NeuroQLab DTI - Probabilistic Parameter Adaption for Efficient Fiber Tracking

Jan Klein[1], Benjamin Geisler[1], and Horst K. Hahn[1]

Fraunhofer MEVIS — Institute for Medical Image Computing, Bremen, Germany,
{jan.klein,florian.weiler,horst.hahn}@mevis.fraunhofer.de

Abstract. NeuroQLab DTI is a software tool which we developed for efficient and robust fiber tractography and fiber quantification. It consists of deterministic and probabilistic fiber tracking algorithms and offers multiple options for seeding and filtering fiber tracts.

This paper shows the fiber tracking results for three different patient data sets, published within the context of the 2015 DTI tractography challenge. All patients suffered from a tumor in the close vicinity of the precentral gyrus. The task of the challenge was to reconstruct the pyramidal tracts (left and right hemisphere) for all three patients. We propose to use a probabilistic approach which adapts its control parameters locally. This allows for a reconstruction of fiber bundles whose geometric properties and whose corresponding underlying diffusion processes vary throughout passing brain regions. For defining seed regions, we utilized a 3D picking mechanism so that seed ROIs can interactively be placed on the brain surface or within the brain.

Our results show that the pyramidal tracts can reliably and efficiently be tracked for the given data sets.

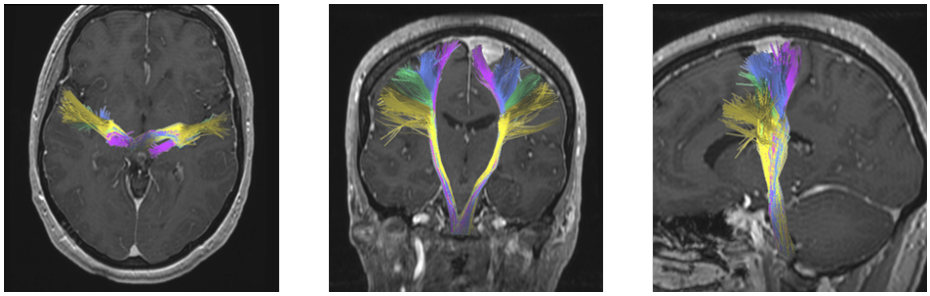

Fig. 1. The pyramidal tract is an accumulation of upper motor neuron fibers that start in the precentral gyrus and terminate either in the brainstem (corticobulbar tract) or in the spinal cord (corticospinal tract). The image data have been provided within the context of the MICCAI tractography challenge 2015 (patient 1).

1 Introduction

The MICCAI 2015 DTI Challenge Workshop on Tractography for Brain Tumor Surgery aims at comparing and evaluating the quality of fiber tracking algorithms with respect of reconstructing the pyramidal tract. The anatomy of this tract which is an accumulation of upper motor neuron fibers that start in the precentral gyrus and terminate either in the brainstem (corticobulbar tract) or in the spinal cord (corticospinal tract) is well-known for healthy brain tissue (Fig. 1). Landmarks like the internal capsule and the cerebral peduncle indicate where these structures have to pass. However, it is a rather challenging task to predict the movement of fiber tracts due to a displacing brain tumor without reconstructing the fibers based on diffusion MRI data.

In 2015, the 5th edition of the MICCAI tractography challenge will be held in Munich, Germany. The past four editions have originated sophisticated approaches and there is a clear trend towards a better understanding of the anatomy by the participating teams. As a consequence, the approaches have been optimized from challenge to challenge. Especially, the reconstruction quality of the corticobulbar tract has been improved which is more difficult to reconstruct due to crossing fibers with the superior longitudinal fascicle.

Hering and Neher [1, 2] presented an approach which does not depend on seed points but only on regions of interest for selecting the pyramidal tract. Masutani et al. demonstrated a tensor field replacement for canceling crossings within the superior longitudinal fascicle [3]. Khan et al. [4] proposed a multi-tensor framework including probabilistic tractography and use a hybrid visualization method which combines streamlines with connection probability maps.

