Rapid and Accurate T2 Mapping from Multi Spin Echo Data Using Bloch-Simulation-Based Reconstruction

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Introduction T2 contrast is an important tool for non-invasive diagnosis and prognosis of pathologies. Although T2 assessment is usually done in a visually-qualitative manner, its quantitative characterization promises additional value for numerous applications including studying biophysical changes in cartilage, cancer detection, cardiac imaging, and investigation of muscle physiology. Genuine T2 quantification, however, remains challenging in clinical practice due to the very long scan times associated with full spin-echo (SE) acquisitions (10’s of min), or, in the case of multi-SE (MSE) protocols, due to an inherent bias of the T2 values resulting from contamination of the echo-train by stimulated and indirect echoes, non-rectangular slice profiles, and inhomogeneous B1+ field profiles. Several T2 mapping approaches have been presented which take these effects into account and offer multi-contrast information. Notwithstanding promising preliminary results, in vivo mapping of T2 values is still challenging in clinical settings. Recently, a new T2 mapping technique – the Echo Modulation Curve (EMC) algorithm – has been introduced, which relies on high-precision Bloch simulations to model the exact signal evolution in MSE pulse-sequence schemes, while preserving the potential for further acceleration via non-Cartesian undersampling strategies. In this work we: 1) investigate the potential of the EMC technique for multiparametric mapping, including proton density (PD), B1+ and T2 values, and 2) evaluate its accuracy and precision for varying levels of noise.

Methods EMC algorithm: Bloch simulations of the prospective MSE protocol were performed using the exact RF pulse shapes and other experimental parameters. Simulations were repeated for a range of T2 and B1+ inhomogeneity values (T2=1...1000ms, B1+ = 50...130 %), producing a database of EMCs, each associated with a unique [B1+,T2] value pair. Experimental data were acquired on four different clinical 3T whole-body scanners for 1) an MnCl2 phantom, and in vivo human 2) brain, 3) prostate, 4) knee cartilage, and 5) spinal cord using full SE and MSE sequences with TR=2.5sec, 3mm slices; (TE: SE: TE=[15...90]ms, NEX=6, res=1.7x1.7mm2, T Spo=26:00:00min), (MSE: Echo-spacing=15ms, ETL=6, res=1.1x1.1mm2, T Spo=2:42:42min (2x GRAPPA acceleration)). T2 and B1+ maps were generated by matching the experimental MSE data to the EMC database via l2-norm minimization of the difference between experimental and pre-calculated EMCs. PD maps were calculated by back-projecting the first echo image to time t=0 using the calculated T2 map. Noise analysis: A representative set of EMCs was extracted from a simulated EMC database and matched back to the database after adding it with different levels of noise (SNR = [10...100]). The process was repeated N=128 times for each EMC (using different noise vectors) to produce an estimate of the accuracy (mean value) and precision (standard deviation) for each [B1,T2,SNR] triplet.

Results The results of our in vivo brain exam in a healthy volunteer are shown in the figure. (a) T2 map derived from single-SE scan and fitted to an exponential model S(t) = S0exp(-t/T2). (b-c) T2 maps obtained from MSE data via (b): fitting to an exponential curve as in ‘a’, and (c): matching to the database of simulated EMCs as proposed in this work. (d-e) B1+ bias map, and PD map produced by the EMC approach. (f-g) Accuracy (mean) and precision (STD) of the EMC matching approach (blue) vs. exponential fitting (red) for different noise levels.

Discussion The EMC algorithm offers accurate, high-resolution, and fast T2 mapping capability, which overcomes the common penalties associated with MSE acquisitions. By modeling the exact pulse-sequence scheme, significantly improved fitting accuracy is achieved vs. exponential fitting, yielding simultaneous T2, B1+ and PD maps in clinically feasible timescales and that are invariant to the sequence and scanner type. This was confirmed through MnCl2 phantom T2 mapping results (not shown) exhibiting consistency over different MRI scanners, pulse-sequence schemes, and imaging parameters. The EMC framework can be further extended to model other contrasts (e.g. T1, diffusion, T2*) to derive multi-component T2 distributions, and support arbitrary acquisition schemes.


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