

Dipy - a novel software library for diffusion MR and tractography

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Authors:

Eleftherios Garyfallidis¹, Matthew Brett², Bagrat Amirbekian³, Christopher Nguyen⁴, Fang-Cheng Yeh⁵, Emanuele Olivetti⁶, Yaroslav Halchenko⁷, Ian Nimmo-Smith⁸

Institutions:

¹University of Cambridge, Cambridge, United Kingdom, ²University of California, Berkeley, Berkeley, United States, ³University of California, San Francisco, San Francisco, United States, ⁴University of California Los Angeles / Cedars Sinai Medical Center, Los Angeles, United States, ⁵Carnegie Mellon University, Pittsburgh, United States, ⁶Bruno Kessler Foundation and University of Trento, Trento, Italy, ⁷Dartmouth College, Hanover, United States, ⁸Medical Research Council Cognition and Brain Sciences Unit, Cambridge, United Kingdom

Introduction:

Dipy[1] stands for diffusion imaging in python and it is a free, open source, python toolbox, which is growing, with an already extensive core. It provides a library or API of methods to give a full pathway from raw diffusion MR data to tractographies, with several novel algorithms for analysing and displaying tractographies.

Dipy operates across all standard platforms, and has been developed by research scientists from a variety of different countries and laboratories. Dipy sits alongside and interoperates with other python based neuroimaging toolboxes of the Nipy suite[2].

The aim of dipy is to make it easier to do better diffusion MR imaging research. It achieves this aim by being clearly written, clearly explained, with a good fit to the underlying concepts in a way that fosters collaborative development.

Methods:

Dipy depends on a few standard libraries: python (the core language), numpy (for numerical computation), scipy (more specific mathematical functions), and cython (for speed when needed). Optionally, it can use python-vtk (for visualisation), pytables (for handling large datasets), matplotlib (for scientific plotting), and ipython (for interaction with the code and its results).

Dipy is multiplatform and will run under standard operating systems such as Windows, Linux and Mac OS X. For visualisation we have provided the fvtk module which is based on the VTK library. With this we have achieved efficient simultaneous rendering of large tractography datasets which can be manipulated (zoomed, rotated) in real time in 3-dimensions.

Dipy overcomes size constraints that come with the very large datasets typical of tractography by a variety of techniques and interoperates with other diffusion imaging software such as FSL[3], Camino [4] and Trackvis[5]. Dipy supports many file formats such as Nifti, Dicom, Trackvis, Dpy, text and all other formats supported by nibabel, numpy, scipy or nipy.

Results:

There are many significant novel applications in dipy. Here we are just a few of them.

Reconstruction algorithms e.g. DTI, GQI: as well as the implementation of standard single diffusion tensor modelling (DTI) there is generalized q-sampling imaging (GQI) which enables the detection and propagation of track crossings [6].

Tractography generation algorithms e.g. EuDX: this is an extended Euler integration method with local streamline directions derived from an input option e.g. principal direction for DTI or multiple QA peaks for GQI (e.g. Fig. 1

lower). Integration stopping criteria can be specified based on metrics such as fractional anisotropy (FA) and quantitative anisotropy (QA). Different tractography algorithms can thus be directly compared.

Intelligent downsampling of tracks: there is redundant information in segments of tracks which lie close to a straight line - tractography datasets can be compressed in size by as much as 8:1 without losing significant information.

Clustering and skeletonization of tractography: similar tracks are grouped in clusters, and highly representative tracks (ones with a lot of other similar tracks, see Fig. 3 upper) become the bones of a skeleton (see Fig. 3 lower).

Resampling datasets with anisotropic voxels to isotropic: or indeed resampling between any two voxel sizes.

