Diffusion Imaging in the Medical Imaging Interaction Toolkit (MITK)

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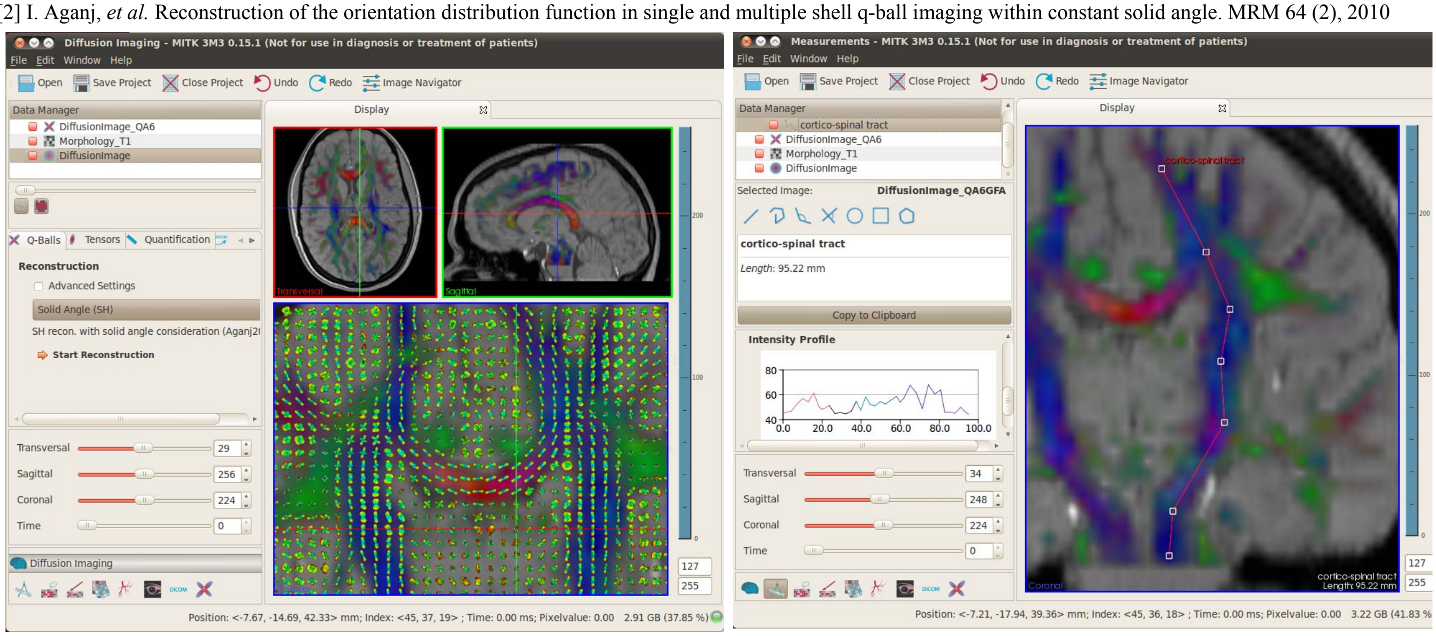
Introduction:
High angular resolution diffusion imaging (HARDI) is a diffusion weighted MRI technique that overcomes some of the limitations of diffusion tensor imaging (DTI) in complex fiber layouts. It provides a unique window on brain anatomy and insights into aspects of brain structure in living 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 fiber architecture and disorders in the brain. 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. Q-ball imaging (QBI) is a HARDI technique that represents the information in each voxel 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 DTI, it significantly raises the complexity of data processing and visualization. Several software toolkits like MedINRIA, Camino, SCIRun, Slicer, or TrackVis 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. The diffusion imaging component (MITK-DI) of the Medical Imaging and Interaction Framework (MITK) [1] 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 is publicly available under a BSD-style open-source license. In contrast to most other frameworks, MITK-DI addresses all aspects of application design including full integration into an OSGi-based 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. It fully benefits from available components such as ROI placement, overlays of multiple contrasts, and quantification. 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.

Materials and Methods
Like the Visualization Toolkit, the Insight Toolkit, 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 that is the 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. MITK-DI supports a range of standard and advanced reconstruction algorithms. It extends the opportunities given by ITK and allows for numerical, analytical, and advanced [2] q-ball reconstruction of HARDI data sets. A core feature of MITK-DI is the possibility to interactively visualize tensors and ODFs in multiple planar views. A visualization scheme for concurrent views of colormaps, ODFs and morphology has been implemented that allows on the fly generation of the scene avoiding to hold the hole ODF 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. The latest version of the source code as well as precompiled binaries for all major operating systems are available at www.mitk.org.

Results
A performance analysis was performed on a Intel Core2 Quad Processor (Q6600 at 2.40GHz each) with 4Gb of RAM. Depending on the applied reconstruction algorithm, q-ball reconstruction for ODFs with 252 directions took around 10s or less (dimensions 96x82x40, 64 directions). Fluent interaction was achieved by the LoD-mechanism even for highly detailed and large datasets. Fig. 1a shows renderings of an *in-vivo* q-ball dataset as overlay over the corresponding T1 morphology. Fig. 1b shows an GFA intensity profile that was extracted along a manually defined path of interest along the cortico-spinal tract.

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 fiber tracking algorithms and further post processing schemes is currently being worked on. Although primarily used as a research tool, diffusion weighted imaging is starting to find its 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.

[1] Wolf I, *et al* The Medical Imaging Interaction Toolkit. Med Image Anal 9 (6), 2005
[2] I. Aganj, *et al.* Reconstruction of the orientation distribution function in single and multiple shell q-ball imaging within constant solid angle. MRM 64 (2), 2010



(a) *In-vivo* q-ball dataset overlaid on T1-image (b) GFA intensity profile along cortico-spinal tract

Fig. 1: Screenshots of MITK-DI running as component in the MITK platform.