

Camino : Open-Source Diffusion MRI Reconstruction and Processing

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www.camino.org.uk



Overview

Camino is an open-source, object-oriented software package for synthesising, reconstructing and processing diffusion MRI data. Camino implements a data processing pipeline, which allows for easy scripting and integration with other software. Camino is written in Java and is documented via Unix man pages. Programs are executed via wrapper shell scripts. The range of standard and cutting-edge tools, combined with the simple user interface, make Camino flexible enough to appeal to a diverse user base.

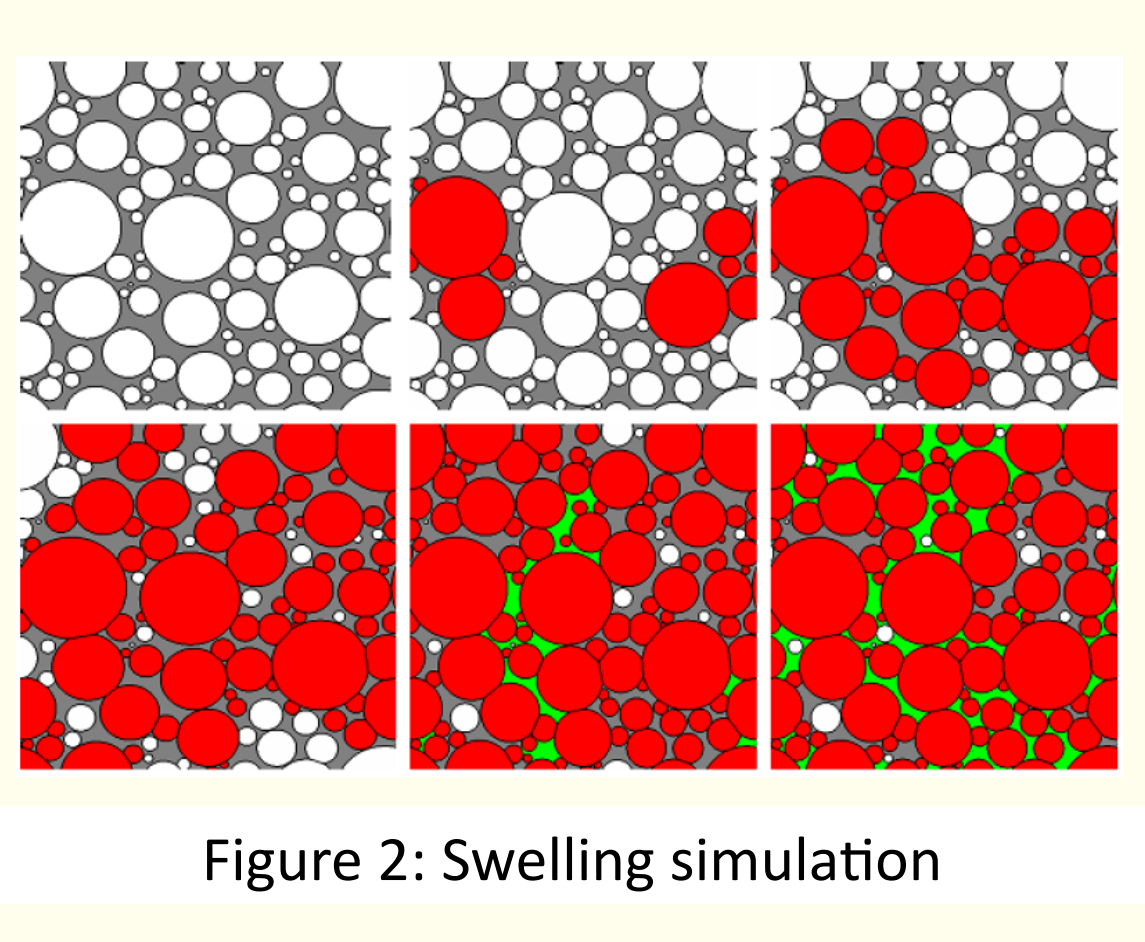
Get the code

The latest Camino release can be downloaded from <http://www.camino.org.uk>
 Wiki available at <http://camino-wiki.pbwiki.com/>
 System requirements:

- Java SDK 1.5.0 or later.
- A Unix environment (native or emulated) for wrapper shell scripts.