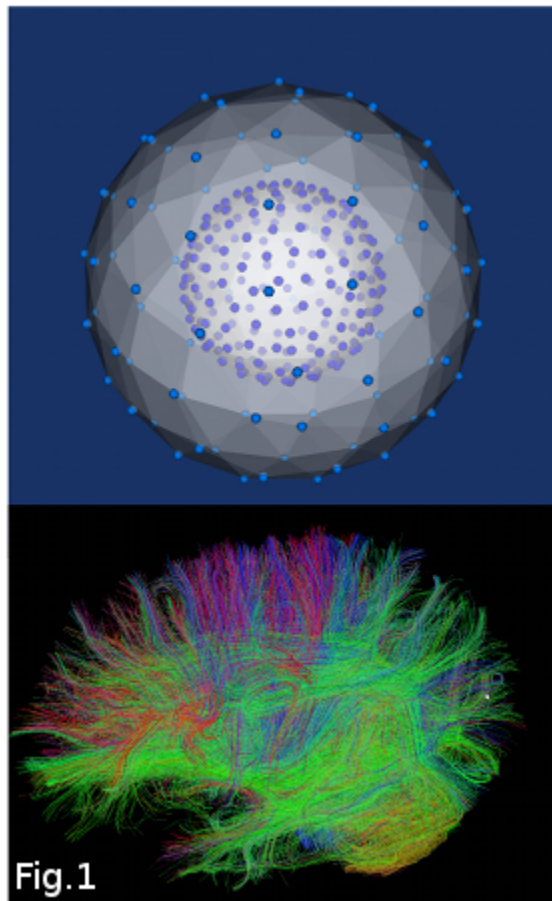
Visualization of multiple brains simultaneously (see Fig. 2 upper and 3 lower) and spherical maps (see Fig. 1 upper)

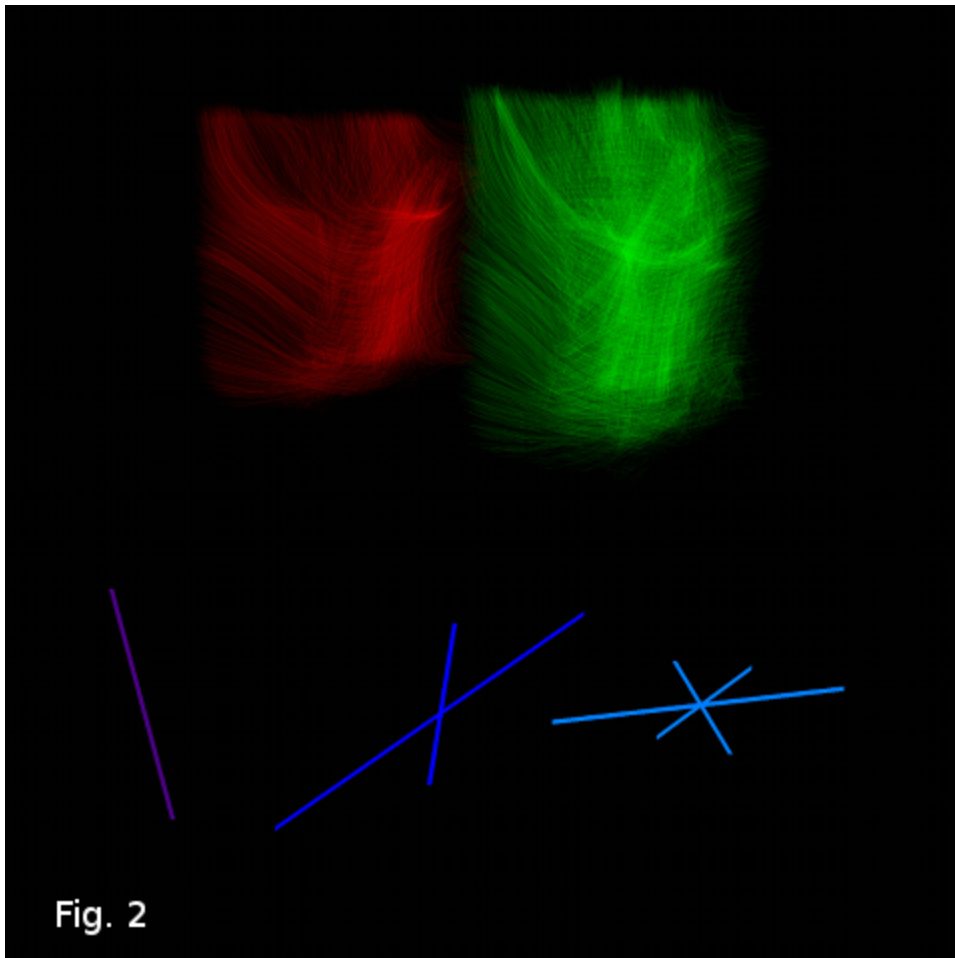
Warping or affine registration of tractographies into another space e.g. MNI space.

Direct correspondence between different tractographies using different distance metrics [7] (see Fig. 3 lower).

Conclusions:

Dipy has the potential to become the software platform of choice for brain scientists who want to be able to explore new approaches to white matter tractography using diffusion weighted MR. Dipy is an international, free, open, clear and welcoming platform to users and developers for the advancement of diffusion analysis employing the most cutting-edge engineering and scientific technologies.





