Piconmat.com version 2.0: A Web-based Probabilistic Tractography Data Service

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INTRODUCTION We are developing web-based software to provide diffusion MRI-derived *in vivo* information about the connections between cortical regions in human and animal subjects, and present the latest version of our software, **`piconmat.com`** version 2.0. By measuring the diffusivity of water along white matter fibre bundles, diffusion MRI and probabilistic tractography allow *in vivo* inferences to be made about the presence of connections between regions of the brain[1]. 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, and the use of appropriate MR sequences and tractography software. To answer many questions of interest it is necessary to characterise connectivity with respect to a population of subjects and across species. For many investigators, such experiments are impractical. One approach is to provide anatomical connection information online, e.g., the CoCoMac database summarises over 400 literature reports on invasive tracer experiments on macaques[2]. These methods are an accepted gold standard, but cannot be used in humans. *In vivo* HARDI-based approaches do not suffer from this drawback. Fig. 1 illustrates a typical tractography result. Version 2.0 of **`piconmat.com`** improves substantially upon the previous version that debuted at the 2009 ISMRM meeting. **WEB-BASED INTERFACE** Conventionally, the strength of connection between all pairs of cortical regions is represented as a symmetrical matrix, which can be visualised as a colour-coded array plot. Our software is based around an interactive connection matrix (Fig. 2), which displays the mean connection strengths between all pairs of regions, where the averaging is performed over all individuals in the **`piconmat.com`** dataset that meet certain criteria. As the user moves the mouse across the connection matrix, a display is updated to show information about the corresponding region pair; this includes: the names of the regions, the mean connection strength, and a coarse histogram of the distribution of strengths. The information about a region pair can be added to a list by clicking on that region pair's matrix element. Associated with each individual is certain metadata (e.g., age, sex, handedness). Controls are provided to allow the user to include or exclude individuals on the basis of these characteristics; the connection matrix and list of selected regions update to reflect changes in the set of individuals of interest. Multiple connection matrices can be simply added to the page, such that visual comparisons of the connection strengths between groups—e.g., males and females aged 25–50—can be made. Finally, once information about interesting region pairs has been selected, the underlying data can be obtained in a format that can be copied and pasted into Excel or statistics software for further analysis. **ACQUISITION & TRACKING** For the human brain data held at **`piconmat.com`**, high angular resolution diffusion data were acquired in human volunteers on a 3T Philips Achieva scanner using an 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 1.875×1.875mm^2, slice thickness 2.1mm, 60 contiguous slices, 61 directions at b=1200s/mm^2, 1 at b=0, SENSE factor = 2.5, correction for susceptibility and eddy current-induced distortion[3]. Tractography connection maps were produced between the aparc+aseg regions defined by FreeSurfer[4,5], using the multi-fibre Probabilistic Index of Connectivity (PICo) method[6]. At each voxel, diffusion probability density functions—generated using constrained spherical deconvolution and a model-based residual bootstrapping method[7,8]—describe fibre bundle orientation 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 connection is defined as the proportion of all streamlines that pass through it. **DISCUSSION & CONCLUSIONS** We have outlined a significant enhancement to previously reported software, **`piconmat.com`**, which we have made publicly available at no cost, as a service to the scientific community. The software uses standard web technologies (HTTP, XHTML, CSS and JavaScript) and requires a high-performance modern browser such as Mozilla Firefox v3.5, Apple Safari v4, Opera v10 or Google Chrome v3. Future work will include improving performance under Microsoft Internet Explorer, the addition of more connection data, and releasing the source code under an open source license. **ACKNOWLEDGEMENTS** Financial support has been provided by the UK's BBSRC (BB/E002226/1), EPSRC (GR/T02669/01) and MRC (G0501632). **REFERENCES 1** Johansen-Berg et al. Curr Opin Neurol, 2006:19;379–85. **2** Stephan et al. Phil Trans Roy Soc Series B, 2001:356;1159–86. **3** Embleton et al. Proc ISMRM #1070, 2006. **4** Fischl et al. Cerebral Cortex, 2008:18;1973–80. **5** Yeo et al. Med Imag Anal, 2008:12;603–15. **6** Parker et al. Phil Trans Roy Soc Series B, 2005:360;893–902. **7** Haroon et al. IEEE TMI, 2009:28;535–50. **8** Haroon et al. Proc ISMRM #362, 2009.

