Reduced-Encoding Imaging of Diffusion Anisotropy

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INTRODUCTION

Characterization of diffusion anisotropy in biological tissues requires high-resolution diffusion-weighted images collected in many diffusion gradient directions. Due to various practical constraints (e.g., motion sensitivity), these images are typically acquired using a single-shot EPI pulse sequence, thus limiting the spatial resolution to several millimeters. The relatively low spatial resolution is a major challenge for white-matter fiber tracking through voxels containing multiple fiber compartments. Conventional DTI, based on a single-tensor model, is unable to correctly estimate fiber orientations in such voxels. More elaborate, higher order diffusion models have been proposed to resolve intravoxel orientation inhomogeneity [1-2]. These methods rely on dense sampling of diffusion directions (or q-space), thus significantly lengthening the data acquisition time, even when a single-shot EPI pulse sequence is used. Parallel to this effort, several groups have used multi-shot EPI pulse sequences to improve resolution [3-4], which also increase data acquisition time. This paper addresses this problem with a new reduced-encoding imaging scheme. This method collects only a few (e.g., 6-10) high-resolution images for some diffusion gradient orientations and a sequence of reduced k-space sets for other diffusion gradient orientations. In image reconstruction, the high-resolution images are used to derive an optimal set of basis functions for a generalized series model that is used to reconstruct high-resolution images from the reduced data sets.

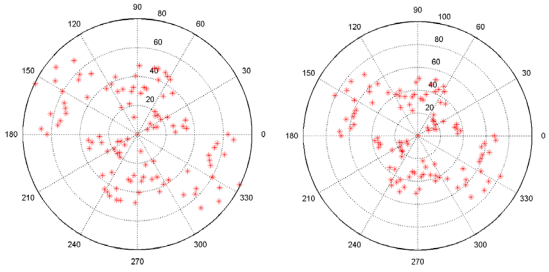
PROPOSED METHOD

The proposed method is aimed at producing diffusion-weighted images in both high spatial and angular resolutions. High spatial resolution is desirable for reducing the chance of having multiple crossing fibers in a single voxel while high angular resolution improves the robustness of fiber tracking. To reduce the data acquisition time, the proposed method samples the (k, q)-space sparsely. Specifically, it covers the "full" k-space for a few selected q values (e.g., 6-10) but only the central region of k-space for all other q-values. The full k-space data sets have the desired spatial resolution while the reduced data sets provide sufficient angular coverage of potential fiber orientations. In image reconstruction, the full k-space data sets are processed using the conventional Fourier reconstruction methods, while images for the reduced data sets are reconstructed using a generalized series model [6]. Specifically, we express the desired image for a particular q-direction as: $\boldsymbol{I}(\boldsymbol{q}, \overset{\rightarrow}{\boldsymbol{x}}) = \sum_{\boldsymbol{n}} \boldsymbol{c_n}(\boldsymbol{q})\boldsymbol{\phi_n}(\boldsymbol{q}, \overset{\rightarrow}{\boldsymbol{x}})$, where the basis functions $\boldsymbol{\phi_n}(\boldsymbol{q}, \overset{\rightarrow}{\boldsymbol{x}})$ are derived from the high-resolution images using the minimal cross-entropy principle. This model effectively utilizes the prior information in the high-resolution images to reconstruct the reduced data sets in a data-consistent way.

RESULTS

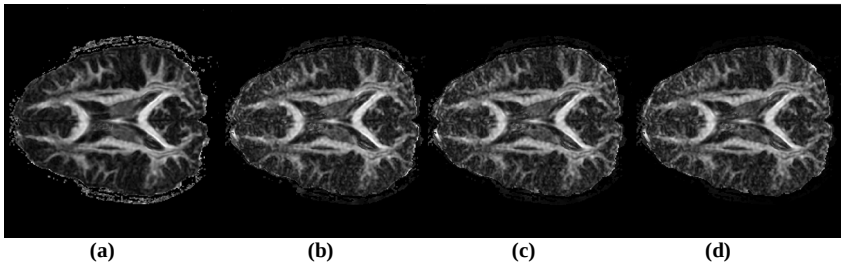
Experimental studies were carried out on a General Electric 3.0T MRI scanner (GE Healthcare, Milwaukee, WI) using a customized DTI pulse sequence. Two datasets were acquired from a healthy human subject. In the first dataset, 55 diffusion gradient directions were evenly distributed in a 2D plane and a coronal image was acquired at each gradient orientation. This dataset was used to analyze the signal distribution as a function of gradient orientation, from which fiber orientations were derived. The second dataset was acquired with 27 diffusion gradient orientations in 3D, as determined using an electrostatic repulsion model [5]. Fractional anisotropy (FA) was calculated from this dataset before and after processing using the generalized series model.

Signal distributions from the 2D dataset with 55 directions are shown in Fig. 1 for a voxel containing crossing fibers of the arcuate fasciculus and the corpus callosum, for (a) a fully-encoded data set and (b) a reduced 64x64 data set. The fiber crossing is clearly resolved in both, though with datasets below 32x32 the detection of the crossing was significantly degraded. For single-compartment voxels, the fiber orientation can be clearly revealed in all cases, even with only 8x8 k-space coverage, as expected. The FA maps of the 3D dataset calculated with different levels of data truncation are shown in Fig. 2. As can be seen, the quality of the FA maps from the reduced datasets is comparable to the one without data reduction, illustrating the robust performance of the proposed technique.



(a) **(b)**

Fig. 1. Signal distributions in 55 directions from a voxel containing crossing fibers: (a) a fully-encoded data set, and (b) a reduced data set with 64x64 encodings.



(a) **(b)** **(c)** **(d)**

Fig. 2. The FA maps of the 3D dataset calculated with different levels of data truncation: (a) 256x256 encodings; (b) 32x32 encodings, (c) 16x16 encodings, and (c) 8x8 encodings.

CONCLUSION

This paper proposes a new reduced-encoding method for measuring diffusion anisotropy in tissues. The method samples the (k, q)-space sparsely and utilizes a generalized series model for image reconstruction. Experimental results show the proposed method can produce high-quality images with as few as 8x8 encodings for each q-frame, and resolving fiber crossings with as few as 64x64 encodings. This technique has the potential to significantly reduce the data acquisition time for measuring tissue diffusion anisotropy.

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