Improved T_2-Quantification with Slice Selective MSE-Sequences

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Introduction: Fast and accurate measurement of the transverse relaxation time T_2 has been the goal of numerous studies. Multiple single-echo spin-echo measurements offer the possibility to estimate T_2 with a high level of accuracy. However, this approach is slow and, thus, in daily practice multi-spin echo (MSE) CPMG measurements are used which are hampered by systematic influencing factors from B_0 and B_1+ inhomogeneities and slice profile effects. Different methods are available to circumvent these shortcomings, including crusher gradients to destroy spurious echo pathways [1], specific phase relationships and phase cycling methods [2,3], or homogenization of the slice profile [4]. However, crusher gradients artificially diminish the echo amplitudes by a factor depending on B_1+ and the slice profile, so that a correction of the measured T_2 values is needed. Furthermore, severe artifacts can result if the crusher scheme does not completely spoil the spurious echoes. Phase balanced CPMG sequences effectively eliminate these artifacts at the cost of a distortion of the pure T_2 decay. Stimulated echoes exhibit T_1 decay and will introduce so called "T_1 mixing". In this study we show the applicability of a method that allows for accurate T_2 mapping in the presence of B_1+ inhomogeneities and non-ideal slice profiles.

Theory & Methods: The signal magnitudes in a CPMG train cannot be analytically expressed in the presence of B_1+ inhomogeneities and non-ideal slice profiles. Nevertheless, an analytical formula in the z-transform domain exists [5]. The so-called generating function formalism (GF) is given in eqn. 1. where M_0 is the equilibrium magnetization, $\kappa_1=\exp(-\tau/T_1)$ and $\kappa_2=\exp(-\tau/T_2)$ the relaxation terms, α the refocusing flip angle, τ the inter-echo spacing, T_1 and T_2 the relaxation times; z is a complex variable in the z-domain. Eqn. 2 is an expansion of the formalism to include non-ideal slice profiles (α_i, i=1..Q) and a noise bias N. Evaluation of this expression for $z=\exp(j\phi)$ ($\phi = 0...2\pi$) and, thereon, applying the FFT yields a discrete time signal corresponding to the echo amplitudes at sampling times $n\tau$. Signals in the frequency domain should be generated for a large number of sample points to prevent truncation artifacts in the FFT. Only the first 32 transformed data points are further used in the fitting algorithm, and the parameters T_2 and M_0 are calculated using a nonlinear least square fitting procedure (Active-set algorithm, Matlab, Natick, USA). The proposed method was validated with phantom and in vivo measurements. Test tubes with a) $MnCl_2$ solution adjusted to physiologic relaxation times and b) Gadobutrol (short T_1 and T_2) served as phantoms. An additional larger phantom ($MnCl_2$) was used to compute an entire T_2 map to show the influence of B_1+ inhomogeneities. For T_2 estimation an MSE sequence (TR/TE/contrasts 7000/12ms/32), an SE sequence (TR/TE/contrasts 7000/12-288ms/6), and single voxel spectroscopy as a gold standard were used. T_1 values were obtained using a TIR sequence (TR/TE/TI/contrasts 7000/7.4/100-3200ms/6). RF field maps were acquired using the double angle method (α=60°, 120°, TR=10000 ms). Fitting to mono-exponential decay models for MSE, SE, and SVS sequences was compared to the GF fitting approach for MSE data. For the large phantom a four parameter fit (including B_1+ and T_1) was calculated. For in-vivo evaluation cerebral scans were used. SE images were produced with a "specific" sequence [6] with constant length of the interval TR-TE (400 ms, TE=10-160 ms). In-vivo B_1+ maps were acquired using the Bloch-Siegert method (Gaussian off-resonance pulse with $B_{1,peak}$=0.11 G, K_{BS}=21.3 rad/G^2/ms, duration 8000 ms, f_{OR}=8 kHz) and the same sequences as for the phantom measurements. Again, mono-exponential and GF fitting were compared. All measurements were performed at 3T (TimTrio, Siemens, Erlangen, Germany) with different head coil setups (1 channel CP, 12 channel). Slice profiles were calculated by applying the forward SLR transform.

