Probabilistic Parameter Adaption for Fiber Tracking of the Corticospinal Tract

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Abstract. The MICCAI DTI tractography challenge is an annual event where teams have the possibility to reconstruct fibers of the corticospinal tract and where the results are evaluated by an internationally renowned jury afterwards. The main goal of the challenge — in contrast to many other challenges — is not to find the ultimate algorithm but rather to build teams and to get inspired by new ideas for improving and evaluating fiber tractography.
Our team uses a probabilistic approach which adapts its control parameters locally by a white matter atlas. This allows for a very time efficient reconstruction of fiber bundles whose geometric properties and whose corresponding underlying diffusion processes vary throughout passing brain regions. For defining seed regions, we developed new 3D interactive selection techniques which allow for segmenting the gyri of interest. Our results show that the corticospinal tract in its entity and the arcuate fascicle can be tracked reliably and efficiently for the given data set.

1 Introduction

The 2014 DTI tractography challenge aims at evaluating the performances of different fiber tracking algorithms on pre-operative and post-operative diffusion MRI data. The main fiber structure to be reconstructed in the challenge is the corticospinal tract, a large bundle which originates in the precentral gyrus and terminates in the spinal cord. The anatomy of this bundle is well-understood and landmarks like the internal capsule and the cerebral peduncle indicate where this structure has to pass. In addition, the arcuate fascicle had to be tracked for patient 2 as its astrocytoma is in the near vicinity of the language pathways.

In 2013, some very interesting and well-working approaches have been presented within the challenge workshop. Masutani et al. presented an approach which is based on tensor field replacement for canceling crossings within the superior longitudinal fascicle [1]. Khan et al. [2] proposed an algorithm which employs fiber-crossing maps to weight the influence if local orientation, allowing to continue unhindered through these regions. A global tracking approach has been presented by Neher et al. [3] which does not depend on seed points but only on regions of interest for selecting the corticospinal tract.

However, the past MICCAI challenges have also shown that, although using advanced diffusion models and fiber tracking approaches, the corticospinal tract is still difficult to determine without having false negatives or positives. Thus, much space is left for improvements, especially with respect to the timings as most groups needed more than 90 minutes for only two cases last year.

2 Materials and Method

2.1 Image Acquisition

Diffusion weighted image (DWI) data two patients has been provided. Patient 1 suffered from a metastatic adenocarcinoma, patient 2 had an astrocytoma W.H.O. grade II, both in the near vicinity of the corticospinal tract. The patients were scanned using the 3T MRI scanner of the "Advanced Multimodality Image Guided Operating" (AMIGO) suite which is the clinical translational test bed of the National Center for Image-Guided Therapy (NCIGT) at the Brigham and Women's Hospital (BWH) and Harvard Medical School. The data has been acquired using 69 gradient directions, 4 b-values, and a 2 mm isotropic voxel size. Additionally, structural T1- and T2-weighted image data has been provided and could be used for anatomical reference.

2.2 Image processing

After motion correction, we propose to perform a supersampling of the data before fiber tracking to an isotropic target voxel size of 1mm using a higher-order filter. This supersampling guarantees for using a simple tri-linear interpolation at the later tracking stage also in case of having non-isotropic data. As proposed in [4], we use a Lanczos-3 filter in the spatial domain that represents a good trade-off between computational speed and filtering accuracy. Finally, we computed the diffusion tensors using the Stejskal-Tanner equation.

2.3 Segmentation of the precentral gyrus

Our fiber tracking algorithms utilizes the whole precentral gyrus as a seed volume for reconstructing the corticospinal tract. For tracking the arcuate fascicle, we use the Broca area for seeding. Last year, we utilized an interactive watershed transformation approach [5] where markers have been placed within 2D FA slices. As this approach was relatively time-consuming, we decided to develop and compare different new method where the precentral gyrus can be segmented interactively in 3D. Basis for all approaches is a skull-stripped brain which we determined by the above mentioned interactive watershed transformation on the T1-weighted image.

