Fast Quantitative T2 Mapping using Simultaneous-Multi-Slice and Model-Based Reconstruction

Tom Hilbert[1,2,3], Jennifer Schulz[4], Lauren J. Bains[4], José P. Marques[4], Reto Meuli[2], Jean-Philippe Thiran[2,3], Gunnar Krueger[2,3,5], David G. Norris[4], Tobias Kober[1,2,3]

1 - Advanced Clinical Imaging Technology (HC CMEA SUI DI BM PI), Siemens Healthcare AG, Lausanne, Switzerland
2 - Department of Radiology, University Hospital (CHUV), Lausanne, Switzerland
3 - LTS5, École Polytechnique Fédérale de Lausanne, Lausanne, Switzerland
4 – Radboud University Nijmegen, Donders Institute for Brain, Cognition and Behaviour, Nijmegen, Netherlands.
5 - Siemens Medical Solutions USA, Inc., Boston, MA, USA

INTRODUCTION:

Despite providing better comparability, the long acquisition times of classical quantitative magnetic resonance imaging sequences have impeded their widespread application in clinical routine and research. Accelerating these acquisitions is important for their broader acceptance. Here, we investigate the combination of two techniques to accelerate T2 mapping: Simultaneous Multi Slice (SMS) together with a model-based undersampling approach. SMS speeds up acquisitions by simultaneously exciting several slices, subsequently disentangling the superimposed signals by using parallel imaging techniques[1,5,6]. We use the PINS ("Power independent of number of slices")[2] SMS pulses due to their advantageous specific absorption rate (SAR) behaviour. The application of MARTINI ("Model-based Accelerated RelaxomeTry by Iterative Nonlinear Inversion")[3] allows for k-space undersampling, which further reduces the acquisition time. Using this combination, our technique enables the sampling of high-resolution whole-brain T2 maps in less than 3 minutes.

MATERIALS & METHODS:

A multi-echo spin-echo sequence (MESE) was modified to acquire SMS data. Since PINS pulses show "excitation aliasing", i.e. infinitely repeat in slice direction, the excitation of the MESE sequence was performed using a multiband SMS pulse[4]. The refocusing pulses were however replaced by PINS pulses, which reduced the SAR load. Gradient blips were added in order to shift slices depending on their z-position ("blipped CAIPI")[5], improving the subsequent parallel imaging reconstruction.

After obtaining written consent from two healthy volunteers, fully sampled k-space data were acquired using the described prototype sequence with four simultaneous slices (ΔTE/TR/TA 12ms/4s/13:37min, resolution $0.7\times0.7\times3mm^3$, slice gap 0.3mm, 40 slices, 33mm distance between simultaneous slices, fat-saturation) on a 3T scanner (MAGNETOM Skyra, Siemens Healthcare, Germany) using a 64-channel head/neck coil. Note that the long TR was chosen to avoid stimulated-echo effects. The obtained data were first artificially undersampled (5x acceleration) using the MARTINI block-sampling scheme[3]. The superimposed and undersampled k-spaces of the different slices were separated with Split-Slice-GRAPPA[4], yielding undersampled k-space datasets for each single slice. Subsequently, MARTINI[3] was applied on the k-space of each slice, thus obtaining quantitative M_0/T2 maps. A flowchart of the algorithm is shown in Fig. 1. As reference, a standard MESE sequence (same parameter as prototype sequence but only 10 slices, TA=13:37min) was acquired. Using the MESE data, a non-linear fitting was conducted to obtain T2 values. In an additional experiment, a multi-purpose phantom (five compartments with different concentrations of MnCl2·4H2O, Siemens E-38-19-195-K2130) was scanned with both the prototype sequence and the reference MESE sequence using the same sequence parameters as in the in-vivo experiments.

