Diffusion Tensor Imaging

Diagnostic Imaging Lab 2

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1   Task 1. Exploring A Breast DTI Scan

This data has 25 gradient direction which can be checked following instructions in the **Slicer**: **Volumes –> Display –> DWI compoent**

2   Task 2. Computing Diffusion Tensor & Associated Scalar Measures

1. 40 axial slices stored in DICOM files originates from a breast DTI scan. DTI information such as gradient direction and b factor are contained in each DICOM file.

2. The length of every direction gradient vector has been computed, which is equal to 1 indicates that direction gradient is represented as an unit vector. The first gradient direction is $[0, 0, 0]^T$, resulting in that the measured image is the baseline image S_0 and now, only diffusion tensor is the unknown item. b is 1000 for each slice except the baseline image. Figure 1a is the baseline image. Figure 1b is the result of fractional anisotropy (FA). Figure 1c is the inverse FA that will be explained in following part. Figre 1d shows the volume ratio (VR). Figure 1e is the result of mean diffusivity (MD).

3. MD, also known as trace, is a scalar feature of the total diffusion within a voxel, which can be computed as Equation 1. FA is a scalar value as shown in Equation 2, from 0 to 1, for describing the degree of anisotropy in a diffusion process. It can be seen from Figure 1b that the region of breast tissue is too dark to be observed. Therefore, the inverse FA (computed as 1 - FA) can be calculated as shown in Figure 1c, in which the breast tissue is more clear. VR, as shown in Equation 3 represents the ratio of the ellipsoid volume over the volume of a sphere of radius MD. In equations, λ_1, λ_2 and λ_3 are eigenvalues of diffusion tensor.

$$MD = \frac{\lambda_1 + \lambda_2 + \lambda_3}{3} \tag{1}$$

$$FA = \frac{\sqrt{3} \cdot \sqrt{(\lambda_1 - MD)^2 + (\lambda_2 - MD)^2 + (\lambda_3 - MD)^2}}{\sqrt{2} \cdot \sqrt{\lambda_1^2 + \lambda_2^2 + \lambda_3^2}} \tag{2}$$

$$VR = \frac{\lambda_1 \cdot \lambda_2 \cdot \lambda_3}{MD^3} \tag{3}$$

4. Equation 4 shows the diffusion signal $S(b)$ that is measured in direction g. Matrix B can be computed as Equation 5.

$$S(b) = S_0 \times exp(-bg^T Dg) \tag{4}$$

$$
g^T Dg = \begin{bmatrix} g_x & g_y & g_z \end{bmatrix} \begin{bmatrix} D_{xx} & D_{xy} & D_{xz} \\ D_{xy} & D_{yy} & D_{yz} \\ D_{xz} & D_{yz} & D_{zz} \end{bmatrix} \begin{bmatrix} g_x \\ g_y \\ g_z \end{bmatrix}
$$

$$
= g_x{}^2 D_{xx} + g_y{}^2 D_{yy} + g_z{}^2 D_{zz} + 2g_x g_y D_{xy} + 2g_x g_z D_{xz} + 2g_y g_z D_{yz}
$$

