Tractography-based method for the estimation of the co-registration error for white matter structures

Christian Ros[1], Hellmuth Ricardo Muller-Moran[2], Daniel Güllmar[1], Martin Stenzel[3], Hans-Joachim Mentzel[3], and Jürgen Rainer Reichenbach[1]
[1]Medical Physics Group, Department for Diagnostic and Interventional Radiology I, Jena University Hospital, Jena, Thuringia, Germany, [2]McGill University, Montreal, Quebec, Canada, [3]Pediatric Radiology, Department for Diagnostic and Interventional Radiology I, Jena University Hospital, Jena, Thuringia, Germany

Introduction – Analysis of Diffusion Tensor Imaging (DTI) data in multi-subject imaging studies is usually performed by analyzing quantitative diffusivity measures (e.g. Apparent Diffusion Coefficient (ADC), Fractional Anisotropy (FA), Eigenvalues, etc.) with Voxel Based Morphometry [1], Tract Based Spatial Statistics [2] or quantitative tractography-based analysis of white matter fiber bundles [3, 4]. For all methods (VBM, TBSS and tract-based analysis) co-registration techniques have to be employed in order to align the individual brains and to extract a common template. Quantitative analysis is then performed in the unique template space. Thus, the most important step for the analysis is the correct alignment of the individual brain in order to compare the correct regions during the analysis. Estimating the spatial co-registration error is therefore essential for the evaluation of co-registration frameworks as well as for determining the optimal registration technique for the data sets. With this contribution we present a new tractography-based estimation technique to determine this error. The method was used to evaluate the ANTs registration framework, in order to determine optimal registration parameters as well as suitable contrasts for the co-registration of white matter regions.

Tractography-based estimation of the co-registration error – In order to perform the estimation of the registration error (see Fig. 1), standard processing of the diffusion weighted data set and fiber tracking is performed first. The resulting data set will be termed gold standard data set (GS). In a separate step (described below), a set of displacement vector fields (DF_1 ... DF_N) is generated describing the translational displacement for every voxel. Each displacement field DF is then applied to the GS data set (including fiber tracts) to obtain new unique prototype data sets (PDS_1 ... PDS_N). Next, the co-registration between the newly generated PDS and the GS is performed to transform the PDS back into the GS space, resulting in transformed prototype data sets ($TPDS_1$ … $TPDS_N$). In order to compute the registration error, these transformations are also applied to the fiber tracts. Due to the fact that there is a one-to-one correspondence between the GS fiber tracts and the TPDS tracts, the exact displacement can be computed for every point of the fiber tracts. Subsequently to the generation of the PDS the back-transformation can be used again to analyze registration techniques in order to find most suitable parameter sets. Hence, the optimal result will be the (unknown) inverse of the original DF (IDF) that was used to generate PDS. If the registration technique is capable of finding the optimal registration (IDF) between PDS and GS the error will be zero and TPDS will be equal to the GS.

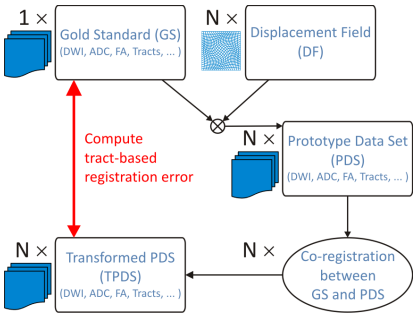

Fig. 1 – Workflow for the tract-based estimation of the co-registration error.

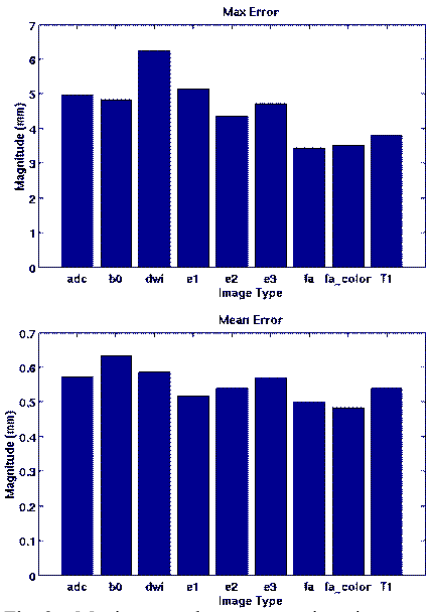

Fig. 2 – Maximum and mean co-registration error for different contrasts.

