

MITK Global Tractography

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ABSTRACT

Fiber tracking algorithms yield valuable information for neurosurgery as well as automated diagnostic approaches. However, they have not yet arrived in the daily clinical practice. In this paper we present an open source integration of the global tractography algorithm proposed by Reisert et.al. into the open source Medical Imaging Interaction Toolkit (MITK) developed and maintained by the Division of Medical and Biological Informatics at the German Cancer Research Center (DKFZ). The integration of this algorithm into a standardized and open development environment like MITK enriches accessibility of tractography algorithms for the science community and is an important step towards bringing neuronal tractography closer to a clinical application. The MITK diffusion imaging application, downloadable from www.mitk.org, combines all the steps necessary for a successful tractography: preprocessing, reconstruction of the images, the actual tracking, live monitoring of intermediate results, postprocessing and visualization of the final tracking results. This paper presents typical tracking results and demonstrates the steps for pre- and post-processing of the images.

Keywords: Global Fiber Tracking, Neuronal Tractography, Diffusion-weighted Imaging, Q-Ball Imaging, Diffusion Tensor Imaging, open source, MITK, ITK, VTK

1. INTRODUCTION

Up to now, diffusion weighted imaging (DWI) is the only technique to noninvasively gain insight into the architecture of the human white matter pathways. Tractography algorithms try to explicitly estimate the underlying fiber pathways from the given voxelwise information. There exists a wide variety of different tractography algorithms that can roughly be divided into the two subgroups of local and global methods. Local methods try to reconstruct a fiber step by step by following the voxelwise information and successively adding segments to the fiber. While local methods are known to be performant, they often struggle with image artifacts or complex fiber configurations like crossings or kissings. Global methods try to reconstruct all fibers simultaneously, searching for a global optimum. While computationally much more challenging, global methods promise more robust results. This work presents the integration of the successful and also computationally efficient² global approach proposed by Reisert et.al. called Gibbs Tracking^{1,3} as well as the tools needed for pre- and postprocessing of the data within the Medical Imaging Interaction Toolkit (MITK), more precisely within the diffusion imaging component MITK-DI.⁴ MITK is a free open-source software system for development of interactive medical image processing software.⁵ The open source application *MITK Diffusion* is available on www.mitk.org.

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2. MATERIALS AND METHODS

In order to maximize reusability and compatibility with other applications, the algorithm itself is realized as an Insight Toolkit (ITK, www.ITK.org) filter object (`itk::GibbsTrackingFilter`) using well established ITK mechanisms like smart-pointers and pipeline processing. New MITK datastructures (e.g. `mitk::FiberBundle`) extend MITK-DI and ensure seamless integration into MITK based applications. This includes extensions to the MITK factory mechanism to support loading, saving, and drag and drop of fiber bundle files using either the MITK xml-based `.fib` file format or the widely used `vtkPolyData` format (ASCII) using `.vfib*`.

2.1 Preprocessing

The tractography algorithm expects orientation distribution functions (ODF) as input data. For high angular resolution diffusion imaging (HARDI) sequences, a Q-Ball reconstruction can be performed directly. If HARDI data are not available, a standard tensor reconstruction can be applied. Afterwards ODFs can directly be calculated from the diffusion tensors. MITK provides several different Q-Ball reconstruction methods: a numerical reconstruction (Tuch et.al.⁶), a spherical harmonics (SH) reconstruction (Descoteaux et.al.⁷), and a SH reconstruction with solid angle consideration (Aganj et.al.⁸). In order to accelerate the tracking process, the search space can be limited by providing a mask image to the algorithm.

2.2 Tractography

The basic idea of the gibbs tracking algorithm is to fit a model M , consisting of directed points (particles) and connections between the particles, to the image data D by minimizing two energy terms. This process is designed as an iterative process introducing random changes into the model M that are accepted with a certain probability calculated from the two energies. The energies tell us how well the model fits the data (external energy) and how well shaped the fibers are (internal energy). The "Gibbs Tracking View" (Fig. 1) allows configuration of the most important parameters which can be saved and loaded using xml-based `.gtp` files:

- Number of iterations
- Particle length/width/weight controlling the contribution of each particle to the model M
- Start and end temperature controlling how fast the process reaches a stable state
- Weighting between the two energies
- Minimum fiber length constraint

Several parameters, like the particle length, width and weight, can be estimated automatically according to the selected image data. The automatically selected parameters usually give a good estimate of the optimal parameters and can be used as a basis for further optimization. To automatically estimate the particle weight, which is an important parameter controlling the sensitivity of the algorithm, the (generalized) fractional anisotropy (FA/GFA) map of the input image is used. The parameter is estimated from the ODFs belonging to voxels that exceed a certain FA/GFA threshold. The particle length and width are simply estimated as $c \cdot \text{minspacing}$, where c is set to 0.5 for the particle width and to 1.5 for the particle length.

