A NEW FIBER TRACT COLOR-ENCODING SCHEME BASED ON DIFFUSION TENSOR MODEL RESIDUALS

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Introduction and purpose

Diffusion Tensor MRI (DTI) and Fiber Tracking (FT) have become important tools for studying white matter (WM) anatomy and pathology [1]. However, interpretation of DTI data is required before drawing conclusions on the underlying WM fiber architecture, i.e., is the observation-of-interest really a true effect or an artifact arising from noise, distortions, subject motion, inadequacy of the model, etc. Due to the high-dimensional multi-component nature of DTI data, distinguishing between real and artifactual observations is often non-trivial, especially in a clinical setting. To bridge this gap between the acquired images and the understanding of the underlying WM microstructural organization, specialized FT visualization methods have been developed that display various WM properties along the fiber tracts (encoded by pathway shape and color) [2-4]. However, none of these visualization approaches reflects the acquired data quality (artifacts) or Goodness-of-Fit (GoF) to the model, which is crucial in interpreting analysis results, as recently emphasized [5]. In this context, we developed a new color-encoding scheme for visualizing fiber tracts, based on the analysis of tensor model residuals, which allows the investigation of data quality and GoF.

Methods

Data acquisition and processing: 2 cardiac-gated DTI data sets (2.4 mm slice thickness; FOV = 23 cm; 96×96 acquisition matrix, reconstructed to a 128×128 image matrix) were collected on a 3 Tesla MR system using a 60 directions gradient sampling scheme with 6 non-diffusion-weighted (DW) images ("data 1": b = 1200 s/mm^2 and "data 2": b = 3000 s/mm^2) [6]. The tensor model was fitted using a non-linear regression procedure [7] and a deterministic FT approach was applied [8].

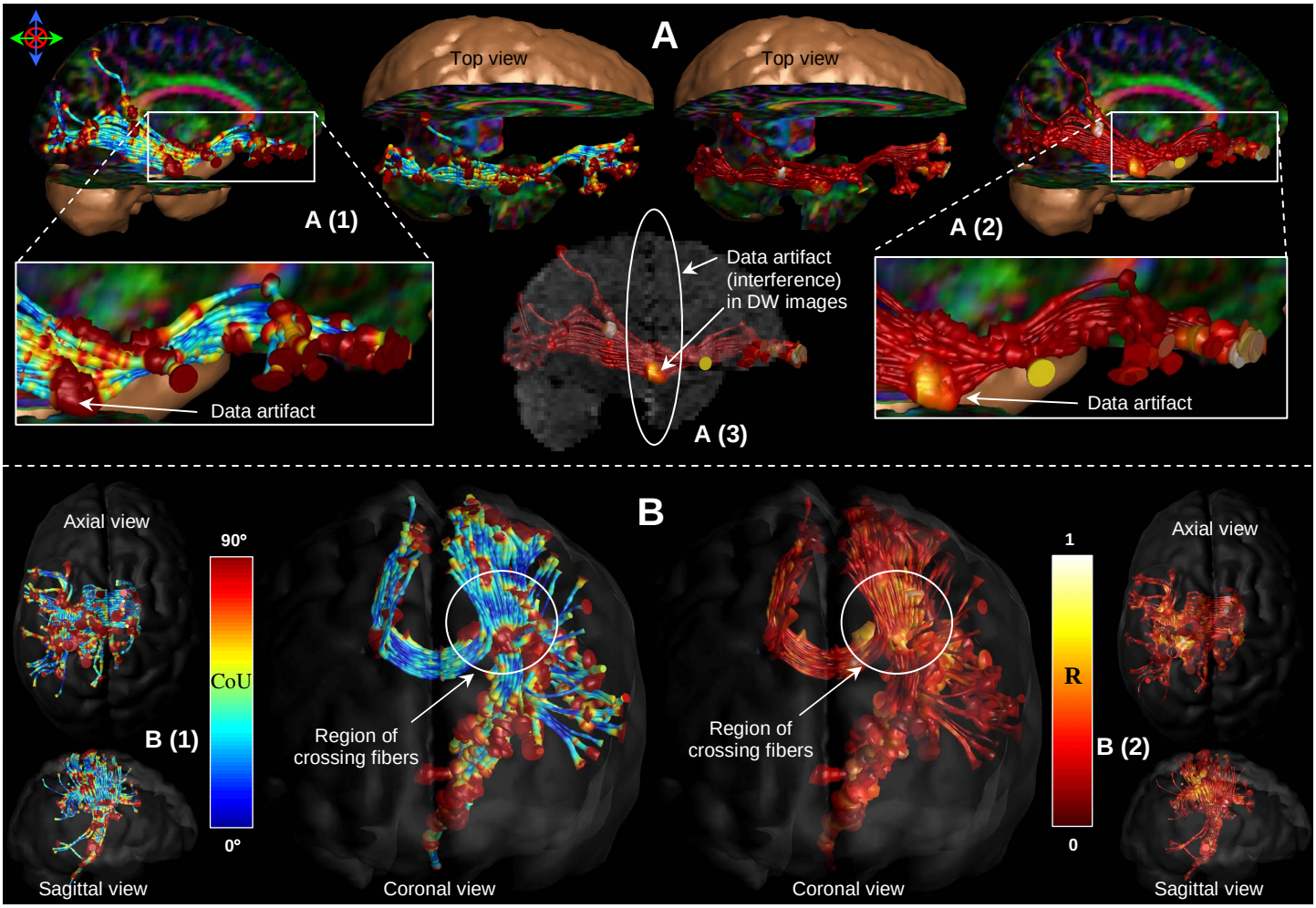
Visualization: fiber pathways were displayed as hyperstreamlines, where the width of the hyperstreamline encodes the 95% 'Cone of Uncertainty' (CoU), i.e. the uncertainty of the first eigenvector [4]. For Fig. A(1) and B(1), this CoU is also color-encoded as shown by the color bar in Fig. B(1). On the other hand, in Fig. A(2) and B(2), the proposed color-encoding represents the normalized median absolute value of the DW residual with respect to the tensor model ('R') for each point along the tract pathway and provides complementary information about data quality ("data 1" → Fig. A) and/or (in)adequacy of the tensor model ("data 2" → Fig. B).

Results and discussion

As shown in Figs. A(1) and B(1), the color-encoding only emphasizes the CoU, which is already represented by the local tract tube width. The following 2 examples show the benefit of our new color-encoding scheme: **1)** In Fig. A, right hemisphere fronto-occipital fibers are reconstructed using "data 1", which suffers from an interference artifact, as indicated in Fig A(3). When comparing the enlarged region of Figs. A(1) and A(2), this artifact is clearly visible in A(2), but can not be differentiated from other regions with a high CoU in A(1). **2)** In Fig. B, fiber tracts were reconstructed using "data 2". As indicated by the region of crossing fibers (originating from the corpus callosum, cortico-spinal tracts, and the superior longitudinal fasciculus), the non-Gaussian diffusion behavior (high b-value), reflected by the high values of 'R' (inadequacy of the tensor model), can be observed in Fig B(2), but not in Fig A(2).

Conclusion

In conclusion, with our new color-encoding scheme, based on the analysis of tensor model residuals, we have demonstrated the potential to investigate data quality and GoF, which is important in interpreting analysis results.



References

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