Instantaneous Signal Loss simulation (InSiL) – An improved algorithm for myocardial T1 mapping using the MOLLI sequence

Jiaxin Shao[1], Yutaka Natsuaki[2], Bruce Spottiswoode[2], Kim-Lien Nguyen[1,3], and Peng Hu[1,4]

[1]*Department of Radiological Sciences, David Geffen School of Medicine, University of California, Los Angeles, CA, United States,* [2]*Siemens Healthcare USA, Inc., IL, United States,* [3]*Division of Cardiology, David Geffen School of Medicine, University of California, Los Angeles, CA, United States,* [4]*Biomedical Physics Inter-Departmental Graduate Program, University of California, Los Angeles, CA, United States*

Target audience: Scientists and clinicians who are interested in myocardial T1 mapping.

Purpose: We propose an alternative T1 map calculation method, Instantaneous Signal Loss simulation (InSiL), based on the standard MOLLI T1 mapping sequence. Myocardial T1 mapping is an emerging technique that assesses diffuse myocardial scar (1-2). Currently, the modified Look-Locker inversion-recovery (MOLLI) sequence has been widely used for T1 mapping. MOLLI uses 3-parameter exponential fitting with Lock-Locker correction for T1 estimation (3), and is known to underestimate myocardial T1 values, especially at longer T1s and/or at higher heart-rate (4-5). We hypothesize that InSiL will improve T1 estimation accuracy and reduce the dependency of T1 estimation on heart rate compared with the MOLLI standard method.

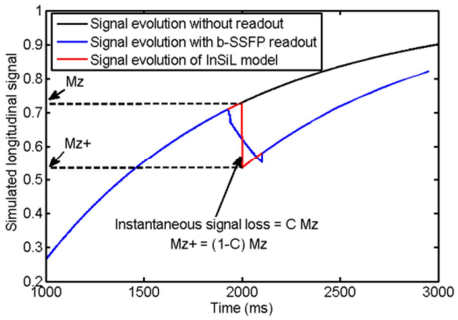

Fig.1. Illustration of the InSiL model. The longitudinal signal perturbation by each single-shot bSSFP imaging is simulated as instantaneous signal loss parameterized by factor C.

Methods: InSiL simulates the signal evolution of the MOLLI sequence for T1 calculation. The effect of longitudinal signal perturbation due to each single-shot imaging readout is parameterized as an instantaneous signal loss in longitudinal magnetization during the central k-space line by an unknown factor of C ($0 \le C \le 1$), as illustrated in Fig.1. The inversion pulse is considered to be applied instantaneously at the end of the inversion with inversion factor δ. Therefore, two approaches are studied in this work: 1) a 3-parameter pixel-wise fitting method (M0, T1, and C) assuming δ is known; 2) a 4-parameter fitting algorithm (M0, T1, C and δ). M0 is the longitudinal signal during equilibrium, and T1 is the T1 value of the particular pixel. The 3 or 4 unknowns can be solved by using the Levenberg-Marquardt algorithm such that the simulated signal matches best with the measured signal for each pixel.

The standard MOLLI 3-(3)-3-(3)-5 was studied on a 1.5T MR scanner (MAGNETOM Avanto, Siemens Healthcare, Erlangen, Germany) using an investigational prototype sequence. The T1 estimation accuracy over different T1 values and heart rates (HR) by InSiL-3-parameter fitting was evaluated against the standard MOLLI approach based on phantom data. Eight 50ml Agar and CuSO4 gel phantoms with T2 around 45ms-75ms, and T1 ranging from 223ms - 1641ms were used for the study. Reference T1, T2 values of phantoms were determined by spin-echo experiments. The inversion factor for each phantom was determined using a new MOLLI scheme 5-(0)-3-(0)-1(which was found to be better for inversion factor estimation compared with the standard MOLLI 3-(3)-3-(3)-5 from phantom study) with InSiL-4-parameter fitting.

