High Resolution 2D ECG-Segmented Slice Interleaved T_1 mapping (STONE) with Reduced Partial Voluming

Jihye Jang[1,2], Tamer Basha[1], Sophie Berg[1], Cory Tschabrunn[1], Elad Anter[1], Sébastien Roujol[1], and Reza Nezafat[1]

[1]*Department of Medicine, Beth Israel Deaconess Medical Center and Harvard Medical School, Boston, MA, United States,* [2]*Computer Aided Medical Procedures, Technische Universität München, Munich, Bayern, Germany*

Introduction/ Purpose: Myocardial T_1 mapping is commonly performed by pixel-wise curve fitting of single-shot images collected during diastolic rest period of cardiac cycle. Single-shot imaging often has limited spatial resolution, requires high acceleration factor and prone to cardiac motion that occurs over >200ms acquisition window during cardiac cycle. This results in partial voluming error and reduced measurement precision in T_1 mapping. We recently developed a free-breathing slice-interleaved T_1 (STONE) [1] mapping sequence which removes the breath-holding constrain and allows efficient simultaneous imaging of multiple slices. In this study, we sought to further extend STONE imaging sequence to allow ECG segmented multi-shot data acquisition to improve spatial resolution. Phantom, ex-vivo and in-vivo experiments are performed to evaluate the proposed sequence.

Methods

Imaging Sequence: **Fig. 1** shows the schematic of the proposed multi-shot STONE sequence, which consists of multiple inversion recovery (IR) prepared imaging blocks with segmented k-space data acquisition. To sample the infinity point of the longitudinal magnetization recovery curve, each slice is first acquired without any inversion pulse. In the following IR blocks, each slice is selectively excited after a single non-selective inversion pulse, and images are acquired over multiple cycles to acquire all k-space segments. This acquisition block is then repeated with different order of slices to sample the signal of longitudinal recovery curve at TI, TI + 1 RR, TI + 2 RR, TI + 3 RR, TI + 4 RR (TI: inversion time, RR: duration of one heart-beat), and finally repeated once more with different TI.

Experimental Validation: The proposed imaging sequence was implemented on a 1.5T Philips Achieva scanner. A phantom experiment was performed using 14 vials of $NiCl_2$ doped agarose phantom with different T_1/ T_2 times to study accuracy, precision, and reproducibility of the segmented STONE T_1 mapping sequence. Images were acquired five times repeatedly using the proposed multi-shot STONE (segmented bSSFP imaging readout, TR/TE=3/1.5ms, flip angle=35, FOV=280x322mm^2, voxel size=1.5x1.5mm^2, slice thickness=10mm, TFE shots=3, TFE factor=28, acquisition window=84ms, linear k-space ordering, 10 linear ramp-up pulses, SENSE factor=2) and compared to a single-shot STONE and a 5-(3)-3 scheme MOLLI [2] which were acquired using similar imaging parameters. Accuracy was defined as the difference between the mean T_1 and the averaged reference T_1 (spin echo) in each vial. Precision was defined as the averaged standard deviation of T_1 in each vial. Reproducibility was defined as the standard deviation of T_1 over five repetitions. Statistical significances between sequences were assessed using a Wilcoxon signed rank test. To demonstrate the feasibility of the proposed sequence, high-resolution T_1 maps were acquired on ex-vivo heart of an infarcted swine model using the multi-shot STONE sequence (segmented bSSFP imaging readout, TR/TE=6/3ms, flip angle=35, FOV=160x160mm^2, voxel size=0.5x0.5mm^2, slice thickness=10, TFE shots=4, TFE factor=35, acquisition window=209.2ms, linear k-space ordering, 10 linear ramp-up pulses, SENSE factor=2) and compared to the high resolution T_1 weighted images (segmented bSSFP imaging readout, TR/TE=6/3ms, flip angle=35, FOV=200x200mm^2, voxel size=1x1x0.5mm^2, TFE shots=904, TFE factor=25, acquisition window=152.8ms, low-high k-space ordering, 5 linear ramp-up pulses). In-vivo measurement was performed in a healthy subject using the multi-shot STONE sequence (segmented bSSFP imaging readout, TR/TE=3.1/1.6ms, flip angle=35, FOV=280x322mm^2, voxel size=1.5x1.5 mm^2, slice thickness=10mm, TFE shots=3, TFE factor=28, acquisition window=88ms, linear k-space ordering, 10 linear ramp-up pulses, SENSE factor=2) and compared to a single-shot STONE (single-shot bSSFP imaging readout, TR/TE=2.9/1.4ms, flip angle=35, FOV=360x352mm^2, voxel size=2.1x2.1mm^2, slice thickness=8 mm, TFE factor=86, acquisition window=247ms, linear k-space ordering, 10 linear ramp-up pulses, SENSE factor=2). Prospective slice tracking was performed and combined with retrospective in-plane image registration [3] to compensate for respiratory motion. T_1 maps were reconstructed by voxel-wise curve-fitting of the signal with a two-parameter fit model.

