Consistency of DT-MRI to Assess Quality of MRI Inter-Subject Registration

F. J. Sanchez Castro[1,2], O. Clatz[2], J. Dauguet[2], J-P. Thiran[1], and S. K. Warfield[2]

[1]Signal Processing Institute, Ecole Polytechnique Federale de Lausanne (EPFL), Lausanne, Switzerland, [2]Computational Radiology Laboratory, Radiology, Children's Hospital, Harvard Medical School, Boston, MA, United States

Purpose:

Several nonrigid registration algorithms have been proposed for inter-subject alignment, used to construct statistical atlases and to identify group differences. Assessment of the accuracy of nonrigid registration algorithms is a crucial issue. Previous validation studies have used synthetic phantoms or sparse landmark correspondence. Synthetic phantoms provide known ground truth but do not capture the variability observed in studies of patients and volunteers. Landmark detection is difficult and subject to inter-rater variability. Recent advances in MR hardware have made it practical to rapidly acquire both high resolution structural MRI and diffusion MRI. Conventional inter-subject registration algorithms utilize only structural MRI.

We propose here that the diffusion MRI provides an independent means of assessing the quality of alignment achieved. Diffusion tensor MRI allows for the comparison of the local position and orientation of regions of white matter that appear homogeneous in conventional MRI. We carried out inter-subject alignment of conventional T1-weighted MRI with two different registration algorithms, and projected DT-MRI of each subject through the same inter-subject transformation. We assessed the quality of the inter-subject alignment by estimating the consistency of the aligned DT-MRI.

Material and Methods:

Data. Nine healthy volunteers enrolled in this study carried out with Institutional Review Board approval. High-resolution MRI was acquired using a 3T Signa System (GE Medical Systems, Milwaukee, WI). The acquired images included the following: line scan diffusion images (TR/ TE = 93/55 milliseconds, field of view [FOV] = 270 cm, matrix size = 256 × 256) using a b = 1000 s/mm^2, 1 baseline (b=5 s/mm^2) and 6 noncollinear and noncoplanar directions, 60 contiguous 2-mm-thick axial sections for each direction; and MPRAGE3D T1-weighted (TR/TE = 8/3.2 ms, inversion preparation time = 725 milliseconds, postdelay time = 1400 ms, FOV = 240 cm, matrix size = 256 × 256), 124 contiguous 1.3-mm-thick sagittal sections.

Alignment and Evaluation Procedure. Intra-subject and inter-subject alignment was carried out. *Intra-subject registration*: rigid registration of the T1-weighted image and the baseline diffusion image of each subject was used to compute a transformation aligning the diffusion MRI with the structural MRI. This transformation was applied to the corresponding diffusion tensor MRI. *Inter-subject registration*: One subject was randomly chosen as a reference and each single patient registered to the reference using a) an affine transformation model and b) a nonrigid transform represented with B-splines. Polar Decompositions of these transformations were used to reorient the tensors as has been previously described and validated [1]. *Evaluation of the alignment*: Using the Riemannian Log-Euclidean framework [2] the Log-Euclidean average tensor was computed at each voxel. Then the Frobenius norm between the average tensor and each registered subject tensor was computed in the log space. The standard deviation of this norm is a consistency measure for the alignment algorithm under consideration. In addition to this global measure of consistency, we visualized the distribution of this error in regions with differing tissue structure by constructing a histogram of the error as a function of the fractional anisotropy (FA) of the reference subject.

Algorithms for Alignment. An affine transformation (with 12 degrees of freedom - translation, rotation, scaling and shearing) and a nonrigid transformation (B-splines with a regular 7x7x5 grid of control points spaced every 27 mm) were identified by finding the transform parameters that maximize the mutual information between the images. A coarse-to-fine pyramidal optimization approach implemented in the Insight Toolkit was used [3].

Results

Figure 1 illustrates the consistency at each voxel of the alignment of the affine transformation and the nonrigid transformation. Figure 2 shows a histogram of this consistency measure. Differences between the two alignment methods are clearly seen around the ventricles and the corpus callosum.
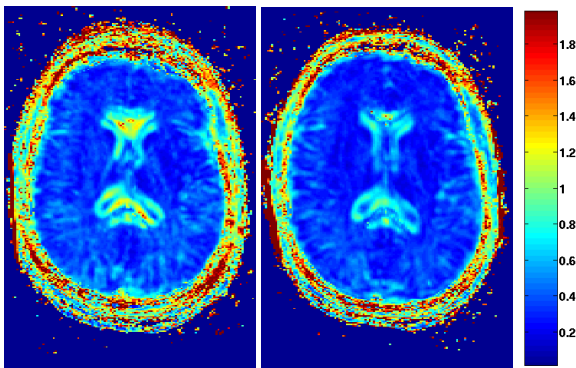

Figure 1. Error to the Log-Euclidean average tensor at each voxel. Left: using Affine registration. Right: using B-splines registration.
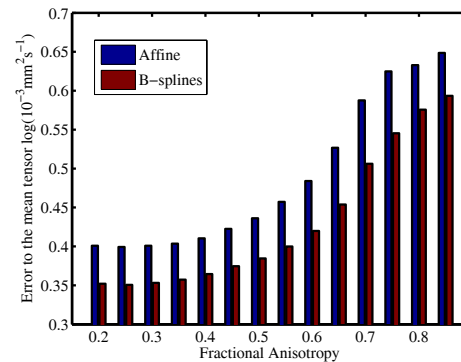

Figure 2. Histogram of the error to the Log-Euclidean average tensor by using affine (in blue) and B-splines (in red) registration methods.

We found a reduction of the global error by 13.5% using B-spline nonrigid registration as compared to affine registration. A t-test comparing the mean error obtained for all voxels for the two registration methods showed significant difference with a p-value smaller than 10^{-4}. A t-test comparing the mean error in each FA bin for the two methods found significant difference in all of the histogram bins, with a p-value smaller than 10^{-3}.

Conclusions and Future Work:

We found that the tensor consistency obtained with the nonrigid registration is quantitatively better than the one obtained with affine transformation. This assessment procedure is a general method to evaluate registration algorithms. Future work will focus on comparing different registration methods and finding the optimal parameters of the methods using the proposed evaluation scheme.

References:

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