Method 1: Spheres-of-influence segmentation This method uses markers which are placed within the precentral gyrus. For each marker, a sphere with a certain radius is determined. The resulting mask is used for masking the FA map which is finally used for a watershed-transformation.

Method 2: Tube-based segmentation This method produces a simple tube by drawing a contour on the segmented brain. The result is comparable with the given pre-segmentation of the contest data. Finally, the tube is mapped onto the FA image from which markers are extracted automatically.

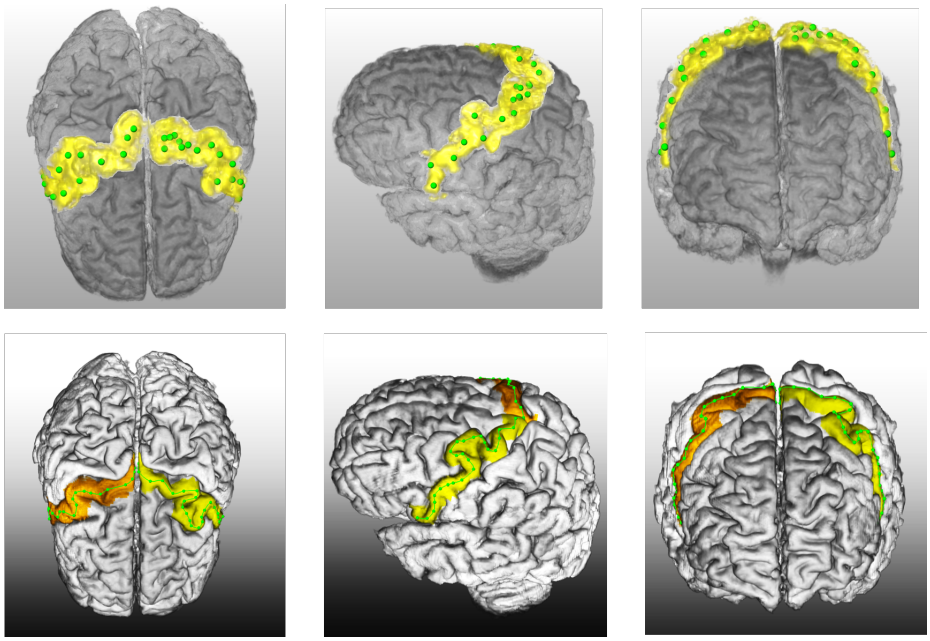

Fig. 1. Upper row: The precentral gyrus has been segmented using spheres-of-influence segmentation. It is rendered together with the T1 skull-stripped data. Markers for defining the spheres are shown in green. Lower row: the segmentation has been done by an interactive gray matter voxel clustering.

Method 3: Interactive gray matter voxel clustering Here, we applied a novel method for precise gyral segmentation. Like in method 2 a contour is drawn in 3D on the brains surface. Starting from this contour, a connected set of white matter voxels in closest proximity is identified. The resulting gyral segmentation is obtained by identifying all gray matter voxels connected to this white matter voxel set by means of a Voronoi diagram of the white matter voxel coordinates. This yields an accurate segmentation of a single gyrus since gray matter voxels are exclusively added based in their connectivity to the white matter, thus, discarding voxels from of neighboring gyri from the segmentation. The advantage of this method is its high precision. The disadvantage is the dependence on a good brain segmentation which is especially difficult if having only post-contrast images.

Using any of the above mentioned methods, the segmented precentral gyrus is mapped on the FA image from which seed points are automatically extracted. Segmentation results can be found in Figure 1.

2.4 Probabilistic parameter adaption

The basis of our local, adaptive fiber tracking algorithm is an advection-diffusion based algorithm, which is integrated into NeuroQLab, a software assistant for

the purpose of neurosurgical planning and quantitative image analysis [6]. In addition to the basic algorithm, our algorithm adapts its control parameters to specific regions of the white matter atlas "JHU-MNI-ss atlas", which is often called "Eve Atlas" [7, 8]. It is based on the T1-MRI data of 152 healthy volunteers and consists of 176 regions. Details of the algorithm can be found in our previous paper [9].

