**Application of Deep Learning to Quantify Brain Microstructure**

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1. Introduction

Diffusion-weighted magnetic resonance imaging (DW MRI) offers valuable insights into cellular structures, making it a powerful tool for the non-invasive evaluation of brain microstructure. This modality is particularly sensitive to natural processes of brain maturation and aging, and various neurological disorders [1]. However, accurate modeling of the DW signal is crucial for extracting quantitative indicators, especially when the acquisition procedure is limited.

1. Description of the problem

Diffusion tensor imaging (DTI) [2] is a widely used technique for modeling the DW signal, but interpreting its data can be challenging as it only captures the primary direction of diffusion [1]. An alternative approach involves using multicompartment biophysical models that assume specific tissue geometries and can directly estimate key microstructural parameters, making data interpretation easier [3]. Two of the most popular biophysical models are Neurite Orientation Dispersion and Density Imaging (NODDI) [4] and the Spherical Mean Technique (SMT) [5] (see Fig.1). Microstructural parameters derived from multicompartment models are typically calculated using numerical optimization procedures. However, these methods require more complex and time-consuming acquisition protocols, including a specific number of DW volumes, than those commonly used in clinical practice. This complexity significantly limits the practical application of biophysical models in clinical settings.



**Fig.1.** Distribution of the total DW signal between different compartments of the A. NODDI and B. SMT models.

1. Related work

Research in the literature has explored the potential application of deep learning to estimate parameters of multicompartment models, especially the NODDI [6,7]. However, these studies are quite limited in scope. They often focus only on the effects of a reduced number of DW volumes, while employing acquisition schemes that are not commonly used in clinical practice.

1. Solution to the problem

The study utilized the HCP WU-Minn data [8], which originally included 90 gradient directions for three b-values (1000, 2000, and 3000 s/mm2). To simulate acquisition protocols more representative of clinical settings [9], the data were downsampled and interpolated using spherical harmonics to generate three separate datasets with b = 1000 s/mm² and 32, 15, and 6 gradient directions. Microstructural parameters were estimated using both traditional numerical optimization techniques and a deep learning-based U-net model. Parameters derived from the original, full-resolution acquisition were used as the ground truth for comparison. Performance evaluation was conducted using the Mean Structural Similarity Index Measure (MSSIM).
A summary of the results is provided in Table 1.

**Table 1.** MSSIM results of the U-Net and a standard numerical method across different acquisition schemes, assessed for various parameters of the SMT and NODDI models.

|  |  |  |  |
| --- | --- | --- | --- |
|  | **32 volumes, b1000** | **15 volumes, b1000** | **6 volumes, b1000** |
| **Microstructural parameter** | **DL model** | **Numerical method** | **DL model** | **Numerical method** | **DL model** | **Numerical method** |
| **vic** | 0.950 | 0.703 | 0.947 | 0.704 | 0.945 | 0.698 |
| **vec** | 0.785 | 0.099 | 0.791 | 0.103 | 0.784 | 0.116 |
| **viso** | 0.884 | 0.484 | 0.887 | 0.488 | 0.867 | 0.495 |
| **vin** | 0.833 | 0.225 | 0.823 | 0.218 | 0.823 | 0.065 |

1. Conclusions and future work

Deep learning models significantly outperform traditional numerical method, achieving MSSIM values over 0.8 for all parameters except vec, even with only 6 gradient directions.

To better assess ability of artificial intelligence to estimate microstructural parameters, we should move beyond U-Net to more advanced models like GANs, and focus on metrics more clinically relevant than MSSIM, particularly in key regions of the brain. It's also crucial to determine if these models can effectively differentiate parameter values between healthy individuals and those with diseases to support accurate diagnosis.

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