Once started, the tracking process runs in a separate worker thread realized by using the mechanisms provided by QTs `QThread` class and therefore does not block the application GUI. In addition to the textual display that provides information about the tracking progress, the whole process can be monitored by visualizing the intermediate tracking results every second. To increase the number of detected fibers and to account for the statistical nature of the process, each image can be tracked several times to combined the results afterwards.

2.3 Postprocessing

To postprocess the fiber tracking results, the MITK-DI component provides the Fiber Processing View. This view integrates all mechanisms necessary to work with fiber bundles like heatmap, envelope and surface mesh generation, visualization of fiber endings and extraction of fiber subsets via ROI placement. The view is visualized in Fig. 2

*.vtk files have to be renamed to `.vfib` in order for them to be recognized as fiber bundle

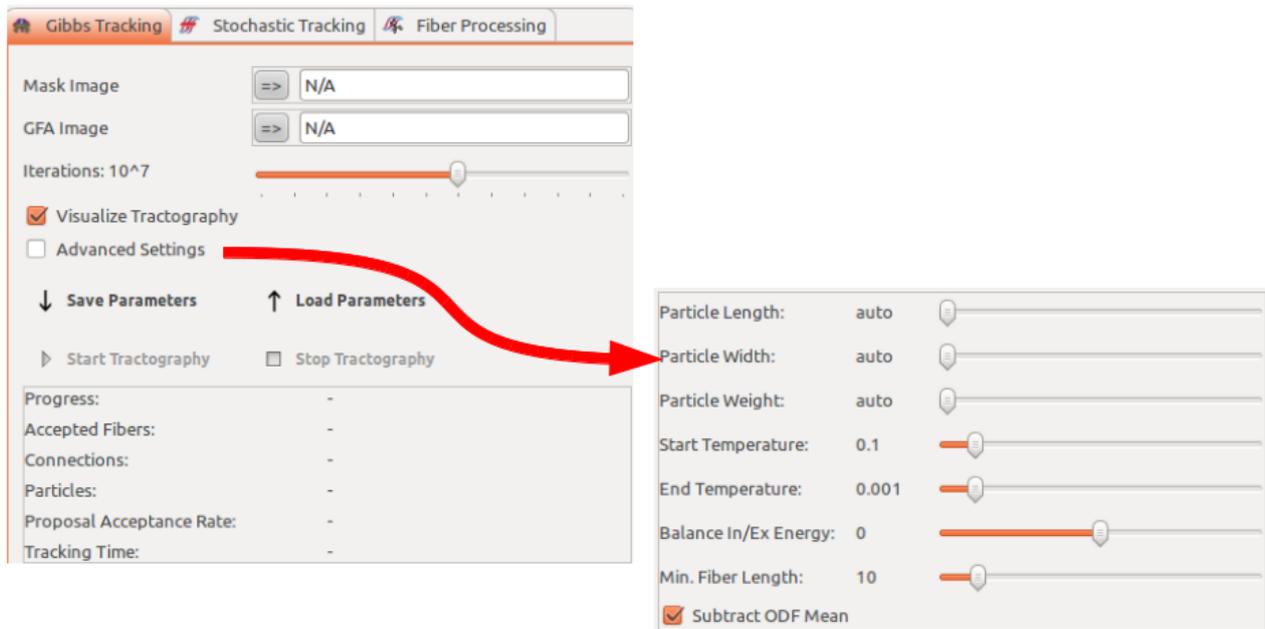


Figure 1. Screenshot showing the "Gibbs Tracking View".

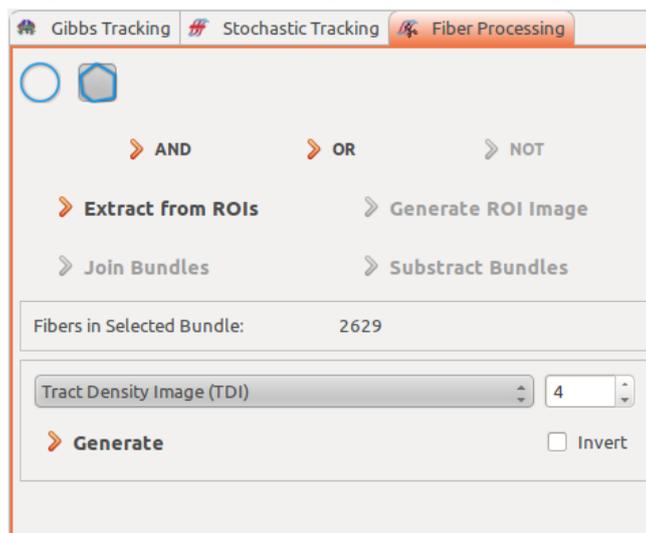


Figure 2. Screenshot showing the "Fiber Processing View".

