Evaluation of a fast T_2 Mapping Method in the Brain

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INTRODUCTION - T_2 measurements provide important information about the mobility and chemical environment of water in the tissue of interest [1-5]. The most frequent method for accurate T_2 quantification uses multi-echo spin-echo (MESE) incorporating multiple refocusing pulses in each repetition time following the CPMG sequence [6]. To cover a wide range of T_2 values, the number of spin echoes and corresponding RF pulses needs to be relatively large, resulting in increased TR, long scan durations, and a high SAR. Recently, a fast T_2 mapping method, reducing the total number of phase encoding steps of a MESE sequence without sacrificing spatial resolution nor the dynamic range of T_2 values, was proposed and evaluated in simulations and pre-clinical experiments [7, 8]. In this work, the accuracy of this acceleration technique for T_2 mapping in the human brain was assessed in a larger group of volunteers.

METHODS - In the proposed fast T_2 mapping method, *k*-space is under-sampled with an alternating pattern, as illustrated in Fig. 1 for a two-fold acceleration. For calibration, a number of consecutive *k*-space lines are acquired without under-sampling. Each missing sample in *k*-space is then reconstructed on the basis of a linear combination of its neighbors in the *kt*-space. In this manner, images free of under-sampling artifacts are reconstructed at each echo time [7].

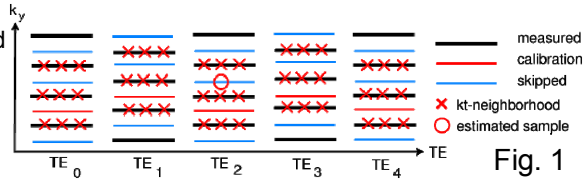
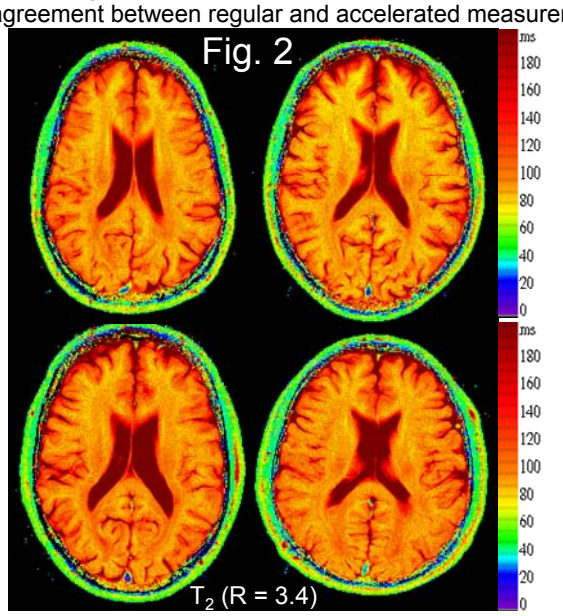
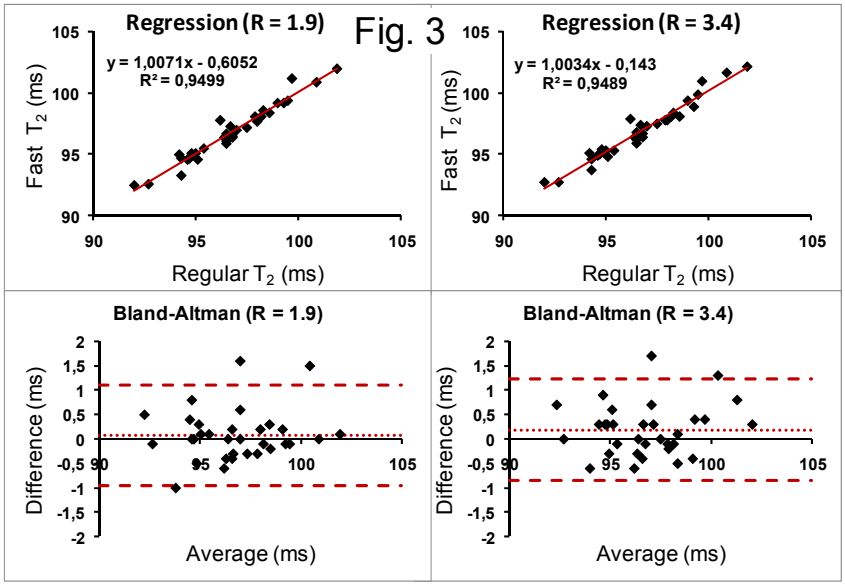


Fig. 1

Brain imaging was performed on a 1.5T MR scanner (Achieva, Philips Healthcare, The Netherlands) in a group of 8 healthy volunteers (mean age: 37.6±3.6 years). The applied protocol consisted of a regular 2D MESE sequence, followed by two fast T_2 mapping sequences with net acceleration factors of R = 1.9 and R = 3.4. The acquisition parameters were: TE = 16, 24, 32, …, 264 ms, TR = 1000 ms, FOV = 220 × 220 x 8 mm^3, data matrix = 256 × 256, transverse orientation. To minimize blood flow artifacts originating from the superior sagittal sinus, a saturation slab was placed above the excited slice, and the phase-encoding direction was chosen left-to-right. After reconstruction, T_2 maps were computed for each data set by means of a non-linear least-squares fitting algorithm assuming mono-exponential T2 decay. Mean T_2 values were computed in four ROIs placed manually around the ventricles. Correlation between the T_2 values obtained with and without acceleration was assessed; regression and Bland-Altman analysis was performed.

RESULTS - Fig. 2 shows four examples of T_2 maps acquired with an acceleration factor of R = 3.4, demonstrating consistent suppression of fold-over artifacts after reconstruction of the under-sampled data. Fig. 3 summarizes the statistical comparison between regular and accelerated mapping methods. For both acceleration factors, the Pearson correlation coefficient is above 0.97, the slopes of the regression curves are close to 1, and the intercept coefficients are almost zero. The Bland-Altman plots confirm the good agreement between regular and accelerated measurements, with a T_2 error standard deviation of 0.5 ms and a negligible positive bias.





DISCUSSION and CONCLUSIONS – Clinical routine application of quantitative relaxometry measurements requires fast and reproducible acquisition protocols. The proposed fast T_2 mapping method yields a significant reduction in acquisition time and SAR by exploiting the redundancy of the MR signal in *kt*-space. This method was here evaluated in the brain in a group of volunteers, where comparison is not hampered by motion. In this setting, it has shown consistent accurate quantification of T_2, for acceleration factors up to 3.4. Its application to T_2 quantification in more challenging organs, such as the prostate, is currently undertaken in clinical research.

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