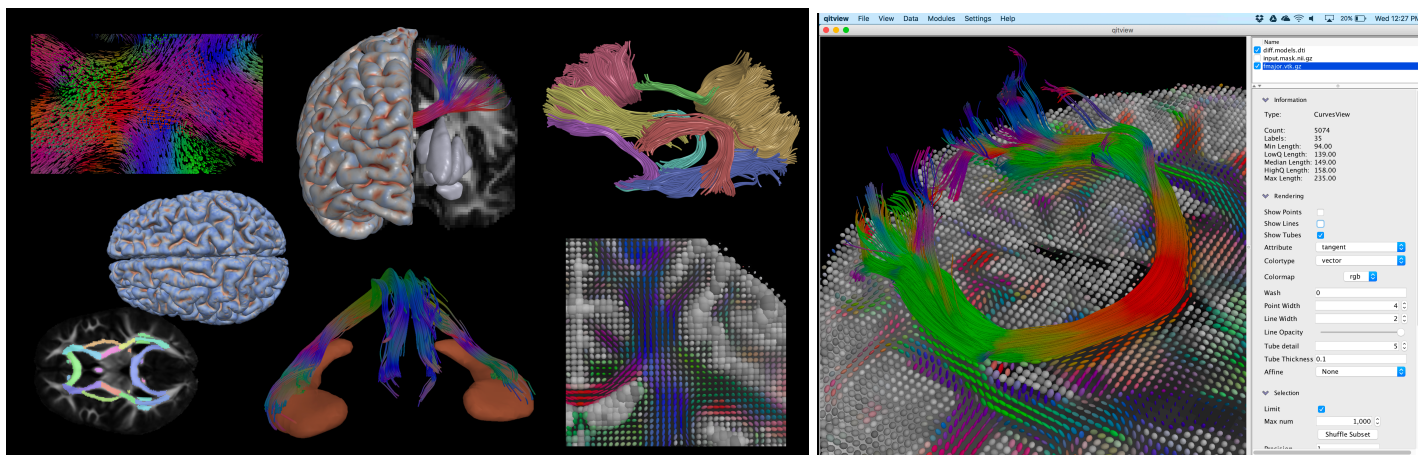# Quantitative Imaging Toolkit: Software for Interactive 3D Visualization, Processing, and Analysis of Neuroimaging Datasets

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Introduction

Computational tools are increasingly important to MR imaging research, as they can make experiments more reproducible, improve our ability to share our findings and methods, and facilitate hypothesis generation. We aim to contribute a software package to the research community named the Quantitative Imaging Toolkit (QIT). QIT was developed to provide tools for 3D visualization, data exploration, and computational analysis of neuroimaging datasets. Beyond this, it is also meant to serve as a platform the development of new methods that can be translated to neuroimaging studies. While meant to be generally useful for neuroimaging, the tools have extensively developed features for diffusion MRI and analyzing large population imaging datasets. Below, we describe the design and relevant features of QIT.

Design

QIT is written in Java and OpenGL and is compatible with macOS, Windows, and GNU/Linux. It includes an interactive 3D rendering application qitview, a command line program qit, and a collection of utilities for processing large datasets. Many data types are supported, including multi-channel volumes, multi-label masks, curves, triangle meshes, vectors, deformation fields, affine transforms, tabular data stores, geometric primitives (boxes/spheres).

QIT includes a module framework for easily adding new functionality. Modules are implemented as a Java class, and the interface and parameters are specified in a declarative way using Java Annotations. Once written, a module can be run interactively in qitview, scripted using qit, integrated into workflows in the LONI Pipeline[3], or shared as an external plugin. A major benefit of the module framework is that file formats are automatically handled, making them easier to develop and use. There is also support for module provenance, in which parameter sets can be saved for archival purposes or for later reuse.

QIT also supports parallel computing with multi-threading and automatic dispatching of large tasks to grid computing

engines. qitview supports a rich user interface, which includes fine-grained control of the visual encoding of data, user-defined colormaps, manual mask drawing, data querying, high resolution off-screen rendering, arbitrary vertex attributes, multi-modal volume visualization, and a python scripting console. Finally, QIT was also designed for easy data exchange with other neuroimaging computing platforms, such as 3D Slicer[4], FSL[6], TrackVis[2], MRtrix[5], MITK[7], DSI Studio[8], BrainSuite[9], and others.
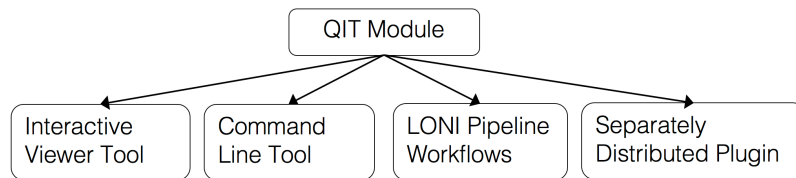
Features

Out of the box, QIT includes many algorithms for processing volumetric and geometric datasets. There are a variety of smoothing and denoising algorithms, including non-local means, mean-shift, anisotropic diffusion, Gaussian blur, median filtering, etc. A variety of segmentation algorithms are supported, included region growing, Gaussian mixture modeling, manual drawing, etc. There are also many operations that can be performed on masks, such as erosion, dilation, skeletonization, connected components labeling, Markov random field restoration, distance transforms, etc. There are also ways to convert between data types, e.g. by extracting contours from slices or extracting isosurfaces from volumes. Mesh and curve operations include smoothing, simplification, clustering, reparameterization, discretization, etc. There is also a statistical framework for summarizing individual data objects and analyzing population imaging dataset[11].

QIT also provides a rich set of tools for diffusion MRI. In contrast to other diffusion MRI toolkits, QIT supports a wide variety of diffusion models: tensors, kurtosis, NODDI, ball and sticks, spherical harmonics, and orientation distribution functions. It provides native model fitting routines for many of these, as well as wrappers around commonly used 3rd part fitting routines. Diffusion models can be visualized as 3D glyphs, and QIT provides a unique interface for arbitrary placement of glyphs, e.g. along tracts or scattered within a volumetric region. There are modules for both deterministic and probabilistic tractography[10], and fiber bundles can be delineated using atlas regions, manually drawn masks, or manually placed geometric primitives. Beyond this, QIT supports many other diffusion MRI features, such as multi-tensor smoothing, ODF peak extraction, Q-space interpolation, signal drift analysis, model reorientation, bundle selection, along tract analysis, tractography simplification, clustering, and outlier rejection.

Conclusion

QIT develop was guided by a number of MR imaging studies of the brain in health and disease, and we hope that by sharing with the community, the tools will catalyze other future brain imaging studies. As we continue development, we also hope for QIT to serve as a platform for developing new methods that can be more directly integrated such studies. QIT can be downloaded from the web, and documentation is available in a wiki, which includes installation instructions, a user manual, and a set of tutorials for learning how to use the toolkit for specific imaging tasks.

Acknowledgements

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