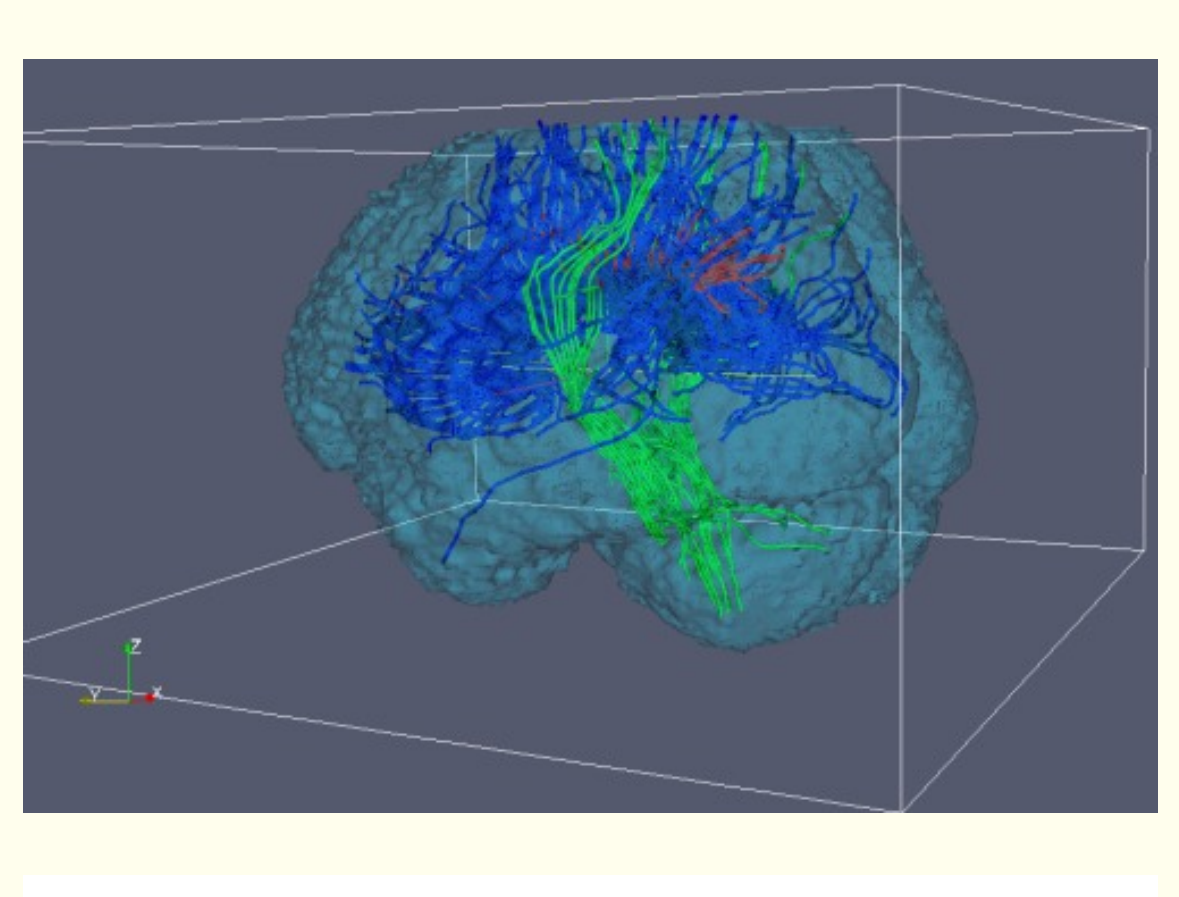
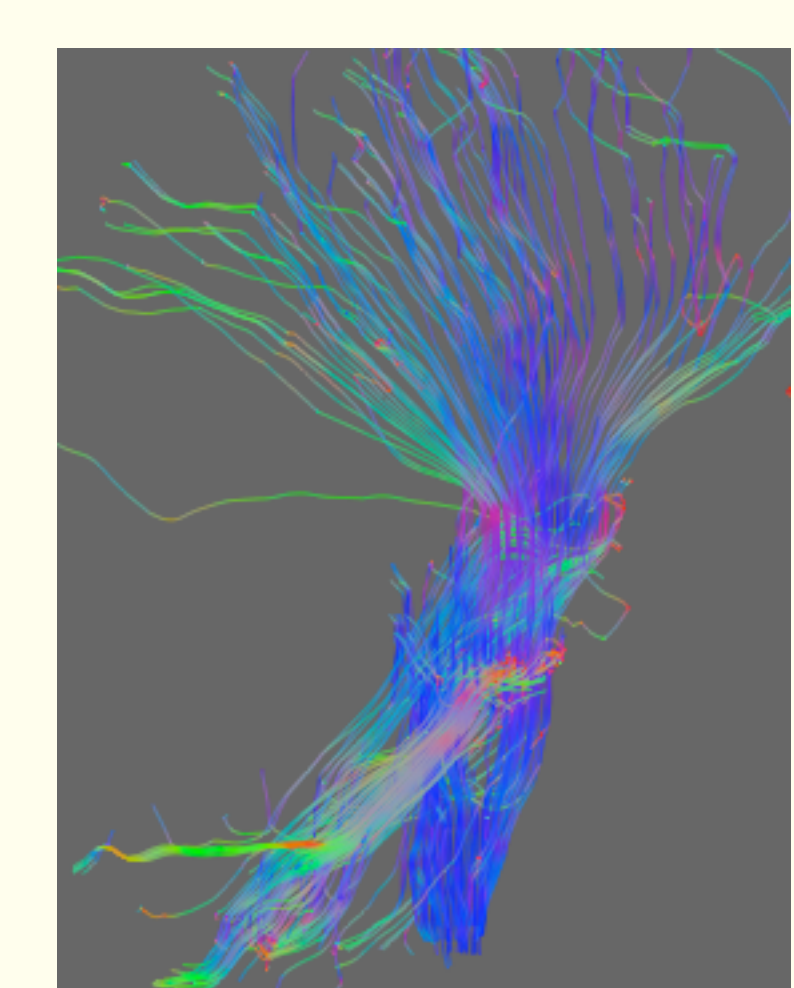
Monte-Carlo Simulation