However, the past MICCAI challenges have also shown that there is still space for improvements, especially by having a closer look at the above mentioned landmarks which define the areas where the pyramidal tract has to pass. Many algorithms lead to fibers which do not end in the brainstem or the spinal cord, but which terminate in other areas in the close vivinity. In addition only few algorithms were able to reconstruct fibers which do not abort during their way from the precentral gyrus downwards.

2 Materials and Method

2.1 Image Acquisition

Diffusion weighted images (DWI) of three patients have been provided together with registered T1- and T2-weighted data as anatomical references. While a tumor description/grading of patient 1 has not been given, patient 2 and patient 3 suffered from a low grade glioma in the near vicinity of the pyramidal tract. The data have been acquired using 30 gradients (patient 1 and patient 2) and 32 gradients (patient 3). Only one repetition of the DWI image acquisition has been made for each patient. The image resolution is 2.2mm isotropic (patient 1) and 2.5mm isotropic (patient 2 and patient 3).

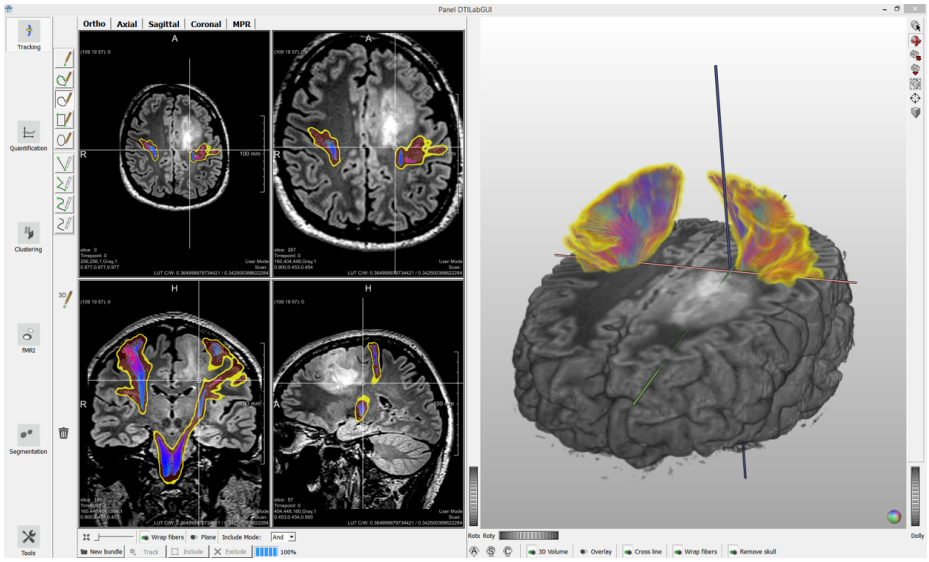

Fig. 2. NeuroQLab DTI - The GUI allows the user for an easy interaction with the image data for reconstructing fiber pathways. The image data have been provided within the context of the MICCAI tractography challenge 2015 (patient 2). Besides fiber tracking, fiber quantification and fiber clustering, a tumor segmentation approach is available.

2.2 Image processing

We propose to perform a supersampling of the data before fiber tracking to an isotropic target voxel size of 1.5mm 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 [5], 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

For reconstructing the pyramidal tracts we propose to segment the precentral gyrus and use it as seed volume. For the 2013 and 2014 contests, we developed various segmentation techniques. The most powerful one is based on a 3D picking mechanism where the user can interactively click on the brain surface within a 3D viewer. 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 [6]. This year, we extended this technique by enabling the user to place seed markers also within the brain. This makes the method more robust, especially for cases where the tumor is close to the brain surface.