2.4 Image Data

In order to demonstrate the value of the proposed application, processing of a typical dataset was performed. The experiment was performed on an Intel Core i7 CPU (2.93 GHz each) with 24 Gb of RAM. The results are documented in the following chapter. The image data used for our experiment consists of a single DWI dataset acquired with an isotropic resolution of 2.5 mm, a b-value of 3500 s/mm^2 , a size of $96 \times 82 \times 40$ and 65 gradient directions.

3. RESULTS

The used DWI was reconstructed using a standard spherical harmonics approach.⁷ The tracking was performed as a single session with 5×10^8 iterations and took about 5 hours. Several white matter tracts like the corticospinal

tract (CST), fornix and cingulum were afterwards extracted from the whole brain tracking result (Fig. 5). The process to extract the CST using several ROIs as well as the whole brain tractography result is visualized in Fig. 3. An overview over the "Fiber Tracking Perspective" of MITK Diffusion is given in Fig. 4.

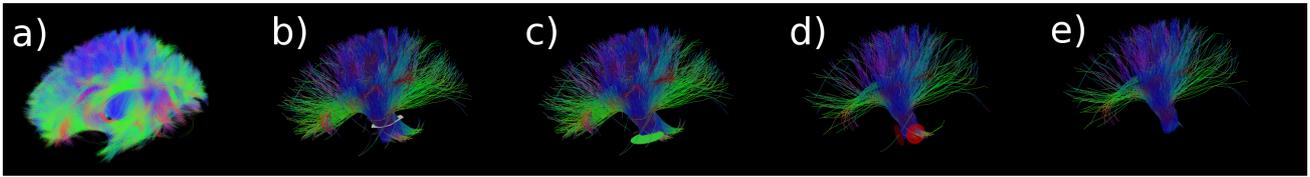


Figure 3. Extraction process for the corticospinal tract. Several positive ROIs (b and c), that retain all passing fibers, and negative ROIs (d), that remove the passing fibers, are used.