- Randomly-packed cylinders with gamma distributed radii
- Abutting, deforming cylinders simulating swelling
- Crossing cylinder substrates
- Arbitrary geometries using triangle meshes



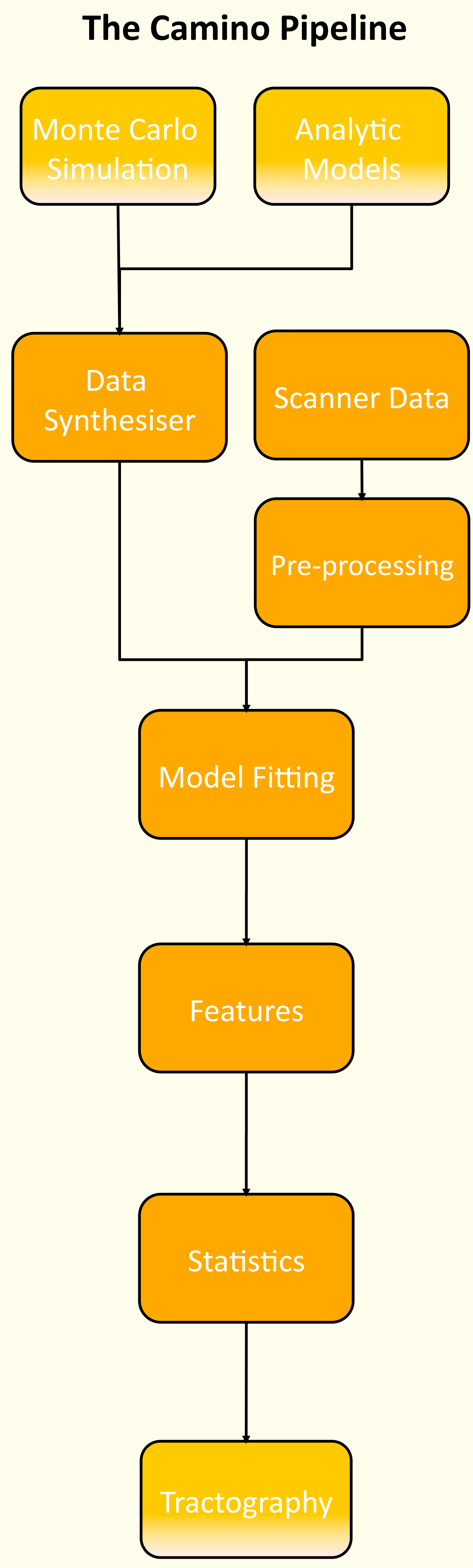
Data

- Input from the scanner or from the data synthesizer (datasynth).
- Synthesises data by emulating the scanner sequence.
 - Twice refocused spin-echo
 - Statistical measures extracted directed from particle dynamics
 - Generation of particle trajectories with separate scan data generation, allowing more than one data set to be generated per simulation
- Use a range of pre-programmed Gaussian test functions (including a two and three compartment model), or specify your own.
- Simulates bootstrap experiments.
- `analyzeheader` creates Analyze 7.5 headers for porting Camino data to other software.



