Improved Accuracy of T1 Mapping Reconstruction Using a Novel Bloch Equation-based Fitting With Graphic Processing Unit Implementation

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Target Audience

Scientists and clinicians who are interested in myocardial tissue characterization.

Purpose/Introduction

Native myocardial T_1 sequences generally use a balanced steady state free precession (b-SSFP) readout[1]. However, the b-SSFP signal is sensitive to many factors including B_0/B_1 field inhomogeneities, T_2, and magnetization transfer[1]. We recently developed the slice-interleaved T_1 (STONE) sequence[2] which we extended to spoiled gradient echo (GRE) imaging. This sequence enables simultaneous acquisition of 5 slices under free breathing conditions. The GRE readout removes the T_2 dependence and the magnetization transfer sensitivity of T_1 estimates, and reduces the overall sensitivity to B_0 field inhomogeneities. Although both 2-point fit model and 3-point fit model can be used for T_1 reconstruction, the 2-point fit model provides improved robustness against artefact and provides higher T_1 precision. However, this model is associated with reduced accuracy induced by its sensitivity to imperfect inversion efficiency and signal disturbances caused by the imaging pulses[1]. In this study, we sought to develop and evaluate an alternative fitting approach using the simulated signal of the entire pulse sequence using Bloch equations as fitting model.

Materials and Methods

T_1 Mapping Sequence: 5 slices are simultaneously acquired under free breathing conditions with prospective slice tracking. Each slice is first acquired without any magnetization preparation pulse to sample the fully recovered longitudinal magnetization. Subsequently, an inversion recovery (IR) experiment is performed where the 5 slices are acquired over the next 5 heartbeats using a slice interleaved ordering. This IR experiment is repeated 5 times using different slice ordering to sample the signal at TI, TI + 1 RR, TI + 2 RR, TI + 3 RR, TI + 4 RR (RR: time between two R-waves, TI: inversion time). This block of 5 IR experiments is finally repeated using a second TI value.

T_1 Map Reconstruction: The magnetization signal is simulated for a range of T_1 ([0 - 2000] ms) using the Bloch equations and the employed sequence design/parameters and actual imaging timing. The fitting is then performed on a pixel basis by maximization of the correlation coefficient between the simulated and the measured signal. Since this operation is computationally intensive and independent for each pixel, this step is offloaded to a graphic processing unit (GPU) where the reconstruction of each pixel is assigned to one thread. A multi-fitting approach is used to ensure correct signal polarity restoration.

Experimental Validation: All data were acquired on a 1.5 T Phillips scanner. The proposed reconstruction was compared to the 2-point fit model in term of accuracy and precision using numerical simulations, phantom experiments, and in-vivo using the slice interleaved T_1 sequence with GRE imaging (TR/TE/α=4.3/2.1ms/10°, FOV=280×272 mm^2, voxel size=2×2 mm^2, slice thickness=8 mm, number of phase-encoding lines=43, linear ordering, 10 linear ramp-up pulses, SENSE factor=2.5, half Fourier=0.75, bandwidth=382Hz/pixel, rest cycle length=3s). Monte-Carlo simulations were used to study the influence of imaging flip angle and rest cycle length for a range of T_1 ([200-1600] ms). Phantom experiments were performed using 14 vials ($NiCl_2$ doped agarose) with different T_1 values and 10 scan repetitions. In-vivo imaging was performed in nine healthy subjects (37±22 years, 3 males).

Data Analysis: In phantom, accuracy was measured as the average (over the 10 repetitions) of the difference between SE T_1 and estimated T_1 in each vial. Precision was measured as the average (over the 10 repetition) of the standard deviation of T_1 estimates in each vial. Measurements and spatial variability of in-vivo native T_1 mapping are reported for each subject in average over the myocardium in the 3 mid-ventricular slices.

