

Diffusion Analysis Using Camino

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Highlights

- Demonstration of diffusion imaging analysis tools in Camino.
- The presentation will focus on analysis of the sample data set.
- See the Camino website at camino.org.uk for more information, where you may
 - Download the software.
 - See documentation and tutorials.
 - Join the Camino users mailing list for additional support.
- See below for an overview of some of the core capabilities of Camino.

About Camino

Camino is an open-source software toolkit for diffusion MRI processing. The toolkit implements standard techniques such as diffusion tensor fitting and streamline tractography. It also contains more specialized and cutting-edge techniques, such as Monte-Carlo diffusion simulation, multi-fibre and HARDI reconstruction techniques, diffusion compartment models, and axon density and diameter estimation.

The microstructure imaging group at University College London lead development and maintenance of Camino. Many of the specialist modules arise from the research of the MIG and collaborating groups within the University of London and at other institutions including the University of Manchester and the University of Pennsylvania.

Camino is distributed under the Artistic License 2.0 for research use only. The full text of the license is on the Camino website.

Installing and running Camino

Camino is designed for a Mac / Unix / Linux command line environment. Windows users typically use a Linux virtual machine or software like Cygwin to use Camino.

Camino is developed and tested using Oracle Java. Other Java implementations may fail to compile Camino. Please see the Camino website for more instructions on installing Camino.

Data reconstruction tools in Camino

Camino contains a variety of tools for model fitting. The most widely used is the diffusion tensor, and there are several options for calculating the DT and derived statistics such as anisotropy. A variety of more advanced models are also implemented for HARDI data.

Diffusion Tensor Imaging

- Diffusion tensor fitting with linear least squares [2].
- Non-linear least squares and RESTORE for robust tensor estimation [3,4].

Multi-fiber models and HARDI

- Spherical harmonic model classification for detection of non-Gaussian diffusion [5].
- PAS-MRI and Maximum Entropy Spherical Deconvolution [6,7].
- Q-ball imaging [8,9].

Compartment models for multi-shell HARDI

- ActiveAx for axon diameter estimation [10].
- Variety of white matter models incorporating isotropic, extracellular and intracellular restricted diffusion [11].

Tractography tools in Camino

Tractography in Camino is based on streamline line propagation through a vector field, using one of several available stepping algorithms [12]. The vector field is estimated once for deterministic tractography, or randomly sampled from some distribution for probabilistic tractography.

Streamline tractography

- Deterministic and probabilistic streamline generation using FACT, TEND and a variety of other stepping algorithms [12, 13, 14].
- Probabilistic algorithms sample from a probability distribution on the fiber orientation in each voxel, using:
 - Parametric spherical PDFs [15,16].
 - Bayesian estimation with Dirac priors [17].
 - Wild bootstrap resampling of DTI residuals [18].
 - Bootstrap resampling of repeated acquisitions of DTI data.

Post-processing of streamlines

- Streamline filtering of streamlines with ROIs and exclusion ROIs.
- Construction of streamline connectivity matrices.
- Output streamline density images (PICO or “connectivity” images).
- Sample image data (eg, fractional anisotropy) along streamlines

Data synthesis tools in Camino

Camino contains a variety of tools for synthesizing data from various models, including the diffusion tensor. These can be used to create many realizations of a single voxel or to synthesize new images. Gaussian or Rician noise can be added to the idealized measurements.

Data synthesis from models

- Diffusion tensor models with user specified properties.
- Multi-tensor mixture models.
- Customizable white matter compartment models can be combined to generate data with a variety of configurations including isotropic, extracellular and intracellular diffusion.

Data synthesis from real data

- Bootstrap resampling of repeated measures of the same acquisition.
- Wild bootstrap resampling from diffusion tensor imaging data.

Data synthesis from diffusion simulation

- Monte Carlo simulation of diffusing particles in customizable simulated tissue environment [19].

References

If you use Camino in published research, we ask that you cite the original Camino abstract (reference 1 below). If you wish to link readers to the software in addition to citing the abstract, please use the permanent address (camino.org.uk). Please also cite the references below for specific tools within Camino, as appropriate. A list of relevant citations is maintained on the Camino website.

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