We adapted the following control parameters:

- $\alpha \in [0, 1]$, which interpolates between streamline ($\alpha = 1$) and deflection-based tracking ($\alpha = 0$)
- window length (mm): length of a window where parameters like curvature and FA are averaged. The averaged values are used for comparing with the minimal allowed FA or the maximal allowed curvature instead of comparing the current values directly. As a consequence, local outliers do not immediately stop the tracking process.
- minimal FA value.
- maximal curvature.
- step width (mm): the step width between two consecutive fiber points.

For each tracking position, the corresponding atlas region is determined. If the tracking is reaching a new region, the parameters are randomly changed from predefined intervals, and thus, the reconstruction is locally adapted. The selection is done randomly in order to avoid missing fibers resulting from discrete samplings. Afterwards, it is tested if one of the stopping criteria is reached and if the tracking process should be aborted. If the fibers are determined for all seed points, the tracking process is repeated until a predefined fiber density is reached or the number of iterations exceeds a predefined threshold.

Finally, the fibers may be filtered with include and exclude ROIs. In contrast to the previous challenge, we optimized our implementation of our filtering algorithm which is now based on mapping fiber points to the plane defined by an ROI.

3 Results

All of our algorithms have been implemented in MeVisLab using C++. The computations have been performed on an Intel Core i7-2600 with 3.40 GHz and 32 GB main memory. The tracking and filtering process of the corticospinal tract of one hemisphere took around 30 seconds. The most time consuming part is the filtering which is done after each iteration, i.e., if fibers have been tracked for all seed points.

The submitted video, the reconstructed tracts and the images in Fig. 4 to 7 show the tracked fibers and their proximity to the tumors. It is demonstrated that the fibers end in the precentral gyrus. Furthermore, it can be seen that no false fibers belonging to the corona radiata have been computed. This has been achieved by using seed points only in the precentral gyrus, and not in the capsula interna or in the brain stem as it can be found in many research papers, e.g., see [10–13].

Task	Avg Time in 2013 (minutes)	Avg Time in 2014 (minutes)
DTI preprocessing	4	4
Skull stripping	5	5
Atlas registration	2	2
Segmentation of precentral gyrus	5 (per hemisphere)	1 (per hemisphere)
Fiber Tracking including the definition of include ROIs and exclude ROIs	14 (per hemisphere)	5 (per hemisphere)
Overall time	49	28

Fig. 2. Timings of our different algorithms and approaches. This year we have improved the segmentation of the precentral gyrus and the filtering process of the fibers resulting in time saving of 20 minutes.

4 Discussion and Conclusions

In the past years, we have developed and implemented several algorithms and techniques for improved fiber tractography ranging from probabilistic Bayesian approaches to global optimization algorithms [14–17]. All of them could not achieve the quality and performance of the probabilistic parameter adaption algorithm which we introduced for the 2013 tractography challenge [9] where we have shown that a reliable tracking of the corticospinal tract is possible if adapting the control parameters of the algorithm to the local regions.

Thus, we decided to use this approach again, but in a revised and improved version. The pure tracking process takes only less than 30 seconds for one hemisphere. However, at the 2013 on-site challenge we needed 98 minutes for only two cases. Table 2 summarizes the timings which we used for the different steps of our processing pipeline. In addition it shows the new timings based on our current implementation where we have improved the segmentation of the precentral gyrus and the filtering of the fibers by regions of interest.

To the best of our knowledge, our approach is the first fiber tracking algorithm which adapts its parameters locally using a white matter atlas. Crossing fibers of the corticospinal tract and the superior longitudinal fascicle can easily be determined by our approach if increasing the step width in the corresponding region. Fibers with a high curvature, e.g., fibers of the corticospinal tract ending in "face area" of the precentral gyrus can be computed if increasing the allowed curvature. Note that in contrast to many other available algorithms, our approach determines non-stopping fibers which all connect the desired regions, e.g., the precentral gyrus and the brain stem.