$$
= \begin{bmatrix} g_x{}^2 & g_y{}^2 & g_z{}^2 & 2g_x g_y & 2g_x g_z & 2g_y g_z \end{bmatrix} \begin{bmatrix} D_{xx} \\ D_{yy} \\ D_{zz} \\ D_{xy} \\ D_{xz} \\ D_{yz} \end{bmatrix} = B \cdot D' \tag{5}
$$
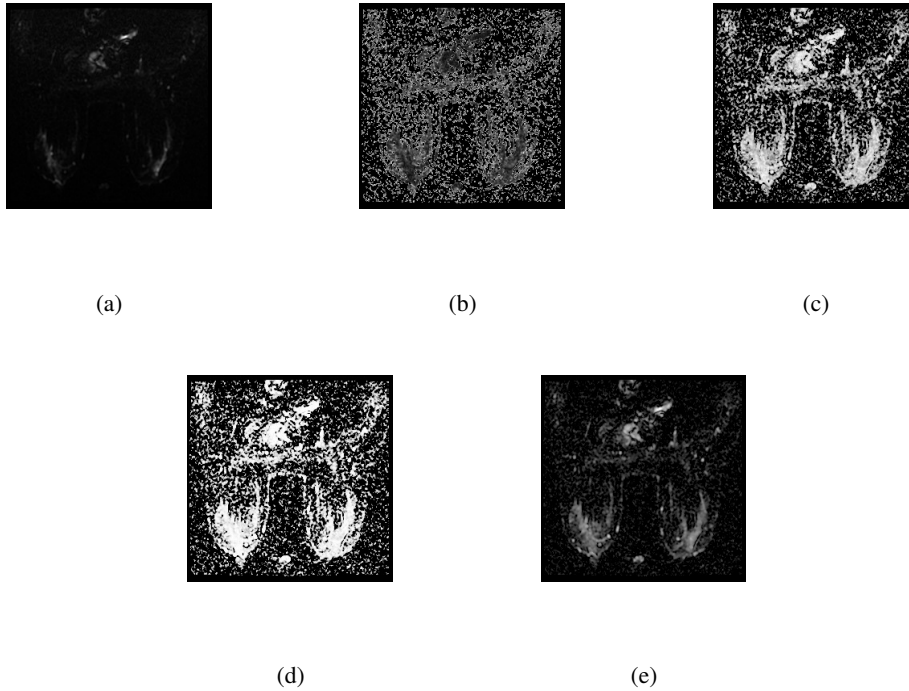

(a)

(b)

(c)

(d)

(e)

Figure 1: Resulting images of Task 2. (a) baseline image (b) FA (c) inverse FA (d) VR (e) MD

3   Task 3. Exploring White Matter Fibers

Question1: The highest FA value is 0.977262, which locates at the vovel $(64, 75, 51)$ in white matter. The main component of gray matter is cell bodies. By contrast, white matter is composed of nerve fibers. The structure of nerve fibers, such as axons and their myelin shield, is able to facilitate the translation of water molecules. Thus, the FA of diffusion tensor in white matter is generally larger than those in gray matter.

Question2: The version of the *Slicer* we used to generate DTI image is 4.6.2. An extension, *SlicerDMRI*, was installed to import some relative moduls. Figure 2 is the required screen capture, it was done by following the tutorials file *DiffusionMRIanalysisTutorial_Slicer4.5_SoniaPujol.pdf*. The tracts are stretched from the green area of the sagittal slice.
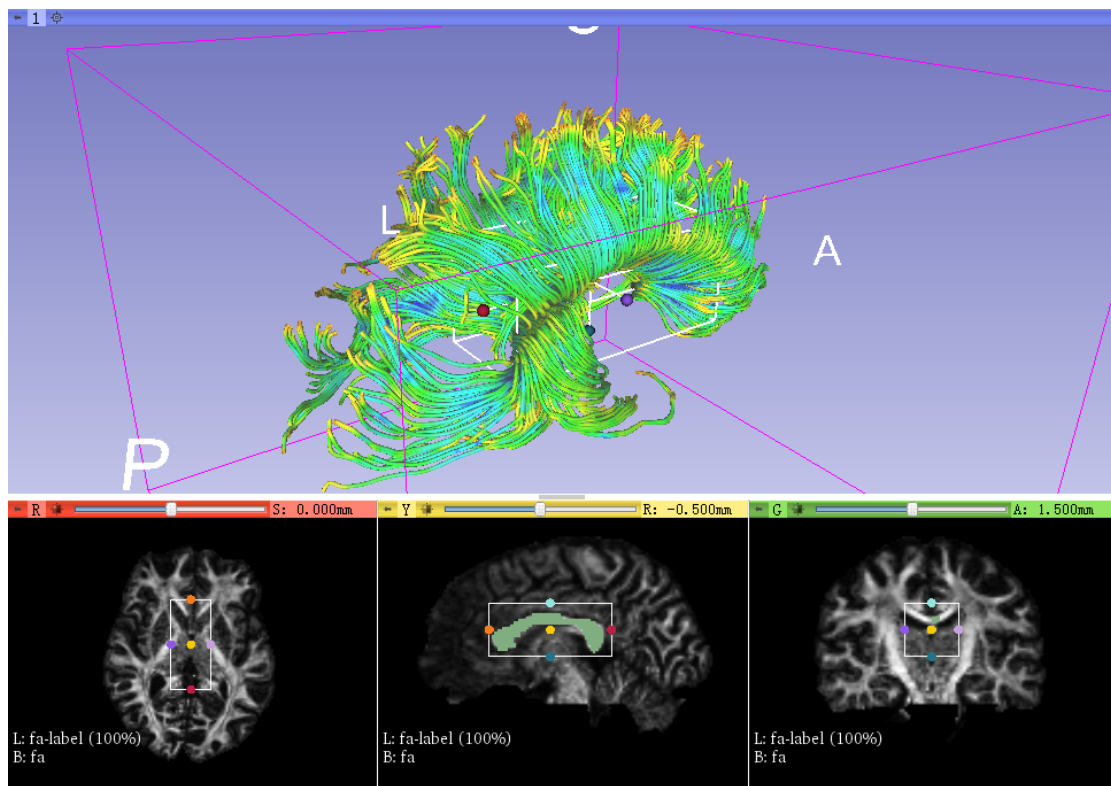

