

# MITK-DI

## A new Diffusion Imaging Component for MITK

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**Abstract.** Diffusion-MRI provides a unique window on brain anatomy and insights into aspects of brain structure in living humans that could not be studied previously. There is a major effort in this rapidly evolving field of research to develop algorithms that provide detailed information on the white matter fibre architecture and disorders in the brain. High angular resolution diffusion imaging (HARDI) provides an extraordinarily high level of detail, including entire manifolds of information at each voxel. The lack of standardized software tools for data I/O, model reconstruction, interactive visualization, feature extraction and statistics impedes development and sustainable evaluation in HARDI research.

In this paper, a new toolkit component of the Medical Imaging and Interaction Toolkit (MITK, [www.mitk.org](http://www.mitk.org)), MITK-DI, is presented and its features are summarized at each stage of the pipeline from raw data processing to comprehensive statistics. MITK-DI aims at integrating novel diffusion imaging techniques into the MITK toolkit to provide a comprehensive software framework for performant data processing, analysis and interactive visualization. An exemplary application of the framework is shown using phantom and *in-vivo* datasets from a clinical MR scanner. Visualizations are presented that reveal details for which there would be no direct way to appreciate using conventional display of scalar- or RGB-images.

## 1 Introduction

Diffusion-MRI provides a unique and sensitive probe for the architecture of biological tissues. The diffusion tensor model, which was introduced in 1994 [1], encapsulates the measured diffusion properties of water molecules as the 3x3 covariance matrix of a Gaussian distribution. The well known limitations of this model in complex fiber configurations have led to the development of high angular resolution diffusion imaging (HARDI) techniques like q-ball imaging (QBI) [2]. Here, the information in each voxel is represented by a manifold, called orientation distribution function (ODF), that resembles the marginal displacement probability of diffusing water molecules after being released at the center of each voxel. While QBI has several advantages over diffusion tensor imaging (DTI), it significantly raises the complexity of data processing and visualization.

Several software toolkits like MedINRIA,<sup>1</sup> Camino,<sup>2</sup> SCIRun,<sup>3</sup> Slicer<sup>4</sup> or TrackVis<sup>5</sup> support processing and visualization of diffusion imaging data. However, display and interaction capabilities are often limited. Camino, for example, uses unix-style command interfaces and manual export of models for viewing in other programs. There is a clear need for software tools that feature proper interactive visualization and quantitative evaluation in HARDI data.

In this paper, we present a new toolkit component of the Medical Imaging and Interaction Framework (MITK, [www.mitk.org](http://www.mitk.org)) [3], called MITK Diffusion Imaging (MITK-DI). MITK-DI aims at supporting cutting edge diffusion imaging techniques, extending the MITK framework in terms of data I/O, processing and visualization of diffusion related images. It will be made publicly available under a BSD-style open-source license in December 2009. As an example of application, several phantom and *in-vivo* datasets were processed and visualized in order to underline the capabilities of the component. In contrast to most other frameworks, MITK-DI addresses all aspects of application design including full integration into an OSGi-based<sup>6</sup> application platform and fluent workflows. While other diffusion imaging toolkits exclusively focus on providing diffusion related functionalities, MITK-DI is tightly integrated into the grown-up platform MITK and therefore allows covering the complete cycle from raw-data to computer-aided diagnosis and statistics.

## 2 Materials and Methods

Standardization is a key issue in medical imaging research and can only be successful with a consistent and flexible software design, the publication of source code and the use of development tools that allow integration in a clinical environment with reasonable effort to prove relevance and, finally, to improve health care. Specific care was taken to these requirements during the design of MITK-DI.

