

BUNDLES OF INTEREST BASED REGISTRATION OF WHITE MATTER TRACTOGRAPHIES

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ABSTRACT

We present an efficient and robust method for direct registration between fiber bundles of interest and the complete White Matter (WM) tractography of the same or another brain. The method does not require any previous registration between the brains, such as DTI registration, and it can be used for both intra and inter-subject registration. The algorithm is inspired by the well known iterative closest point method. Here, 3D points are replaced by feature vectors representing WM fibers, and the neighborhood is determined by the efficient approximation framework of the locality sensitive hashing. Initial results demonstrate the successful application of the proposed registration method to the automatic extraction of anatomical WM structures in unsegmented brain tractographies

Index Terms—White matter, DTI, tractography, registration, Iterative closest point

1. INTRODUCTION

In the last ten years, Diffusion Tensor Imaging (DTI) and tractographic reconstructions are changing the way we perceive White Matter (WM) in MRI brain [1,2]. As is the case with structural MRI, registration tools are required to enable the comparison between several DTI studies. The main difference between the registration of scalar and tensor images, is that in addition to the estimation of a geometrical deformation, DTI registration must also take care of re-orienting each tensor to maintain consistency with the surrounding anatomical structure [3,4]. A classical approach is to perform DTI registration and then compute tractographies in the warped and target brain. Alternatively, scalar DTI images such as fractional anisotropy can be aligned and the recovered transformation applied directly to the fibers. A joint clustering step of the tractographies is then implemented to obtain cluster level correspondences [5]. More recently, the statistical analysis of fractional anisotropy along fiber tracts has been proposed for quantitative analysis of DTI [6]. It includes the generation of a mean fiber tract by co-registration of its fibers using a Procrustes analysis. The registration is limited to fibers belonging to a single tract of a single subject (intra-subject registration). The main contributions of this paper are: 1)

Given a *bundle of interest* (hereafter termed BOI) extracted from a brain tractography, extract automatically the anatomically corresponding bundle in any other brain tractography. 2) The method is robust and efficient. 3) No need for previous registration of the original DTI scans. This paper is organized as follows: In section 2 we will describe the proposed algorithm. Experimental results on both synthetic and real data will be presented in section 3, followed by a summary and conclusions in section 4.

2. ALGORITHM DESCRIPTION

Denote by M_i , $i=1..n$ and T_j , $j=1..m$ a model and target set of fibers, respectively. Each fiber is described by a sequence of 3D coordinates describing its trajectory between the extremities it connects. In this work, the sets M and T are obtained by tractographic reconstruction of the DTI data using DtiStudio [7]. The model and target sets may originate from the same brain, as in the case of intra-subject registration for longitudinal studies. Alternatively, the sets may belong to distinct brains for inter-subject registration. For the target set, we will consider the full set of WM fibers reconstructed by tractography. For the model set we will consider WM structures such as the Corpus Callosum or the Corticospinal tract that may constitute anatomical BOIs. Our goal is to match between model and target fibers by finding for each model fiber M_i , the target fiber T_j that best corresponds. At the same time, we want to perform spatial registration between the corresponding fiber sets. If we think of a fiber as a point in some feature space, the matching-registration problem can be viewed as a (feature) point sets matching-registration. We adopt this approach by extending the well known iterative closest point (ICP) algorithm for 3D point sets [8] to an iterative closest fiber (ICF) algorithm for tractographic fiber sets. The main ICF steps are: 1) Represent each model and target fiber by a distinct feature vector. 2) For each model fiber M_i find the “closest”, that is most similar, target fiber T_j . 3) Given the set of fiber correspondences found in 2), fit a linear geometric transformation between model and target fibers. 4) Warp the model fiber set using the transformation computed in 3). 5) Repeat from point 2) until convergence or a maximum number of iterations is reached. 6) Return the final correspondence set between model and target fibers

together with the combined geometric transform between original (non-warped) model and target sets.

2.1. Fiber Representations

We now define two feature space representations of the fibers that will be motivated and used in the following steps of the algorithm.

2.1.1. Spatial Coordinates Sequence

The fibers generated by DtiStudio are represented by a variable number of points. Therefore, we re-sample each fiber f along its trajectory at a fixed number n of uniformly distributed points. Each fiber is now represented by the same number of points n . By linearly appending the re-sampled coordinate sequence, (x_i, y_i, z_i) , we obtain the $1 \times 3n$ feature vector :

$$f_{cs} = [x_1, y_1, z_1, \dots, x_n, y_n, z_n] \quad (1)$$

The number of samples, n , is an empirical compromise between dimensionality and fidelity of the fiber representation.