RESULTS & DISCUSSION:

The phantom T2 values obtained by PINS-MARTINI are in good agreement with the reference MESE acquisition (c.f. Table 1), except for the compartment with very short T2 (~19ms). The observed overestimation is probably due to a long ΔTE=12ms, rendering the ill-posed fit of such short T2 values even more sensitive to noise. The sequence protocol could be optimized for shorter T2 values by shortening the ΔTE; however, we target T2 values of white and grey matter, which are typically in the range of 70ms to 120ms.

A juxtaposition of T2 maps estimated using the reference method, fully sampled and 5-fold undersampled PINS-MARTINI is shown in *Fig. 2*. The T2 map of PINS-MARTINI resembles the reference. However, an increase in noise is visible which can be explained by the 5-fold undersampling and noise amplifications caused by the slice-GRAPPA reconstruction. It should be noted, however, that the increase in noise is acceptable considering the high acceleration (13:37min, 10 slices versus 2:42min, 40 slices).

Fig. 3 shows four M_0 and T2 maps that were simultaneously acquired using 4x5-fold accelerated PINS-MARTINI, corresponding to an acquisition time of 2:42min (note that undersampling was still artificial). No inter-slice leakage or undersampling artifacts are visible within the brain.

Using a PINS instead of multi-band pulse has the advantage of decreasing the power deposition of the sequence, facilitating the acquisition of whole brain datasets within the SAR limits. For example, an acquisition with the proposed sequence parameters reaches ~50% of the SAR limit whereas it may be exceeded using a standard MESE sequence to acquire the same amount of slices. Furthermore, PINS pulses do not cause magnetization-transfer, thus provide a better SNR and the M_0 map becomes more proton density weighted.

CONCLUSION:

Using the complementary acceleration techniques PINS and MARTINI, high-resolution (0.7x0.7x3mm³) whole-brain (40 slices) T2 mapping can be performed in clinically acceptable acquisition times of less than 3 minutes. In the value range expected in brain tissue, the obtained T2s are in good agreement with a gold-standard reference fitting.

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| Concentration	T2 MESE	T2 PINS-MARTINI
10 mg	176.7+-2.7 ms	175.7+-3.6 ms
20 mg	95.8+-2.0 ms	96.4+-2.5 ms
40 mg	48.3+-1.5 ms	50.1+-2.4 ms
70 mg	27.0+-1.3 ms	31.0+-2.2 ms
120 mg	18.5+-1.5 ms	42.3+-3.5 ms