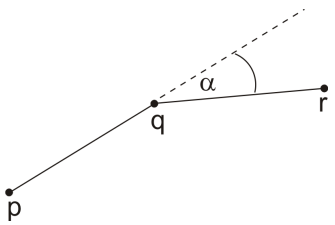

Fig. 3. The maximal curvature is one of the parameters which is modified depending on the selected brain region. Assume, the fiber points p and q have already been tracked and it should be decided if the point r should be added to the current fiber or if the tracking should be stopped. If $\sin(\alpha) \leq$ maximum curvature, then r will be added, otherwise tracking is stopped.

2.4 Probabilistic parameter adaption

Our adaptive fiber tracking algorithm utilizes an advection-diffusion based algorithm [7, 8] which is integrated into NeuroQLab DTI (see Fig. 2), a software tool for neurosurgical planning and quantitative image analysis [9, 10].

In contrast to the basic fiber tracking approach, our algorithm adapts its control parameters to brain regions defined by a white matter atlas ("Eve Atlas" [11, 12]). The atlas has been built using T1-MRI data of 152 healthy volunteers and consists of 176 regions. Details of the algorithm can be found in our previous papers [13, 14]. In contrast to the previous challenges in 2013 and 2014, we also tested the possibility to replace the atlas by a discretized FA map which consists of 176 different grey values larger than zero. The idea behind this is that the FA map reflects the different brain regions quite well where different diffusion processes predominate.

We adapted the following control parameters:

- $\alpha \in [0, 1]$, which interpolates between streamline ($\alpha = 1$) and deflection-based tracking ($\alpha = 0$)
- window length $\in [1.5, 6]$ (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 $\in [0.1, 0.45]$.
- maximal curvature $\in [0.2, 0.65]$. The situation is explained in Fig. 3.
- step width $\in [0.5, 7]$ (mm): the step width between two consecutive fiber points.

For each tracking step, the corresponding atlas region is computed. 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 to overcome timing issues and 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 has to be aborted. If the fibers are determined for all seed points, the tracking process is repeated until

a predefined fiber density is reached or until the number of iterations exceeds a predefined threshold.

Finally, the fibers are filtered with include ROIs and exclude ROIs.

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 20 seconds.

The reconstructed tracts visualized in Fig. 5 to 9 show the tracked fibers and their proximity to the tumors. It is demonstrated that the fibers end/originate 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 internal capsule or in the brain stem as it can be found in many research papers, e.g., see [15–18].

From our point of view, patient 3 was the most interesting and most challenging data set. On the one hand, the tumor was very close to the pyramidal tract so that the fibers were shifted away to the frontal part, on the other hand the image data had a relatively coarse resolution and it was quite difficult to reconstruct the fibers on the healthy hemisphere for the corticobulbar tract (high curvature, low FA close the crossings of superior longitudinal fasciculus, corpus callosum and corticobulbar tract).

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 [19–24]. All of them could not achieve the quality and performance of the probabilistic parameter adaption algorithm which we developed for the 2013 and 2014 tractography challenges [13, 14] where we have shown that a reliable tracking of the pyramidal tracts is possible by 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 most powerful improvement was the extension of the selection of seed regions in a 3D viewer so that also regions within the brain can be used and not only 3D volumes along the surface of the cortex.

To the best of our knowledge, our approach is the only 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 representing 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.