Non-contrast MOLLI image sets were acquired in 10 healthy volunteers. Post-contrast MOLLI image sets were acquired at different time points after contrast injection on two volunteers. Both InSiL-3-parameter fitting and the MOLLI standard approach were used to calculate in-vivo T1 values for comparison. The inversion factor was estimated using the MOLLI scheme 5-(0)-3-(0)-1 with InSiL-4-parameter fitting at selected ROIs on myocardial tissues in 9 healthy volunteers and was set to be 0.84.

Results: Fig. 2 shows the T1 error in T1 estimation using both MOLLI and InSiL at different HRs as compared to reference T1 values in phantom studies. The maximum absolute error by InSiL is less than 12ms, while that by MOLLI is more than 300ms for T1 values from 223ms to 1641ms. The benefits of InSiL is greatest at HR ≥ 80bpm and T1>1000ms, and InSiL reduced MOLLI T1 absolute error from 197ms to 4ms on average. Based on data from 10 volunteers, the native myocardial T1 values by InSiL were greater than that by the MOLLI standard approach by 238.0±9.0ms (1166.0±23.1 ms vs. 928.1±21.8ms, relative 25.7±1.2%, $p<0.001$) at an average heart rate of 63.7±11.2bpm. The pre- and post-contrast myocardial T1 maps obtained from one normal volunteer using MOLLI and InSiL are shown in Fig. 3. The T1 maps by InSiL method show similar image quality (SNR) to that by the standard MOLLI approach.

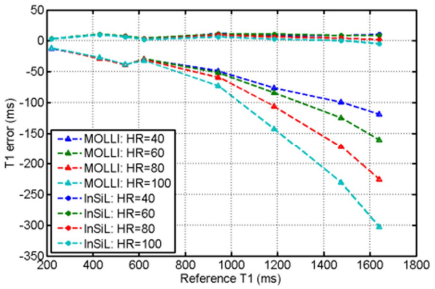

Fig.2. Phantom study results in InSiL and MOLLI T1 estimation at different heart rates as compared to reference T1 values. InSiL provides more accurate T1 values(upper 4 plots), and is less dependent on heart rate compared with the MOLLI standard approach(lower 4 plots).

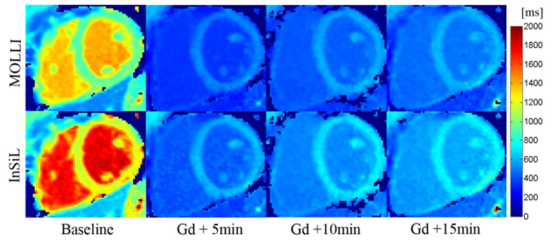

Fig.3. Short axis T1 maps of normal myocardium using MOLLI by original T1 calculation algorithm (top row) and by the proposed InSiL algorithm (bottom row) at 1.5T at the baseline and the following Gd-DTPA administration at different times. T1 values of pixels where data doesn't fit well (R^2 <0.98) were set to zero. InSiL provides similar image quality (SNR) as MOLLI for T1 mapping, but higher T1 values than MOLLI.

Discussion: Underestimation of T1 values using standard MOLLI mainly results from the following three factors: (1) imperfect inversion; (2) approximation of Look-Locker correction and (3) Neglecting possible incomplete recovery before the following inversion pulse. InSiL was proposed to address these issues by simulating the signal evolution of the standard MOLLI sequence by using a simplified model of Bloch simulation. Results show that InSiL generates greater and more accurate T1 values compared with MOLLI, and is less dependent on heart rate.

Conclusion: Compared the original 3-parameter exponential fitting algorithm, the proposed InSiL T1 mapping algorithm provides better T1 calculation accuracy, and can reduce the dependence on heart rate variations across subjects. InSiL allows the standard MOLLI pulse sequence to be used while giving the option to retrospectively correct for T1 errors in existing MOLLI datasets.

References: 1. Moon JC et al. J. Cardiovasc. Magn. Reson.,2013; 15(1):92. 2. Broberg CS et al. Circ. Cardiovasc. Imaging. 2010; 3(6):727-734. 3. Messroghli DR et al. Magn. Reson. Med. 2004; 52(1):141-146. 4. Gai ND et al. Magn. Reson. Med. 2013; 69(2):329-336. 5. Piechnik SK et al. J. Cardiovasc. Magn. Reson. 2010; 12:69.