An Intuitive Model of Several Factors Affecting Accuracy of MOLLI $T_1$ Values
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INTRODUCTION The MOdified Look-Locker Inversion recovery (MOLLI) sequence (1) and its variants are commonly used for quantitative cardiac $T_1$ mapping to detect myocardial fibrosis. However, MOLLI sequences have been shown to have systematic $T_1$ errors dependent on factors such as heart rate (2), $T_2$ values (3), $T_1$ values (4) and inversion efficiency (4). The interaction of these effects is not well understood and potential dependencies on other pulse sequence parameters have not been considered. We propose a model for predicting systematic MOLLI errors that incorporates the effects of $T_1$, $T_2$, and other sequence parameters to provide an intuitive understanding of how these factors affect MOLLI $T_1$ errors.

THEORY The MOLLI sequence consists of several “Look-Locker sets”, each containing a single inversion pulse followed by several single-shot balanced steady-state free precession images at various inversion times (TI), separated by several heartbeats for magnetization recovery. $T_1$ values are calculated by fitting a three-parameter exponential recovery model and applying the “Look-Locker correction” (5), intended to account for magnetization attenuation from multiple imaging readouts after a single inversion pulse.

We propose that the errors in MOLLI $T_1$ values are directly related to the magnitude of magnetization perturbation caused by imaging. The perturbation of imaging readouts can be characterized by comparison to pure $T_1$ recovery that would occur over the same time period in the absence of an imaging readout. Specifically, $M_{\text{diff}}$ is defined as the difference in normalized longitudinal magnetization following first imaging readout as compared to pure $T_1$ recovery over the same time (Fig. 1). The degree of perturbation is determined by both tissue properties such as $T_1$ and $T_2$ as well as imaging parameters such as repetition time and the number of k-space lines acquired.

METHODS Phantoms: 14 NiCl2 doped agarose phantoms with a wide range of physiologic $T_2/T_1$ values simulating pre- and post-contrast blood and myocardium were imaged on a 1.5T Siemens Avanto. Spin echo experiments using a 10 s TR with 16 TIs spanning 100–5000 ms and 6 TEs spanning 11–200 ms were used to calculate gold standard $T_1$ and $T_2$ values respectively. Three variations of a “3-5” Shortened MOLLI (6) sequence were performed: 1) typical parameters with TE/TR of 1.03/2.43 ms and 86 acquired k-space lines per image, 2) rate 2 GRAPPA parallel imaging with 57 acquired k-space lines, and 3) a longer TE/TR of 1.24/3.06 ms. All 3 variations shared other common pulse sequence parameters: 2 inversion sets of 3 and 5 images with 3 recovery heartbeats between sets, 140 ms TI value, 57 acquired k-space lines, and 3) a longer TE/TR of 1.24/3.06 ms. All 3 variations shared other common pulse sequence parameters: 2 inversion sets of 3 and 5 images with 3 recovery heartbeats between sets, 140 ms TI increment, 6/8 partial Fourier, 75% phase resolution, 35º flip angle, and a 60 bpm simulated heart rate. $T_1$ values were calculated using in-line $T_1$ maps with Look-Locker correction.

Simulations: Bloch equation simulations of the MOLLI sequence were used to calculate $M_{\text{diff}}$ as described in the Theory and Figure 1. Simulations were performed in MATLAB for each phantom experiment using an adiabatic hyperbolic secant inversion pulse, spin echo $T_1$ and $T_2$ values, and actual imaging sequence parameters.

RESULTS Phantoms had a wide range of spin-echo $T_1$ (276–1453 ms) and $T_2$ (46–199 ms) values. MOLLI generally underestimated $T_1$ values compared to spin echo with a wide range of accuracy from a 12% underestimation to a 7% overestimation. Errors in MOLLI $T_1$ values were strongly related to $M_{\text{diff}}$, with increasing errors at larger $M_{\text{diff}}$ values (Fig. 2). $M_{\text{diff}}$ values varied greatly between phantoms due to a wide range of $T_2/T_1$ values (50/1145 – 122/276 ms), with larger perturbations for smaller $T_2/T_1$ ratios. Phantoms with $T_2$ and $T_1$ values similar to pre- and post-contrast blood and myocardium (circled markers in Figure 2) have widely different systematic errors ranging from a 10% underestimation in pre-contrast myocardium to 5% overestimation in post-contrast blood. $M_{\text{diff}}$ and systematic $T_1$ errors were also affected by sequence parameter changes, with greater errors for longer readouts and up to 2% of errors in any given phantom were the result of parameter changes alone.

DISCUSSION AND CONCLUSION Large systematic errors in MOLLI $T_1$ values were strongly correlated with $M_{\text{diff}}$, a measure of magnetization perturbation caused by the imaging readout. $M_{\text{diff}}$ is affected by both intrinsic tissue $T_2/T_1$ values and also commonly altered sequence parameters, such as TE/TR and the number of RF pulses. The Look-Locker correction factor is intended to correct for the effects of magnetization perturbation, although our data show that significant errors remain even after correction. The $M_{\text{diff}}$ concept provides an intuitive understanding of how tissue relaxation and sequence parameter affect accuracy of MOLLI $T_1$ values, although other confounders such as heart rate may present yet additional sources of systematic errors.

REFERENCES
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Fig. 1 $M_{\text{diff}}$ with pre-contrast myocardium-like $T_1$ and $T_2$ values. Dashed blue line shows pure $T_1$ recovery following inversion. Solid red line shows a bSSFP readout with linearly ramped opening RF pulses and a closing α/2 pulse.

Fig. 2 MOLLI $T_1$ errors as a function of $M_{\text{diff}}$ for all phantoms for different sequence parameters. Data for pre- and post-contrast blood and myocardium-like phantoms are shown with enlarged data points.