstructed from 25 encoding steps or more has similar results.

Introduction

Diffusion tensor imaging (DTI) has been recognized as an important tool to reveal axonal fiber tracts in cerebral white matter noninvasively. By probing the translational displacement of water molecules, it provides the primary direction of water molecular diffusion which is correlated to the main pathway of fiber bundles. The eigenvector of the diffusion tensor at each location in the cerebral white matter represents the fiber orientation at the same location. Based on this information, 3D reconstruction and visualization of white matter fiber pathways can be produced by tractography.

While development of a robust tractography algorithm and its applications are currently under active research, the optimum condition for DTI gradient encoding is not clear. Jones et al. used Monte Carlo simulation to study the dependence of the number of encoding gradients on the orientation uncertainty of the first eigenvector of the diffusion tensor [1]. They found that the uncertainty reduced dramatically as the number of gradient steps increased from 6 to 30, and that little benefit was gained when gradient steps of more than 30 were used. However, the effect of the number of encoding steps on the tract orientation as a whole is still unknown. Therefore, this work aimed to address this question by comparing the tractography results among three different DTI encoding schemes, i.e., 7, 25 and 43 icosahedrally-oriented gradient steps.

Methods

A healthy volunteer was scanned on a 3T MRI system (Trio, Siemens, Germany). A diffusion EPI sequence was used to acquire transaxial images encompassing the whole brain. Isotropic spatial resolution was obtained by setting FOV = 360 mm x 360 mm, matrix size = 128 x 128 and slice thickness = 2.8 mm. Diffusion-weighted images using the diffusion sensitivity (b-value) = 900 s/mm^2 were acquired with TR/TE = 7900/120 ms. Three different DTI encoding schemes were used, i.e., 7, 25, and 43 icosahedrally-oriented steps. To have comparable scan times and signal-to-noise ratio, repetitions of 14, 4, and 2 were prescribed for 7, 25 and 43 encoding steps, respectively. The scan time for each DTI data set was about 18 minutes.

An in-house tractography algorithm was developed using a similarity interpolation approach in which the vector orientations of the neighboring pixels were incorporated to determine the direction of the next propagation step [2]. We quantified the effects of different gradient encoding steps on the tractography in terms of a coherence index. The coherence index was a measure of similarity of an individual tract with respect to the gold standard tractography obtained from 75 encoding steps, i.e., the total data of 7, 25 and 43 steps. Specifically, we computed the inner product of the propagation vector at each step divided by the distance between the step positions of two tracts. The coherence index of the two tracts was the summation of these ratios along the entire tracts. Tractography of corpus callosum was used to compare the coherence indices among three different encoding schemes. In addition, the first eigenvectors of the diffusion tensors in the white matter pixels were selected from the three DTI data sets. Deviation angles between these eigenvectors and the standard eigenvector derived from the 75 encoding steps were computed and compared.

Results and Discussion

Tractography results reconstructed from 7, 25, 43 and 75 encoding steps are shown in Fig. 1. Although the pictures look similar, subtle difference can be seen, for instance in the tapetum. Higher similarity of the tractography in the 43 and 75 encoding schemes is noted. A total of 20267 pixels in the white matter were selected to study the deviation angle between the first eigenvector of the diffusion tensor derived from the 75 encoding steps and the eigenvectors derived from the three different encoding schemes. The deviation angles for 7, 25 and 43 encoding steps were 9.67(4.85), 7.40(3.84), and 4.00(2.35), respectively (Fig. 2a). The difference was significant between any two schemes ($p<0.05$). A total of 403 fiber tracts in the corpus callosum were compared between different encoding steps. The coherent indices for 7, 25 and 43 encoding steps were 25.86(8.00), 27.17(8.00) and 27.80(7.83), respectively (Fig. 2b). The difference between 7 and 25 encoding steps was significant (p=0.02), whereas the difference between 25 and 43 encoding schemes was not significant (p=0.26).

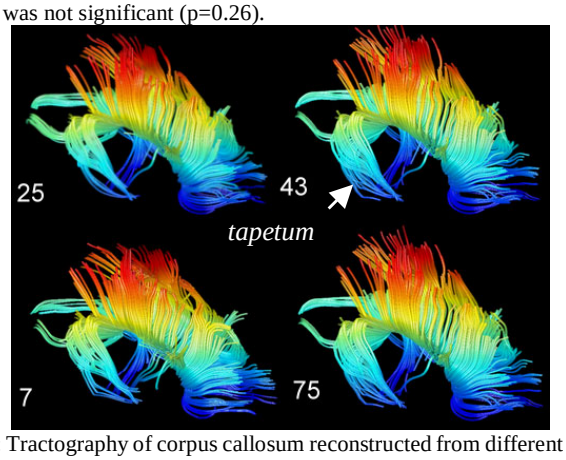

Fig. 1: Tractography of corpus callosum reconstructed from different DTI data sets using 7, 25, 43 and 75 encoding steps.

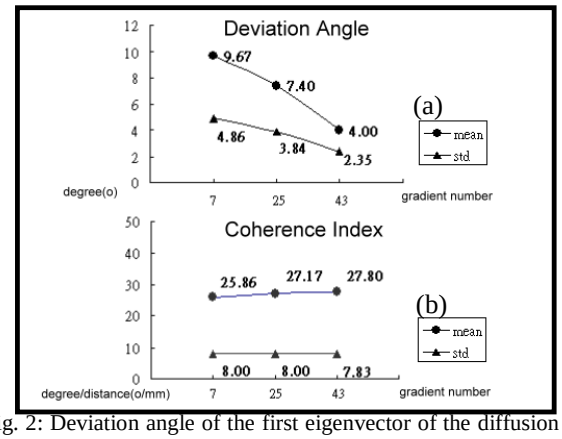

Fig. 2: Deviation angle of the first eigenvector of the diffusion tensor (a), and the coherence index of the fiber tractography (b), compared among different DTI data sets using 7, 25, 43 and 75 encoding steps.

Conclusions

Our results indicate that given the same scan time, encoding steps of more than 7 in DTI acquisition produces better fiber tractography. Tractography reconstructed from 25 encoding steps or more has similar results.

References

[1] Jones DK et al. 2003. *Proc ISMRM* p72. [2] Mori S et al. *NMR Biomed*. 2002, 468-480.