Comparison of Myocardial T1-mapping Protocols: Accuracy and Precision

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Introduction: T1-mapping in the myocardium may be used to detect both focal and diffuse disease processes that result in an elevation of T1. Both the accuracy and precision of T1-mapping are important for quantitative measurements and reliable detection of abnormal elevation of T1. Accuracy reflects the systematic or bias errors while precision reflects the random error due to noise. Accuracy is affected by a large number of parameters including the sequence, protocol, tissue T1 and T2, fitting method, and scanner adjustments such as center frequency. Precision of T1 estimates is a function of the number and timing of measurements along the T1-recovery curve, signal-to-noise ratio (SNR), tissue T1, method of fitting, as well as other protocol and sequence parameters. The accuracy and precision of several popular methods are investigated in detail using a waveform level Bloch simulation to assess accuracy, and Monte-Carlo method of repeated trials to assess precision. Simulations are confirmed with phantom measurements. Methods include 2 optimized inversion recovery protocols based on MOLLI [1] and a saturation recovery method originally known as SAP-T1 [2], referred to here as SAturation-recovery single-SHot Acquisition or SASHA [3].

Methods: T1-mapping using inversion recovery approaches such as MOLLI [1] are based on performing a 3-parameter fit at each pixel to measurements of the inversion recovery at multiple inversion times. The 3-parameter model yi = A – B exp(-ti/T1*), is used to estimate the apparent time constant T1*, and the T1 is subsequently estimated as T1*(B/A -1). The so-called Look-Locker correction (B/A-1) for the influence of the readout is known to cause errors which depend on T2 [4] as well as center frequency. An alternative saturation recovery based (SR) approach [2,3] applies a SR preparation for each measurement thus eliminating the need for the Look-Locker correction and minimizing the associated error. For ideal saturation, the SR approach may be used in conjunction with a 2-parameter fit to yi=A(1-exp(-ti/T1)) thus reducing the degrees of freedom and reducing random error. A relatively small bias error will result due to the effect of the readout which may be largely eliminated by a 3-parameter fit at the cost of increased random error (i.e., loss of precision). A simulation of the Bloch equations was used to determine the accuracy of both IR and SR approached. A Monte-Carlo simulation using N=65,536 trials was used to compute the standard deviation of T1 as a function T1 for a large number of protocols. Specific protocols reported here are: (a) MOLLI 5(3)3 sampling, 8 images/11 heartbeats, TImin=105 ms, TIshift = 80 ms, FA 35°, (b) MOLLI 4(1)3(1)2 sampling, 9 images/11 heartbeats, TImin=105 ms, TIshift = 80 ms, FA 35°, and (c) SASHA with 1 steady state acquisition and 10 SR prepped images each subsequent heartbeat, 11 images/11heartbeats, TI min 105 ms, TIshift = 80 ms, FA 70°. All protocols used SSFP readout. The raw steady state SNR for MOLLI was assumed to be 20 based on in-vivo measurements, and for SASHA was 34 as a result of the higher readout FA. Experimental validation was performed using CuSO4 doped agar gel phantoms with varying concentrations resulting in T1 and T2 in the expected range for myocardium.

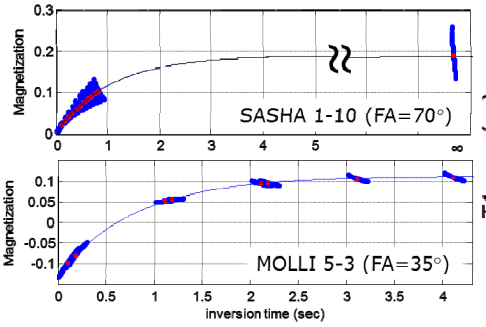

Figure 1. Illustration of SASHA (top) with FA=70 acquiring 10 SR images plus 1 initial steady state, and MOLLI (bottom) using FA=35 IR prepped with 5-3 sampling scheme.

