

Camino: Open-Source Diffusion-MRI Reconstruction and Processing

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Introduction Diffusion-MRI is a rapidly evolving research field that has produced a wealth of algorithms for the analysis of white matter fibre architecture and disorders in the brain. Camino is a free, open-source toolkit designed to make a selection of this technology available and convenient to use for the diffusion MRI research community. Camino implements a data processing pipeline, which allows for easy scripting and flexible integration with other software. This abstract summarises the features of Camino at each stage of the pipeline from the raw data to the statistics used by clinicians and researchers.

Design Camino is written in Java, and designed for a Unix-style interface. The user documentation is in the form of Unix manual pages, and each program has a shell wrapper, so users do not require any knowledge of Java. The data pipeline provides flexibility, by allowing data to be imported and exported to other software, and transparency, because the output of each Camino program can be analyzed in detail. Fig. 1 illustrates the pipeline. Camino processes all data in voxel order, where the measurements for each voxel are stored together. This ordering facilitates the data pipeline model and allows each voxel to be processed independently, which simplifies parallel processing. All of Camino's output is in a documented raw binary format. The tractography module optionally outputs Analyze images for easy integration with visualisation software.

Data The data source for Camino can be raw data from a scanner or from Camino's data synthesiser. The data synthesiser emulates scanner sequences and provides synthetic data from a range of customisable test functions. Data from scanners is not typically in voxel order, so Camino contains tools for rearranging data into the correct format. Associated with each data file is the scheme file, which is a text file that describes the acquisition parameters for each measurement.

Reconstruction The reconstruction stage takes as input raw data and reconstructs information about the diffusion in each voxel. Camino supports a range of standard and advanced reconstruction algorithms. The simplest and fastest inversion is the linear diffusion tensor fit, in which the elements of the diffusion tensor are calculated from a standard linear least-squares fit to the log of the measurements. With the `dtfit` program, a linear diffusion tensor fit takes about two minutes for a $128 \times 128 \times 60$ voxel data set, on a standard Pentium IV 2.4 GHz workstation. Nonlinear fitting is slower but potentially more accurate. Camino supports nonlinear least-squares diffusion tensor fitting and the RESTORE method [1]. Camino also supports non-tensor based diffusion reconstruction, including mixture modelling [2], PAS-MRI [3], Q-ball [4] and spherical deconvolution [5]. Spherical harmonic voxel classification [6] detects non-Gaussian diffusion. The thresholds used in classification can be set interactively (Fig. 2) and the classification can be used to drive reconstruction, fitting multi-fibre models only where the diffusion tensor is not suitable.

Features and statistics Voxel-based statistics of the diffusion can be extracted from the reconstructed data. For tensors, two common statistics are the trace (computed by `trd`) and the fractional anisotropy (computed by `fa`). The `dteig` program outputs the entire eigen system of the tensor. The `shredder` program extracts periodic chunks from composite data sets, for example it can create an image containing the largest eigenvalue of each tensor in a volume, given the output of `dteig`. All of these programs handle one, two or three tensors per voxel. Statistics on populations of voxels include the mean and variance of scalar measures such as anisotropy, or the concentration of fibre orientations.

Tractography Camino supports deterministic and probabilistic streamline tractography. Streamlines can be calculated quickly from diffusion tensor data, since the `track` program can read the output of `dtfit` directly. Streamlines can also be calculated from the output of `sfpicks`. Camino's probabilistic tractography uses the PICo algorithm [7] with improvements and refinements as described in [8]. The calibration of PICo is automated and carried out once per scanner sequence (rather than per subject). The raw streamlines can be written in raw or OOGL (Geomview) format, while PICo connection probability maps (Fig. 3) are written as Analyze images.

Example We demonstrate the user interface with a simple example. Starting with scanner data from a scan with 60 measurements per voxel, stored as raw binary floats in `SubjA.Bfloat`, we convert to voxel order, fit the diffusion tensor (the scheme file is `A.scheme`), and extract an FA map (Fig. 2).

```
cat SubjA.Bfloat | scanner2voxel -components 60 -voxels 983040 | dtfit - A.scheme | fa > SubjA.fa.Bdouble
```

Availability The latest version of the source code is available from the Camino web site: <http://www.cs.ucl.ac.uk/research/medic/camino>.

Reference

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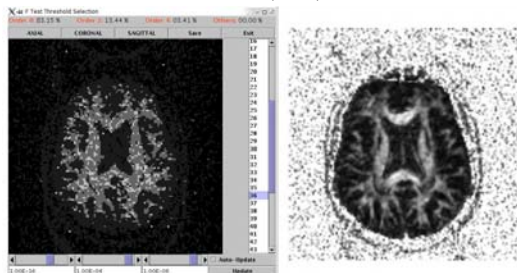


Fig 2: The `vcthrshselect` tool (left) allows interactive voxel classification. The fractional anisotropy map for the same data is shown on the right.

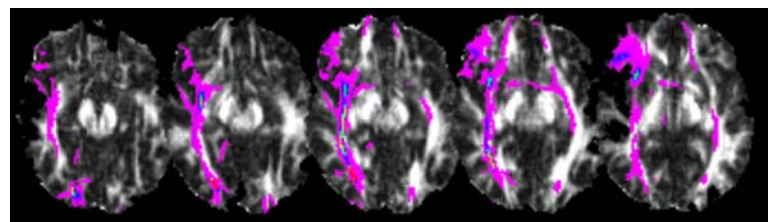


Fig 3: PICo connection probabilities from `track`, visualised in MRICro.

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