

NeuroQLab – A Software Assistant for Neurosurgical Planning and Quantitative Image Analysis

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Abstract. Neuroimaging techniques produce large amounts of data capable of displaying a wide variety of structural and functional properties of the brain. A large number of specialized image analysis and visualization tools exist that aim at helping the physician in analyzing and dealing with the data. We present a flexible and extendible software assistant covering a number of typically required tools for evaluating neuroimaging studies. It comprises tools for preprocessing tasks such as registration, skull-stripping or non-uniformity normalization as well as some dedicated packages for quantitative analysis of anatomical images, a toolkit for DTI analysis as well as a tool for analyzing fMRI studies. The software assistant is built upon an established platform for rapid-prototyping, which facilitates fast integration of new features by user request as well as the adaption of given features to concrete clinical questions. In this paper, a brief overview of the basic underlying software architecture is given accompanied by a presentation of selected tools offered by the software.

1. Overview

Neuroimaging is a continuously evolving medical discipline that covers the large variety of imaging techniques required for all medical fields associated to the brain and its pathologies, which includes at least neurology, neuroradiology, neurosurgery and neuropsychology. Besides the different nature of these medical fields, the required tools for image analysis and data visualization techniques for the underlying data are often similar. Common processing tasks include registration of different modalities or imaging sequences to a reference image as well as segmentation of prominent structures such as the brain, the ventricular system or the vascular system from different datasets. Additionally, since there usually exists a number of different datasets for a given patient which show different properties of the same brain, a commonly desired feature is the possibility to combine multiple available datasets in such a manner that the relations between individual properties of the brain become clear. For example, the fusion of activation areas determined by functional magnetic

resonance imaging (fMRI) with white matter fiber tracts derived from diffusion tensor imaging (DTI) may enhance the neurosurgical planning process.

These circumstances strongly motivate the desire for software assistants capable of dealing with the available data in a flexible manner by providing both basic tools for general processing tasks as well as dedicated tools custom tailored to specific clinical problems. In this paper, we give an overview of *NeuroQLab*, a software assistant aiming to offer all the basic tools typically required for processing and working with MR images of the brain, as well as a number of tools specifically targeted at certain clinical problems. Its primary purpose is to facilitate the application of state-of-the-art technologies and research results from the field of medical image processing in clinical trials and studies.

2. Underlying architecture

The software assistant is build upon a dedicated application framework designed specifically for rapid prototyping of clinically applicable software assistants with a focus on research and study evaluation. The framework, which is built on top of MeVisLab [MeV09], consists of multiple hierarchically structured layers providing a number of fundamental functionalities for dealing with medical image datasets, handling patient information and storing processing results. Additionally, a modular plug-in concept allows for integration of packages dedicated to concrete clinical questions. An additional communication layer allows for exchanging events and data between different applications allowing for reuse and combination of results stemming from different processing steps within the pipeline. Key features of the application framework include:

- a dynamic and extendible multi-layered architecture allowing for short development cycles for both the addition of new features to existing tools as well as the inclusion of completely new tools
- a mature case handling concept managing all relevant data of a case within one data structure based on the Extensible Markup Language (XML)
- integration into clinical environments by means of PACS communication and handling of standard medical image data formats (DICOM)

A detailed description of the application framework can be found in [Rex08]. The multi-layered approach is an adaption of the widely used *Model-View-Controller (MVC)* pattern known from software engineering. It provides the key functionality for integrating rapid-prototyping techniques into the development process of medical software assistants, which allows for seamless integration of the user, i.e. the clinical expert, into the process of software development.

3. Components

The following section will give a brief overview of some of the most important tools included within the software assistant. They can be categorized into three groups, *Preprocessing*, *Visualization* and *Advanced Processing*.

3.1 Preprocessing

The *Preprocessing* section includes tools typically required before performing any advanced analysis or data processing. One essential element of this section is the registration tool, which allows for manual or automatic linear registration of all images within a case. Here, any image can be registered to any reference image from the same case, which means that the user is free to choose which image to use as a reference image for further processing steps.