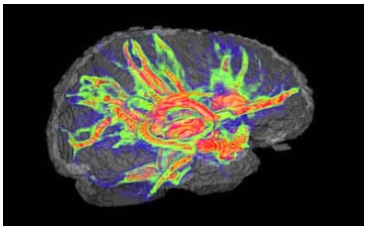

Figure 1 *A visualisation of the result of probabilistic tractography.*

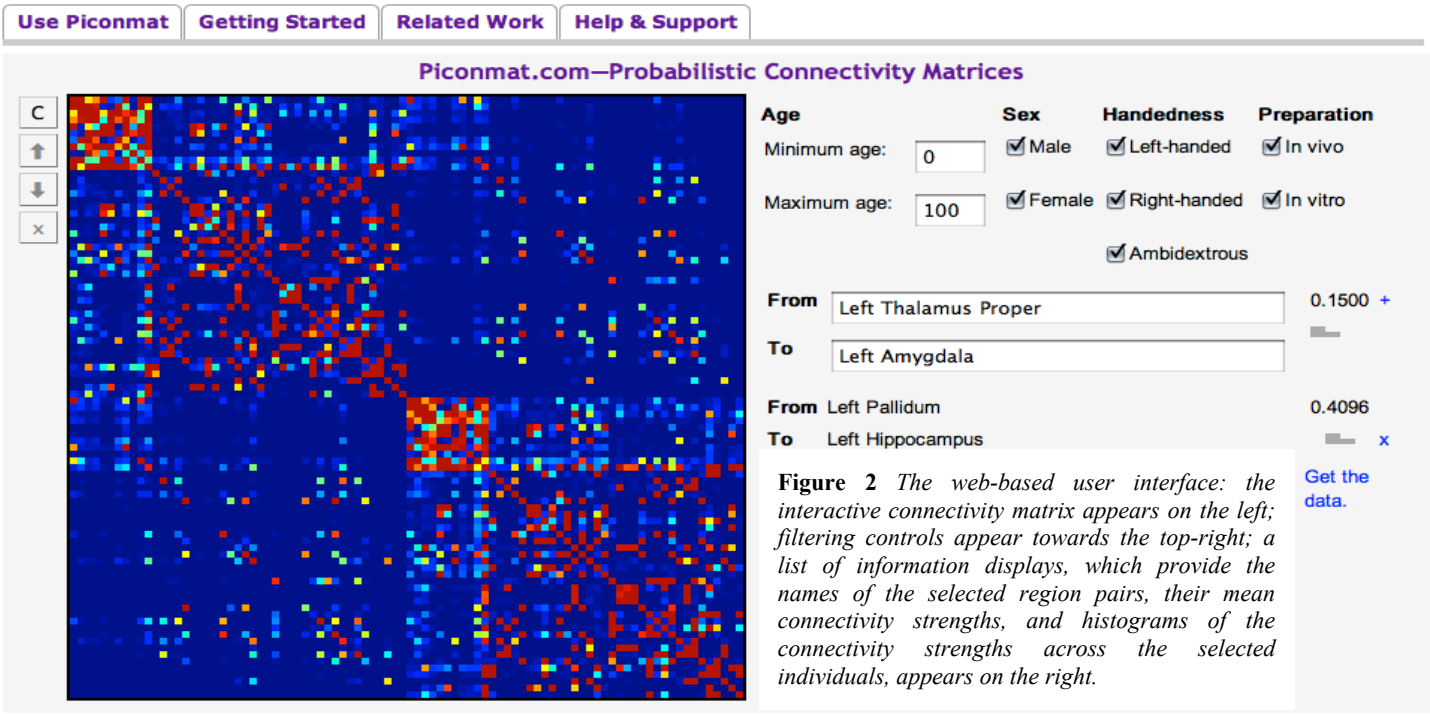

Figure 2 *The web-based user interface: the interactive connectivity matrix appears on the left; filtering controls appear towards the top-right; a list of information displays, which provide the names of the selected region pairs, their mean connectivity strengths, and histograms of the connectivity strengths across the selected individuals, appears on the right.*