Effects of Diffusion Gradient Direction Numbers on DTI-derived Metrics: A Real Image Data Study

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Introduction: In recent years, effect of diffusion gradient sampling scheme on the accuracy of final DTI-based metrics, such as FA and Trace, has been evaluated by different groups [1,2]. Meanwhile, with increasing clinical use of DTI, it becomes more important to achieve a better compromise between data accuracy and scanning time. Inspired by the conclusion of Jones's recent publication based on Monte Carlo simulation [3], we measured the variations of DTI derived metrics between different clinical DTI protocols with real DTI data sets, and evaluated requirements for measurement accuracy and scanning time for typical clinical studies.

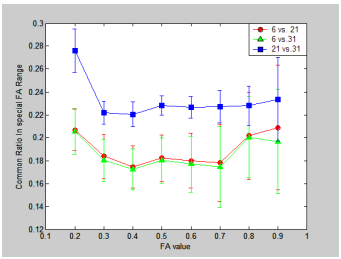
Material and Methods: We scanned 13 healthy normal volunteers on a GE 1.5T scanner (Excite11). For each volunteer, three brain DTI images data sets were acquired with three protocols. Except the difference in diffusion gradient directions (6, 21 and 31), each data set has exactly the same imaging parameters (128x128x28 matrix, TR/TE=6000/80 ms and b-value=1000s/mm^2) and exactly the same slice position. In order to keep SNR of all three data sets the same, different average numbers were used for different protocols and the total numbers of images were kept the same. Before evaluating the equivalence between protocols, pre-processing has been taken to carefully remove eddy current effects and motion artifacts. Comparisons are made between every pairs of the three data sets. Image pixels were categorized into subgroup according to the FA value with the stepwise increase of 0.1. Pixel-wise comparison were made based on three criteria: (1) Identity of commonly used diffusion metric like FA and Trace from two protocol images (Paired-t test); (2) Matching of measured diffusion tensor shape metrics: C_L(linearity), C_P(Planarity) and C_S(Sphericity)[4]; (3) Matching of diffusion tensor orientation (evaluated by difference of principal eigenvector), between images from two protocols. For the pixel subgroups from different protocols but within same FA range, only those pixels occupying the same spatial locations in both data sets were used.

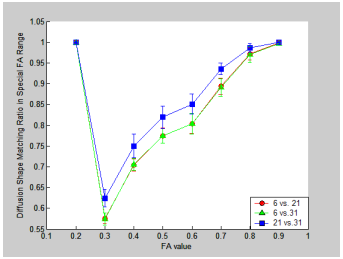
Several quantitative indices were calculated in assist of evaluating criterion 2 and 3: Common Ratio: $CR = \frac{N_{com}}{N_{P1} + N_{P2}}$ $(N_{com} = N_{P1} \cap N_{P2})$, measures the overall matching between two protocols (P_1,P_2). Orientation discrepancy: $\Delta\theta = \frac{1}{N_{com}}\sum(\theta_i^{P1} - \theta_i^{P2})$ and $\Delta\phi = \frac{1}{N_{com}}\sum(\phi_i^{P1} - \phi_i^{P2})$, with θ, ϕ being orientations of the principal diffusion eigenvector. These orientation discrepancy measures were further subcategorized for pixels that are interpreted as different shape: cigar (C_L), pancake (C_p) and sphere shape (C_s) [5]. To evaluate the specificity of protocol for diffusion shape detection, discrepancy of diffusion orientation in terms of azimuth angle difference is only taken into account for pixels that are interpreted as the same shape in both protocols. Therefore, based on the three criteria above, only those protocols which not only result in statistically identical FA and Trace values but also matched tensor shape and orientation interpretation are treated as equivalent.