Table 1: *T2 values estimated using a multi-echo spin-echo (MESE) and the proposed method (PINS-MARTINI) within the compartments of a multi-purpose phantom with different concentrations of MnCl2·4H2O (in mg per 1000g distilled water).*
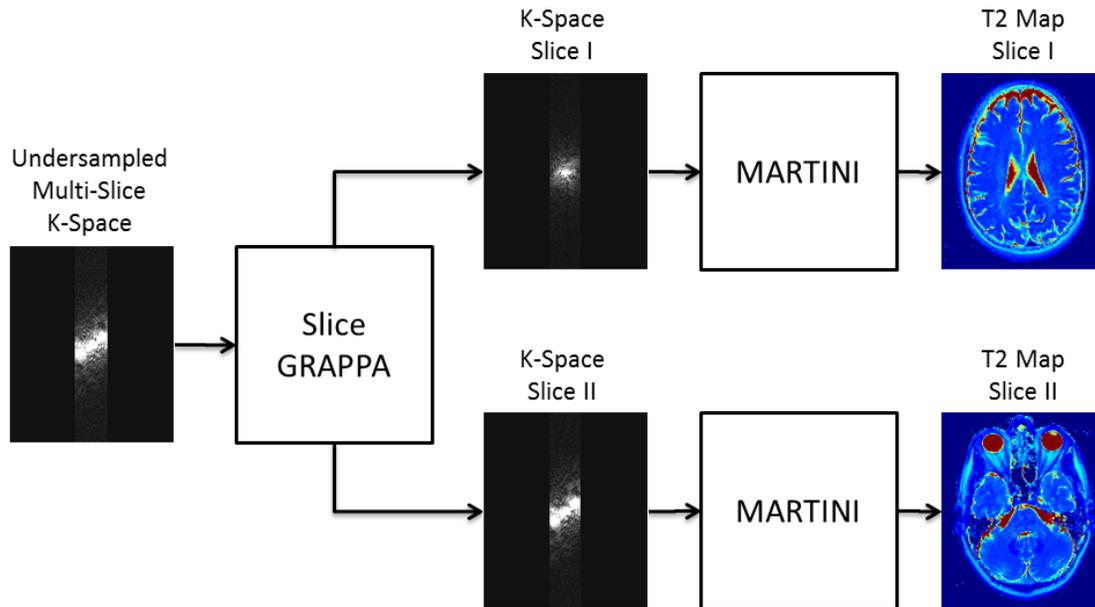
Fig. 1: *Workflow of the proposed algorithm for fast quantitative T2 mapping using simultaneous-multi-slice and model-based reconstruction.*
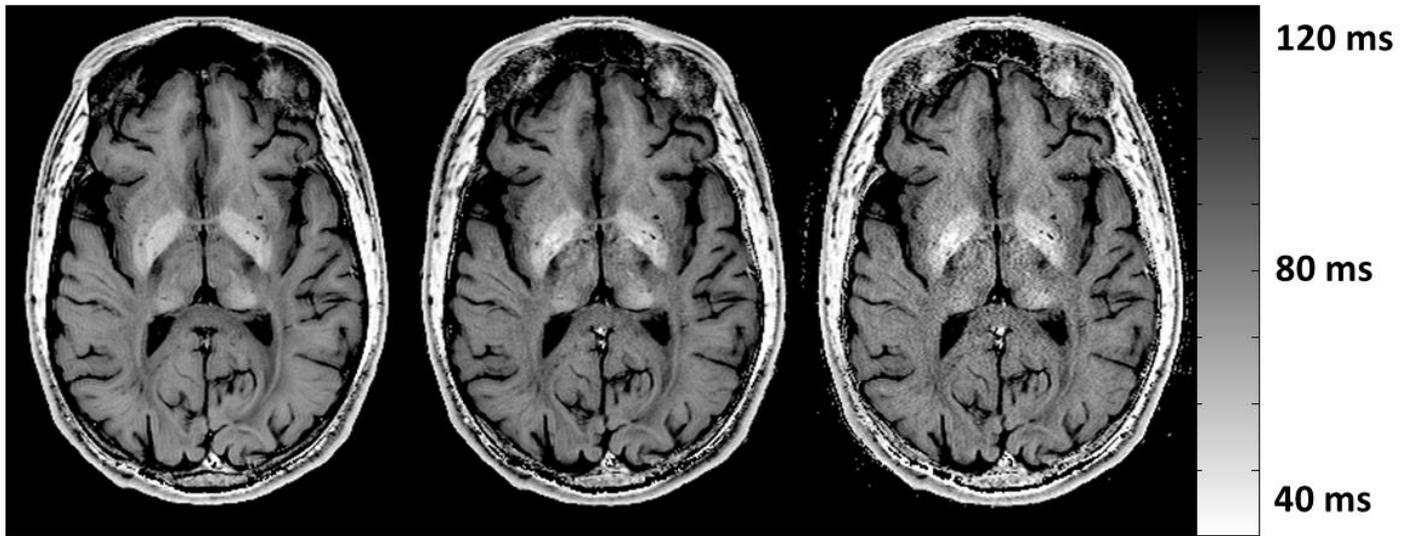
Fig. 2: In-vivo T2 values estimated using a fully sampled multi-echo spin-echo sequence (left, TA 13:37min, 10 slices) and the proposed method with a 4x multi-slice acquisition fully sampled (middle, TA 13:37min, 10 slices) and 5x artificial undersampling (right, TA 2:42min, 40 slices).
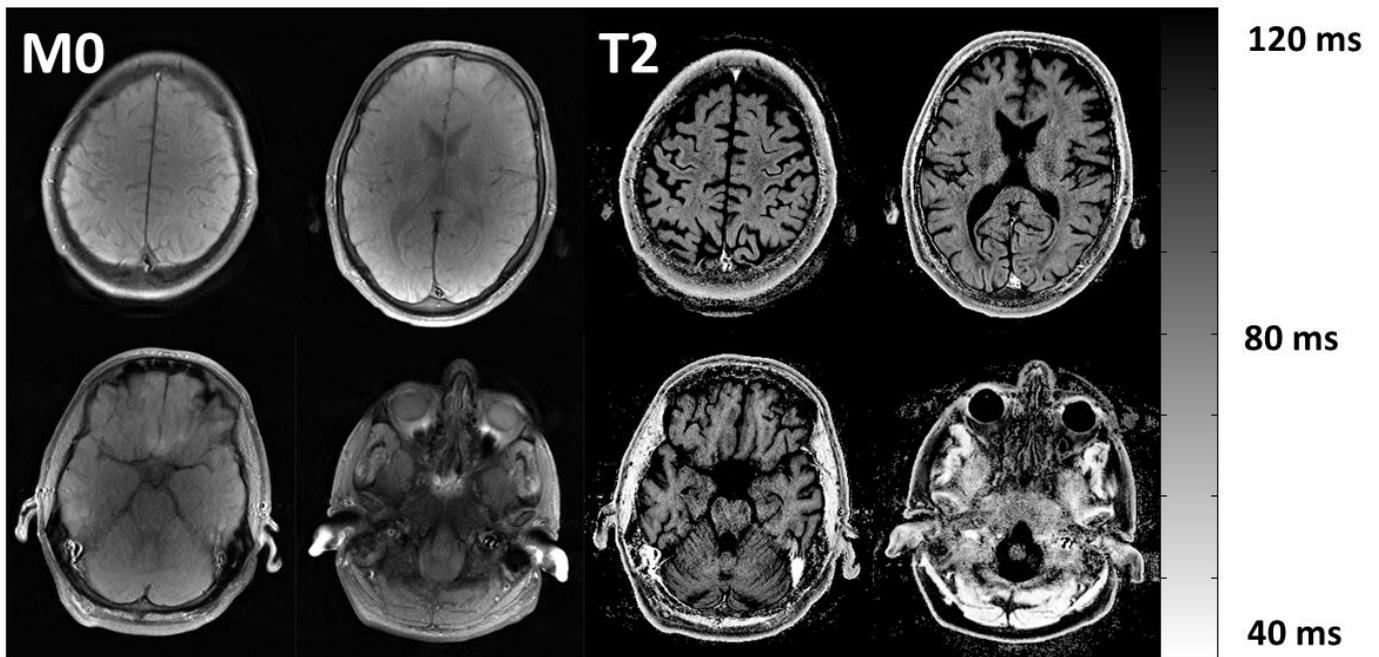
Fig. 3: The reconstructed M0 and T2 maps of four slices that were acquired simultaneously and estimated with a model-based iterative reconstruction on a 5x undersampled k-space.

Synopsis: Long acquisition times of quantitative magnetic resonance imaging (qMRI) are one obstacle that prevents qMRI to be used in clinical routine. Acceleration methods, such as simultaneous-multi-slice and model-based iterative reconstruction proved in the past to allow high acceleration factors in MRI. Here we suggest combining these two methods to allow fast quantitative T2 mapping, yielding a high-resolution (0.7 x 0.7 x 3 mm³) whole brain (40 slices) acquisition within a clinically acceptable acquisition time of less than 3 minutes. T2 values of the proposed method are similar to the values of the standard method as it is shown on phantom experiments.