DR-TAMAS: Diffeomorphic Registration for Tensor Accurate alignMent of Anatomical Structures

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Synopsis

Spatial alignment of diffusion tensor MRI data is of fundamental importance for voxelwise statistical anaysis and creation of population specific atlases of diffusion MRI metrics. In this work, we propose DR-TAMAS, a novel diffusion tensor imaging registration method which uses a spatially varying metric to achieve accurate alignment not in only in white matter but also in gray matter and CSF filled regions. Our tests indicate that DR-TAMAS shows excellent overall performance in the entire brain, while being equivalent to the best existing methods in white matter.

Purpose

Spatial normalization of Diffusion Tensor MRI (DTI) data is of fundamental importance for both voxelwise statistical anaysis and creation of population specific atlases from diffusion MRI metrics. Most available DTI-based spatial normalization algorithms emphasize alignment of anisotropic structures. In this work, we propose DR-TAMAS, a novel framework for inter-subject registration of DTI datasets which is designed to achieve optimal alignment of gray matter (GM) and cerebro-spinal fluid (CSF) boundaries, in addition to white matter (WM) structures. Moreover, DR-TAMAS also is able to include information from anatomical MRIs in the registration. This framework is optimized for brain data and its main goal to ensure accurate alignment of all brain structures is achieved by incorporating a locally varying weighting of its similarity metrics.

Materials

Data from 11 volunteers were collected on a 3T MRI system equipped with a 32-channel coil. DWIs were acquired with a single-shot spin-echo EPI sequence (FOV=256x256 mm, slice thickness=2mm, matrix size=128x128, 78 slices, TR/TE=9981/90ms). Diffusion acquisitions consisted of 4 volumes with b=0 s/mm^2, 12 volumes with intermediate b-values and 62 volumes with b=1100 s/mm^2. DWIs were corrected for motion, eddy-currents distortions[1] and EPI distortions[2].

Methods

Registration method: DR-TAMAS uses the SyN diffeomorphic transformation model[3] and three similarity metrics: trace similarity, the deviatoric tensor similarity and cross-correlation similarity of anatomical images. The trace similarity metric ξ_1 aims to align GM and CSF filled regions. The deviatoric tensor[4] similarity, ξ_2 has been shown to lead to accurate WM alignment in terms of

Figures

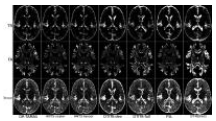

Figure 1. Voxelwise variance maps for TR and tensors computed on a slice o registered images across the populati for each method. Lowest variance (da the images) corresponds to the best registration performance.

Table 1. Average of voxelwise FA,TR, a tensor variance measures over all bra voxels. Lower values indicate better performance.

Table 2. Average of voxelwise principa eigenvector orientation dispersion measures computed in several WM R(Lower values indicate better registrati performance.

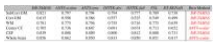

Table 3. DICE overlap measures in var brain regions. Higher values indicate better registration performance.

anisotropy and orientation[5], hence, is the metric choice for these regions. With this metric, the tensor orientations are explicitly optimized using the finite-strain method[6] with the corresponding deformation fields ϕ. Cross-correlation ξ_3 of additional anatomical images is used if further fine alignment of GM regions is needed . At each optimization iteration *n*, for each voxel **x**, the displacement field updates from each metric are fused with a spatially varying weight factor w as:

$$\phi(\mathbf{x})^{n+1} = \phi(\mathbf{x})^n + w_1(\mathbf{x})\frac{\partial \xi_1}{\partial \phi}(\mathbf{x}) + w_2(\mathbf{x})\frac{\partial \xi_2}{\partial \phi}(\mathbf{x}) + \sum_i^N w_3^i(\mathbf{x})\frac{\partial \xi_3^i}{\partial \phi}(\mathbf{x})$$

where N is the number of anatomical image pairs. The weight for the deviatoric tensor similarity, w_2 is a function of voxelwise FA. In anisotropic regions, the large w_2 causes the deviatoric tensor similarity metric to be dominant, whereas in regions with isotropic diffusion, the remaining weight $(1 - w_2)$ is distributed evenly among the trace and structural similarity metrics to favor the alignment of GM and CSF regions.

Registration validation: We compared the performance of DR-TAMAS to those of six well-known tensor and scalar image based registration methods: 1) ANTS-scalar (FA and TR)[3], 2) ANTS-tensor (6 tensor components), 3) DTITK-dev (deviatoric tensor similarity)[5], 4) DTITK-full (full tensor similarity), 5) FSL[7] (FA) and 6) DT-REFinD[8]. DR-TAMAS and the reference methods were used to create a DTI atlas and several quality measures were computed using the warped images of the 11 subjects. These measures were FA/TR/tensor variances, principal eigenvector orientation dispersion (PEOD)[9], and DICE overlap measure used on warped label maps initially extracted on the native space of each subject.

Results

Tensor (TCOV), FA and TR variance maps are displayed in Figure 1. TR maps showed that the methods using only anisotropy information, such as DTITK-dev and FSL showed poor performance at the GM/CSF boundaries. This is particularly evident at the level of the head of the caudate nucleus. Moreover, with ANTS and FSL, TCOV is relatively high in the splenium of the CC, despite low FA variance. This is due to their lack of tensor reorientation during optimization. Table 1 reports the average of these voxelwise variance values. Methods that use anisotropy information directly, ANTS-scalar, DTITK-dev and FSL, produced the lowest FA variances. However, DTITK-dev and FSL achieved this at the cost of very large variance values for the trace. DR-TAMAS showed a very balanced behavior, producing close to optimal results for both metrics. Moreover, DR-TAMAS was the best performing method in terms of the tensor variance. With the PEOD metrics (Table 2), DR-TAMAS and DTITK-dev are the best performing methods with similar performances in all the WM ROIs tested. The DICE overlap metrics (Table 3) indicate that DR-TAMAS performed very well, being the best method in subcortical and cortical GM, WM and CSF label map alignment.

Conclusion

The proposed method shows excellent overall performance in the entire brain, while being equivalent to the best existing methods in white matter. The use of TR information along with spatially varying weight factors proved to lead to the robust performance of DR-TAMAS across the whole brain.

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