A Web-based Probabilistic Tractography Database

C. J. Rose¹, D. Ellard¹, D. Morris¹, H. Haroon¹, K. Embleton^{1,2}, N. K. Logothetis^{1,3}, M. A. Lambon Ralph², and G. J. Parker¹

¹Imaging Science and Biomedical Engineering, School of Cancer and Imaging Sciences, The University of Manchester, Manchester, United Kingdom, ²School of Psychological Sciences, The University of Manchester, Manchester, United Kingdom, ³Max Planck Institute for Biological Cybernetics, Tübingen, Germany

INTRODUCTION By measuring the diffusivity of water along white matter fibre bundles, diffusion tensor imaging (DTI) and probabilistic tractography allow *in vivo* inferences to be made about the presence of connections between regions of the brain¹. Tractography results are useful to a range of communities, from those working in MR, through biologists, psychologists and physicians. However, tractography requires access to MR scanning facilities, the use of appropriate MR sequences and tractography software, placing the technique beyond the reach of many who would benefit from the technique. One approach to easing this problem is to provide anatomical connectivity information online, e.g. the CoCoMac database, which summarises over 400 literature reports on invasive tracing experiments on macaques². These methods are an accepted gold standard, but cannot be used in humans. *In vivo* DTI-based approaches do not suffer from this drawback. Fig. 1 illustrates a typical tractography result.

This abstract describes a new Internet-based system that allows researchers to obtain anatomical connectivity information—derived from DTI and probabilistic tractography³⁻⁵—for a number of human and animal subjects. A database stores information about the subjects that have been scanned (including age, sex and handedness etc.), and the standard atlases that have been used to provide cortical parcellations that serve as tracking start and target regions. This allows users to obtain anatomical connectivity information according to attributes of interest using the vocabulary of the relevant atlas. The system has two interfaces: a browser-based interface that is suited to manual exploration, and a programmatic interface that is suited to batch processing.

ACQUISITION & TRACKING High angular resolution human and animal DTI data were acquired (example human acquisition parameters: 3T Philips Achieva scanner (Philips Medical Systems, Best, Netherlands), 8-element head coil. PGSE EPI with TE=59ms, cardiac gating, G_{max} =62mT/m, partial Fourier factor 0.679, 112×112 matrix reconstructed to 128×128, reconstructed resolution 1.875×1.875mm², slice thickness 2.1mm, 60 contiguous slices, 61 directions at b=1200s/mm², 1 at b=0, SENSE factor = 2.5, correction for susceptibility and eddy current-induced distortion⁶). Tractography connectivity maps were produced using the multi-fibre Probabilistic Index of Connectivity method⁴. At each voxel, probability density functions—generated using a residual bootstrapping method²—describe tract direction uncertainty. We used 1000 streamlines and a step size of 0.5mm. Streamlines were terminated on doubling back or on leaving the brain volume. A voxel's connectivity is defined as the number of streamlines that pass through it.

BROWSER INTERFACE We have developed a web browser interface to our software, available at http://piconmat.com, that allows users to select specific brain regions—from subjects with particular characteristics (such as species, age, sex)—for which to calculate tractography connectivity information. A screenshot of this interface is presented in Fig. 2. Results are displayed as a symmetrical matrix.

PROGRAMATIC INTERFACE We have also developed a web service that allows researchers to write software that can extract tractography results from the database. This allows large numbers of results from our tractography software to be

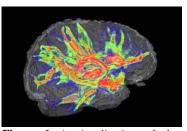


Figure 1 A visualisation of the result of probabilistic tractography.

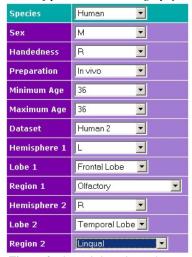


Figure 2 The web-based interface.

used within experiments without manual web-based interaction. An obvious experiment might involve running specific queries on different datasets (experimental subjects) to identify differences that are caused by factors such as gender, handedness, age etc. The programmatic interface is accessed using hypertext transfer protocol (HTTP) requests; results are returned in Javascript Object Notation (JSON) format⁸, which is human-readable and easily parsed using one of the many software libraries available for the programming languages commonly used in scientific research (C, Matlab, Perl, Python etc.). The connectivity information could then be exported to Excel, for example. There are two programmatic interfaces: the http://piconmat.com/query interface allows a user to query the database to determine what data are available, and the http://piconmat.com/get-connectivities interface allows a user to obtain the probabilistic tractography connectivity information between a given pair of regions.

The query interface requires one or more arguments in (key, value) pairs, which can be constructed by appending a HTTP query string to the base URL (see below). The interface mandates one argument, the key get, which allows the user to specify what they want to query: e.g. if a user was interested in the species that are available, they would specify the value species and perform an HTTP GET on the URL http://piconmat.com/query?get=species. The result might be the JSON string ["Human", "Macaque"], indicating that tractography results are available for both species. The full list of keys that are currently supported is: species, atlas, sex, handedness, preparation, age_min, age_max, dataset, hemisphere, lobe and region. The interface is specified in full online.

The get-connectivities interface requires the keys species, atlas, ..., dataset as above and the keys hemisphere1, lobe1, region1, hemisphere2, lobe2, region2—all with values determined using the query interface—specifying for which two regions tractography results should be returned, and the key response with the value json, which specifies that the result must be returned in JSON format (rather than hypertext markup language, HTML). This interface returns the connectivity strengths as a JSON array encoding the symmetrical connectivity matrix.

DISCUSSION & CONCLUSIONS We have developed an Internet-based system to allow DTI-based probabilistic tractography information to be made widely available, particularly to those communities that would otherwise not benefit from these methods. We currently have data for human and macaque subjects. Our system can currently provide connectivity information between any two regions, and we plan to extend this to an arbitrary number of regions as part of ongoing development that will include expansion of the set of query keys, refinement of the manual interface and the addition of human and animal data.

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