

Two-Tensor Residual Bootstrapping on Classified Tensor Morphologies

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Introduction: The residual-bootstrap method [1] using a single diffusion tensor is an alternative to conventional bootstrapping for characterising uncertainty in DTI and for reconstructing white matter fibre tracts. Multi-tensor imaging can classify multiple intra-voxel fibre configurations within regions of complex white matter architecture. In this study, a fast and clinically feasible residual bootstrapping algorithm using a two-tensor diffusion model is employed for estimating uncertainty in fibre orientation and probabilistic tractography. Voxels are classified based on tensor morphologies before applying single and two-tensor residual bootstrapping algorithms. The classification of tensor morphologies allows the tensor morphology to be considered when selecting the most appropriate bootstrap procedure. We use a constrained two-tensor model [2] for planar voxels, using the information present in the single-tensor fit. Acquisition times can be greatly reduced compared to other multi-tensor approaches, facilitating widespread clinical use. We evaluated the algorithm using images of a physical phantom containing complex fibre configurations.

Two-Tensor Residual Bootstrapping Algorithm: We first fit a single-diffusion tensor using linear least squares for the acquired DW-data, and then decide which voxels are suitable for single-tensor or two-tensor fit based on classifying tensor morphology algorithm. We compute the residuals to the fitted model (single-tensor or two-tensor) for each voxel. The residual bootstrapping approach assumes that all residuals have similar distributions and freely resamples among them. Repeating these steps, resampling and estimation, builds up a collection of tensors called a residual bootstrap distribution. The generated residual bootstrap volumes contain a combination of single-tensor and two-tensors as appropriate for the nature of the particular voxel.

Classifying Tensor Morphologies: The use of bootstrap methods to quantify uncertainty in estimating fibre orientation is determined primarily by tensor morphology [3]. The three types of degenerate tensors are isotropic (I) ($\lambda_1 = \lambda_2 = \lambda_3 > 0$), oblate (O) ($\lambda_1 = \lambda_2 > \lambda_3 > 0$), or prolate (P) ($\lambda_1 > \lambda_2 = \lambda_3 > 0$) where λ_i ($i=1,2,3$) are the three eigenvalues of the tensor. We verified three equalities based on the testing procedure of Zhu et al. [4], sequentially to classify tensor morphologies (TM) at each voxel. Two-tensor residual-bootstrapping algorithm was applied to oblate (TM=O) voxels and single-tensor residual bootstrap algorithm to the other voxels.

Two-Tensor Estimation: A geometrically constrained two-tensor model [2] was used to find the two diffusion tensors and reduce the degrees of freedom in the original multi-tensor model. This model assumes that both fibre tracts are constrained in the plane spanned by the first two principal eigenvectors from the single-tensor fit. The equation $E(q_i) = S_i/S_0 = fe^{-b\tilde{g}_i^T D_A \tilde{g}_i} + (1-f)e^{-b\tilde{g}_i^T D_B \tilde{g}_i}$ [2] becomes a system of nonlinear equations and minimises $\sum_i (E(q_i) - E(q_i))^2$, which gives the estimated tensor elements D_A , D_B and the fraction f . In each gradient direction i , a residual ε_i is calculated according to $\varepsilon_i = E(q_i) - \hat{E}(q_i)$. Two-tensor estimation was performed using the Levenberg-Marquardt optimisation algorithm.

Probabilistic Fibre Tractography: Having generated n tensor volumes for residual bootstrapping methods, for individual bootstrapped trajectories; a simple fourth order Runge-Kutta streamline tracking algorithm was used to propagate streamlines bidirectionally from given seed points. The algorithm was repeated for each of the n volumes to generate n tracts for each seed point. If the seed point is in a region of crossing fibres then two separate trajectories are generated from the seed point using two fibre orientations. The deterministic tracking algorithm is then used to propagate the trajectories to the next position. We use two tensors per position in the planar tensor morphology regions, and also the two principal eigenvectors to determine which if any of the trajectories should be followed. For each position, we choose the diffusion tensor which has the smallest angular difference to the principal eigenvector calculated from the previous position.

Physical Phantom: 3T DTI data was acquired from a physical phantom [5] with $3 \times 3 \times 3$ mm³ voxel resolution, b value = 1500 s/mm² and 64 diffusion directions. We applied the two-tensor residual bootstrapping algorithms to the phantom data, and generated 1000 residual bootstrap volumes. The probabilistic tractography algorithm was applied to the residual bootstrap volumes from 3 pre-defined seed positions and a comparison of the results of our method with that of the single-tensor residual bootstrapping applied on the same starting points.

