Partial Volume Corrections of Myelin Water Fraction values

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INTRODUCTION: Multi-component relaxometry of fast- and slow-T_1 and T_2 has previously been used to quantify aspects of tissue microstructure in brain tissue[1,2], notably – the myelin water fraction (MWF). The myelin water content is estimated by attributing the short T_2 relaxation component to the water trapped within the myelin sheath. However, the amount of partial volume contamination from cerebral spinal fluid (CSF) is unknown and until now, with methods such as mcDESPOT[1,2] there is not method to check for or correct for partial volume errors (PVE). Here, we investigate the effects of partial volume contamination due to CSF or free water and propose a novel approach to correcting the problem of PVEs in mapping myelin water content. To measure free water contamination we used the procedure detailed in[3], to extract a free water contamination map from diffusion imaging data. However, it has been shown that diffusion images are affected by partial volume of brain tissue with free water[3] causing artifactual elevations in mean diffusivity and reductions in anisotropy. By correcting diffusion data with FWC maps has been shown to improve the robustness of this method[3]. This can be ameliorated by fitting two tensors to the diffusion-weighted signal – a) "Tissue" tensor and b) "CSF" tensor. The relative volume fractions then indicate the level of partial volume. Here, we show how this correction factor can then be sued to correct MWF for partial volume.

Methods: Healthy volunteers (*N*=28, 31.1 ± 6.7 y) were studied using a 3T MRI scanner (HDx system GE Medical Systems, Milwaukee, WI). Cardiac-gated DTI data were acquired with a single-shot spin-echo EPI sequence with the following parameters: b-value = 1200 s/mm^2 along 60 gradient directions; six non-DW images; 60 axial slices, with effective TR = 20 R-R intervals[4]. Sequence specific parameters for mcDESPOT-SPGRs were: TE/TR = 2.1/4.7 ms, flip angle (α) = [3,4,5,6,7,9,13,18]; mcDESPOT-bSSFPs were: TE/TR = 1.6/3.2 ms, α = [10.6,14.1,18.5,23.8,29.1,35.3,45,60][5]. All participants gave written informed consent to participate in this study under a protocol approved by the local Ethics Committee/IRB.

Free water voxel estimation was applied to each diffusion dataset resulting in a free water correction (FWC) maps[3]. The MWF map was then non-linear registered to the fractional anisotropy map using an in house optimization scheme prior to FWC application to MWF data. MWF correction data were calculated by dividing the measured MWF by the FWC measurement, thus giving us a measure of uncontaminated MWF values. The affect on MWF within WM was investigated by masking the WM by a mask created by FMRIB's automated segmentation tool brain segmentation (FAST)[6].

RESULTS: The difference between corrected MWF and uncorrected MWF values demonstrate high difference in areas close to ventricles and sulci, as expected (Fig 1). However, it should be noted that in other parts of the brain there is still up to a 10 percent difference. To further investigate this difference between corrected and uncorrected MWF values, we graphed a histogram of MWF values in white matter for the slice shown in Fig 1. The histogram demonstrates a upward shift in MWF values within the white matter (Fig 2). Notability, there is a change in the peak height and location MWF value in this histogram demonstrating that FWC is not a linear correction throughout white matter. However, in Fig 3 the MWF values along the corpus callosum, tracts, which are expected to be highly affected by free water contamination, appear to have the same heterogeneity in MWF values, further demonstrating this correction can affect white matter tracts differently.

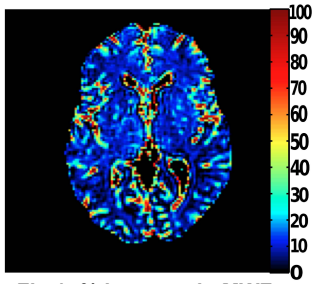

Fig 1: % increase in MWF

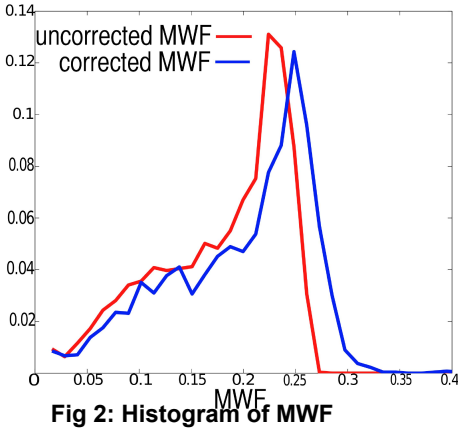

Fig 2: Histogram of MWF

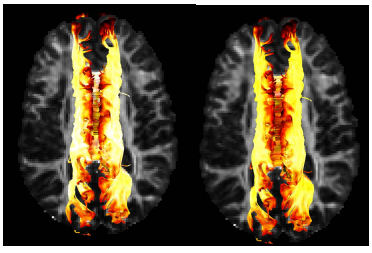
Fig 3: A)corrMWF B)MWF

DISCUSSION: MWF measurements are affected by free water contamination in particularly in areas near ventricles and sulci. This will have negative impact on ROI-based, histogram based, VBM-style tractography based analysis – if not corrected for. This results however shown using tracgraphy and mcDESPOT can be applied to any analysis or sequence protocol to correct MWF values. In particular current pathological studies, such as in MS, where uncorrected MWF histogram peak location and height changes are used to determine the patient's WM integrity. This is particularly a concern in studies comparing MWF in controls and pathology/ageing/development where FWC effects may be even more pronounced. Further work is being done to test the affect of FWC on MWF in different white matter tracts and participants with abnormal MWF measurements.

REFERENCES: [1]Deoni SC et al. (2008) HBM, Melbourne, Australia. p. 269. [2]Deoni SCL et al (2008) JMRI **27:**1421-9 [3]Pasternak O et al. (2009) MRM.62:717-30 [4]Whittall *et al* (1997) MRM. 37:34 [5]Deoni et. al. (2008) MRM. 60:137. [6]Zhang Y. et al. (2001)IEEE TMI. 20:45