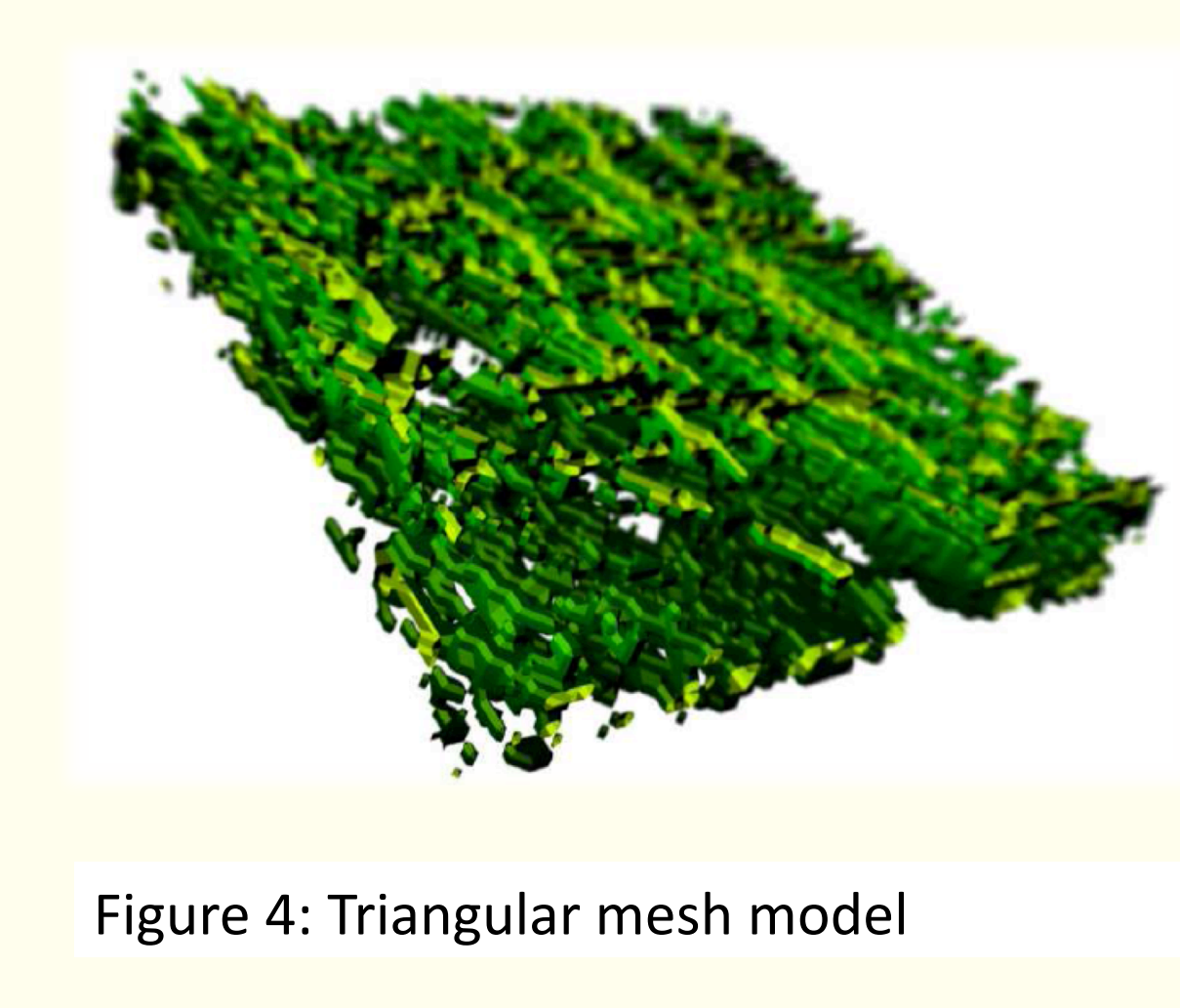
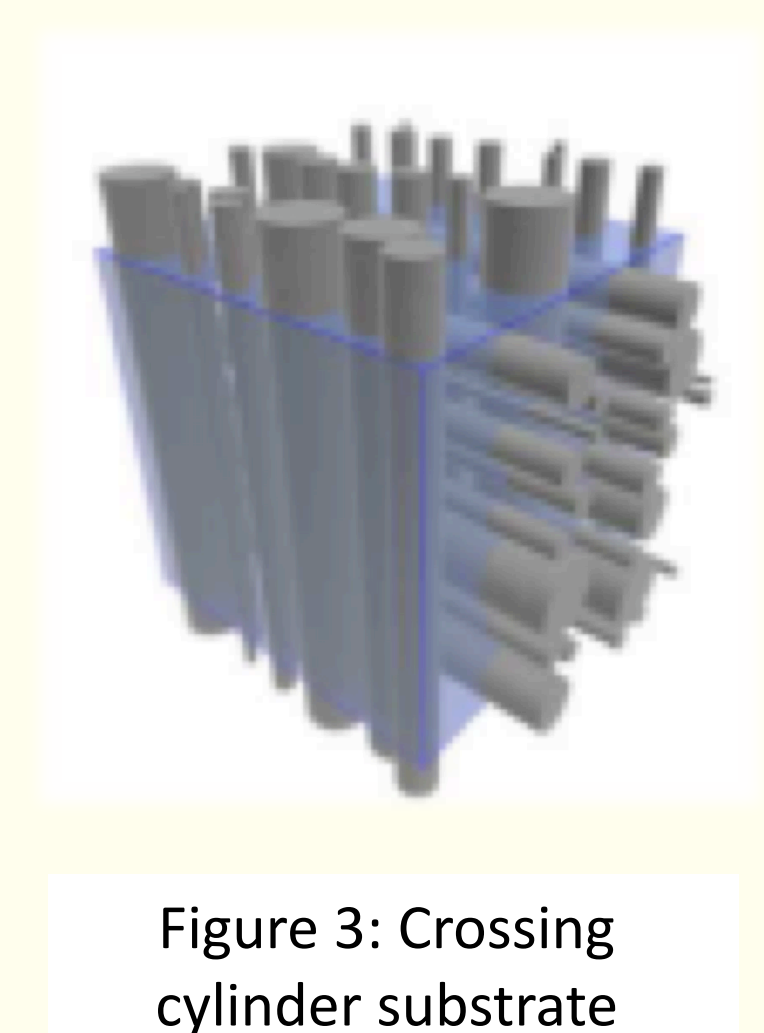
Tractography

- Deterministic and probabilistic tractography. Streamlines can be computed from raw data in just three steps: `cat A.Bdouble | dtfit -scheme A.scheme | track [options]`. Streamline output is in raw binary format or OOGL vectors (as used by Geomview).
- PICO tractography [6] with single or multi-fibre models of the voxel PDF. Outputs connection probability images, or raw streamlines.



