Model order estimation in DTI

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Introduction

Diffusion Tensor Imaging (DTI) allows the noninvasive visualization of white matter fiber tracts in the human brain. One of the main difficulties in fiber tracking is the existence of voxels containing several crossing fibers. The usual DTI model, based on a single diffusion tensor, is unable to correctly estimate fiber directions in such voxels. More elaborate, higher order diffusion models have been proposed to resolve intravoxel orientation heterogeneity [1,2]. These methods rely on high angular resolution sampling of diffusion directions, as opposed to the original DTI model, which requires fewer directions (e.g., 6). White matter fiber tract orientations can then be estimated for each voxel using model fitting techniques such as expectation-maximization or gradient descents. However, the problem of estimating the model order (number of fiber tracts) in a given voxel remains an important one. Here we propose an approach based on the statistics of the estimated diffusion tensor as a function of the directions employed to estimate it.

Methods

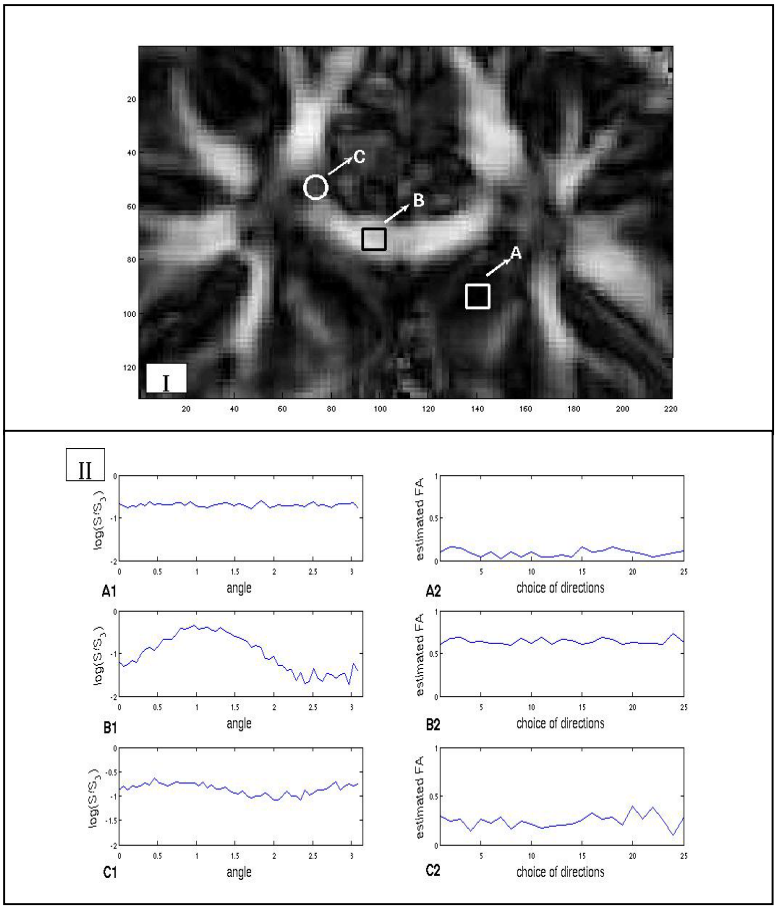
Assuming that data from a number of diffusion directions is available, we can estimate the diffusion tensor *D* using a subset of these data. If the single component model is correct, one diffusion tensor will be enough to describe the data, which can be expressed as $S(\vec{q}) = S(0)\exp(-b \cdot \vec{q}^T D \vec{q})$ for each diffusion direction $\vec{q}$, where *S(0)* is the signal collected without diffusion weighting. In this case, the estimated diffusion tensor will not depend on the choice of diffusion directions employed to estimate it, except for the noise present in each measurement. When a voxel contains several fiber tracts, the estimated diffusion tensor does depend on the choice of diffusion directions employed for estimation (more than just because of noise), as already noted in [3]. The MRI signal from such a voxel can be expressed as:

$$S(\vec{q}) = S(0)\sum_{j=1}^{M} c_j \exp(-b \cdot \vec{q}^T D_j \vec{q})$$

Thus, in voxels containing more than one fiber, the estimated FA will present a lower SNR. This has been confirmed through simulations using various numbers of components and different levels of noise.

In [4], the variance of the FA estimate is analytically computed in terms of the noise power. In this case, assuming that several equally well-conditioned combinations of diffusion directions are picked to produce estimates of FA, the sample variance of FA will be larger than predicted, since in addition to the noise, there is variation due to the choice of orientations.

This method could be used in addition to a multiresolution approach. Voxels would thus be analyzed first using low resolution, low noise data and resort to higher resolution when there is evidence of several fibers within one voxel.



Results

For experimental validation, a DW data set was acquired on a healthy human subject at 1.5T Signa MR scanner (GE Medical Systems), using a single-shot EPI pulse sequence with b = 1000 s/ mm^2, TE = 70 msec, and 55 gradient directions restricted to the X-Y plane. Figure I shows an FA map of part of a coronal slice (where white regions indicate high anisotropy), indicating three points at which experiments were conducted. The results for these points are shown in figure II. Figs. II-A1, II-B1 and II-C1 show the MRI signal $\log(S(\vec{q})/S(0))$ as a function of the diffusion weighting direction at points A, B and C, respectively. In each case, we estimated the two-dimensional diffusion tensor D using various groups of 3 measurements. For each estimated D we computed the Fractional Anisotropy (FA), which is shown in Figs. II-A2, II-B2 and II-C2 for 27 different combinations of measurements. Voxel A presents isotropic diffusion. Voxel B shows one main diffusion direction. It can readily be seen that in voxels with a single fiber direction (B) the estimated FA does not change greatly with the choice of orientations employed. Figs. II-C1 and II-C2 show the signal and estimated FA for a voxel likely to contain crossing fibers. As shown in the figures, a larger number of components produce more variance in the estimated FA, relative to its mean, i.e., an increase in σ_{FA}/μ_{FA}. Thus, thresholds can be placed on this value to estimate the model order for a given voxel. As the number of distinct fibers within a single voxel increases, the estimated FA approaches that of isotropic diffusion (no fibers present).

Several fibers with similar orientations are difficult to distinguish from a single fiber. The minimum angle between distinct fibers so that they are separable depends on the level of noise and the diffusion anisotropy in the fibers. If the fibers have low diffusion anisotropy (i.e., small values of FA) they need to be separated by a large angle in order to be separable with DTI. Better results are expected when combining information from neighboring voxels instead of using just local estimation from each voxel.

References

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