Inversion Recovery DTI In Vivo at 7T in the Human Brain

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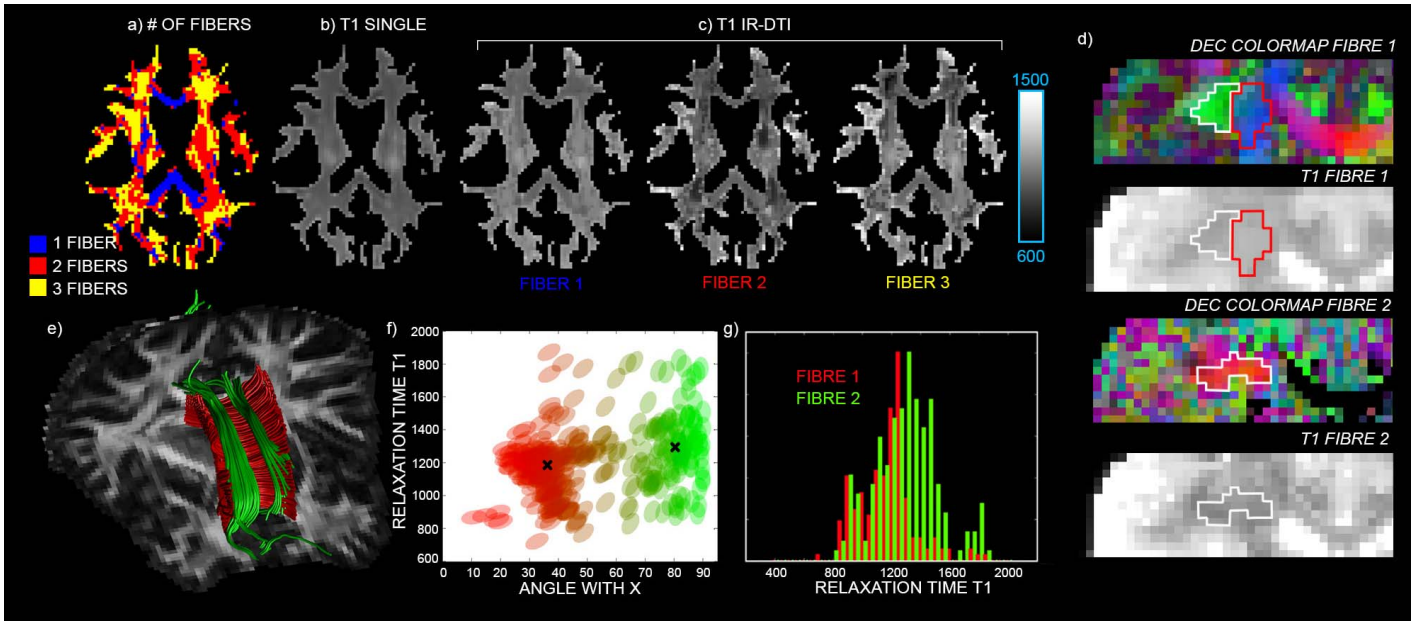
PURPOSE AND TARGET: White matter (WM) microstructural properties can be described by at least two distinct attributes: the axonal features (e.g., axonal diameter and density) and the myelination. MRI techniques have proven to be capable of characterising WM attributes in recent years: diffusion MRI allows estimation of the diffusion tensor [1], reflecting largely axonal properties but modulated by myelin, while relaxometry allows quantification of myelin content [2-3], both averaged over the image voxel. As more than 90% of WM voxels contain complex fibre architecture [4], increasing specificity to distinct WM attributes requires disentangling quantitative metrics from the fibre *architectural paradigm* and estimating them per individual fibre tract. Recently, a new MRI technique combining inversion recovery and DTI (IR-DTI) was introduced to provide fibre-specific estimates of the relaxation time T1 and of the diffusion tensor [5]. The technique was previously applied on fixed tissue of an animal model. Here, we successfully apply this technique *in vivo* to the human brain for the first time. To reduce the experimental times, we develop IR-DTI model fitting using orientation information from independently acquired HARDI data. In addition, we use a model selection step [4] to decide voxel-wise how many T1-diffusion compartments are supported by the data. **Target audience** is basic scientists interested in modelling microstructure and clinical scientists interested in WM diseases.

METHODS: The IR-DTI protocol comprises several inversion recovery prepared diffusion MRI series acquired for different inversion times (TI). 3 healthy subjects underwent an IR-DTI protocol at 7T using the following parameters: TI=200,300,400,500,700,1000,1500 ms, b-value 1000 s/mm^2, 30 directions for each TI, TE=50.8ms, TR>10 s, GRAPPA factor=2. A separate HARDI scan was also acquired using 60 gradient orientations, b-value 2000s/mm^2 and 6 b0, TE=57.6 ms, TR=5 s, GRAPPA factor=3. The resolution of all scans was 2 mm isotropic. Data were corrected for motion and distortion and processed using in-house Matlab scripts. First, HARDI data were processed to obtain the fibre orientation density (FOD) using constrained spherical deconvolution (CSD) [5]. Then, up to three FOD maxima, thought to correspond to the main underlying fibre orientations, were extracted using a numerical optimization procedure [4]. The orientational information was then fed into the IR-DTI script that fits a T1 value for each fibre population present in the voxel by the model: $S/S0=\Sigma_i f_i*(1-2*\exp(-TI/T1_i))*\exp(-b*D_i)$. To demonstrate that the analysis can return fibre specific values in crossing areas, the corpus callosum (CC) and the cingulum (CING) bundle were reconstructed by tractography and fibre-specific T1 histograms were computed.



RESULTS AND DISCUSSION: Fig a) reports the number of distinct fibre populations in each WM voxel for one representative subject. Fig b) and c) show, for the same subject, the maps of single T1 (calculated using conventional inversion recovery) and the fitted T1 specific to each fibre population, respectively. Fig. d) shows qualitatively that in areas likely belonging to the same fibre tract (here the CC, corticospinal tract and superior longitudinal fasciculus), the fitted tract-specfic T1 maps are also homogeneous, with adjacent tracts showing clearly distinct values of T1. Fig e) shows the tractography of CC and CING bundle. Fig. f) is a scatterplot of the angle to the L-R direction versus T1 in the area of crossing of CC and CING. The two crosses represent the calculated cluster centroids. The two bundles show a clear separation on both axes, with the cingulum having larger T1 values than the corpus callosum. This is also shown in the histogram of Fig. g). The results are consistent with the fact that the corpus callosum is more myelinated than the cingulum [7] and myelin is inversely correlated with T1. The results are consistent across all subjects.

CONCLUSION: We demonstrate the feasibility of in-vivo IR-DTI analysis on the human brain identifying fibre tract specific T1 values. IR-DTI has great potential for application in the clinic, for instance in detecting very early tract specific alterations of myelination in crossing fibre areas that might not be detected using other MRI-based approaches.

REFERENCES: [1] Basser et al. *J Magn Reson B* **103** :247 (1994) [2] MacKay et al *MRM* **31**:673 (1994) [3] Deoni et al. *MRM* **60**:1372 (2008) [4] Jeurissen et al. *HBM* **34**:2747 (2013) [5] De Santis et al. Proc. ISMRM (2014) [6] Tournier et al. *NI* **23**:1176 (2004) [7] Dean et al. *NI* **84**:742 (2014)