Future work may examine whether advanced registration techniques can further improve the results. At the moment, only a rigid registration with an allowed scaling is performed. Furthermore, it could be investigated if our approach can benefit from advanced diffusion models like spherical harmonics or Q-ball representations.

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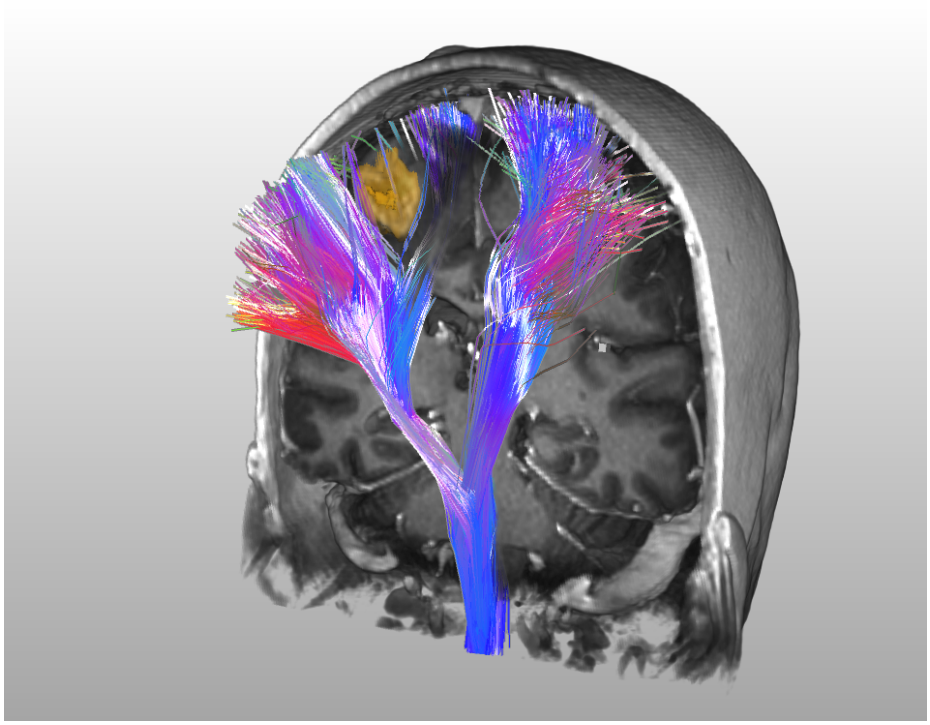

Fig. 3. Patient 1. Tracked fibers of the corticospinal tract with a volume rendering of T1 data.

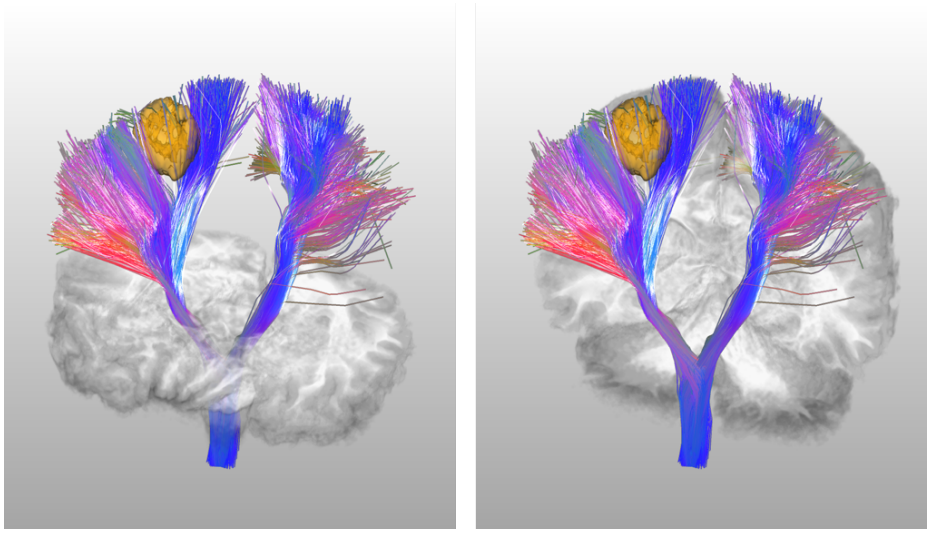

Fig. 4. Patient 1. Tracked fibers of the corticospinal tract with a volume rendering of T1 skull-stripped data.

