Rapid and Accurate T_2 Mapping from Multi Spin Echo Data Using Bloch-Simulation-Based Reconstruction

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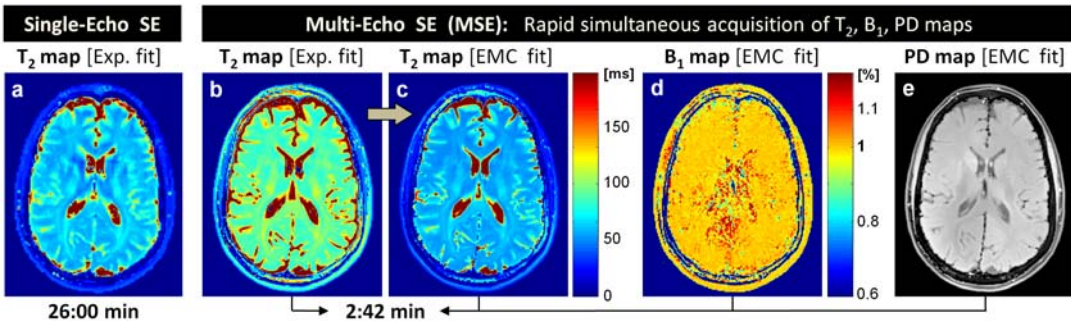
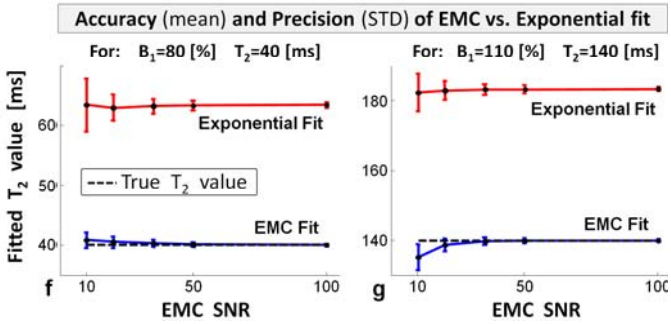
Introduction T_2 contrast is an important tool for non-invasive diagnosis and prognosis of pathologies. Although T_2 assessment is usually done in a visually-qualitative manner, its quantitative characterization promises additional value for numerous applications including studying biophysical changes in cartilage[1], cancer detection[2,3], cardiac imaging[4], and investigation of muscle physiology. Genuine T_2 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 T_2 values resulting from contamination of the echo-train by stimulated and indirect echoes, non rectangular slice profiles, and inhomogeneous B_1^+ field profiles. Several T_2 mapping approaches have been presented which take these effects into account and offer multi-contrast information[5-11]. Notwithstanding promising preliminary results, in vivo mapping of T_2 values is still challenging in clinical settings. Recently, a new T_2 mapping technique – the Echo Modulation Curve (**EMC**) algorithm – has been introduced[12], which relies on high-precision Bloch simulations to model the exact signal evolution in MSE pulse-sequence schemes, while reserving 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**), B_1^+ and T_2 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 T_2 and B_1^+ inhomogeneity values (T_2=1…1000ms, B_1^+ = 50…130 %), producing a database of EMCs, each associated with a unique $[B_1^+,T_2]$ value pair. Experimental data were acquired on four different clinical 3T whole-body scanners for **1)** an $MnCl_2$ 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; {*SE:* TE=[15…90]ms, N_{TEs}=6, res=1.7x1.7mm^2, T_{acq}=26:00min}, {*MSE*: Echo-spacing=15ms, ETL=6, res=1.1x1.1mm^2, T_{acq}=2:42min (2x GRAPPA acceleration)}. T_2 and B_1^+ maps were generated by matching the experimental MSE data to the EMC database via l_2-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 T_2 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 $[B_1,T_2,SNR]$ triplet.

Results The figure summarizes the results of an exemplary in vivo brain exam in a healthy volunteer. (**a**) T_2 map derived from single-SE scan and fitted to an exponential model $S(t) = S_0\exp(-t/T_2)$. (**b-c**) T_2 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**) B_1^+ 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 T_2 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 T_2, B_1^+ and PD maps in clinically feasible timescales and that are invariant to the sequence and scanner type. This was confirmed through **$MnCl_2$** phantom T_2 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. T_1, diffusion, T_2^*), to derive multi-component T_2 distributions, and support arbitrary acquisition schemes.

References **[1]** Pan J et al. *Radiology*. 2011; 261(2): 507-15. **[2]** Liu W et al. *MRM*. 2011; 65(5):1400-6. **[3]** Farraher SW et al. *J Magn Reson Imaging*. 2006; 24(6):1333-41. **[4]** Usman AA et al. *Circ Cardiovasc Imaging*. 2012; 5(6): 782-90. **[5]** Zur Y. *J Magn Reson*. 2004; 171(1):97-106. **[6]** Warntjes J et al. *MRM* 2007; 57(3): 528-37. **[7]** Lukzen NN et al. *J Magn Reson*. 2009; 196(2): 164-9. **[8]** Lebel RM, et al. *MRM*. 2010; 64(4):1005-14. **[9]** Doneva M et al. *MRM* 2010; 64(4): 1114-20. **[10]** Prasloski T et al. *MRM* 2012; 67(6): 1803-14. **[11]** Ma D et al. *Nature* 2013; 495(7440): 187-92. **[12]** Ben-Eliezer N et al. ISMRM 21, 2013 p 2453.

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