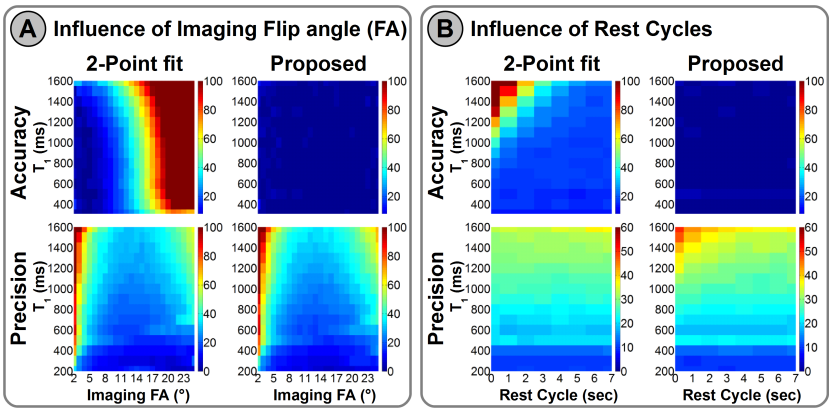

Figure 1. *Numerical simulations obtained for different T_1 times with various imaging flip angle (a) and rest cycle length (b). The proposed technique provided overall improved accuracy and similar precision than the 2-point model fit.*

Results

The propose technique provides higher T_1 accuracy than the 2-point fit model and is independent from the choice of imaging flip angle and rest cycle length. Furthermore, the technique can simultaneously improve the precision over the 2-point model fit by optimal selection of imaging parameters (in the current sequence design using an imaging flip angle (~15°)). In Phantom, the proposed approach provided higher accuracy (15±12ms vs. 29±19ms, p<0.001) and similar precision (5.8±1.9ms vs. 5.7±1.9ms) than the 2-point fit model. Higher in-vivo native myocardial T_1 times (1126±26ms vs. 1092±24ms, p<0.001), and similar spatial variability (65±11ms vs. 62±10ms) were achieved using the proposed approach.

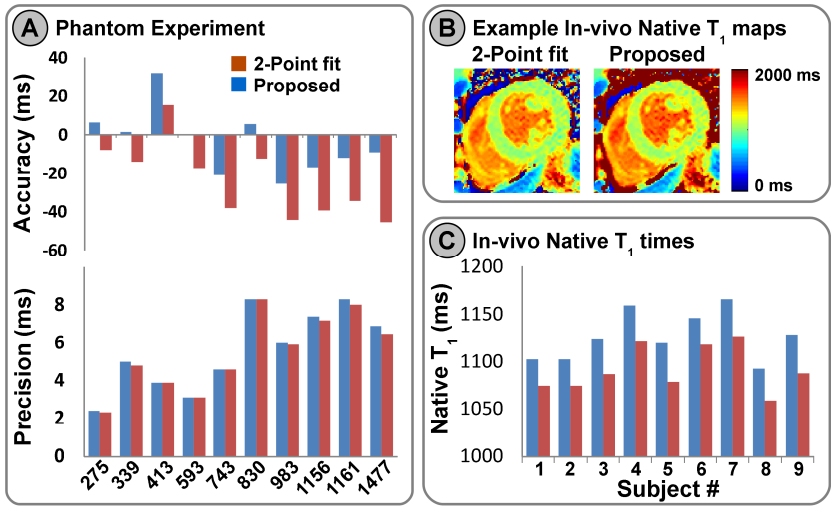

Figure 2. *Phantom experiments (a) example of native T_1 maps (b) and in-vivo analysis (c). The proposed sequence provided higher accuracy and similar precision than the 2-point fit model.*

Conclusions

The proposed approach provides higher accuracy than the conventional 2-point fit model and is independent from imaging parameters such as imaging flip angle and rest cycle length. Furthermore, this technique shows promise to simultaneously improve the precision over the 2-point fit model by flexible selection of imaging parameters.

Acknowledgements

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References

[1] Kellman, JCMR, 2014 [2] Weingartner, MRM, 2014