Silent Myelin Imaging using Magnetization Prepared RUFIS

Tobias C Wood[1], Emil Ljungberg[1], Ana-Beatriz Solana Sanchez[2], and Florian Wiesinger[1,2]

[1]Department of Neuroimaging, King's College London [2]ASL Europe, GE Healthcare, Munich Germany

Introduction Myelin is a crucial part of a healthy nervous system. Fortuitously, it is also a major but not the only contributor to MR contrast between grey and white matter. Hence development of sequences that are specific and not just sensitive to myelination are of great interest for clinical usage.

Myelin is a complex layered semi-solid structure that exhibits many interesting MR phenomena. In particular, the saturation behaviour of myelin is different when irradiated with a dual-frequency RF pulse compared to a single-frequency pulse[1]. We refer to this as dipolar-coupled Magnetization Transfer (dcMT), but it is also referred to as inhomogeneous MT (ihMT) in the literature [2]. dcMT appears to be unique to myelin within the brain and hence can be exploited as a myelin specific contrast.

One major clinical drawback of MR scans is the high acoustic noise inherent in many sequences, including the gradient echo sequences generally used with dcMT. Patient comfort can be increased using a zero echo-time (ZTE) radial sequence such as RUFIS [3]. Recently Mchinda et al showed that the dcMT effect can be significantly increased using a preparation train and segmented readout [4]. As radial sequences can be easily segmented, we hence combined RUFIS with dcMT to produce a silent myelin weighted imaging sequence.

Methods A flexible MT-prep module was implemented in a RUFIS sequence and used to scan a volunteer on a GE MR750 3T scanner. The prep module had 12 0.5 ms Tukey pulses separated by 0.5 ms, with an average B1 of 7 $\mu\mathrm{T}$ applied at an offset of 7 kHz. The readout was acquired at 1.5 mm isotropic resolution over a 24 cm field-of-view, flip-angle 3 degrees and 128 readouts per segment. Scan time was 1 minute 28 seconds per volume. Five volumes were acquired: one with no saturation power (REF), one with pulses applied at +7 kHz (P), one at -7kHz (M), and two with alternating offsets (PM & MP). The input images were smoothed with a Gaussian kernel FWHM 1 mm. From these volumes the standard MT Ratio (MTR) was calculated as (1 - (M+P)/(2*REF)) and the dcMTR was calculated as (1 - (MP + PM)/(2*REF)) - MTR.

Results & Discussion Figure 1 shows slices through the raw unweighted, MT-weighted and dcMT-weighted images. Figure 2 shows the calculated dcMTR, with exquisite myelin contrast. Values of around 6% are observed in white matter and 3% in grey matter. The achieved contrast is lower than Mchinda et al, despite an identical preparation sequence. We postulate that this is because semi-solid protons with very short T2 values (tens of $\mu\mathrm{s}$) are visible in ZTE sequences while they are invisible in standard cartesian sequences. As these protons have a short T1 value [5], they likely recover during the readout and contribute some signal towards the end of the segment, which reduces the dcMTR.

References

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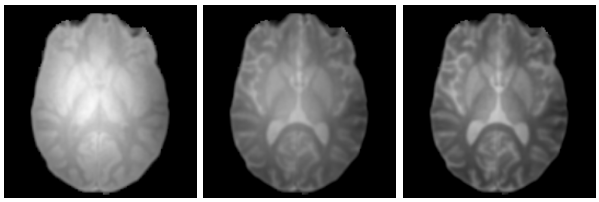

Figure 1: Example slices through the PD-, MT- and dcMT-weighted volumes.

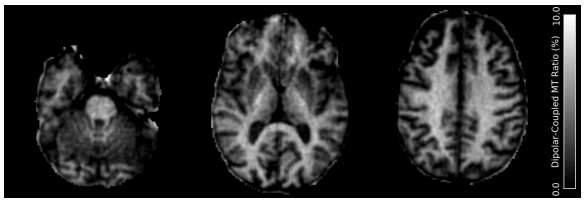

Figure 2: The Dipolar-Coupled MT Ratio, showing excellent specificity for myelin.