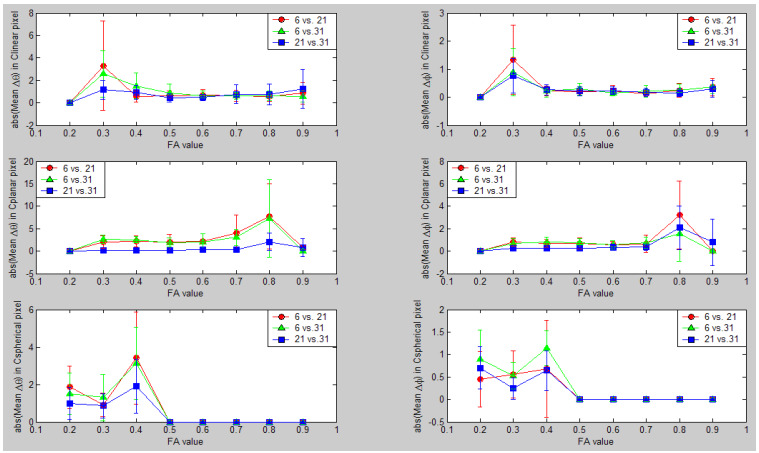
Results and Discussion: (1). Figure-1 shows the common ratio (CR) of different protocols in each range of FA. In all the range, protocols with 21 directions (P_{21}) and with 31 directions (P_{31}) illustrate better overall matching of FA map than with 6 directions (P_6). (2). As for tensor shape and orientation interpretation, Figure-2 shows the overall diffusion shape matching ratio between P_{21} and P_{31} is also better than the ratios between any other two protocols' combination. Figure-3 gives detail information of orientation discrepancy of special diffusion parameters between two protocols. Judged by the given plot, P_{21} and P_{31} result in much closer description of diffusion in all the range of anisotropy. (3). Results from paired-t test on FA and Trace varied with different FA range as well as different subjects. However, when anisotropy increase (FA>0.7), paired-t test show three protocols give us the statistically identical FA and Trace map (For details refer to [6]). The potential advantages of more diffusion directions are also suggested by our results. In Figure-3, for FA ranging from 0.3 to 0.4 where the diffusion shape changes substantially (C_L changes from 0.08 to 0.15, C_p from 0.15 to 0.23 and C_s from 0.78 to 0.64). This range corresponds to complicate environments such as fiber crossing or partial volume effects. In this range, 21directions and 31 directions give less uncertainty compared to 6 directions.

Conclusions: (1). In terms of three criteria discussed above, our results show that overall variation of diffusion metrics between 21-direction and 31-direction protocols is smaller than with 6-direction protocol. More accurate definition of diffusion directions will provide better interpretation of diffusion properties in vivo. Our results support the Jones' statements on effect of gradient number on FA uncertainty [3]. (2). Even though in high anisotropic region, FA and Trace distributions from three protocols are statistically identical, measurements with more diffusion directions lead to better diffusion orientation interpretation. Therefore, for applications that are largely depend on orientation information like fiber tracking, more diffusion directions may be desirable. Further investigations on potential applications with many diffusion gradient directions as the routine clinical DTI study need to take into consideration other factors such as partial volume effects, to achieve a better compromise between accuracy and time efficiency.

Figure-1 (below left): Common Ratio (CR) between protocols.
Figure-2 (below right): Diffusion Shape Matching Ratio (DSMR) between protocols in different range of FA. *DSMR=($N_{sameshape}$/N_{total_pixel})*.
Figure-3 (far right): Diffusion Orientation Discrepancy (OD) of different diffusion shapes between protocols. OD is described by azimuth angles' difference of principal eigenvector for pixels that are occupied same spatial location in both protocols, within the same FA range and interpreted as the same diffusion shape. Absolute values of the mean angle difference (Mean OD) of all 13 subjects are presented here.







Acknowledgments: This work was partially supported by the NIH under Grants NS32024 and NS41048.

Reference: [1]. Jones DK *et al*. *Magn Reson Med* 1999; 4:515-525; [2]. Papadakis NG *et al. Magn Reson Imaging* 2000; 18:671-679; [3]. Jones DK. *Mag Reson Med* 2004; 51:807-815; [4]. Westin C-F *et al*. *Proc ISMRM* 1997, p. 1742. [5].Alexander AL *et al. Magn Reson Med* 2000; 44:283-291. [6]. Ni H. *et al*, RSNA 2004.