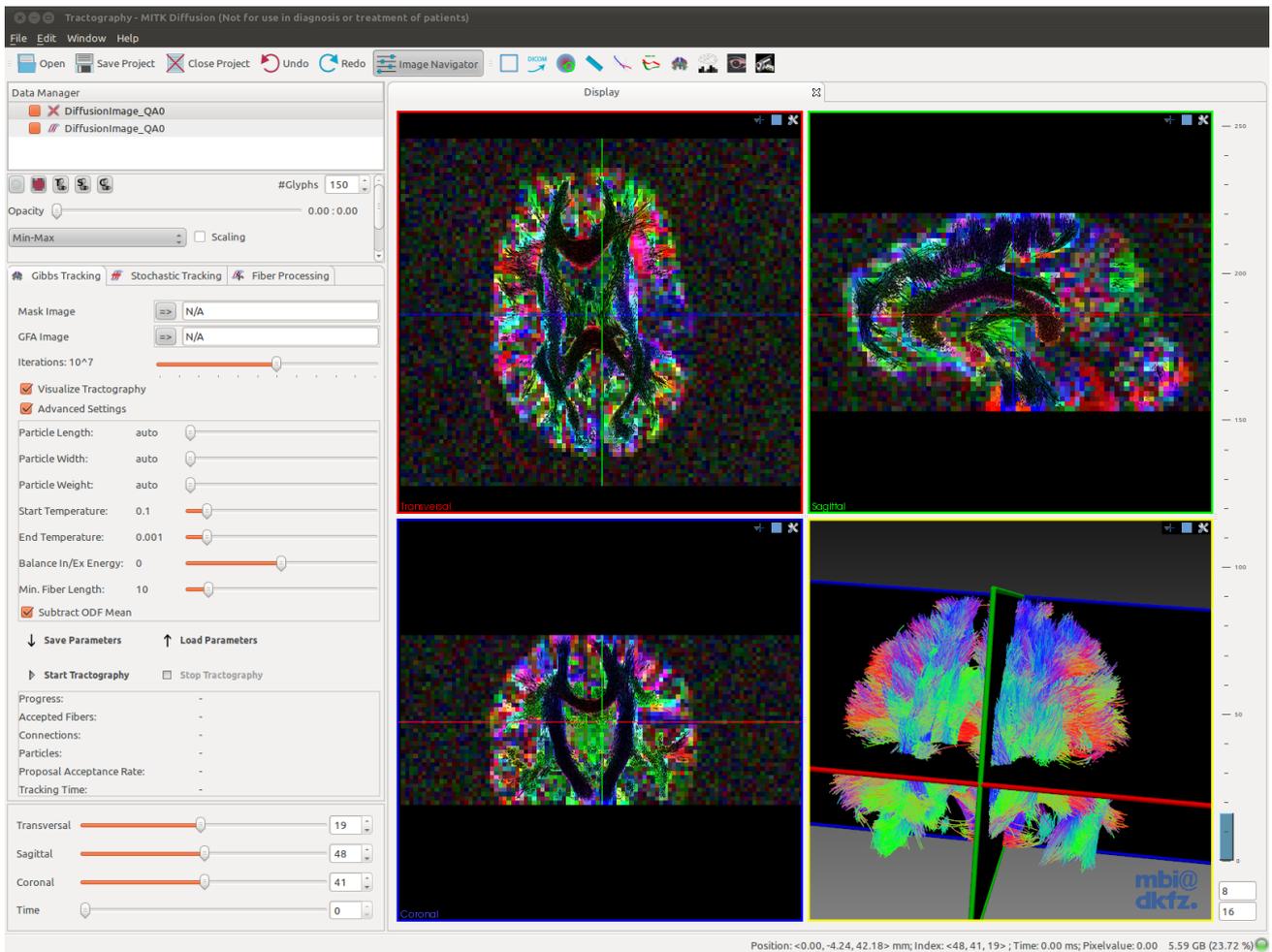


Figure 4. Screenshot of the "Fiber Tracking Perspective" as well as a Q-Ball und fibervisualization, embedded into MITK Diffusion.

4. CONCLUSION AND OUTLOOK

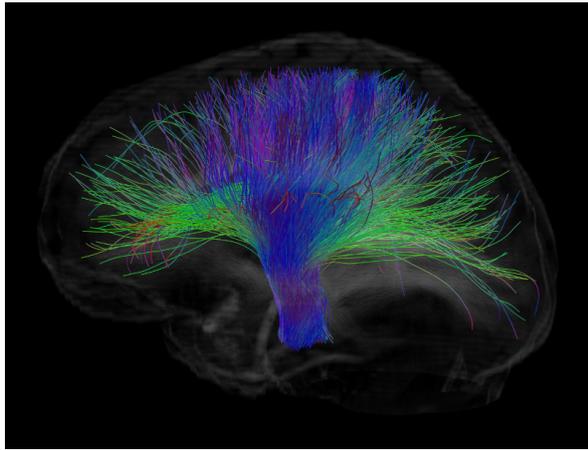
Global tractography algorithms are known to be computationally challenging but at the same time more promising regarding the tracking quality and robustness compared to local methods. In this paper we presented an implementation of the algorithm presented by Reisert et.al.¹ and the tools used for pre- and postprocessing of the data within the diffusion imaging component MITK-DI of the Medical Imaging Interaction Toolkit. To

our knowledge this is the first efficient open source implementation of a global tractography algorithm in an established framework like MITK. This ITK-style implementation allows convenient integration into other ITK compliant projects due to the standardized ITK filter architecture. Therefore it is an important addition to the currently available and reusable repertoire of open source tracking algorithms. Support of commonly used data formats ensures comparability and usability of the tracking results and raises impact to the community. The application executables are downloadable for free under www.mitk.org.

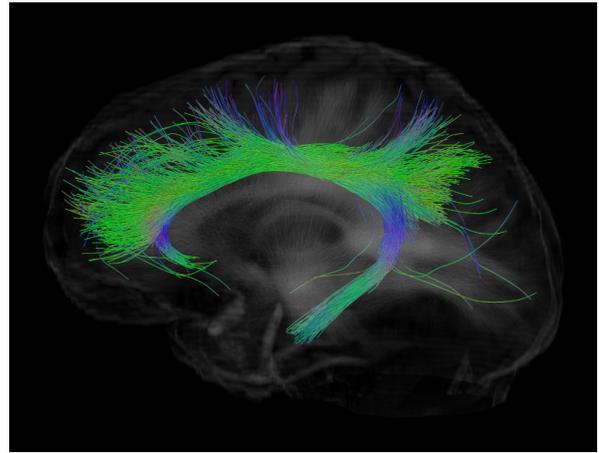
The application of the algorithm as well as the extraction of several white matter tracts from the resulting whole brain tracking results were successfully tested on an in-vivo dataset. Further work will concentrate on the performance and also on the qualitative improvement of the tractography approach for example via parallelization and integration of prior anatomical knowledge.