Results and Discussion: Ideally, one would expect the tractography trajectories starting from the seed point (Fig. 2-1st row and Fig. 2-3rd row) to cross the regions 1,2 and 3 (Fig. 1 (a)); instead as they enter the fibre crossing region the fibre tracts diverge in the wrong direction. With our method the trajectories correctly cross the fibre crossing region and tracts are similar to the expected ground truth. The seed point (Fig. 2-2nd row) selected as a target shows the branching ability of the two-tensor residual bootstrap algorithm. The estimated pathways of single-tensor residual bootstrapping have leaked and are dispersed, which makes the main pathway of connectivity more difficult to comprehend. Based on our experimental evaluations, first, we can use data which is routinely available from clinical scans to implement this approach and unlike previous bootstrap methods with other multi-fibre modalities our algorithms show improved computational efficiency, making them clinically feasible. Secondly, our bootstrap algorithms are implemented on appropriate tensor morphology voxels to increase the validity of the probabilistic bootstrap distribution. Thirdly, our algorithms can accurately reconstruct the fibre-paths and are also able to recover complex fibre configurations.

References : 1.Chung et al., 2006, NeuroImage, 33, 531–541. 2. Peled et al., 2006, Magn. Reson. Imag., 24, 1263–1270. 3. Ying et al., 2008, IEEE Trans. Med. Im., 27, 1506-1514. 4. Zhu et al., 2006, Magn. Reson. Imaging, 24, 569–582. 5. Poupon et al., 2008, Magn. Reson. Med., 60, 1276–1283.

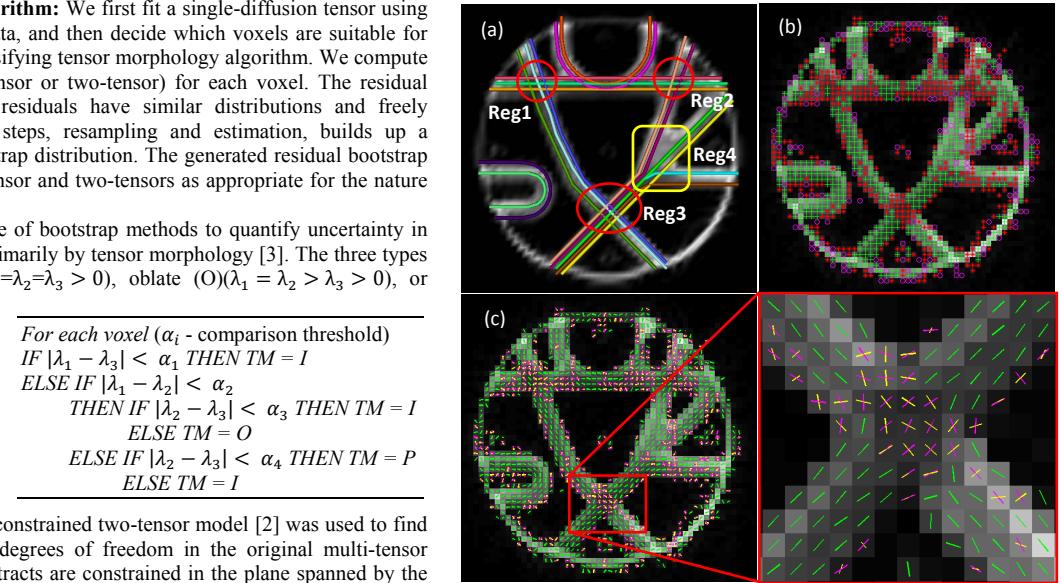


Fig. 1. (a) Ground-Truth and selected crossing regions (in red circles) and a branching region (in yellow rectangle) (b) classification (linear (+), planar(*) or spherical (o) shape) (c) constrained two-tensor model estimation.

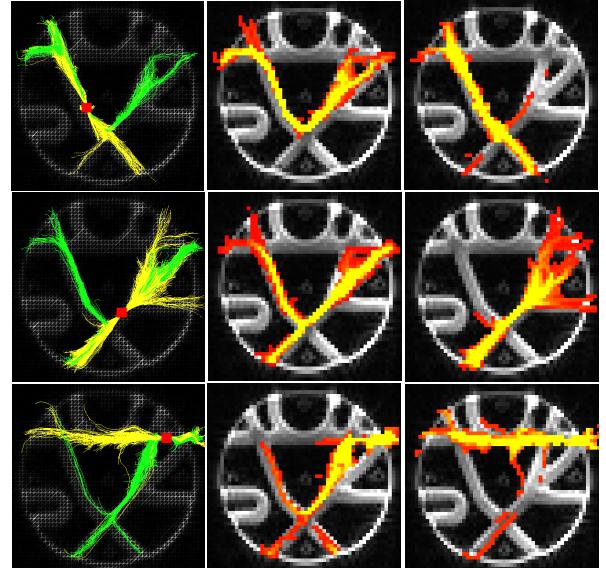


Fig. 2. Tracking Results from 3 seed points (Seed points are illustrated in the red square) in each row. First column: Residual bootstrap results: Single-tensor (green) and Two-tensor (yellow) second column: probability map of single-tensor residual bootstrapping and third column: probability map of two-tensor residual bootstrapping.