

The effect of atlas selection on voxel based analyses of DTI data

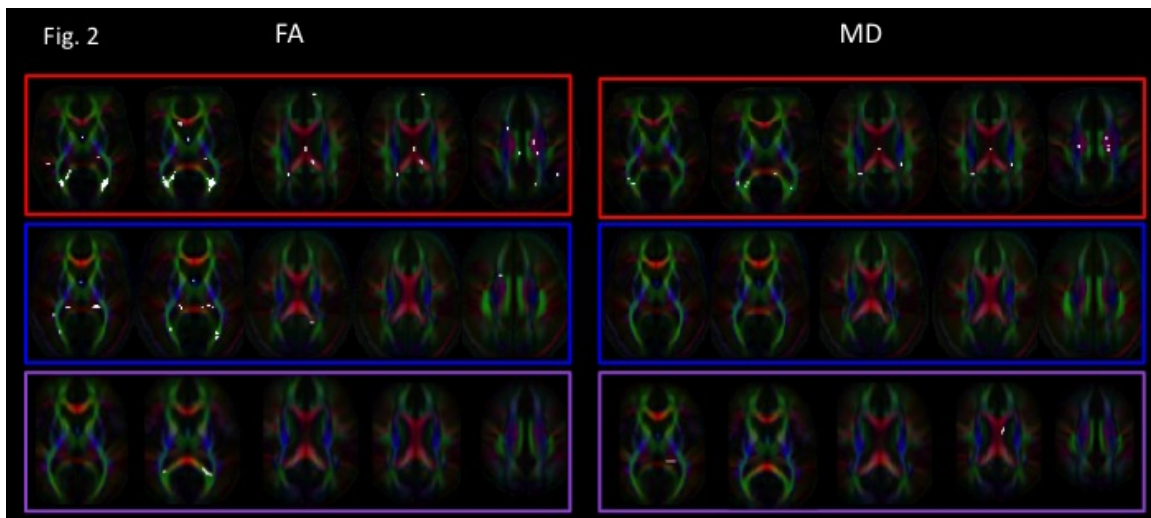
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Introduction: In recent years, voxel based analysis (VBA) studies have demonstrated the potential of diffusion tensor imaging (DTI) to detect white matter (WM) damage in patients with various neurological or psychiatric disorders. In VBA, all DTI data sets are transformed to an atlas or template, whereafter the diffusion measures of control subjects and patients are evaluated in each voxel. In most VBA studies of DTI data sets, a standard template, such as the Montreal Neurologic Institute (MNI) atlas, is used. The advantage of the MNI atlas is that it contains coordinate, anatomic, and cytoarchitectonic labels and that the VBA results can be easily compared across studies using the MNI coordinates. However, since this atlas is not study-specific, it might fail to provide a good representation of the population that is studied, thereby potentially resulting in residual image misalignment after coregistration of the DTI data sets to this reference space. Mori et al. (2008) introduced a stereotaxic WM template (the ICBM-81 atlas) that was constructed from 81 DTI data sets of healthy subjects that were normalized with an affine transformation to the ICBM-152 template [1]. This template contains the tensor elements, so that they can be used in a multi-channel coregistration approach. Recently a population based, study specific DTI atlas was introduced, whereby the magnitudes of the deformation fields that are needed to warp the different images to the atlas are minimized, potentially leading to a decreased image misalignment in VBA [2]. The goal of this work was to examine the effect of the atlas selection on the reported VBA results. To this end, DTI data sets of multiple sclerosis (MS) patients and control subjects are examined with VBA using different DTI templates. These templates are (i) a study-specific population-based template (PA), (ii) a study-specific subject-based atlas in MNI space (SA), and (iii) the ICBM-81 template of Mori et al. (2008) (MA).

Methods: 20 healthy subject and 20 MS DTI data sets were acquired and aligned to the PA, SA, and MA atlases using an affine and a non-affine registration method, based on a viscous fluid model that includes all tensor information [3]. After the image registration to the atlases, the data sets were smoothed with an anisotropic kernel with a FWHM of 3 mm. FA and MD values were then compared between the healthy and the simulated DTI data sets in atlas space using a non-parametric Mann-Whitney U test and a multiple comparisons correction based on the Benjamini-Hochberg false discovery rate of 0.05 was applied. The PA was constructed based on the method of [2]. The SA was created by aligning and averaging 40 healthy subject DTI data sets (acquired with the same protocol as the 20 healthy and 20 MS data sets of the VBA study) to MNI space with an affine and non-affine registration based on the viscous fluid model.

Results: In order to evaluate the image alignment accuracy, the coefficient of variance (COV) and corresponding cumulative distribution function (CDF) are displayed for both FA and MD in all atlas spaces (Fig. 1). These results demonstrate higher image alignment accuracy in the PA compared to the SA and MA for both FA and MD. In Fig. 5, the VBA results are displayed after coregistration to the SA, MA, and PA. The VBA results clearly depend on the atlas space to which all data sets are normalized.



Discussion: Our results suggest that the selection of the DTI template for a VBA group analysis affects the sensitivity and specificity to detect FA and MD changes. The results of Fig. 1 clearly demonstrate that a higher registration accuracy is obtained after alignment of the data sets to the PA space, compared to the SA and MA space. This can be explained by the fact that this atlas is a better representation of the subject group that is studied.

References: [1] Mori et al., 2008 (NeuroImage); [2] Van Hecke et al., 2008 (NeuroImage); [3] Van Hecke et al., 2007 (IEEE TMI)