

Fiber Tractography within MITK Diffusion

Peter F. Neher, Division of Medical Image Computing, German Cancer Research Center (DKFZ)
Heidelberg, p.neher@dkfz.de,

Klaus H. Maier-Hein, Division of Medical Image Computing, German Cancer Research Center (DKFZ)
Heidelberg, k.maier-hein@dkfz.de

The publication of scientific software and algorithms as open source stands at the core of reproducible science and is increasingly pursued in many fields, including medical image processing. Especially in the area of diffusion-weighted magnetic resonance image (dMRI) processing, many research groups follow this paradigm and publish their methods as ready to use software tools, such as MRtrix, DIPY and our own work *MITK Diffusion* [1]. *MITK Diffusion* offers selection of image analysis methods for dMRI processing. In this abstract we outline the capabilities of *MITK Diffusion* and present recent additions to the application focusing on neuronal fiber tractography.

The core functionalities of *MITK Diffusion* are (1) easy data handling by supporting the im- and export of most file formats common in the area of dMRI processing and fiber tractography, (2) quantification and modelling of dMRI signals, (3) various types of fiber tractography methods, (4) processing and quantification of tractograms as well as (5) simulation of realistic dMRI images. Most of these functionalities are available via the graphical user interface of *MITK Diffusion* as well as via the corresponding command line tool, which enables easy batch processing of larger data collectives. The following paragraphs describe the functionalities outlined above in more detail.

(1) *Data handling*: *MITK Diffusion* supports most standard medical image formats such as NIFTI, NRRD and DICOM as well as common tractography file formats such as vtk/fib, trk, tck, and tractography DICOM (supplement 181 of the DICOM standard). The latter is for example supported by the neuro-navigation software of Brainlab. By supporting tractography file formats native to other tools (e.g. 3D Slicer, MRtrix, DIPY) and by offering interfaces for many specialized file types, such as for peaks, ODFs or spherical harmonic coefficients, *MITK Diffusion* integrates seamlessly into complex workflows involving other software tools.

(2) *Signal modeling*: A crucial step in most dMRI studies is the ability to quantify and model the diffusion-weighted signal. *MITK Diffusion* provides methods to calculate tensor and Q-ball model fits of the data as well as scalar maps derived from these models (GFA, FA, RD, AD, etc.) or from the raw signal (ADC, IVIM and kurtosis maps). To extend the range of models usable for fiber tractography, the results of signal models implemented in other toolkits, such as CSD (MRtrix), multi-tensor (Camino), or ODFs reconstructed with DIPY using methods such as a SFM or a 3D-SHORE based reconstruction, can be imported into *MITK Diffusion*.

(3) *Fiber tractography*: *MITK Diffusion* offers multiple types of tractography, which can be categorized into global, originally proposed by Reisert et al. [2], and streamline tractography. The latter is available in many flavors (see Figure 1) including peak, tensor (TEND, FACT), multi-tensor, ODF, as well as the recently presented machine learning based tractography [3]. Streamline tractography can be run in a whole-brain or seed-region based manner as well as interactively by placing and moving a spherical seed region in the image where each parameter and position change triggers a real-time tractography update. The streamline integration can be performed deterministically or probabilistically as well as based only on the current streamline position or including neighborhood information [3]. The resulting tractogram can be presented as classic fibers or alternatively as heatmap, which is a feature often used in conjunction with probabilistic tractography.

(4) *Fiber processing*: A common task after successful tractography is to filter, dissect or otherwise post-process the tractogram. In *MITK Diffusion*, tractograms can be automatically filtered by length, curvature or direction. To extract parts of a tractogram, static mask images can be used as inclusion or exclusion regions for fibers passing through or ending inside the mask. Furthermore, circular and polygonal inclusion ROIs can be drawn dynamically and combined using logical operations to perform complex tract-surgery. Besides these dissection tools, *MITK Diffusion* enables the combination and subtraction of tractograms, resampling and compression of fibers, as well as different colorization (directional, by curvature, by weight, by scalar map, uniform) and visualization modes (lines, tubes, ribbons).

(5) *dMRI simulation*: Using simulated datasets for the validation of new methods is a common approach in medical image processing. To this end, *MITK Diffusion* includes the dMRI simulation tool Fiberfox [4]. Fiberfox enables the straight-forward simulation of dMRI images on the basis of complex but well-defined fiber configurations. Fiberfox gives the user full control over many parameters of a typical dMRI acquisition as well as artifact generating effects not controllable in real acquisitions, while providing a gold-standard with respect to the underlying fiber configuration and volume fractions. A whole-brain diffusion-weighted MR image simulated with Fiberfox was for example employed in the ISMRM tractography challenge 2015 [5] (http://www.tractometer.org/isrmr2015_challenge/).

In this work we focused on fiber tractography and related functionalities but there is much more to discover, such as connectomics and manual segmentation, the description of which was unfortunately beyond the scope of this abstract. Some of the features presented here are newer than the latest binary release 2017.07, which can be downloaded on <http://mitk.org/wiki/DiffusionImaging>, but all features including the most recent developments are available as ready-to-build source code on <https://phabricator.mitk.org/source/mitk.git>. With this contribution we want to follow good scientific practice and emphasize the importance of publishing scientific methods open source by contributing to the openly available collection of software tools that are crucial for advances in the research field of dMRI processing.

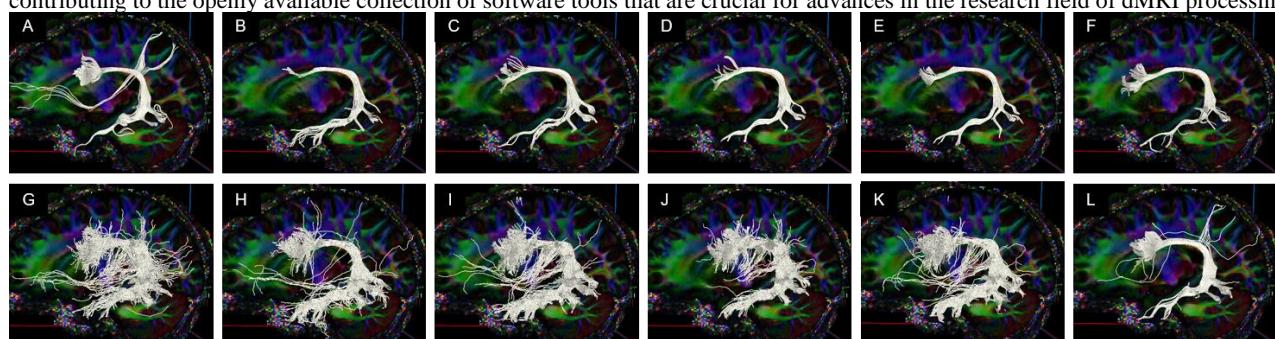


Figure 1: Tractograms obtained with *MITK Diffusion* using the same seed region (4 voxels in the superior longitudinal fasciculus) with different diffusion models and streamline integration. The figures illustrate the capability of *MITK Diffusion* to easily run and compare a multitude of tractography methods. It also highlights the large variability introduced by the different signal modelling and streamline integration methods. Tractograms A-F and L were obtained with deterministic, G-K with probabilistic streamline integration. Diffusion models were DTI (A,G), CSA Q-ball (B,H), 3D-SHORE (C,I), SFM (D,J), CSD (E,K), CSD Peaks (F) and Two-tensor (L).

References

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