Generating Simulated DT-MRI Dataset

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INTRODUCTION: DIFFUSION TENSOR IMAGING

Diffusion tensor magnetic resonance imaging (DT-MRI), also known as diffusion tensor imaging (DTI), needs post processing by adequate image analysis and visualization tools. White matter tractography using DTI is becoming a routine MR technique to study white matter properties, connectivity, and alterations of fiber integrity due to pathology. The success of the method depends on the accuracy of the tracking algorithms. The disadvantage on the evaluation of such methods is that there is no gold standard regarding the true geometry of the brain anatomy or fiber bundles reconstructed in each particular case.

Considering the increasing number of reports on DTI post-processing research, it is observed that most of the methodology is applied only to real data, acquired from human or animal test subjects. This approach has the following drawbacks: (i) the true anatomy of each imaged subject is not known in detail, (ii) the image noise is of little control, (iii) cost of scanner time is usually high, (iv) the comparison of the methods and the results from different studies is difficult because the data has been acquired on various MR scanner hardware, and often scanned with different imaging protocols, and finally, (v) the test data is collected from different subjects, each having unique characteristics in gross anatomy and tissue micro-architecture. In order to reduce these problems, a synthetic DTI dataset with known geometric and signal properties has been developed.

The accuracy of white matter anatomical maps obtained by DTI is still unclear due to the general inability of the diffusion tensor model describing a single voxel with multiple orientational maxima. Verification and validation of the synthetic data analysis' aims to elucidate the white matter fiber tractography in eliminating the uncertainty areas and understanding the connectivity more clearly and reliable.

A model must describe how water diffuses in the synthetic dataset. For simplicity, we have in this work considered only two very basic models. In this work two separate models with different geometric properties characterized by anisotropic Gaussian diffusion are specified. These models are sampled and their output is similar to those obtained from MR scanners are generated. The efficient calculation of the diffusion tensor is achieved from that output. It is used to generate several common measures and visualizations describing Gaussian water diffusion. The project covers the geometric model, discrimination, sampling, tensor calculation, parameter calculation, and the visualization.

BACKGROUND

DT-MRI Pulse Sequences: Encoding for Diffusion

Diffusion-weighted images are the raw data source used to calculate the diffusion tensor. In DTI, each voxel is assigned a tensor that describes local water diffusion. The relationship between the loss of phase coherence in the transverse spin radio frequency (RF) signal S_0 and S_i, and the gradient pulse $g=[g_{ix}\, g_{iy}\, g_{iz}]^T$ with $\hat{g}_i^T D\hat{g}_i$ the apparent diffusivity along g_i is given by the Stejskal-Tanner equation (Stejskal, 1965):

$$S_i = S_0 e^{-b\hat{g}_i^T D\hat{g}_i} \qquad (1)$$

A Stejskal-Tanner imaging sequence may be implemented by adding diffusion encoding gradients to standard anatomical MRI pulse sequences (Ciccarelli et al., 2003).

By systematically applying diffusion gradients in multiple directions, a mathematical construct known as the diffusion tensor, D, could be estimated at each

point in the tissue. The utility of the diffusion tensor is that it provides the direction in three dimensional space in which the rate of diffusion is greatest (Basser, Pajevic, Pierpaoli, Duda, & Al-droubi, 2000; Borisenko & Tarapov, 1979).

Estimation of the Diffusion Tensor

Derivation of structural information follows a measured displacement characteristic related by means of a model to the physical and geometrical properties of the tissue. Diffusion coefficients and shapes of semipermeable membranes of compartments in the system are these related characteristics. The behavior of the MR signal and the measured *apparent diffusion coefficient* (ADC) as anisotropic diffusion indexes are greatly affected by the cellular architecture of a tissue, mainly because cellular membranes are relatively impermeable to water.

The relationship between loss of phase coherence in the transverse spin RF signal and the gradient pulse *g* is given by the Stejskal-Tanner equation (1), where *b* is the diffusion weighting factor (Ciccarelli et al., 2003) given by:

$$b = \gamma^2 \delta^2 \left[\Delta - (\frac{\delta}{3}) \right] |g|^2 \qquad (2)$$

Here, γ is the gyromagnetic ratio, δ is the gradient pulse width, Δ is the time between the gradient pulses, $|g|$ is the strength of the diffusion gradient pulses.

Basser (Basser, Mattiello, & Le Bihan, 1994), building on the work of Stejskal and Tanner (Stejskal, 1965), has shown that the diffusion tensor can be calculated from knowledge of signal attenuation and magnetic gradient strengths applied during a diffusion weighted spin echo experiment using the following equations;

$$\ln\left(\frac{A(b)}{A(b=0)}\right) = -\sum_{i=1}^{3}\sum_{j=1}^{3} b_{ij} D_{ij} = \qquad (3)$$

$$-\left(b_{xx}D_{xx} + 2b_{xy}D_{xy} + 2b_{xz}D_{xz} + b_{yy}D_{yy} + 2b_{yz}D_{yz} + b_{zz}D_{zz}\right)$$

$$Trace(D) = D_{xx} + D_{yy} + D_{zz} = 3\langle D \rangle = \lambda_{xx'} + \lambda_{yy'} + \lambda_{zz'} \qquad (4)$$

where *A(b)* is the voxel attenuated signal (echo) intensity recorded in the presence of gradients (3), *A(0)* is the gradient-free, unattenuated echo intensity, D_{ij} is the (symmetric, positive definite, 3 by 3) diffusion tensor (3), and b_{ij} is a matrix specified by the magnetic field gradients applied during the spin echo. In eq. 3:

$$\sum_{i=1}^{3}\sum_{j=1}^{3} b_{ij} D_{ij} \equiv b : D$$

is the standard scalar product of two tensors. This so called *b-matrix* (2, 3) has the form: $A = A_0 e^{(-b:D)}$.

Tensor Analysis and the Diffusion Tensor: PCA

Principal component analysis (PCA) is a classical statistical method widely used in data analysis and compression. PCA is based on the statistical representation of a random variable. The method reduces data dimensionality by performing a covariance analysis between factors. PCA method is based on linear transformations; however, nonlinear extensions exist. PCA is a technique for reducing second-order dependencies in the data by rotating the axes to correspond to orthogonal directions of maximum covariance (decorrelation).

From a symmetric matrix such as the covariance matrix, an orthogonal basis by finding its eigenvalues and eigenvectors can be calculated. The diffusion tensor *D* is a real, symmetric second order tensor, represented in matrix form as a real, symmetric 3x3 matrix (5).

$$D = \begin{bmatrix} D_{xx} & D_{xy} & D_{xz} \\ D_{yx} & D_{yy} & D_{yz} \\ D_{zx} & D_{zy} & D_{zz} \end{bmatrix} \qquad (5)$$

The diagonalization of the positive definite and symmetric diffusion tensor results in a set of three eigenvalues, $\lambda_1, \lambda_2, \lambda_3$, listed in decreasing order. The eigenvectors e_i and the corresponding eigenvalues λ_i are the solutions of the diagonalization of *D* (5), where the eigenvectors e_i are the principal diffusion directions e_i *(i* = 1, 2, 3*)*. The eigensystem of the diffusion tensor may be interpreted graphically as an ellipsoidal surface with semimajor axis oriented in the e_1 direction and semiminor axis oriented in the e_2 and e_3 directions regarding to $De_i = \lambda_i e_i$.