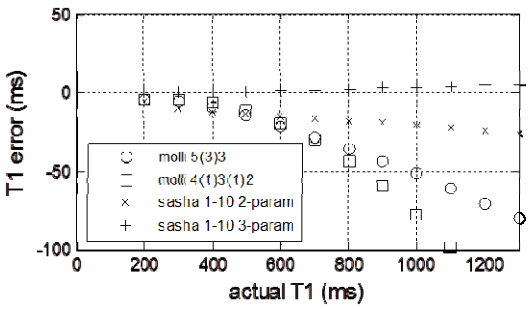

Figure 2. T1 measurement error for various T1-mapping protocols.

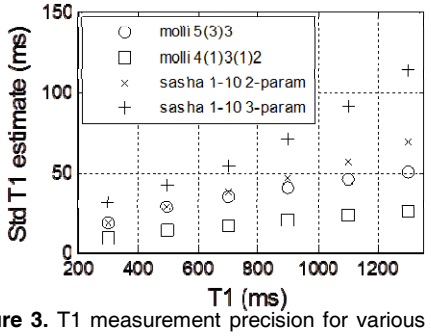

Figure 3. T1 measurement precision for various T1-mapping protocols based on Monte-Carlo measurement of repeated trials.

Results: IR methods have a greater dynamic range than SR (0.2M0 vs 0.16M0), however, the steady state magnetization of SR is greater (0.19M0 vs 0.11M0) results in a 1.7:1 advantage in raw SNR for SASHA, a result of the larger FA. At T1=1000ms, the error in T1 (Fig 2) was 50 ms for MOLLI 5(3)3, 20ms for SASHA with 2 parameter fit, <5 ms using SASHA with a 3-parameter fit. The MOLLI 4(1)3(1)2 protocol is proposed to be used for measurements after Gd contrast at shorter T1, whereas the 5(3)3 protocol is proposed for native myocardial T1. The precision of SASHA with 3-parameter fit is considerably worse than 2-parameter fit or MOLLI (Fig 3). The SASHA 2-param method has improved accuracy with only slightly worse precision than MOLLI for native T1, while the MOLLI 4(1)3(1)2 protocol achieves the best precision for post-contrast T1 with good accuracy. Measurement of T1 in phantoms (Fig 4) are consistent with simulations. The upper right tube T1=1109, 1196, 1233 (left to right) with corresponding standard deviations, 17, 28, 51 ms, respectively.

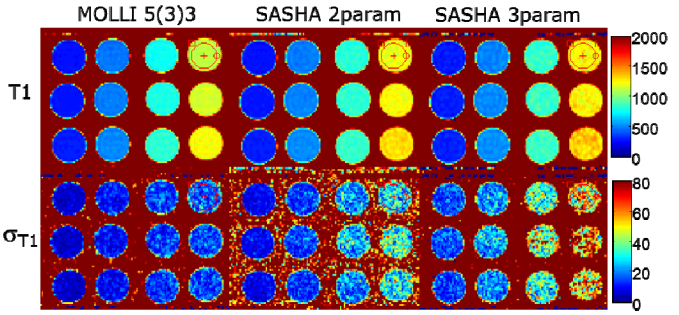

Figure 4. Phantom measurement of T1-maps and standard deviation maps (σ_{T1}) confirm accuracy and precision trade-offs between IR and SR approaches to T1-mapping.

Discussion and Conclusions: T1-mapping protocols are compared from the standpoint of both accuracy and precision. Improved accuracy may be achieved with reduced precision in MOLLI using decreased FA and in SR methods such as SASHA by incorporating more degrees of freedom in fitting. Accuracy and precision trade-offs predicted in theory are confirmed with experimental measurements in phantom.

References: [1] Messroghli, et al J Magn Reson Imag. 2007, 26:1081–6. [2] Higgins DM, et al, Medical Physics. 2005;32(6):1738. [3] Chow K, et al. ISMRM 2012 p395 [4] Gai ND, et al, Magn Reson Med. 2012 Mar 27. doi: 10.1002/mrm.24251