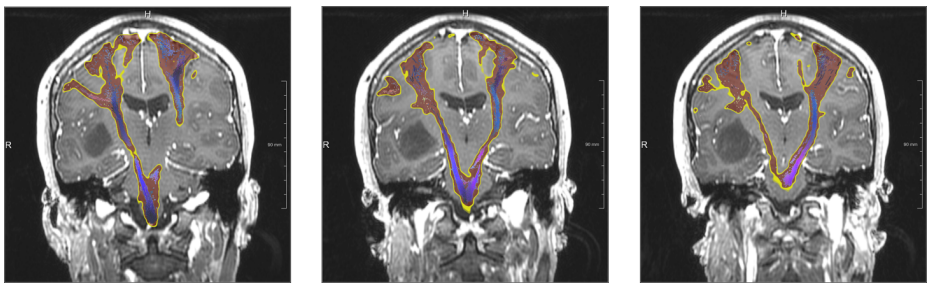

Fig. 5. Patient 2. Wrapped fibers of the corticospinal tract along different coronal slices.

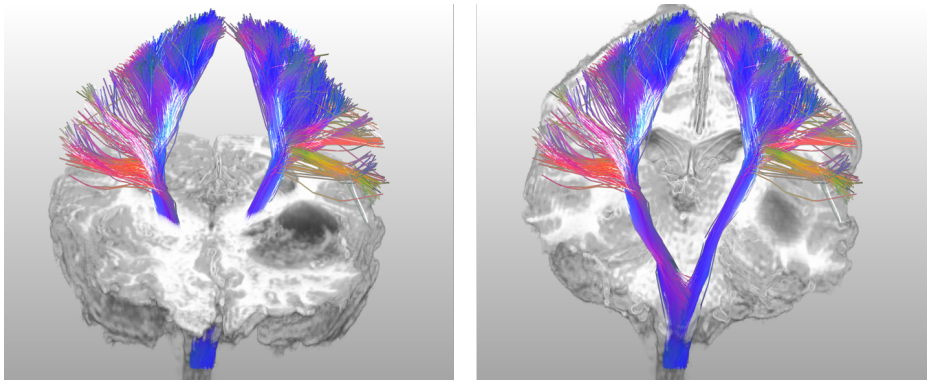

Fig. 6. Patient 2. Tracked fibers of the corticospinal tract with a volume rendering of T1 skull-stripped data.

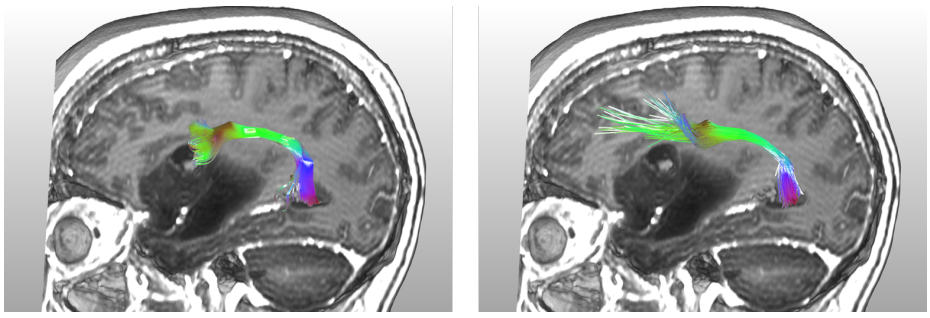

Fig. 7. Patient 2. The arcuate fascicle has been tracked because a tumor is in the vicinity of the language area. Left: standard deflection fiber tracking has been used. Fibers do not end in Broca's area, but do abort earlier due to the crossing corticospinal tract. Right: our proposed approach also tracks fibers which end in the Broca area.