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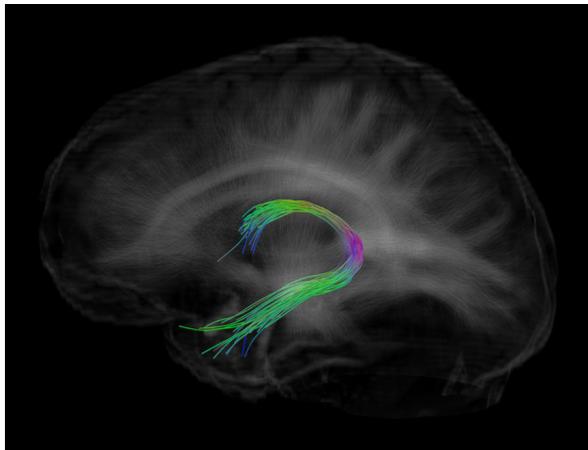
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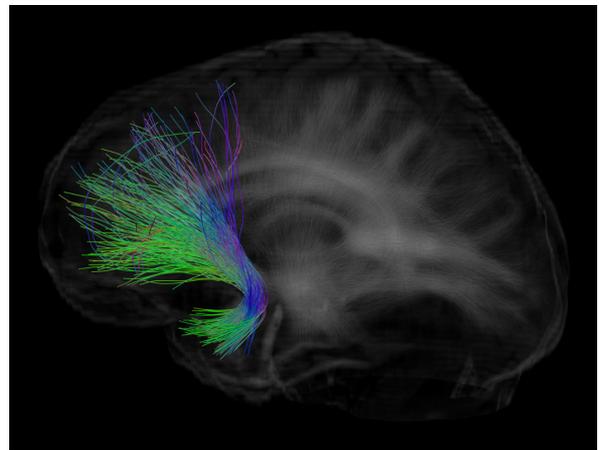
(a) Corticospinal Tract



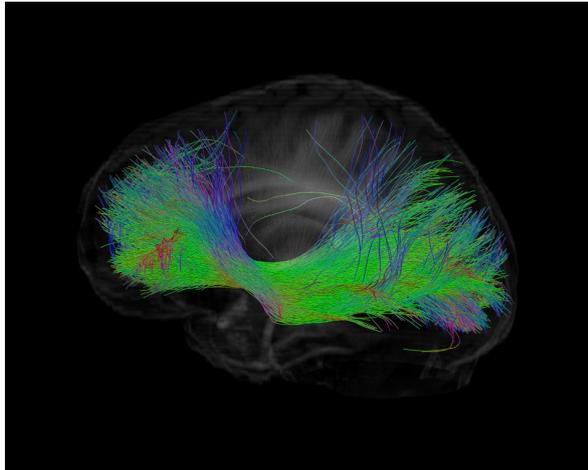
(b) Cingulum



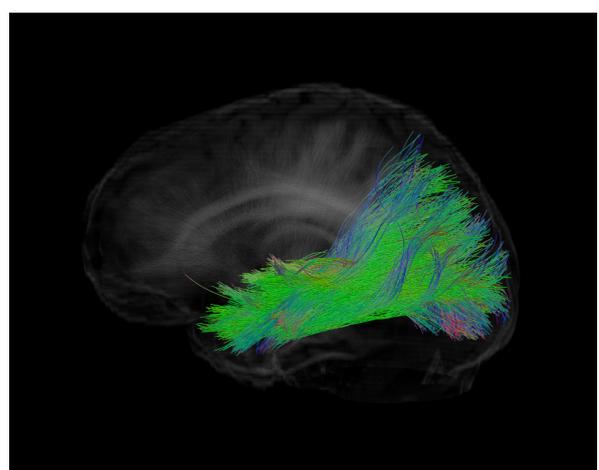
(c) Fornix



(d) Uncus



(e) Inferior Occipitofrontal Fasciculus



(f) Inferior Longitudinal Fasciculus

Figure 5. Selection of the structures extracted from the whole brain tracking result.