Figure 2: Screen capture of computed tracts as tubes coloured

4 Task 4. Analysis of MRI Data: Diffusion Signal Curve Fitting

4.1 Compulsory Task

It can be observed that there is an outlier in S Normal signal. This outlier is replaced by the mean of the previous data and the next data as shown in Figure 3. All results of fitting curves are displayed in Figure 4, in which L-Fit data indicates the the curve fitted by least-square method with data whose b factor is less than 1000 s/mm^2. NL-Fit data shows the results of non-linear fitting curves that estimated by computing the same data with in L-Fit. NL-Fit method, in this case, has degree of freedom of 14 (16 - 2, where 16 is the number of data samples, 2 is the number of parameters to be estimated). The curve fitted by non-linear method with all data is displayed as NL-Fit data.

All these three methods are applied to fit S Normal and S Tumor data, presenting the result in regular y-scale and logarithmic y-scale. The sum of square residuals for S Normal fitted data is 60309, and for S Tumor fitted data is 74897. However, in our opinion, the best result is the S Tumor data fitted by non-linear method with all data since it is more consistent with original data both in regular y-scale and in logarithmic y-scale.
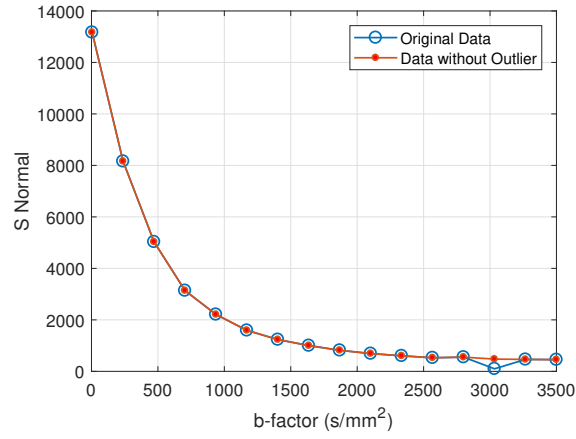
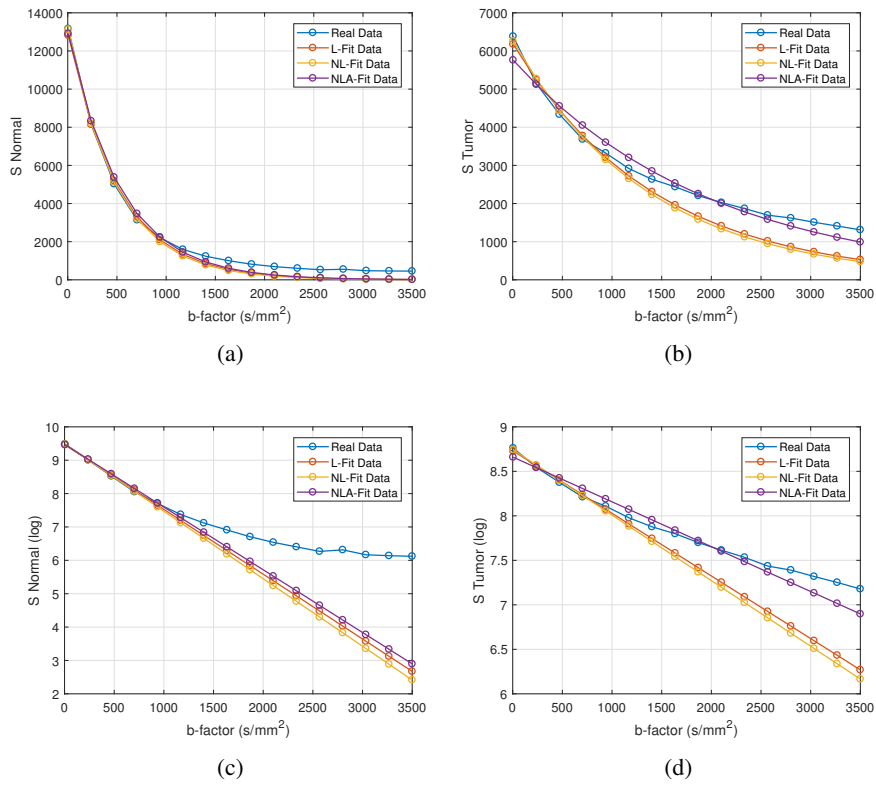*Figure 3: Original S Normal data and S Normal data removed outliers*