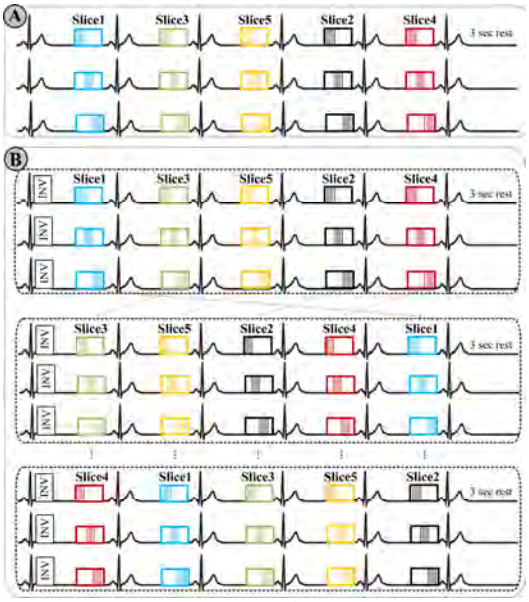

Figure 1. *Sequence scheme of the proposed multi-shot STONE sequence. (a) Each slice is first acquired without any magnetization preparation pulse (b) Each IR block consisted of non-selective inversion pulse and slice-selective excitation is repeated for all segments and the order of slices is shifted cycled-through.*

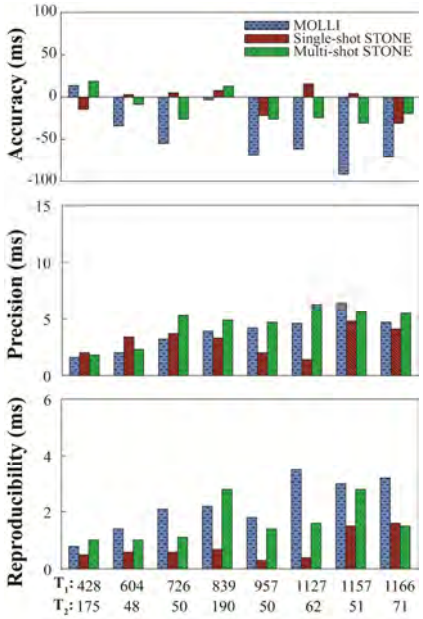

Figure 2. *Accuracy, precision, reproducibility of the multi-shot STONE compared to a single-shot STONE and MOLLI in the phantom experiment.*

Results: Phantom results show that multi-shot STONE has similar accuracy, precision, and reproducibility ($p>0.05$) compared to single-shot STONE, but, higher accuracy ($p<0.001$) and reproducibility ($p=0.005$) with lower precision ($p=0.034$) compared to MOLLI (**Fig. 2**). The high spatial resolution of the proposed segmented data acquisition allows detection of the myocardial scar in the post-Gd T_1 map similar to high resolution T_1 weighted images (**Fig. 3**). **Fig. 4** shows 3 mid-ventricular slices from multi-slice in-vivo native T_1 maps acquired using the multi-shot and single-shot STONE.

Conclusion: The proposed segmented data acquisition for myocardial T_1 mapping allows higher in-plane spatial resolution and reduces data acquisition window in each cardiac cycle which potentially reduces the partial voluming error in myocardial T_1 measurement.

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References: [1]Weingärtner,MRM,2014, [2]Messroghli,MRM,2004, [3]Roujol,MRM,2014.

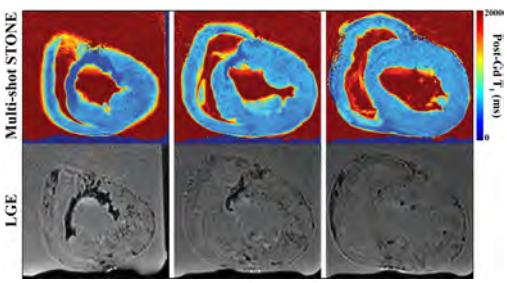

Figure 3. *Ex-vivo heart of an infarcted swine model imaged using the multi-shot STONE compared to the high resolution T_1 weighted images.*

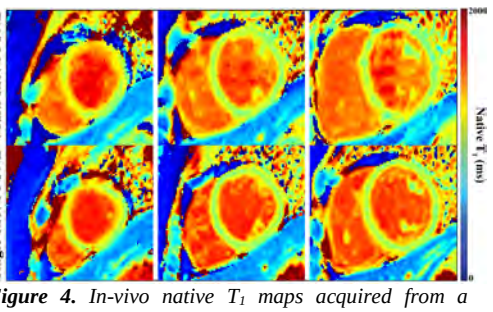

Figure 4. *In-vivo native T_1 maps acquired from a healthy subject using the multi-shot STONE compared to a single-shot STONE.*