References

1. Hering, J., Neher, P.F., Stieltjes, B., Maier-Hein, K.H.: Dti tractography challenge 2014 - mitk global tractography. In: MICCAI Workshop (MICCAI 2014 DTI Challenge). (2014)
2. Neher, P.F., Stieltjes, B., Fritzsche, K.H.: Dti tractography challenge 2013 - mitk global tractography. In: MICCAI Workshop (MICCAI 2013 DTI Challenge). (2013) 70–74
3. Masutani, Y., Suzuki, Y., Ino, K.: Tracking corticospinal tract with diffusion tensor field replacement for cancelling crossing with superior longitudinal fasciculus. In: MICCAI Workshop (MICCAI 2013 DTI Challenge). (2013) 3–8
4. Khan, A.R., Goubran, M., Lau, J.C., Eagleson, R., Peters, T.M., de Ribaupierre, S.: Probabilistic multi-tensor tractography and noddi tumour characterization for neurosurgical planning. In: MICCAI Workshop (MICCAI 2014 DTI Challenge). (2014) 4–14
5. Hahn, H., Klein, J., Nimsky, C., Rexilius, J., Peitgen, H.O.: Uncertainty in diffusion tensor based fiber tracking. Acta Neurochir. Suppl. **98** (2006) 33–41
6. Hahn, H.K.: Morphological Volumetry — Theory, Concepts, and Application to Quantitative Medical Imaging. PhD thesis, University of Bremen (2005)
7. Barbieri, S., Klein, J., Nimsky, C., Hahn, H.: Assessing fiber tracking accuracy via diffusion tensor software models. In: SPIE Medical Imaging. (2010) 762326–762326–9
8. Klein, J., Groetsch, A., Betz, D., Barbieri, S., Friman, O., Stieltjes, B., Hildebrandt, H., Hahn, H.: Qualitative and quantitative analysis of probabilistic and deterministic fiber tracking. In: SPIE Medical Imaging. (2010) 76232A–76232A–8
9. Klein, J., Weiler, F., Barbieri, S., Hirsch, J.G., Geisler, B., Hahn, H.K.: Novel features of neuroqlab - a software assistant for evaluating neuroimaging data. In: Proceedings of European Congress on Radiology (ECR 2012). (2012)
10. Weiler, F., Rexilius, J., Klein, J., Hahn, H.: Neuroqlab-a software assistant for neurosurgical planning and quantitative image analysis. In: GI Jahrestagung. (2009) 1352–1358
11. Mori, S., Oishi, K., Jiang, H., Jiang, L., Li, X., Akhter, K., Hua, K., Faria, A.V., Mahmood, A., Woods, R., Toga, A.W., Pike, G.B., Neto, P.R., Evans, A., Zhang, J., Huang, H., Miller, M.I., van Zijl, P., Mazziotta, J.: Stereotaxic white matter atlas based on diffusion tensor imaging in an ICBM template. NeuroImage **40**(2) (2008) 570–582
12. Oishi, K., Zilles, K., Amunts, K., Faria, A., Jiang, H., Li, X., Akhter, K., Hua, K., Woods, R., Toga, A.W., Pike, G.B., Rosa, P., Evans, A., Zhang, J., Huang, H., Miller, M.I., Van, P.C.M., Mazziotta, J., Mori, S.: Human brain white matter atlas: Identification and assignment of common anatomical structures in superficial white matter. Neuroimage **43** (2008) 447–457
13. Klein, J., Meuschke, M., Geisler, B., Hahn, H.K.: Local atlas-based adaptive fiber tracking. In: MICCAI Workshop (MICCAI 2013 DTI Challenge). (2013) 59–69
14. Klein, J., Weiler, F., Hahn, H.K.: Probabilistic parameter adaption for fiber tracking of the corticospinal tract. In: MICCAI Workshop (MICCAI 2014 DTI Challenge). (2014) 33–41

