Two-tensor model-based bootstrapping on classified tensor morphologies: estimation of uncertainty in fiber orientation and probabilistic tractography

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Abstract

In this manuscript, fast and clinically feasible model-based bootstrapping algorithms using a geometrically constrained two-tensor diffusion model are employed for estimating uncertainty in fiber orientation. A Monte-Carlo-based tensor morphology voxel classification algorithm is initially applied using single-tensor bootstrap samples before the use of a two-tensor model-based bootstrapping algorithm. Classification of tensor morphologies allows the tensor morphology to be considered when selecting the most appropriate bootstrap procedure. A constrained two-tensor model approach can greatly reduce data acquisition and computational times for whole bootstrap data volume generation compared to other multifiber model techniques, facilitating widespread clinical use. For comparison, we propose a new repetition-bootstrap algorithm based on classified voxels and the constrained two-tensor model. Tractography with these bootstrapping algorithms is also developed to estimate the connection probabilities between brain regions, especially regions with complex fiber configurations. Experimental results on synthetic data, a hardware phantom and human brain data demonstrate the superior performance of our algorithms compared to conventional approaches.
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1. Introduction

Diffusion magnetic resonance (MR) tractography has rapidly become an important clinical tool for investigation of white matter architecture in the human brain. Diffusion tensor imaging (DTI) [1] is most commonly used to extract fiber orientations for tractography from diffusion-weighted MR imaging (DW-MRI) data sets. However, this single-diffusion-tensor model does not correctly express the microstructure in voxels that contain more than one fiber orientation. In such regions, the orientation extracted from the diffusion tensor is unreliable, which may cause the tracking process to terminate or tracking to switch to an unrelated adjacent tract [2]. The development of new models based on high-angular-resolution diffusion imaging (HARDI) seeks to provide solutions to this problem. However, HARDI requirements are not always easy to meet in a clinical environment.

Clinical feasibility means that the diffusion MR data acquisition and analysis must be suitable for a clinical environment. Generally, clinical feasibility depends on the speed of image acquisition, practicality of imaging and the speed of the analysis. HARDI-based methods, including multitensor models [3], spherical deconvolution [4] and Q-ball imaging (QBI) [5], require longer acquisition times than conventional DTI and are generally not suitable for clinical applications. The estimation of these models and the tracking processes using them are demanding in terms of memory requirement and processing time (e.g., persistent angular structure (PAS)-MRI [6]) and are sometimes impractical. The high b values utilized in some cases increase sensitivity to subject motion, which is also undesirable in a clinical setting. Constrained spherical deconvolution (CSD) [7] has shown good results when applied to relatively low-angular-resolution DW data; however, only orientational

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