Buy One, Get Two for Free: Simultaneous Knee T2 Mapping and Morphological Analysis On Synthetic Images Using GRAPPATINI

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Synopsis (100 words)

A fast quantitative T2 mapping technique that additionally provides synthetic images for morphological assessment was validated by two experienced radiologists regarding (1) the T2 values through a phantom experiment and (2) the image quality through a quantitative and qualitative assessment for the knee joint in five healthy volunteers.

Introduction:

Today, intermediate-weighted (IW) and T2-weighted (T2w) Turbo Spin Echo (TSE) sequences with fat suppression are most commonly used to clinically assess morphological abnormalities of joint structures[1]. In addition, quantitative analysis of the musculoskeletal system using MR relaxometry techniques such as T2 mapping has gained interest in recent years. This is in particular the case for imaging of osteoarthritis, since T2 values can be used as a non-invasive biomarker of early degenerative disease of cartilage and meniscus[2-4]. The acquisition of both morphological and quantitative sequences is however time consuming. We suggest using a fast quantitative T2 mapping technique that allows the generation of synthetic images with different TEs, allowing a significant decrease in acquisition time while preserving image quality in comparison to the consecutive acquisition of morphological and quantitative sequences.

Methods:

A multi-echo spin-echo (MESE) sequence was modified in order to acquire undersampled k-spaces. Generalized autocalibrating partially parallel acquisition (GRAPPA)[5] and Model-based Accelerated Relaxometry by Iterative Non-linear Inversion(MARTINI)[6] can be subsequently applied to estimate the transverse relaxation T2 and the equilibrium magnetization M_0, a method termed GRAPPATINI[7]. Synthetic TSE images with any T2-weighting can then be generated using the M_0/T2 maps in the forward signal model.

Phantom experiments were performed to validate the T2 estimation. To that end, the prototype GRAPPATINI and product MESE sequences were used to estimate the T2 values within tubes with different concentrations of Gadolinium and Agar using the same acquisition parameters as in the in-vivo experiments. A single-slice single-spin-echo product sequence was used to achieve reference T2 values using a standard log-linear fit onto various fully sampled acquisitions with different TEs=12,24,36,60,100ms.

Subsequently, the prototype GRAPPATINI sequence was used to estimate T2 and M_0 maps of the knee joint at 3T (MAGNETOM Skyra, Siemens Healthcare, Germany) using a 15-channel knee coil in five healthy volunteers (3 males, age 30.2±3.3 years). Additional synthetic

contrasts with TE=34ms and TE=80ms were generated on the scanner. For comparison, standard IW (TE=34ms) and T2w (TE=80ms) morphological TSE images were acquired. The detailed acquisition parameters are listed in Table 1.
The synthetic morphological images were validated quantitatively and qualitatively in comparison to the conventional TSE images.
ROIs of at least 15mm^2 were placed on fluid, muscle, meniscus and cartilage and copy-pasted between comparative images. SNR and CNR (cartilage/fluid and meniscus/fluid) were calculated.
Qualitative analysis was performed by two radiologists in consensus blinded to the employed sequence by comparing the synthetic images and the corresponding TSE side-by-side in random order. A five-grade scale was used for the comparison (-2: first image significantly worse than second, -1: moderately worse, 0: no difference, +1: moderately better, +2: significantly better). Each of the following anatomical structures was assessed: cartilage, menisci, cruciate ligaments, bone marrow, muscle, joint fluid, quadricipital and patellar tendons. Furthermore, image contrast, noise, artifacts, and global diagnostic value were also compared.

Results and Discussion:
Error! Reference source not found. shows the T2 values of the phantom experiment. T2 values found by GRAPPATINI are slightly overestimated in comparison to the reference method, which is most likely due to stimulated echoes, a typical problem for T2 mapping using MESE sequences. The fully-sampled MESE sequence experiences a stronger overestimation which can be explained by the much shorter TR (1.6s versus 4.88s) causing an even stronger stimulated-echo effect due to increased T1 influences in the signal decay[8].
The quantitative analysis showed similar SNR and no statistically significant difference between the synthetic and conventional sequences (average SNR=9.9 for both sequences, p=0.99). CNR values were not statistically different between the two sequences (cartilage/fluid: 6.2 vs. 6.6, p=0.62; meniscus/fluid: 11.3 vs. 11.6, p=0.81).
The qualitative analysis showed no difference in global image quality (cf. Fig 2) or of any of the anatomical structures that were evaluated (average score of 0, 95%CI=[0; 0.4]). Artefact scores were slightly higher for the synthetic sequences (average of -0.1, 95%CI=[-0.002;-0.6]), while visual noise and contrast were slightly better for the synthetic sequences (average score of 0.1, 95%CI=[0.002;0.6]).

Conclusions:
The GRAPPATINI sequence provides accurate T2 values, as well as synthetic sequences that are quantitatively and qualitatively similar to conventional TSE sequences. Using this technique, T2 maps, IW and T2w sequences can all be obtained in 6.22min compared to 12.13min, corresponding to the sum of the acquisition times obtained with the standard technique.