(a)

(b)

(c)

(d)

Figure 4: Curve fitting of (a) S Normal, (b) S Tumor, (c) logarithmic S Normal, (d) logarithmic S Tumor.

4.2 Optional Task

4.2.1 Task 2. Diffusion Tensor Imaging

The FA and PDD for known diffusion tensor D is shown as below.

$$\mathbf{D} = 10^{-4} \cdot \begin{bmatrix} 17 & 0 & 0 \\ 0 & 7 & 0 \\ 0 & 0 & 4 \end{bmatrix}, \mathbf{FA} = 0.6266, \mathbf{PDD} = \begin{bmatrix} 1.0000 & 0.0000 & 0.0000 \end{bmatrix}$$

In Step (2), Gaussian noise is added into the measured signal, which will be used to estimate a new diffusion tensor $\widehat{D}$. The $\widehat{FA}$ and $\widehat{PDD}$ of $\widehat{D}$ is also calculate, as well as the angular error (AE) between

PDD and $\widehat{PDD}$. In Step (3), repeat Step (2) 100 times, the mean of $\widehat{FA}$ and the mean of AE is shown as follows:

mean $\widehat{FA}= 0.6252$, **mean** $AE= 0.0129rad$

When repeat Step (3), the obtained results are not exactly same as previous ones, since in each repetition, different noise in Gaussian distribution is generated and added into the measured signal. Repeat Step (3) 100 times, the 95% confident intervals (CI) for 100 mean $\widehat{FA}$ and 100 mean AE are calculated. It can be observed that though the mean $\widehat{FA}$ and the mean AE changes in each iteration, the range of CI is limited into a small scope. Because the noise that meets Gaussian distribution with zero mean, the noise will be counterbalanced when multiple signals are superposed.

CI for **mean** $\widehat{FA}$: $\begin{bmatrix} 0.6262 & 0.6268 \end{bmatrix}$

CI for **mean** AE: $\begin{bmatrix} 0.0127 & 0.0130 \end{bmatrix}$

If the SNR is increased, variance σ^2 would be reduced, resulting in that fewer noise will be added into the signal. Thus, the mean $\widehat{FA}$ and the estimated $\widehat{PDD}$ is likely to be more closer to the real values. The invariant parameter is FA if we have the same diffusion tensor but in a different orientation. Since, FA has no connection with eigenvectors of the diffusion tensor.

If S_0 is unknown, the diffusion tensor can be estimated on the basis of the modification of Equation 4 and Equation 5, which is shown as 6. Now, there are seven parameters that can be estimated by least-square method.

$$log(S(b)) = log(S_0) - bBD' = \begin{bmatrix} 1 & -bB \end{bmatrix} \cdot \begin{bmatrix} log(S_0) \\ D' \end{bmatrix} \tag{6}$$