2.1.2. Direction vectors Sequence

An alternative representation is derived from (1), by replacing every two successive points in the feature vector with the unit direction vector (u_i, v_i, w_i) they define. Note that n sample points defining a fiber in the previous representation will result in $n-1$ unit direction vectors. The corresponding $1 \times 3(n-1)$ feature vector is obtained, as before, by linearly appending the direction vectors sequence:

$$f_{ds} = [u_1, v_1, w_1, \dots, u_n, v_n, w_n] \quad (2)$$

Note that (2) is inherently a shift and scale invariant representation of a fiber

2.2. Fiber Similarity

Consider a given pair M_i, T_j of corresponding model-target fibers before the first iteration. For the sake of simplicity we will consider that both model and target sets are extracted from the same brain. Since M_i and T_j are corresponding fibers, we must have:

$$\arg \max_n (S(M_i, T_n)) = j \quad (3)$$

where S is an appropriate fiber similarity function. At this stage, however, the relative orientation, position and scale differences between model and target sets are still arbitrary. Therefore, S should mainly rely on shape to provide a meaningful similarity score. We define $R(U, V)$, the vector correlation coefficient (VCC) between two 3-dimensional random vectors $U=(u_x, u_y, u_z)$ and $V=(v_x, v_y, v_z)$ on a unit sphere, as [9]:

$$R(U, V) = \frac{\det(k^{-1} \sum_{i=1}^k U_i V_i^t)}{[\det(k^{-1} \sum_{i=1}^k U_i U_i^t) \det(k^{-1} \sum_{i=1}^k V_i V_i^t)]^{1/2}}, \quad -1 \leq R \leq 1 \quad (4)$$

Where U_i and V_i are the sequences of $k=n-1$ realizations of random vectors U and V , respectively. For perfect correlation, R approaches +1 if the sequences are in the same order or to -1 if they are in reversed order (reflection). As correlation decreases, $abs(R)$ moves towards 0. The feature vector of (2) is actually a sequence of unit direction vectors, therefore it can be viewed as a sequence of random vectors on a unit sphere and we can compute the VCC between any pair of model and target fibers represented by (2). The VCC is shown to be rotation invariant [9]. The shift and scale invariance of (2) combined with rotation invariance of the VCC are particularly useful for the first iteration of the ICF algorithm, when the fiber sets are still arbitrarily misaligned. On the other hand, when iterations proceeds and misalignment progressively decreases, position orientation and scale information may be important in order to increase the specificity of the similarity function. In example, let's suppose that a given fiber shape appears in several identical instances in the target brain but at slightly different positions or orientations. A fiber similarity measurement exclusively based on the VCC would be indifferent to these position/orientation shifts, making the preferred match ambiguous and limiting the matching accuracy. At the first iteration, VCC robustness to large misalignment prevails over its limitations. As misalignment decreases, however, trading up VCC invariance for more specific l_2 distance leads to higher matching accuracy. This suggests a two-fold strategy for fiber similarity measurement. For the first iteration we take as similarity function, S , the VCC between model and target fibers in the feature vector representation of (2). We delimit the range of tolerated position, orientation and scaling misalignment, (DP, DR, DS) by multiplying VCC with a threshold function, $TF(DP, DR, DS)$, that forces S to zero for extreme misalignments:

$$S^{it=1}(M_i, T_j) = abs(R(f_{ds}(M_i), f_{ds}(T_j))) * TF(\Delta P, \Delta R, \Delta S) \quad 0 \leq S^{it=1} \leq 1 \quad (5)$$

For the following iterations, we define S as a decreasing function of the normalized l_2 distance between model and target fibers in the feature vector representation of (1):

$$S^{it>1}(M_i, T_j) = 1 - \frac{\|f_{cs}(M_i) - f_{cs}(T_j)\|_2}{C} \quad 0 \leq S^{it>1} \leq 1 \quad (6)$$

where C is a normalizing constant. In practice, as we look for the nearest target fiber for every model fiber, we replace the naïve computation of l_2 distances with a fast approximate nearest-neighbor (NN) computation provided by the locality sensitive hashing framework (LSH) [10]. With LSH, the target data is embedded in the bins of several hash tables in a pre-processing step. The hash functions have the property of assigning neighboring feature points to the same bins with an elevated probability. The resulting speed-up with regard to naïve NN computation is of at least two orders of magnitude in our application.

