

Tractography and connectivity analysis with the TractoR software package

Jonathan D Clayden¹, Susana Munoz Maniega², Amos J Storkey³, Martin D King¹, Mark E Bastin⁴, and Chris A Clark¹

¹Institute of Child Health, University College London, London, United Kingdom, ²Division of Clinical Neurosciences, University of Edinburgh, Edinburgh, United Kingdom, ³School of Informatics, University of Edinburgh, Edinburgh, United Kingdom, ⁴Centre for Clinical Brain Sciences, University of Edinburgh, Edinburgh, United Kingdom

Intended Audience: Researchers analysing imaging data, particularly those interested in connectivity analysis with diffusion MRI

Purpose: A range of software packages are presently available for processing diffusion MRI (dMRI) data, performing tractography and white matter tract segmentation, and analysing the results. In this abstract we describe a recently developed package called TractoR, which notably provides reference implementations for a number of fully automated tract segmentation methods described previously [1,2], as well as tools for standard dMRI preprocessing, estimation of diffusion tensors, DICOM to NIfTI file format conversion and so on. The package is mainly written using R, a free, high-level language and environment for data analysis and statistics [3] which is gaining significant traction as a platform for medical image analysis [4]. Users are not obliged to use R, however, since a simple interface is also provided. TractoR is free and open-source software, with a publicly accessible code repository, available under the GNU Public Licence from <http://www.tractor-mri.org.uk>. The package is regularly updated, but a substantial effort is made to ensure that releases are backwards-compatible.

Methods: TractoR maintains a hierarchy of files associated with individual scanning sessions, each under its own directory on disk. This makes it easy to perform common tasks without individually specifying the locations of large numbers of files. For example, full preprocessing of a diffusion data set, beginning only with a set of DICOM files representing a dMRI acquisition, may be achieved using the command

```
tractor dpreproc
```

from within the directory containing the files. This will perform DICOM to NIfTI format conversion, correction for eddy current induced distortions and brain extraction, prompting for further information where needed. Tractography may be performed using seed points or masks, using the algorithm described by Behrens et al. [5], and “neighbourhood tractography” may also be simply performed for automated, consistent segmentation of tracts in groups [1,2]. An algorithm for handling false positive streamlines in tractography using a tract shape model is also available within TractoR [6], as are various visualisation tools. The platform is easily extensible with user scripts, and it is interoperable with other dMRI-focussed software packages using standard file formats.

TractoR aims to minimise the amount of information that must be provided by the user, whilst at the same time offering considerable flexibility in analyses. A full set of self-tests and a test data set is provided, along with documentation in various forms. Parallel processing on multicore and grid systems is supported for the most demanding tasks. There is also an active users’ mailing list.

Results: Fig. 1 demonstrates the visualisation capabilities of TractoR, in this case showing the principal directions of fibres in and around the forceps minor. Voxels in which there is evidence of anisotropy show a fibre direction, and those with data supporting two fibre populations show two overlapping directions, colour coded by orientation, with their lengths representing the corresponding volume fractions. Fig. 2 shows the ability of neighbourhood tractography methods integrated into TractoR to segment specific connective pathways of interest. This method can automatically segment white matter structures, using a predefined reference tract along with a probabilistic tract shape model [2]. The group maps highlight the consistency of the method across individuals, and by using the model to reject false positive streamlines, the common problem of fewer streamlines appearing distal to a seed point (cf. Fig. 3) is also alleviated.

Discussion & Conclusion: Here we have described a software package for connectivity analysis using dMRI, called TractoR. The package is freely available and ready for application to studies of white matter in health and disease (e.g. [7]). Future development aims to extend the capabilities of the package to provide tools for working with connectivity information derived from other MRI-based sources.

References: [1] J.D. Clayden et al., *NeuroImage* 33:482 (2006); [2] J.D. Clayden et al., *NeuroImage* 45:377 (2009); [3] <http://www.r-project.org>; [4] K. Tabelow et al., *NeuroImage* 55:1686 (2011); [5] T.E.J. Behrens et al., *NeuroImage* 34:144 (2007); [6] J.D. Clayden et al., *Lect Notes Comp Sci* 5762:150 (2009); [7] L. Penke et al., *J Neurosci* 30:7569 (2010).

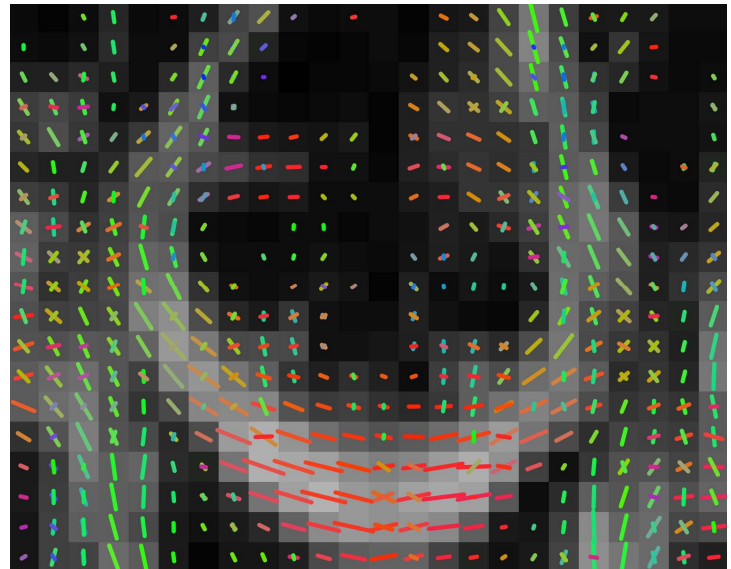


Fig. 1: Principal directions in part of a data set under a model allowing up to two anisotropic compartments per voxel. The background image is a fractional anisotropy map. Visualised using the “dirviz” TractoR script.

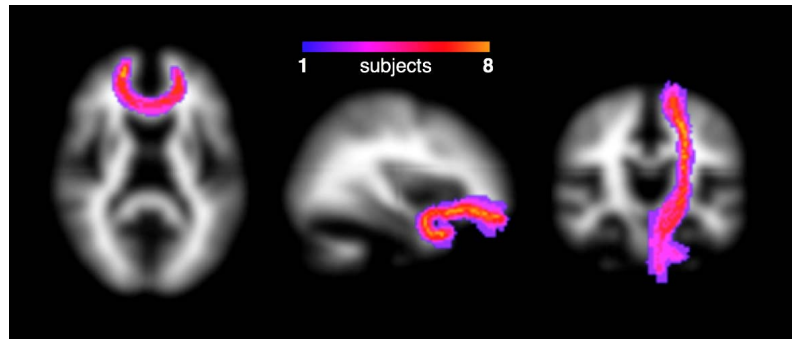


Fig. 2: Group maps of “neighbourhood tractography” segmentations of the forceps minor (left), uncinate fasciculus (middle) and corticospinal tract (right) in a group of eight healthy young adults, visualised using TractoR’s “gmap” script. A very high degree of segmentation consistency across subjects can be observed.

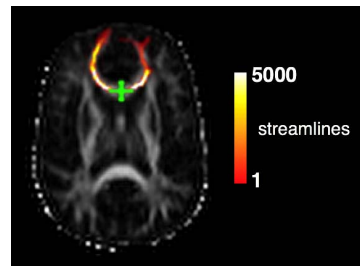


Fig. 3: Tractography visitation map for the forceps minor, shown as an axial maximum intensity projection, illustrating the tendency for fewer streamlines to visit voxels further from the seed point (green cross). Created using TractoR’s “track” script.