15. Lee, J.S., Han, M.K., Kim, S.H., Kwon, O.K., Kim, J.H.: Fiber tracking by diffusion tensor imaging in corticospinal tract stroke: Topographical correlation with clinical symptoms. NeuroImage **26**(3) (2005) 771 – 776
16. Niizuma, K., Fujimura, M., Kumabe, T., Higano, S., Tominaga, T.: Surgical treatment of paraventricular cavernous angioma: Fibre tracking for visualizing the corticospinal tract and determining surgical approach. Journal of Clinical Neuroscience **13**(10) (2006) 1028 – 1032
17. Qazi, A.A., Radmanesh, A., O'Donnell, L., Kindlmann, G., Peled, S., Whalen, S., Westin, C.F., Golby, A.J.: Resolving crossings in the corticospinal tract by two-tensor streamline tractography: Method and clinical assessment using fmri. NeuroImage **47, Supplement 2** (2009) T98 – T106
18. Sivaswamy, L., Rajamani, K., Juhasz, C., Maqbool, M., Makki, M., Chugani, H.T.: The corticospinal tract in sturgeweber syndrome: A diffusion tensor tractography study. Brain and Development **30**(7) (2008) 447 – 453
19. Barbieri, S., Bauer, M.H., Klein, J., Nimsky, C., Hahn, H.K.: Segmentation of fiber tracts based on an accuracy analysis on diffusion tensor software phantoms. Neuroimage **55**(2) (2011) 532–544
20. Barbieri, S., Bauer, M.H., Klein, J., Nimsky, C., Hahn, H.K.: A Variational, Non-Parametric Approach to the Fuzzy Segmentation of Diffusion Tensor Images. In: Proc. of MICCAI workshop on Computational Diffusion MRI. (2010) 134 – 145
21. Klein, J., Barbieri, S., Stuke, H., Bauer, M., Egger, J., Nimsky, C., Hahn, H.K.: On the Reliability of Diffusion Neuroimaging. Neuroimaging (2010) 1 – 24
22. Klein, J., Koehler, B., Hahn, H.K.: Efficient global fiber tracking on multidimensional diffusion direction maps. Proceedings of SPIE Medical Imaging 2012 **8314** (2012) 83140M–1–83140M–8
23. Koehn, A., Weiler, F., Klein, J., Konrad, O., Hahn, H., Peitgen, H.: State-of-the-art computer graphics in neurosurgical planning and risk assessment. In: Proc. of Eurographics Short Papers and Medical Prize Awards. (2007) 117–120
24. Klein, J., Koehler, B., Hahn, H.: Efficient global fiber tracking on multi-dimensional diffusion direction maps. In: SPIE SPIE Medical Imaging 8314. (2012) 83140M–1–83140M–8