A commonly required prerequisite for analyzing MR images of the head is the segmentation of the brain from the head, a problem generally referred to as skull-stripping. NeuroQLab comes with an interactive skull-stripping tool using a marker-based watershed transformation, which allows for efficient segmentation of the brain even in the presence of serious pathologies such as malignant brain tumors [Hahn00]. The algorithm consists of an initialization phase followed by interactive placement of markers to include or exclude parts of the image in the segmented mask. The initialization requires about 10 seconds calculation time on a current standard PC, the placement of markers is fully interactive, which makes it a highly efficient as well as flexible tool for segmentation of the brain. Typically, a good segmentation can be achieved by placing 5 to 10 markers in the dataset.

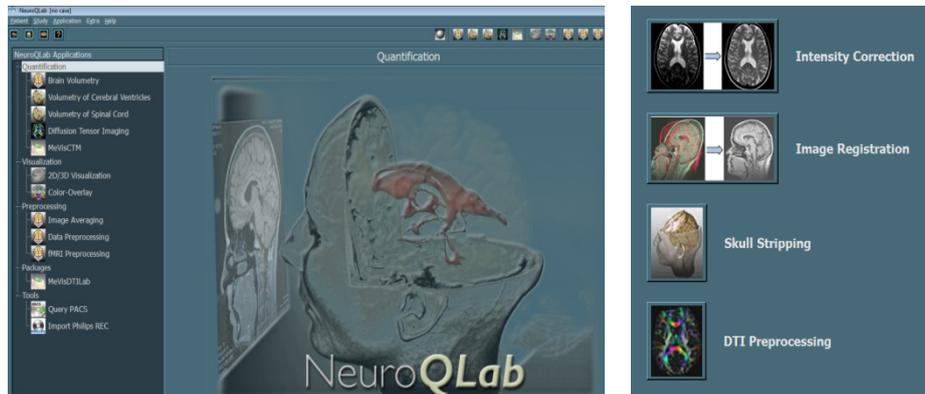


Fig. 1. Two screenshots showing the main screen with application selection and the sub-menu for selection of preprocessing tools.

For dealing with signal inhomogeneities inherently present in MR images, NeuroQLab provides an implementation of the *non-parametric non-uniformity normalization (N3)* algorithm [SZE98]. Further tools in the preprocessing section

provide functionality for preprocessing DTI data, or performing motion correction and filtering on fMRI datasets.

3.2 Visualization

Data visualization is an important aspect when dealing with medical image data. A conventional slice wise gray level presentation of raw datasets is often inferior to dedicated visualization tools build to enhance individual aspects of the input data. This includes, e.g., using color overlays of multiple images possibly stemming from different modalities or MR sequences in both two and three dimensions as well as 3d-volume renderings of datasets in combination with clip-planes and opaque or semi-transparent objects rendered through iso-surfaces.

NeuroQLab features several advanced viewers including synchronized 2d- and 3d-viewers capable of displaying overlays such as fiber tracts or fMRI activation data [KWK07]. Also, dedicated volume rendering modes are included within selected analysis tools, custom tailored to the visualization requirements of the chosen tool.

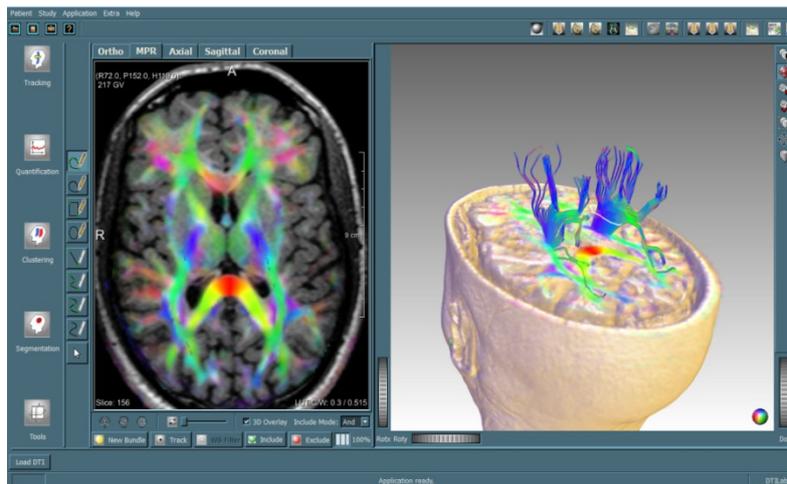


Fig. 2. An example of synchronized 2d- and 3d-viewers, in this case showing DTI color-coded data and some reconstructed fiber tracts.