2.3. Geometric Transformation Fitting

At each ICF iteration we estimate a 12 parameters 3D affine transformation that best warps, in the least squares sense, the model fibers set into the corresponding target fibers found in the previous step. The choice of the affine transform is motivated by our goal of matching corresponding fibers from the model and target sets. For this purpose we need enough flexibility to compensate for global orientation, position and (per-axis) scale differences between the sets. The affine model offers this flexibility while remaining very easy to fit. Higher order transforms can be considered to allow for local deformations. For fiber matching however, perfect warping between model and target fiber is not required. Similarly, when building a statistical WM atlas from a number of aligned tracts, local deformations would discard precious inter-subject variability information.

We implement the affine transform fitting using the RANSAC [11] method to ensure robustness against outliers.

3. EXPERIMENTS

In this section we provide initial experimental results for the application of the presented method. The input data consists of fiber sets generated by tractographic reconstruction on real DTI images with DtiStudio. All the fibers are re-sampled to have $n=20$ representative points, leading to a 57-dimensional f_{ds} and a 60-dimensional f_{cs} feature vectors per fiber. The spatial coordinates in f_{cs} feature vectors were converted to mm and then normalized to a unit less $[0,1]$ range. We consider two experiments: 1) model and target fiber sets belong to the same brain, the target set being a synthetically warped version of the model set. This simulates the intra-subject registration of a longitudinal study. 2) Model and target belong to different subjects, thus corresponding to inter-subject registration. In the first case the ground truth is known so quantitative results for the fiber matching and the recovered transform accuracy can be obtained. In the second case, as the brains are different, no ground truth is available and we will give qualitative results.

3.1. First Experiment: intra-Subject Registration

In this experiment, the model and target fiber sets are extracted from the same DTI brain. Target fibers are obtained by combining a 10 degrees rotation of the model fibers around x-axis with an x-wise translation vector (amplitude =10% of the volume width, about 26 mm). The raw data consists of 31 DWI volumes and 1 reference (B0) volume. Each volume has 56 axial slices of 256 x 256 pixels acquired on a 3T Ge Signa machine with a voxel size of 1x1 mm in axial plane and 2.6 mm in z direction without gap. In the following we will refer to this data as brain#1. DtiStudio was used for all the pre-processing, from tensor computation to tractographic reconstruction of the WM. The target fiber set has 247300 fibers (figure 1(a)),

corresponding to the full WM tractography of brain#1 and warped by the above defined rigid transform. The model (figure 1(b)) is a set of 10280 fibers extracted manually from the target set before the warping. Model fibers are selected to represent mainly the Corpus Callosum tracts. Figure 1(c) shows, the set of corresponding model (green) - target (red) fiber pairs, found at the first ICF iteration before the warping step. At this point, due to the large initial misalignment, only 330 matching fiber pairs were found. After the second iteration, however, full matching with zero error in model-target assignments is achieved. Figure 1(d) shows the corresponding registration between model (green) and matched target (red). The recovered transformation is also identical to the ground truth at working precision. To assess the robustness against noise, we repeated the same experiment following the addition of Gaussian noise ($\mu=0, \sigma=0.03$)¹ to the target fibers coordinates. In figure 1(e), we plot the number of successfully matched fiber pairs with (purple) and without (black) noise addition. We can see that noise has limited the correct matching to 9540 target fibers out of 10280 model fibers, giving a 92.8 percent success rate. The ground truth transformation was recovered after 7 iterations. Figure 1(f) shows the registration obtained with noise addition after seven iterations.

3.2. Second Experiment: Inter-Subject Registration

We now consider model and target originating from different subjects. The target fiber set is identical to that extracted from brain#1 in previous experiment except that no synthetic warping is applied to the fibers. The model set is extracted from another DTI brain, hereafter called brain#2, acquired on the same machine with 43 axial slices of 256x256 pixels, a voxel size of 1x1 mm in axial plane and 3 mm in z direction without gap. For brain#2, only 16 gradients were used for diffusion weighting. The model set consists of 23070 fibers from brain#2 that correspond to several anatomical structures, including the corticospinal tract. Figure 2(a,b) show the model (green) in overlap with the target (red) before registration. The initial misalignment, both in position and scale, is clearly observable. After 7 ICF iterations, the recovered set of model-target fiber pairs has converged, no more re-assignments are observed between iterations and the recovered affine transform remains unchanged at working precision. Figures 2(c,d) show the model (in green) in overlap with the target (red) after registration by 7 ICF iterations. Among 23070 model fibers, 16400 (=71%) found a unique match in the target set. The remaining 6670 were assigned to previously matched target fibers as “second choice” correspondences and were not considered in the geometric transformation fitting. Here, ground truth does not exist due to inter-subject anatomical

¹ The standard deviation is in normalized units, where 1 corresponds to the largest linear dimension of the volume.

variability. Therefore we cannot assess if a given match is correct. Nevertheless, the registered and matched fiber plots in figures 2(e,f) look very consistent.