Analytic Models

- DTI
- Multi-tensor
- Hierarchy of two-compartment models



Pre-processing

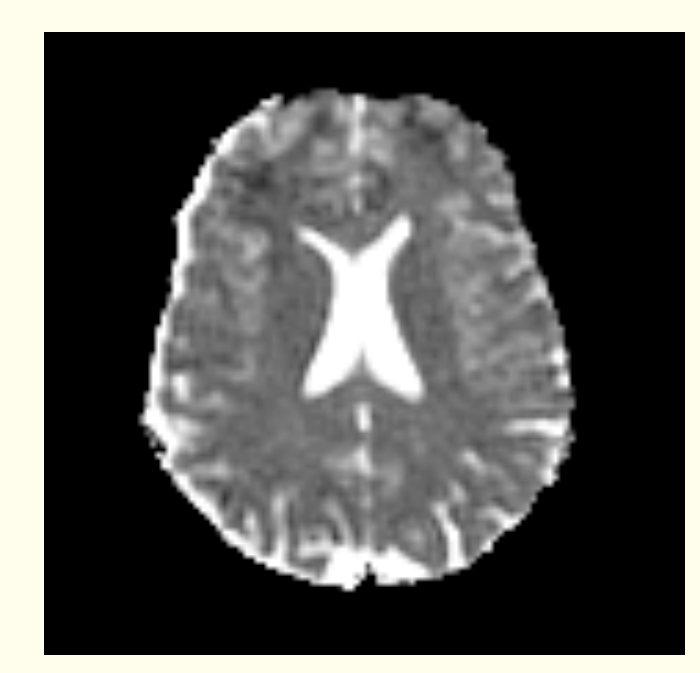
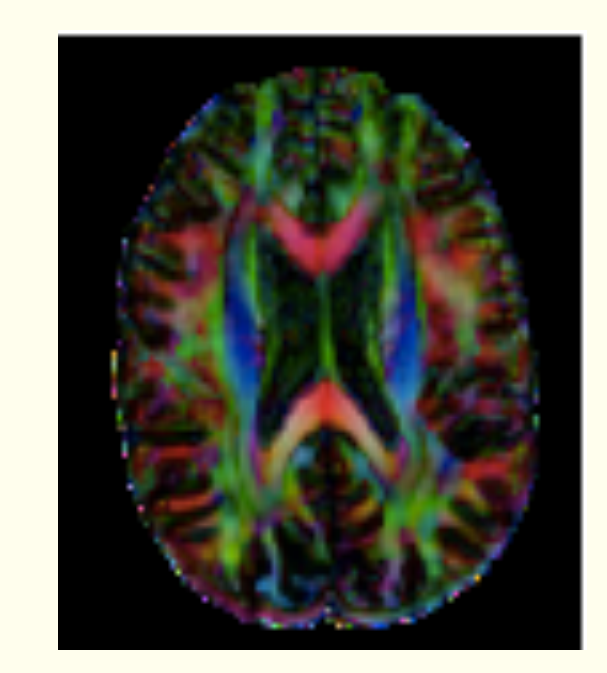
- `mbalign` performs model-based DWI alignment [10]

Model Fitting

- Single and multi fibre reconstruction algorithms.
- Single fibre: Linear diffusion tensor fit, Nonlinear diffusion tensor fit, RESTORE [1].
- Multiple fibre: Two tensor, three tensor, PAS-MRI [2], Spherical Deconvolution [3], DOT [4], Q-ball [5].

Features

- `trd` computes trace of diffusion tensors.
- `fa` computes fractional anisotropy from tensors.
- `dteig` computes full tensor eigensystem.
- `sfpeaks` finds principal directions from non-tensor data.



Statistics

- Mean and variance of scalar data.
- Mean orientation and concentration of principal directions.
- Statistics on success of multiple-fibre reconstruction routines.
- HARDI shape statistics
- HARDI peak finding

References

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