The initial displacement vector fields (DF_1 ... DF_N) can be generated in various ways, whereas the most convenient way is to use the displacement fields that are automatically computed during the template generation (as long as more than one data set is available). Hereby, *M* individual data sets are non-linearly co-registered to extract a common template. For every brain, a unique displacement field is obtained that describes the transformations to the template. These displacement fields can then be employed to generate the prototype data sets. In order to circumvent any side effects only non-corresponding DF and GS are used to extract the PDS. Hence, for every GS data set, a total of *(M-1)* DF was used to extract *(M–1)* PDS.

Materials and Methods – In order to demonstrate the feasibility of the proposed technique, 30 DTI data sets were acquired on a clinical 3 T MR-Scanner (Magnetom Tim Trio, Siemens Healthcare, Erlangen, Germany), using a conventional twice refocused Echo Planar Imaging (EPI) sequence [5]. A 12 channel head coil was employed and the following parameters were used: T_E=113 ms, T_R=7900 ms, α = 90°, iPAT=2, matrix of 96×96, 55 slices with a thickness of 2.5 mm, resulting in a voxel size of 2.5×2.5×2.5 mm³. Five b_0 images without diffusion weighting as well as 70 diffusion weighted images sampled with different gradient directions at b=1000 s/mm² were acquired. In-plane interpolation was performed on the MR-Scanner, resulting in a voxel size of 1.25×1.25×2.5 mm³. In addition, a T1-weighted MPRAGE data set with 1.0×1.0×1.0 mm³ was acquired as well. The Diffusion Toolkit [6] was utilized to perform whole brain fiber tractography. By using the FA maps, non-linear co-registration was performed for all data sets with the ANTs framework [7] and a common template was extracted. The 30 GS data sets were used to estimate the co-registration error (see previous section) for various parameters of the ANTs framework as well as various image contrasts (ADC, B_0, DWI, Eigenvalues (E1, E2 and E3), FA, FA (color-coded) and T1).

Results – Various parameter sets for the ANTs framework were evaluated. From the available metrics (mutual information, mean squared difference, pure cross-correlation and fast cross-correlation), we observed that the fast cross-correlation worked best for our data sets. We also discovered that FA and color-coded FA maps lead to the results with lowest mean and lowest maximum error (Fig. 2). For 95.5% of the data the error was less than 1mm. This was consistent across all subjects. Even though the registration error was equally distributed it was usually more pronounced in peripheral parts of the brain (see Fig. 3).

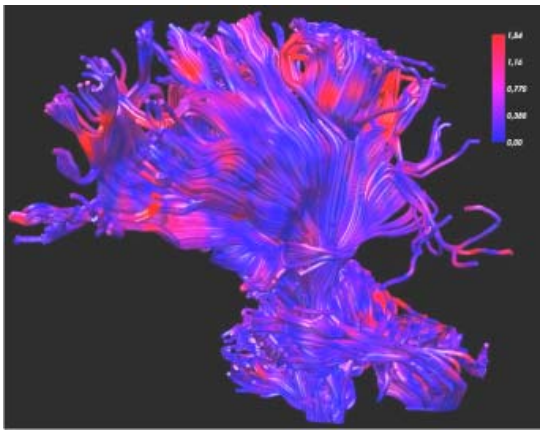

Fig. 3 – Co-registration error along selected fiber tracts.

Discussion & Conclusion – We presented a new method for the assessment of the co-registration error based on fiber tracts and an effective way to analyze co-registration techniques. Due to the use of fiber tracts, we can analyze the displacement not only for the whole brain but also for individual fiber tracts or anatomical white matter fiber bundles. Even though this method works fully automatically, it can only be used to determine the error in white matter. However by employing automated gray matter segmentation techniques, the method can be adopted to work for gray matter as well. To which extent the results of this study can be incorporated into quantitative analysis of white matter structures is unknown and should be observed in future studies.

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