### 2.1 Software Design and Application-level Support

Like the Visualization Toolkit (VTK, [www.vtk.org](http://www.vtk.org)), the Insight Toolkit (ITK, [www.itk.org](http://www.itk.org)) and MITK, MITK-DI is an object-oriented, cross-platform component implemented in C++. Most classes are derived from top-level classes of ITK, reusing all smart-pointer-, time-stamp-, pipeline- and parallel processing mechanisms. The component extends MITK using the provided module-mechanism. Application-level classes are implemented as bundles for the BlueBerry application platform (<http://www.blueberry-project.org/>) that is the

<sup>1</sup> <http://www-sop.inria.fr/asclepios/software/MedINRIA/>

<sup>2</sup> <http://www.cs.ucl.ac.uk/research/medic/camino/>

<sup>3</sup> <http://www.sci.utah.edu/>

<sup>4</sup> <http://www.slicer.org/>

<sup>5</sup> <http://www.trackvis.org/>

<sup>6</sup> <http://www.osgi.org/>

basis for all current MITK applications. Applications run on Windows, Mac OS X and Linux with native look and feel and 64-bit support. All MITK-DI bundles feature an intuitive GUI front-end with the support for multiple dataset processing.

## 2.2 Datastructures

MITK-DI includes algorithms for direct DICOM import and reading and writing of the widely used NRRD<sup>7,8</sup> format. MITK-DI defines new classes that represent diffusion weighted images (`mitk::DiffusionImage`), q-ball images (`mitk::QBallImage`) and tensor images (`mitk::TensorImage`). All these data types make use of the MITK factory mechanism and can be handled via drag and drop on the application level using the file extensions `.dwi`, `.qbi` and `.dti` respectively.

## 2.3 Model Reconstruction

MITK-DI supports a range of standard and advanced reconstruction algorithms. It extends the opportunities given by ITK and allows for linear least squares, nonlinear least squares, weighted least squares and maximum likelihood fitting of diffusion tensors making use of the teem library.<sup>9</sup> It also allows for numerical q-ball reconstruction of HARDI data sets [4].

## 2.4 Visualization

A core feature of MITK-DI is the possibility to interactively visualize tensors and ODFs in multiple planar views. A mapper for concurrent visualization of colormaps and ODFs has been implemented that allows on the fly generation of the scene avoiding to hold the whole image representation in memory. A level-of-detail (LoD) mechanism allows for fluent navigation in the datasets. Different options for normalization and scaling can be configured during runtime. Rendering of vector images (e.g. principal diffusion direction) and the raw diffusion signal is possible.

## 2.5 Image features and statistics

Standard scalar measures such as the tensor's fractional anisotropy or relative anisotropy or the ODF's generalized fractional anisotropy can be computed. MITK's interactive segmentation framework and the image statistics bundle provide powerful tools for performing statistics on populations of voxels in certain ROIs.

<sup>7</sup> <http://teem.sourceforge.net/nrrd/format.html>

<sup>8</sup> [http://wiki.na-mic.org/Wiki/index.php/NAMIC\\_Wiki:DTI:Nrrd\\_format](http://wiki.na-mic.org/Wiki/index.php/NAMIC_Wiki:DTI:Nrrd_format)

<sup>9</sup> <http://teem.sourceforge.net/>

## 2.6 Image data and experiments

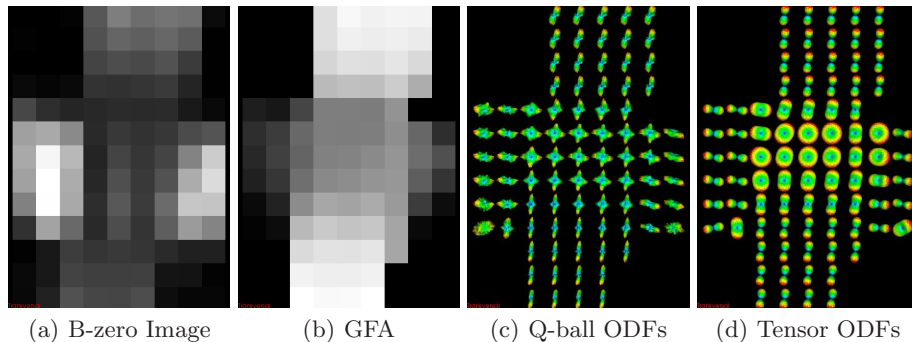
Diffusion weighted MR images were acquired on a 3.0 T MR scanner (Magnetom TRIO, Siemens Medical Solutions, Erlangen, Germany) using a single shot, spin echo, echo planar imaging sequence. Phantoms were constructed in analogy to the production process described in [5]. The phantom imaging parameters were: FOV =  $200 \times 200$  mm<sup>2</sup>, in plane resolution =  $1 \times 1$  mm<sup>2</sup>, TR = 3.4 s, TE = 118 ms, 5 averages,  $b = 3500$  s/mm<sup>2</sup>, 252 gradient directions. *In-vivo* imaging parameters were: FOV =  $240 \times 205$  mm<sup>2</sup>, resolution =  $2.5 \times 2.5 \times 2.5$  mm<sup>3</sup>, TR = 5 s, TE = 120 ms, 2 averages,  $b = 3500$  s/mm<sup>2</sup>, 64 gradient directions.