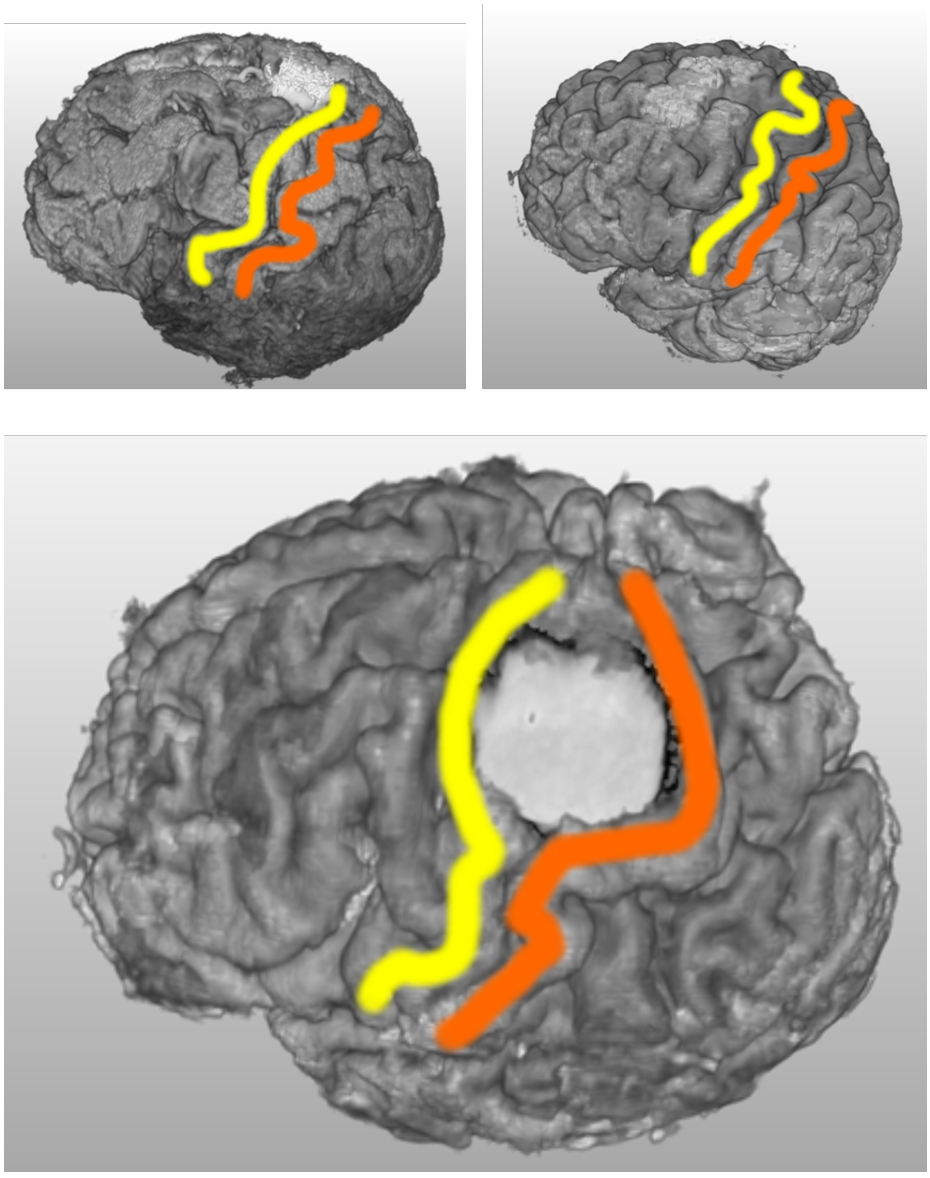

Fig. 4. The precentral gyrus and the postcentral gyrus are marked for all three patients (top row left: patient 1, top row right: patient 2, bottom row: patient 3. While the tumor is very close to the pyramidal tracts for patient 1 and patient 3, the distance is larger for patient 2.

