Quantitative Improvement of Diffusion Spectrum Imaging Tractography using Statistical Denoising

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Introduction

The diffusion spectrum imaging (DSI) technique can map intravoxel heterogeneity of molecular water diffusion and depict complex fiber architecture within tissue structures [1]. Theoretically, an extremely high maximum *b*-value (i.e., > 10000 s/mm^2) is necessary for good DSI reconstruction, though this is difficult to achieve due to limited signal-to-noise ratio (SNR). Previously, an optimized q-space sampling scheme with fewer encoding points and a lower maximum *b*-value was proposed for DSI on clinical MRI systems [2]. While this scheme is potentially useful for clinical applications, low SNR is still a critical issue which affects the accuracy of mapping fiber orientations and tractography. Therefore, in this study, a joint statistical denoising algorithm [3;4] was applied to DSI data. The effect of noise reduction was investigated quantitatively according to a systematic angular analysis based on subsampled *in-vivo* data. An improvement to fiber tractography for several important tracts was also demonstrated through visual comparison of results from the original and denoised DSI datasets.

Materials and Methods

Diffusion data were obtained from five healthy volunteers on a 3T MRI system (Tim Trio, Siemens, Erlangen, Germany). To reduce eddy current effects, a twice-refocused balanced echo diffusion EPI sequence was used for data acquisition [5]. A total of 203 diffusion-weighted images with a maximum *b*-value of 4500 s/mm^2 were acquired on a 3D grid in q-space [2]. Isotropic voxels were obtained with an in-plane resolution and slice thickness of 2.5 mm. A total of 56 slices were acquired, and the total scan time was approximately 30 minutes. To remove noise from the DSI images, a statistical model was used that incorporates an implicit shared line-site prior based on spatial edge features [3;4]. The algorithm was applied to the magnitude of diffusion images, which sacrifices some of the theoretical characterization of the approach, but leads to significantly simpler data processing. The parameters of the denoising algorithm were set to achieve between a 1.4 and 1.7-fold improvement in SNR, equivalent to averaging between 2 and 3 times. DSI analysis was based on the Fourier relationship between the measured signal S($\boldsymbol{q}$) and the diffusion probability density function P($\boldsymbol{r}$) (PDF), i.e., S($\boldsymbol{q}$) = FT{P($\boldsymbol{r}$)} [1;6]. An orientation distribution function (ODF) was computed by integrating P(r) r^2 along each radial direction. Using the theoretical symmetry of q-space, each 203-point DSI dataset was divided into two complementary half-sampled 102-point datasets (Figure 1), and the reproducibility of ODF reconstruction was evaluated by calculating the angular precision (Pa) and dispersion (D) between both datasets [2]. A threshold on the number of the main orientations from one of the original half-sampled DSI datasets was used to divide the voxels into single-fiber and crossing-fiber groups. Angular analysis was performed using in-house program written in MATLAB (The Mathworks, Natick, MA, USA) [2]. Finally, using in-house software (DSI studio, http://dsi-studio.labsolver.org/), a streamline-based fiber tracking algorithm was applied to the DSI data and three specific tracts were selected by using the region-of-interest (ROI) method.

Results

The results of angular analysis were consistent for all five subjects, and are shown in Figure 2. For the single-fiber group, the denoised data had a Pa of 6.52° ± 0.72°, which is significantly lower than the Pa of 8.88° ± 0.99° for the original data. Similarly, for the crossing-fiber group, the Pa of the denoised data was 28.78° ± 2.71°, which is significantly lower than the Pa of 34.94° ± 2.53° for the original data. The angular dispersion values for the single-fiber group were 0.9378 ± 0.0089 for the original data and 0.9578 ± 0.0066 for the denoised data. For the crossing-fiber group, angular dispersion was 0.6208 ± 0.0294 and 0.6900 ± 0.0323 for the original data and denoised data, respectively. These numbers show that the denoised data consistently had significantly better angular dispersion in both the single-fiber and crossing-fiber groups than the original data. Tractography results using the original and denoised datasets with 203 encoding points from a single subject are shown in Figure 3, with large differences indicated by white arrows. Three white matter tracts, namely the cortico-spinal tract, corpus callosum, and arcuate fasciculus, are shown in this figure to demonstrate the utility of noise reduction for fiber tracking. As can be seen, the noise in the original data leads to interrupted or fewer fibers compared with the results from the denoised data.

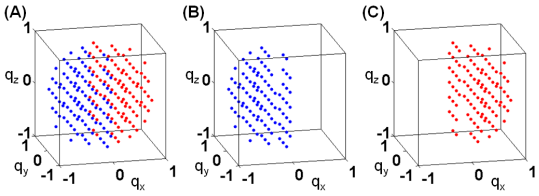

Figure 1. DSI encoding schemes. (A) The fully-sampled 203-point scheme, and (B-C) two complementary half-sampled 102-point schemes.

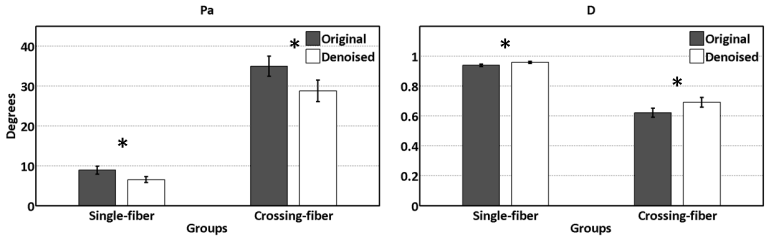

*Figure 2. The results of angular analysis from in-vivo data. (left) Pa and (right) D, for original and denoised datasets (Number of subjects = 5, * p < 0.05)*

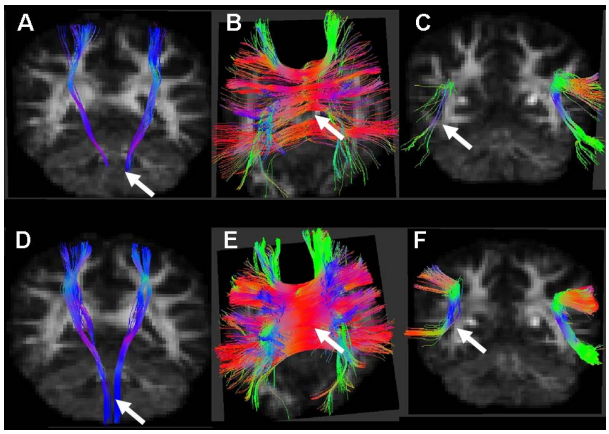

Figure 3. The tractography results using the original (upper row) and denoised (lower row) datasets from a single subject. Three specific tracts are shown here: (A,D) cortico-spinal tract, (B,E) corpus callosum, and (C,F) arcuate fasciculus.

Discussion and Conclusion

In this study, the utility of a statistical denoising algorithm was investigated quantitatively for DSI. The improvement in the angular precision and dispersion was consistent with the expected gain in SNR. As for the tractography results, the reduction of noise significantly improved the precision of fiber tracking. In future work, we will further analyze the relationship between SNR improvement and the precision of fiber tractography. In addition, we will investigate how the increase in SNR may be used to achieve higher spatial resolution and reduce partial volume effects, or to reduce acquisition time and improve patient throughput.

References

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