## 2.7 Availability

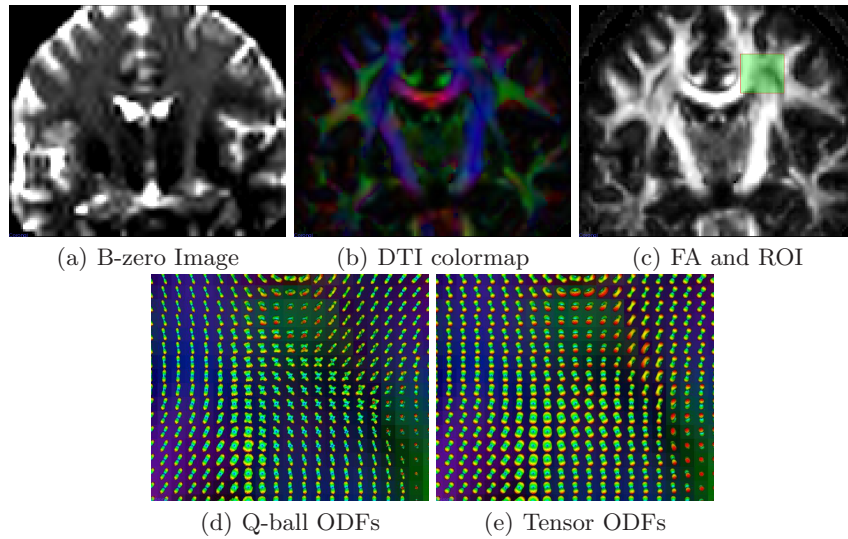
The latest version of the source code is available from the MITK web site: <http://www.mitk.org>.

## 3 Results

A Performance analysis was performed on a Intel Core2 Quad Processor (Q6600 at 2.40GHz each) with 4Gb of RAM. Q-ball reconstruction for ODFs with 252 directions took 12.91s (image dimension 96x82x40, 64 directions). A linear diffusion tensor fit took 2.81s for the same volume. Fluent interaction was achieved by the LoD-mechanism even for highly detailed and large datasets. Fig. 1 and Fig. 2 show renderings of the phantom acquisition and the *in-vivo* dataset respectively. It can be seen that q-ball ODFs provide significantly more detail than the tensor ODFs especially in crossing regions.



**Fig. 1.** Visualized HARDI acquisition of the 90° crossing fiber phantom.



**Fig. 2.** Coronal slice of the *in-vivo* HARDI acquisition with a detailed view on the crossing of corpus callosum and cortico-spinal tract, which is highlighted in 2(c).

## 4 Discussion

We have introduced a new set of tools for processing and interactive visualization of diffusion MRI datasets. MITK-DI implements DTI and HARDI techniques and features display of intricate details in combination with fluent interaction. We will be applying these visualization tools to understanding aspects of HARDI imaging to examine disease characteristics. The integration of fibertracking algorithms and further reconstruction schemes is currently being worked on. Although primarily used as a research tool, diffusion weighted imaging is starting to find it's way to clinical application. MITK-DI is an attempt to bundle up and standardize current techniques in the field in a single framework and, following the open-source spirit, to enable other researchers to contribute and build upon it. Participation is welcome.

## References

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