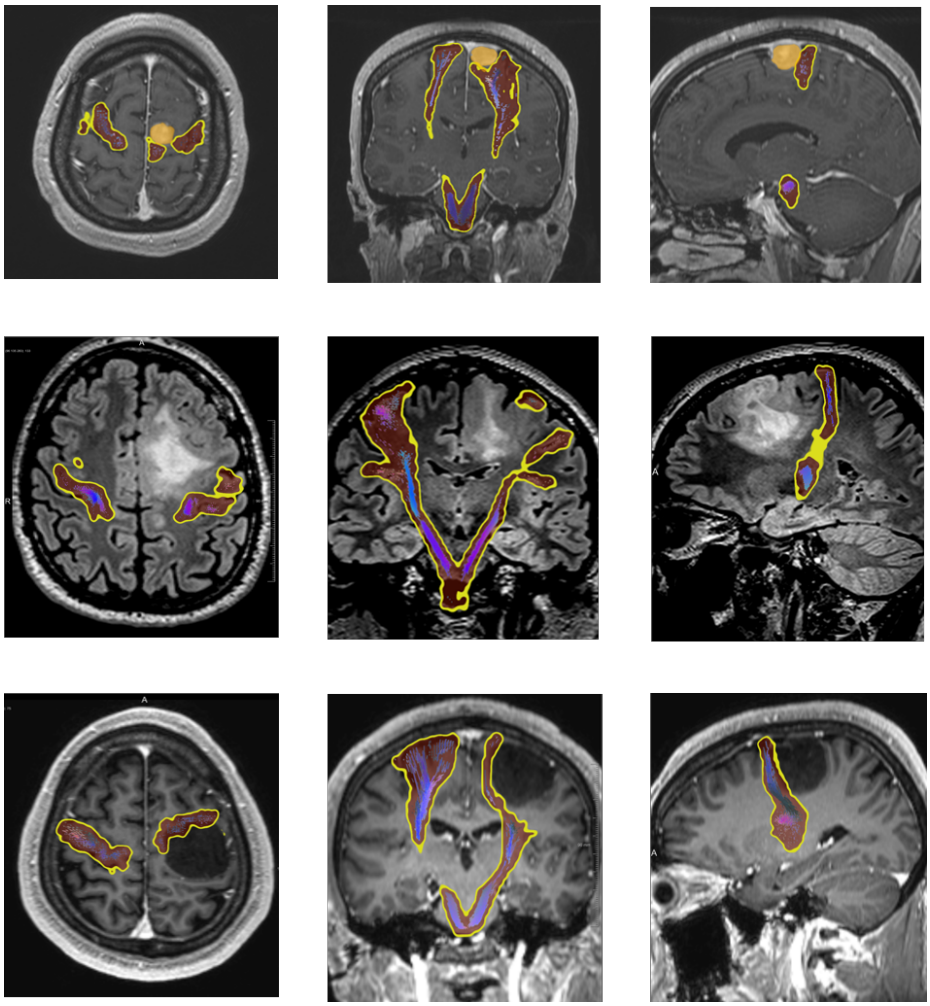

Fig. 5. Wrapped fibers of the pyramidal tracts are shown for all patients. Upper row: patient 1, center row: patient 2, bottom row: patient 3. Note that in contrast to Fig. 1 only those fiber segments are shown which are in the close vicinity of the shown 2D slice.

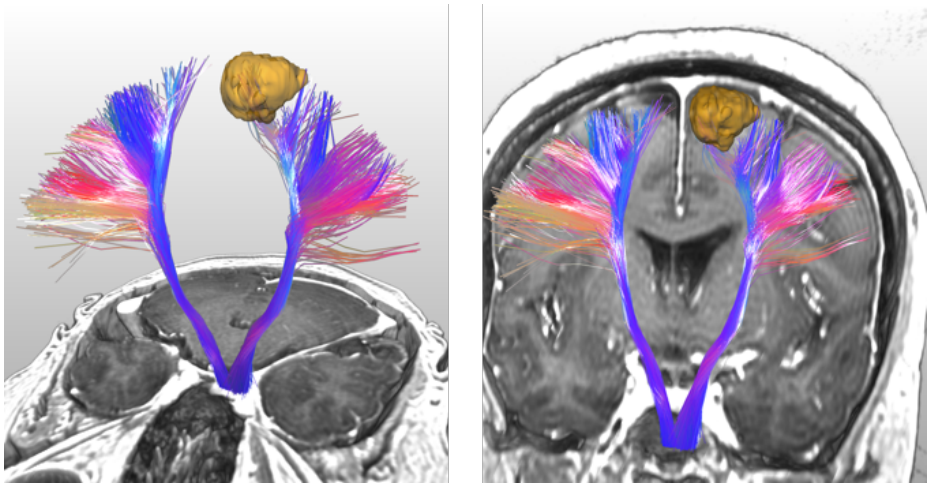

Fig. 6. Patient 1: Tracked fibers of the corticospinal and corticobulbar tract with a volume rendering of T1-weighted image data.

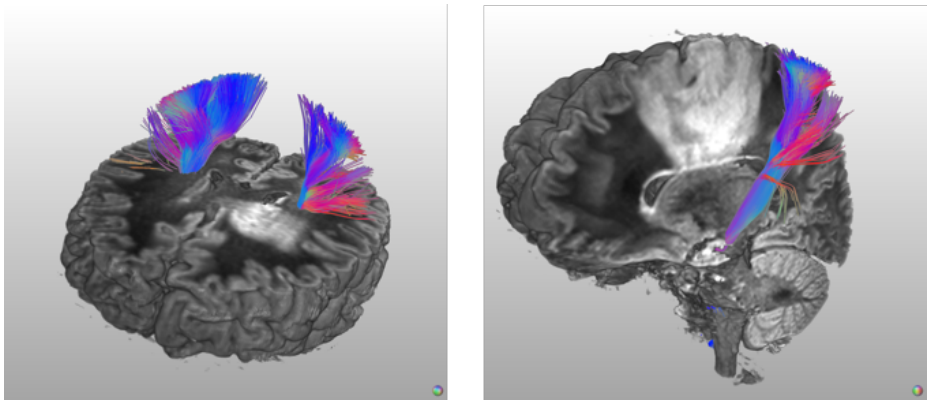

Fig. 7. Patient 2. Tracked fibers with a volume rendering of T2 skull-stripped data.