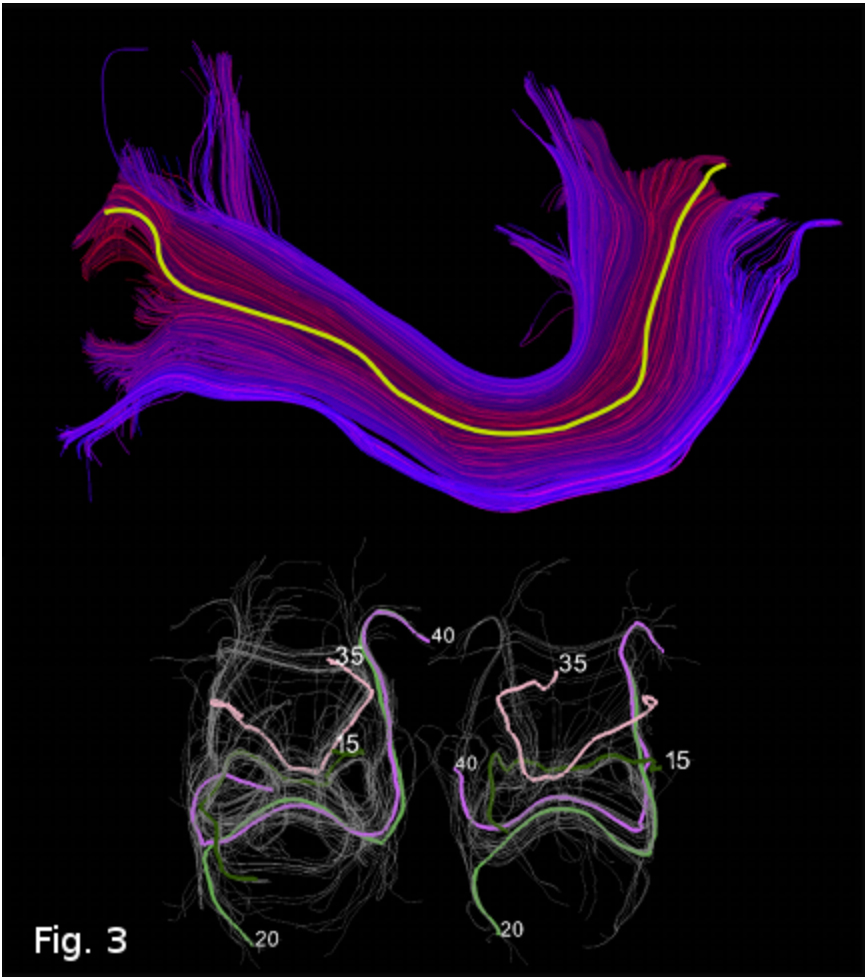


Fig. 1

Up: a 2-shell HARDI acquisition paradigm rendered as a spherical map using our fvtk toolbox.

Down: a whole brain tractography based on data from a 101 direction GQI paradigm. The tractography was based on EuDX with multiple directions derived from GQI peaks.

Fig. 2

Up: the tracks generated using Single Tensor Model principal directions (left, red) and Generalised Q-Imaging peak directions (right, green) for a region of interest in the same dataset. The GQI tractography exhibits a more complex structure derived from the evidence of crossings in the multiple peak directions.

Down: the peak GQI directions for 3 voxels with 1 (left, indigo), 2 (centre, blue) and 3 (right, azure) peaks.

Fig. 3

Up: tracks in the arcuate fasciculus colour coded for degree of similarity to their most representative track (gold).

Down: correspondences between tractographies for two different brains. Tracks over 200mm in length were compared and pairs where the MAM (mean average minimum distance) < 5mm were selected and highlighted.

Modeling and Analysis Methods

Diffusion MRI Modeling and Analysis

Abstract Information

References

- [1] <http://www.dipy.org>
- [2] <http://www.nipy.org>
- [3] <http://www.fmrib.ox.ac.uk/fsl/>
- [4] <http://www.camino.org.uk>
- [5] <http://www.trackvis.org>
- [6] Yeh, F-C. (2010), 'Generalised Q-Sampling Imaging', IEEE-TMI, Sep;29(9):1626-35.
- [7] Garyfallidis, E. (2010), 'Identification of corresponding tracks in diffusion MRI tractographies', Proc. Intl. Soc. Mag. Reson. Med. 18