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Sequence	Resolution	Number of Slices	TR	TE	Fat Suppression	TA
GRAPPATINI	0.4x0.4x3mm^3	36	4880 ms	34 / 80 ms	On	6:22 min
					Total Acq. Time:	**6:22 min**
IW - TSE	0.4x0.4x3mm^3	36	3790 ms	34 ms	On	2:52 min
T2w - TSE	0.4x0.4x3mm^3	36	3790 ms	80 ms	On	2:52 min
MESE	0.5x0.5x3mm^3	36	1630 ms	ΔTE 13 ms	Off	7:09 min
					Total Acq. Time:	**12:13 min**

Table. 1: *Acquisition parameters of the GRAPPATINI sequence in comparison to the acquisition parameters of subsequently acquiring the different contrasts.*

Solution	T2 SE	T2 GRAPPATINI	T2 MESE
Agar 2%	68.9+-1.2	73.2+-2.5	77.3+-3.4
Agar 3%	66.3+-1.1	70.1+-2.1	72.4+-2.8
Agar 4%	54.8+-0.6	58.2+-1.7	60.4+-2.3
Agar 5%	42.6+-0.7	45.9+-1.4	48.5+-2.3
Gd 0.25%	37.1+-0.6	39.0+-0.7	41.3+-1.1
Gd 0.5%	37.5+-0.5	39.8+-0.7	40.6+-0.7
Gd 1%	33.0+-0.2	34.5+-0.6	35.5+-0.6
Gd 5%	26.4+-0.3	27.5+-0.5	28.6+-0.7

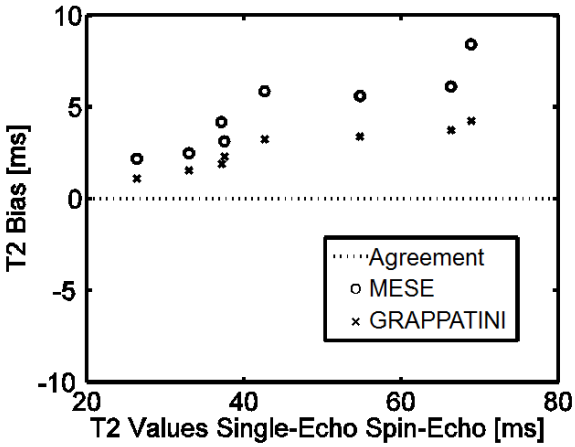

Fig. 1: *Estimated T2 values using different methods within tubes containing different concentration of Gadolinium (Gd) and Agar gel showed in a table and in an agreement plot.*

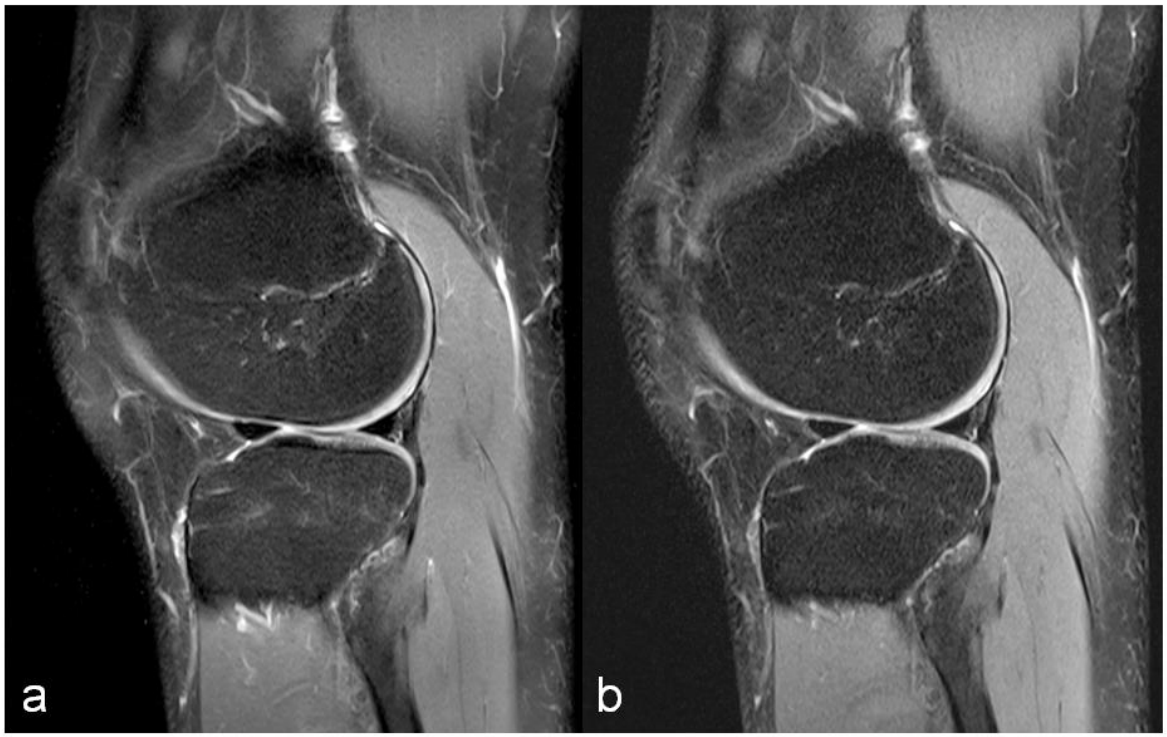

Fig. 2: *Synthetic image (TE=34ms) derived from GRAPPATINI sequence with fat suppression (a) compared to conventional fat-suppressed TSE IW sequence (TE=34ms)(b). No significant difference is seen in terms of subjective image quality, or for the depiction of anatomical structures.*