Compensating Diffusion Bias of Quantitative T_2 on High-Field MRI Scanners

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Introduction: In high-field scanners imaging gradients (RO, PE and SS) are significant, leading to amplification of diffusion weighting and spurious attenuation of the signal, especially in spin-echo (**SE**) based acquisitions where the effect of diffusion accumulates along the echo train. Thus, T_2 mapping on preclinical scanners is challenged by both diffusion and stimulated echoes. Furthermore, different parameter sets will produce different diffusion and stimulated-echoes signal bias, impairing reproducibility of measured values. In this work we implement diffusion correction of SE and multi echo SE (**MESE**) protocol data in the echo modulation curve (**EMC**) algorithm [1] to unravel the unbiased T2 values of the tissue.

Methods: Effective b-value [2,3] is developed according to the applied **MSME** sequence gradients, it is evaluated per echo based on the subset of coherence pathways that contributed to the signal [4], thus incorporating the effects of stimulated echoes in the diffusion attenuation assessment.

$$effective\ b-value = \gamma^2 I = \gamma^2 \int_0^t \left(\int_0^{t'} g^*(t'')dt'' \right)^2 dt' \qquad \text{Eq.1}$$

A phantom containing concentrations of $MnCl_2$ was imaged on a 9.4T Bruker Biospin. Spectroscopy was performed to achieve unbiased T_2 values. **SSE** and **MSME** imaging sequences were applied with varied parameters. ADC: 2.29 x 10^{-5} cm^2/s. **MSME** data was fitted using the **EMC** algorithm after the diffusion attenuation was corrected. An in-vivo scan was conducted on a 7T Bruker Biospec with **MSME** protocol and high-resolution scan parameters.

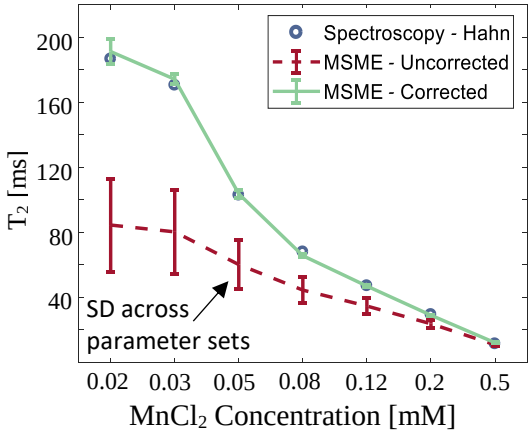

Fig. 1: qT2 from MSME scans of $MnCl_2$ phantom. The green line shows the results after correction of diffusion bias. The bars show the SD over the different parameter sets (varied resolution, slice thickness and BW).

Results: For the 0.02 mM tube, uncorrected results were up to 76% lower than spectroscopy results, after correction max deviation was lowered to 4%; CV value was reduced from 24% to 4% (see Fig. 1 for all concentrations). In-vivo results: corrected T_2 values were raised by 20% in the hippocampus, and by 11% in the cortex and corpus callosum.

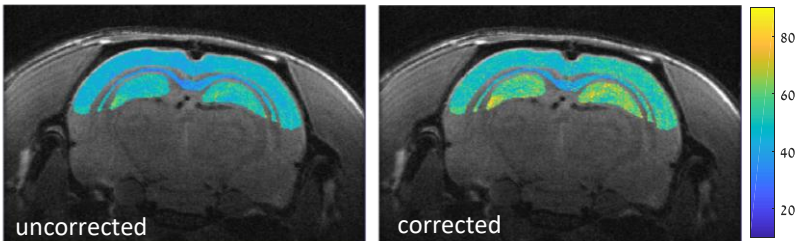

Fig. 2: High resolution in-vivo rat's brain. The segmented areas show T_2 maps [ms] of the cortex, corpus callosum and the hippocampus.

Conclusion: Correction is necessary for high-field / high-resolution qMRI since diffusion effect intensifies as resolution increases. The suggested solution improves accuracy, eliminates the variability observed at different resolutions and slice thicknesses and provides reproducible, steady T2 values.

References: [1] Shepherd, NeuroImage: Clinical. (2017). [2] Abragam, Oxford (1961). [3] Torrey, Phys. Rev. (1956). [4] Hennig, Magn. Reson. (1988).