Visualisation of CSI metabolite concentrations along specific white matter tracts

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Introduction: Diffusion Tensor Imaging (DTI) is a non-invasive method to visualise gross white matter architecture and probe microstructural integrity of both normal and pathological brain[1]. Equivalently, quantitative Magnetic Resonance Spectroscopy (MRS) is a non-invasive technique used to measure metabolic concentrations, changes of which have been documented in several neurological disorders[2]. The two techniques have been combined in recent studies investigating the correlation between MRS and DTI parameters, revealing significant correlations between N-acetyl-aspartate (NAA) and Fractional Anisotropy (FA), and NAA and Apparant Diffusion Coefficient (ADC) and furthering our understanding of the pathological basis for neurological disorders[3; 4]. Here preliminary work that combines MRS Chemical Shift Imaging (CSI) with DTI-tractography is presented. Our aim is to assess the feasibility of performing tract-specific measurements of MRS brain metabolites along the left arcuate fasciculus (AF).

Methods: Acquisition: All datasets were acquired from a normal right-handed male adult on a 3T GE HDx TwinSpeed MR scanner. Whole brain DTI data were acquired using a peripherally gated twice-refocused spin echo EPI sequence, with diffusion gradients applied in 30 isotropically-distributed directions ($b=1300 smm^{-2}$) and 3 B=0 images, 2.4mm slice thickness and 1.797mm in-plane resolution. For acquisition of the MRS-CSI data, a sagittal $16cm^2$ ROI was positioned on the left hemisphere from a sagittal T1W-SPGR, to capture the majority of the AF fibres (Figure 1). CSI was performed using a PRESS sequence, 15.6mm slice thickness, 32x32 matrix, TR/TE=1200/144. A linewidth of 15Hz was achieved. The total imaging time was 1 hour. Analysis: The DTI data were first corrected for motion and eddy current induced distortions using in-house software and then the diffusion tensor was estimated for each voxel[5]. A continuous field was fit to the tensor data using a B-spline approach and streamline fibre-tracking was performed using a two-ROI approach[6]. The CSI data was processed using SAGE and LCModel to estimate metabolite concentrations of NAA, Choline (Ch) and Creatine (Cr) using a phantom for calibration. Coregistration: The non-diffusion weighted images were registered to the SPGR volume using an affine registration (FSL), with normalised mutual information as the cost function. Visual inspection revealed good alignment within the CSI ROI, and the CSI grid was then transformed to DTI space using the same affine transformation. An atrophy correction was applied using the percentage of CSF in each voxel from the segmented SPGR. The NAA, Ch, and Cr were linearly interpolated at each vertex (0.5mm intervals) along the tract, and visualised using streamlines in MATLAB.

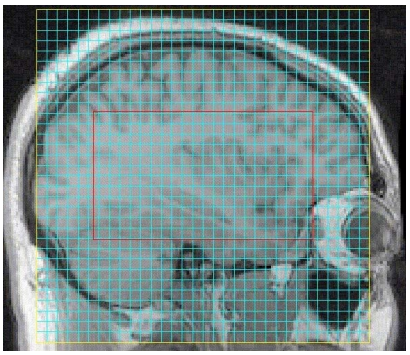

Figure 1: CSI ROI overlaid on the SPGR

Results: The NAA, Cr and Ch concentrations vary along the AF, and are consistent with values reported in the literature. Selected results are shown in Fig 2, showing the FA (left) and NAA (right) spatial distribution along the AF. There is considerable change in the NAA values along the tract, higher values are observed in the central & posterior part, where lower FA values are observed.

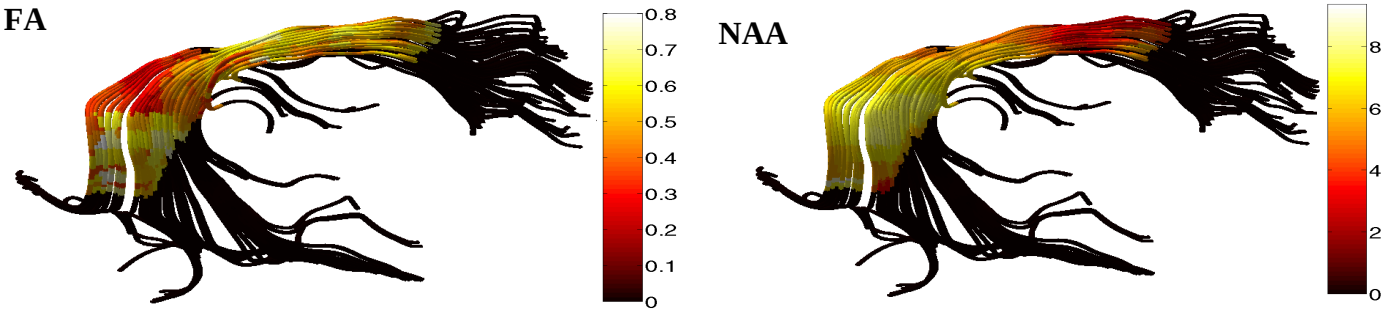

Figure 2: Tractography reconstruction of the AF, colour coded by FA values (left), and NAA mM concentrations (right). Streamtubes coloured black are those that lie outside the CSI volume.

Discussion: In this study we showed that it is possible to combine MRS and DTI to obtain tract-specific measurements of white matter metabolites within clinically acceptable scanning time. The simultaneous characterization of the MRS and DTI offers complementary information about the metabolic composition and the microstructural milieu of the tract. Thus, for example, in zones with low FA the concomitant detection of high NAA concentrations suggests the presence of crossing fibres. One limitation of this approach is the relatively large volume of the CSI, which may contain both grey and white matter. Hence, changes in the NAA concentration could reflect variations in the grey/white matter composition within the CSI voxel, not necessarily reflecting white matter only[7]. Linear regression analysis, covarying for the relative proportions of grey and white matter in the CSI voxels, could partially overcome this limitation. The application of this method to focal degenerative disorders affecting perisylvian language pathways could be helpful in assisting the neurologist and the neuroradiologist in the differential diagnosis and treatment response.

References: 1. Catani, M. Curr Opin Neurol 19 (2006). 2. Kreis, R.J Prog in Nuc Res Speec 31 (1997). 3. Nitkunan, A, et al. NMR Biomed 19 (2006). 4. Irwan, R, et al. Magn Reson Imaging 23 (2005). 5. Pierpaoli, C, et al. Radiology 201 (1996). 6. Catani, M, et al. Neuroimage 17 (2002). 7. Manton, DJ, et al. NMR Biomed 8 (1995).