Deep Learning-Based Algorithm for Reconstructing Diffusion Tensor Distribution Imaging Parameters

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Introduction: Traditional diffusion magnetic resonance imaging (dMRI) methods struggle to characterize multiple diffusion properties within a single voxel. In contrast, diffusion tensor distribution (DTD) imaging provides diffusion tensor distribution for each voxel, offering more precise information on tissue diffusion characteristics. From the diffusion tensor distribution, essential metrics related to tissue diffusion can be computed, such as the expected values of isotropic and anisotropic diffusion, their variances, covariance, and the expected values of isotropic and anisotropic diffusion of three properties (gray matter, white matter, cerebrospinal fluid) delineated by the distribution[1]. Currently, Monte Carlo (MC) inversion remains the most prevalent method for obtaining diffusion tensor distribution. However, it faces challenges: it requires expensively computational resources and entails lengthy solution times, limiting its practical application. Moreover, MC methods independently handle each voxel without considering the spatial continuity of diffusion properties.

Methods: To address these issues, we propose a deep learning model called DTDMapper. This model takes dMRI signals as input and generates DTD metrics in an end-to-end manner. Figure 1 illustrates the model framework.

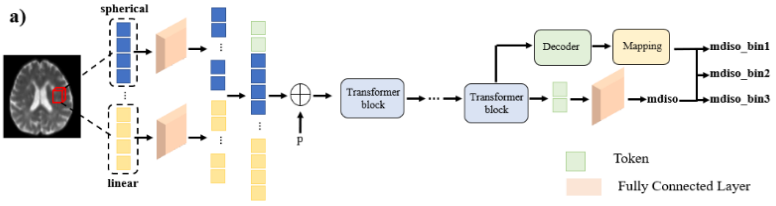

Figure1. The network framework consists of three parts: encoder, decoder. an encoder employs attention mechanism to capture relationships between central and neighboring voxels; a decoder utilizes multiple threshold and convolutional layers to emulate sparse dictionary construction and lookup.

Results and discussion: In Figure 2, the left figure illustrates the process of calculating the signal fractions using DTD, while the right side compares the model predicted results with those obtained from MC inversions. Across all parameters, SSIM surpasses 0.9. Compared with MC, our model achieves nearly a 15-fold reduction in parameter prediction time and smoother results.

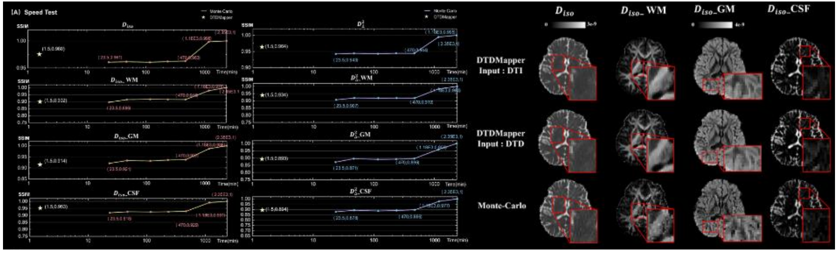

Figure 2 (A) Speed Test experiment. The horizontal axis represents the required computation time (minutes), while the vertical axis shows the SSIM compared the results of 1, 2, 5, 10, 20, 50, 100 times MC and DTDMapper (star) with reference. (B) Analysis of Output Accuracy experiment. Comparison of isotropic and anisotropy metrics of healthy subjects sub017 (male, 23 years old, MRI) under DTDMapper and Monte Carlo methods.

Conclusion: This study introduces the first application of a deep learning model for computing diffusion tensor distribution parameters, effectively addressing computational complexity and spatial continuity issues inherent to Monte Carlo methods. Our approach holds promise for widespread adoption in clinical and research settings.

References: 1. Topgaard D. Diffusion tensor distribution imaging. *NMR Biomed.* 2019;32(5):e4066. doi:10.1002/nbm.4066