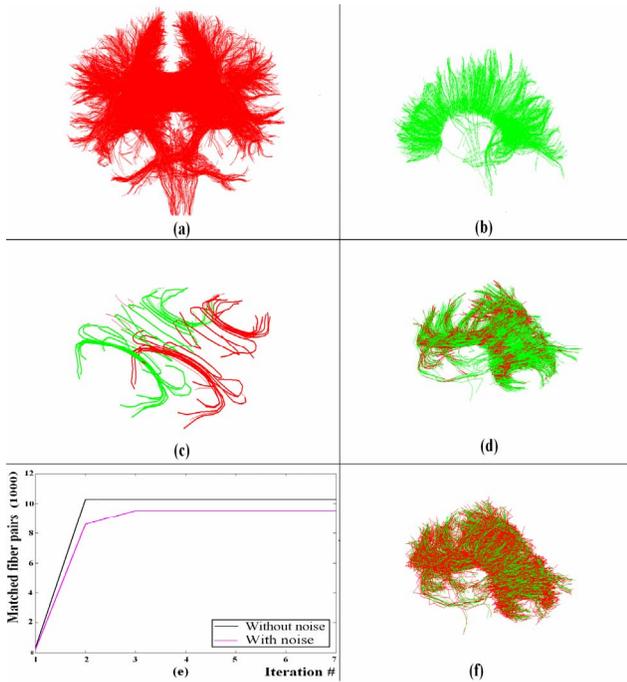


Figure 1 : (a) Target fiber set; (b) Model fiber set; (c) Set of corresponding model (green) – target (red) fiber pairs found at the first ICF iteration; (d) Registration after second iteration; (e) Number of successfully matched fiber pairs with (purple) and without (black) noise addition; (f) Registration obtained with noise addition after seven iterations.

4. SUMMARY AND CONCLUSIONS

We have presented a new robust and efficient method for direct registration and matching of tractographic fiber BOIs without requiring any previous registration step of the original MRI scans. The BOIs can be defined arbitrarily, giving more flexibility in comparison to clustering based methods (such as [5]), in which the BOIs are defined from the obtained clusters. Initial results were presented for both intra and inter-subject scenarios. The method showed promising results in both cases. In its current matlab implementation, the running time for each registration experiments was about 20 minutes. In our case, as the ICF is mainly a large loop of independent operations, a C/C++ multi-threaded implementation on a multi-core PC may reduce significantly the running time. In future work we intend to perform an extensive quantitative validation using expert defined ground-truth, and proceed to the following research: 1) The construction of tractographic atlases of healthy populations. 2) The detection of abnormal fiber shape as “outlier” to the registration-matching framework

and its correlation with potential underlying pathological processes.

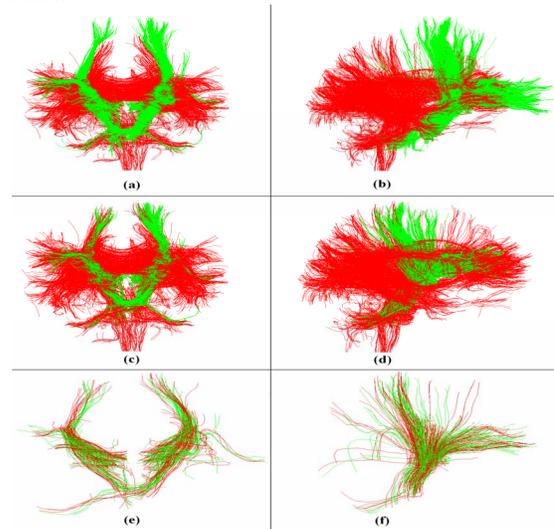


Figure 2 : (a) Model (green) in overlap with the target (red) before registration, coronal view ; (b) Sagittal view; (c) Model (green) in overlap with the target (red) after registration, coronal view; (d) Sagittal view; (e) Registered and matched fibers in coronal view; (f) Sagittal view.

ACKNOWLEDGEMENTS

This work was in part supported by a Strategic Research Directions grant of the Israeli Ministry of Science.

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