3.3 Advanced Processing Packages

As an example of an advanced processing package included within NeuroQLab, we will now present *DTILab*, our software package for DTI-based white matter fiber tracking and quantification. For performing fiber tracking, two modes are available. The so-called *seed-ROI* based approach requires the user to first choose a ROI which is used by the algorithm as a starting point for tracking. This way, all tracts can be reconstructed that emerge from the user chosen ROI. Alternatively, a *whole-brain*

tracking mode is included. Here, tracking for the whole DTI dataset is performed as a preprocessing step. Once this has finished, the user can interactively choose a ROI and immediately visualize all fibers passing through this ROI. Usually, the whole-brain tracking yield qualitatively better results, since it can reconstruct all tracts running through an input ROI as opposed to the seed-ROI based approach.



Fig. 3. Color enhanced rendering of the results of quantitative brain volumetry [HJK04].

The tracking itself can be performed using two different algorithms. First a deterministic deflection-based tracking algorithm and second a non-deterministic algorithm based on probabilistic methods for white matter fiber tract reconstruction [FFW06]. Probabilistic fiber tracking is a relatively new technique that aims towards handling the intrinsically existing uncertainty inherent to DTI based fiber tracking, since it not only reconstructs the tract itself, but at the same time generates a probability map indicating how likely a tract belongs to the reconstructed anatomical structure.

A unique feature of DTILab is its capability of performing quantitative analysis of DTI parameters along reconstructed fiber tracts [KSR08]. This allows for reproducible quantification of fiber bundles based on average values for fractional anisotropy, diffusion strength, axial diffusivity or radial diffusivity. The technique has been used e.g. in the context of multiple sclerosis (MS) for the correlation of white matter fiber integrity with outcomes of psychiatric test based on the *expanded disability status scale* (EDSS) [FKL09].

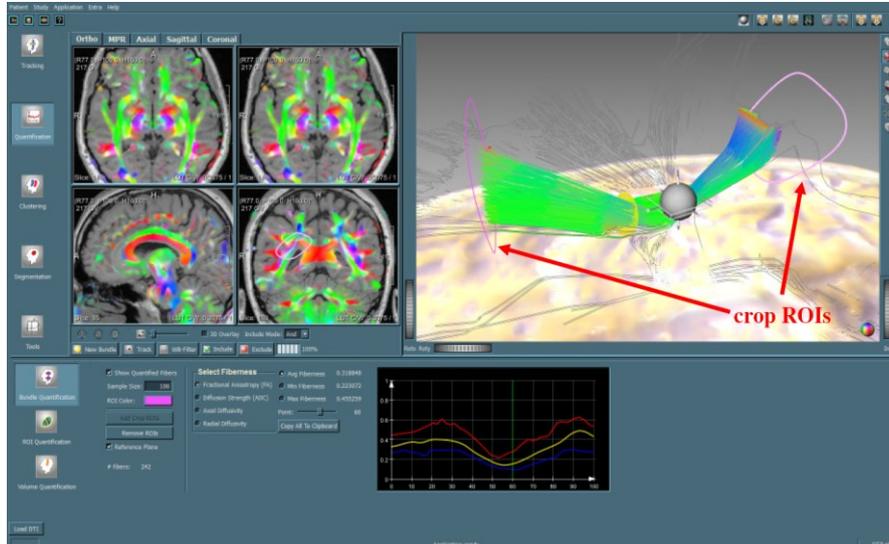


Fig. 4. DTI-based fiber tract quantification.

4. Conclusion

In this work, we have presented a software assistant for use in neuroimaging studies. It comprises a number of tools for both basic processing steps and advanced analysis techniques required in a variety of neuro-related medical disciplines such as neurology, neuroradiology, neurosurgery and neuropsychology. It is currently used by about 20 clinical research partners of our institute in the context of a variety of clinical questions. Further, it has been used as the technical basis for numerous studies resulting in a variety of clinically driven scientific publications.

The number of tools and features of the software assistant is being constantly enhanced with techniques being included continuously. Our focus for current and future developments is on the inclusion of new methods for fiber tracking based on *High Angular Resolution Diffusion Imaging (HARDI)* techniques, non-linear registration methods, new quantitative measuring tools based on cortical thickness mapping for monitoring and diagnosing dementia and related neurodegenerative diseases. Further, a software link to operation microscopes and neuro-navigation systems is planned for better integration of our software in the operation room for intra-operative software support.

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