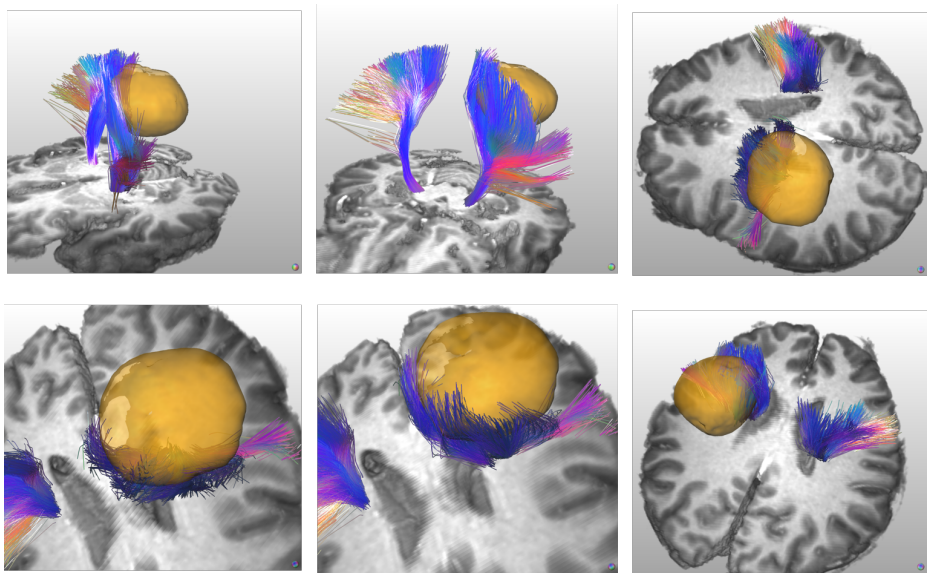

Fig. 8. Patient 3: Tracked fibers with a volume rendering of T1 skull-stripped data. It is demonstrated that the pyramidal fibers are moved to the frontal part of the brain by the relatively large tumor.

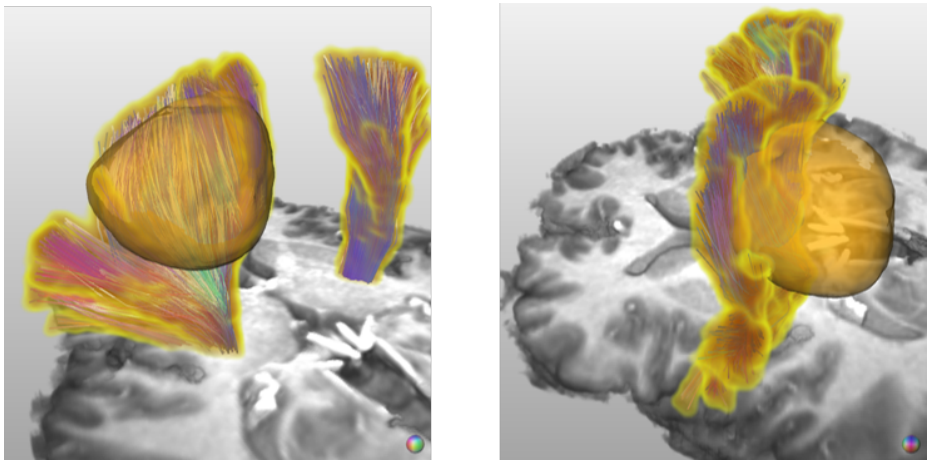

Fig. 9. Patient 3: Pyramidal tracts which are wrapped by hull. These hulls might be integrated into a planning system instead of showing single fiber tracts which might lead to clutter.