$$(1)\quad F(z)=\frac{M_0}{2}\left(1+\sqrt{\frac{(1+z\kappa_2)\left[1-z(\kappa_1+\kappa_2)\cos\alpha+z^2\kappa_1\kappa_2\right]}{(-1+z\kappa_2)\left[-1+z(\kappa_1-\kappa_2)\cos\alpha+z^2\kappa_1\kappa_2\right]}}\right)\qquad (2)\quad F_{SP}(z)=\frac{1}{Q}\sum_{i=1}^{Q}F(z,\alpha_i)+N$$

Results: Compared to the spectroscopic measurement the errors for SE T_2 evaluation were minor being maximally 4.2 %. An exception in this series was the phantom where T_1 and T_2 were quite long. Fitting to a MSE echo signal by discarding the first echo generally overestimates T_2 and yields much higher errors of -15.7 to -29.2%. Fitting to the GF Model yielded errors of comparable size as the errors of single-echo T_2 evaluation. For the Gadolinium phantom T_2 could be estimated with all methods with relatively constant accuracy. The T_2 map of the large phantom revealed the influence of the actual flip angle and slice profile. Fig. 1 (a-c) shows T_2 maps obtained by different methods. The "gold standard" multiple SE measurement (b) produced a homogeneous map. In MSE data some modulation of T_2 resulting from B_1+ inhomogeneity as well as a strong bias due to slice profile effects was observed (c). The map calculated with the GF approach (a) lacked this bias and comprised only minimal modulation. Flip angle deviations across the phantom are shown in (d). The T_2 profiles (e) show that the bias becomes minimal for flip angles of 180°. For the 4 parameters fit B_1+ could be roughly estimated, whereas T_1 could not be determined. Fig. 2 shows in-vivo results. The mono-exponential fitting to multi-echo data tended to overestimate T_2 values, while the GF and the single-echo fitting provided similar results.

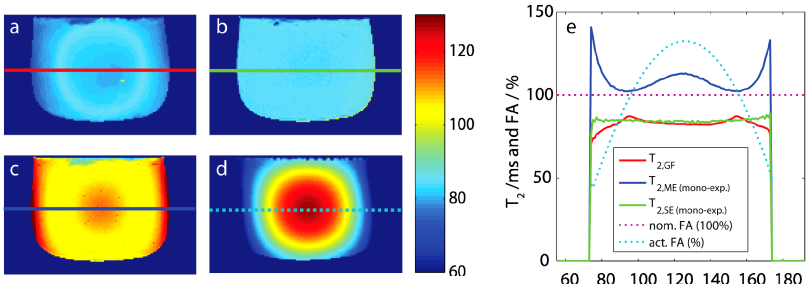

Fig. 1: T_2 maps created with different fits (in ms) (a) GF, (b) SE mono-exp., (c) MSE mono-exp. (d) corresponding B_1+ map (in % of nominal FA) (e) T2 profiles

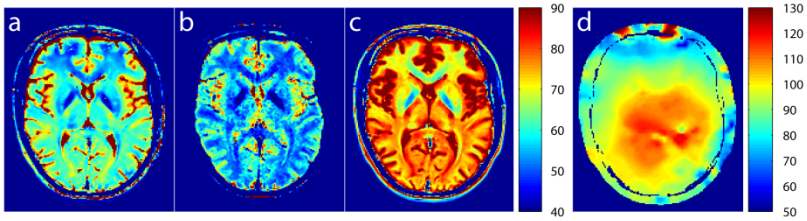

Fig. 2: T_2 maps of the brain (a) GF fit, (b) SE mono-exp. fit, (c) ME mono-exp. fit in ms (d) corresponding B_1+ map (in % of nom. FA)

Discussion and Conclusion: As T_2 is frequently used in quantitative studies the reduction of systematic errors is very important. With phase compensated MSE sequences T_2 tends to be overestimated. With the proposed method it is possible to minimize T_1 mixing and get T_2 values similarly as with multiple SE measurements. This robust algorithm can also be used to improve the analysis of existing measurements as the B_1+ maps are not mandatory and T_1 values from the literature are sufficient for substantial improvement.

References: [1] Poon CS et al. JMRI 1992;2:541, [2] Levitt MH et al. JMR 1981;43:65, [3] Zur Y et al. JMR 1987;71:212, [4] Pell GS et al. JMRI 2006;23:248, [5] Lukzen NN et al. JMR 2007;185:71, [6] Sussman MS et al. MRM 2010;64:536.