

## Can Modified Look Locker Imaging (MOLLI) Provide Accurate T1 Values?

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**Target Audience:** Researchers and clinicians interested in T<sub>1</sub> mapping for myocardial tissue characterization.

**Background:** Myocardial T<sub>1</sub> mapping has been regarded as instrumental for quantification of myocardial fibrosis (1) and infiltrative cardiomyopathies such as amyloid (2). A widely used T<sub>1</sub> mapping technique is Modified Look Locker Imaging (MOLLI) (3-6). However, MOLLI has increased error in estimated T<sub>1</sub> for short T<sub>2</sub> tissues and in the presence of imperfect inversion pulses (7,8). Additional error sources in MOLLI can include the non-rectangular flip angle profiles typically used in fast 2D imaging (9) and magnetization transfer (10). Here we systematically evaluate the inaccuracies of the MOLLI fitting method. We propose a new fitting method, bMOLLI, that utilizes the Bloch equations to model the SSFP signal evolution and account for the flip angle profile and inversion efficiency to provide accurate T<sub>1</sub> estimates.

**Theory:** MOLLI uses single shot inversion prepared SSFP readout to interrogate tissue's T<sub>1</sub> relaxation time (3). In MOLLI, the relaxation is modulated by SSFP readout. There have been efforts using a three parameter fit of the measured signal curve:  $S_{MEAS} = A - Be^{-(T/T_1)^*}$  [Eq. 1] and correcting for T<sub>1</sub><sup>\*</sup> with:  $T_1 = T_1^*(B/A-1)$  [Eq. 2] to obtain the true T<sub>1</sub> (3). This correction is based upon SPGR Look-Locker (LL) imaging (3,11). While the signal evolution during true LL imaging with either SPGR or SSFP readout follows an exponential curve, the signal obtained from MOLLI fundamentally cannot be described by a simple exponential function (Fig.1). Accordingly, Eq.2 only provides an approximation with limited accuracy (8). Furthermore, this correction does not account for non-ideal imaging conditions, including the non-rectangular flip angle profile (9) and the imperfect inversion efficiency (7), which is common when adiabatic pulses are used in tissues with short T<sub>2</sub> (12).

The proposed bMOLLI method used a Bloch equations based fitting (9) which follows the signal evolution of the MOLLI acquisition. In bMOLLI, Eq. 3, the MOLLI signal evolution  $S_{MODEL}$ , which is a function of T<sub>1</sub>, T<sub>2</sub> and M<sub>0</sub>, is simulated using the Bloch equations and the difference between the  $S_{MODEL}$  and the  $S_{MEAS}$  is minimized at all inversion times (TI). Integration of the  $S_{MODEL}$  over the slice profile,  $\alpha(z)$ , is performed numerically to correct for slice profile effect. From the additional acquisition of an inversion efficiency ( $\gamma$ ) map, adiabatic inversion efficiency is also included in the Bloch simulation.

$$[3] \quad T_1, T_2, M_0 = \arg \min_{T_1} \sum_{TI} (S_{MEAS}(TI) - S_{MODEL}(TI, T_1, T_2, M_0, \alpha(z), \gamma))^2$$

**Methods:** MOLLI data was acquired in the calf muscle of N=7 volunteers. In addition, inversion recovery spin echo (IR-SE) data was acquired as a gold standard and was also used to calculate adiabatic inversion efficiency. MOLLI data was acquired at 30°, 60° and 90° to investigate the effect of the readout flip angle on T<sub>1</sub> accuracy. Cardiac MOLLI data was also acquired in N=5 volunteers at a 30° flip angle. For gold standard T<sub>1</sub> values in the heart, a cardiac gated inversion recovery fast spin echo sequence was used.

All data was fit for an ROI in the soleus muscle (calf) or in the septal myocardium (heart). Data was fit using the standard MOLLI (Eq. 1-2) and proposed bMOLLI (Eq. 3) algorithms.

**Results:** In the calf muscle, bMOLLI provided more accurate T<sub>1</sub> values and better fitting residuals vs. standard MOLLI at all flip angles (figure 2) when compared to IR-SE (T<sub>1</sub> = 990 ± 22 ms). Standard MOLLI significantly underestimated T<sub>1</sub> at all flip angles (p<.05) up to 16.4% (figure 2a) and had increased fitting residuals indicating worsening fits at higher flip angles (figure 2b). While T<sub>1</sub> accuracy varies with flip angle using the standard MOLLI correction, the proposed bMOLLI provided consistently accurate T<sub>1</sub> values over the flip angle range of 30° - 90°. Adiabatic inversion efficiency in the soleus muscle was 85 ± 2%.

Cardiac ROI analysis shows accurate T<sub>1</sub> with the bMOLLI fit (1057 ± 35 ms) when compared to the reference of IR fast spin echo (1088 ± 72 ms) while the standard MOLLI correction underestimated T<sub>1</sub> (961 ± 32 ms). On average, the standard MOLLI correction had 11.5 ± 3.9% error compared to 3.3 ± 3.4% error with bMOLLI. An example of a T<sub>1</sub> map for one volunteer is shown in Figure 3. One volunteer was excluded from ROI analysis because of major flow artifact in the myocardium.

**Conclusion:** Our results demonstrate that improved T<sub>1</sub> accuracy can be obtained from MOLLI data using the proposed bMOLLI method. However, this requires knowledge of the adiabatic inversion efficiency.

**References:** (1) Iles, et al. JACC 2008;52(19):1574-1580. (2) Maceira et al. JCMR 2008;10:54. (3) Messroghli et al. MRM 2004;52(1):141-146. (4) Kawel et al. JCMR 2012;14(1):71. (5) Kawel et al. JCMR 2012;14(1):71. (6) Kellman et al. JCMR 2012;14:64. (7) Chow et al. ISMRM 2012. (8) Gai MRM 2012. (9) Ehnes et al. MRM 2012. (10) Cooper et al. MRM 2012;68(5):1579-1585. (11) Deichmann et al. JMR 1992; 96(3):608-612. (12) Norris et al. JMR 1991;92(1):94-101

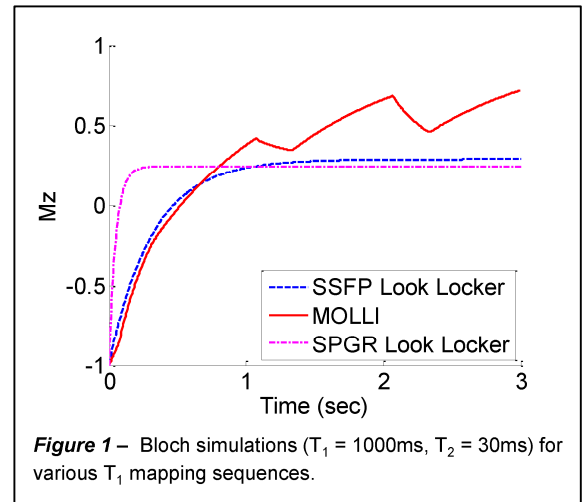


Figure 1 – Bloch simulations (T<sub>1</sub> = 1000ms, T<sub>2</sub> = 30ms) for various T<sub>1</sub> mapping sequences.

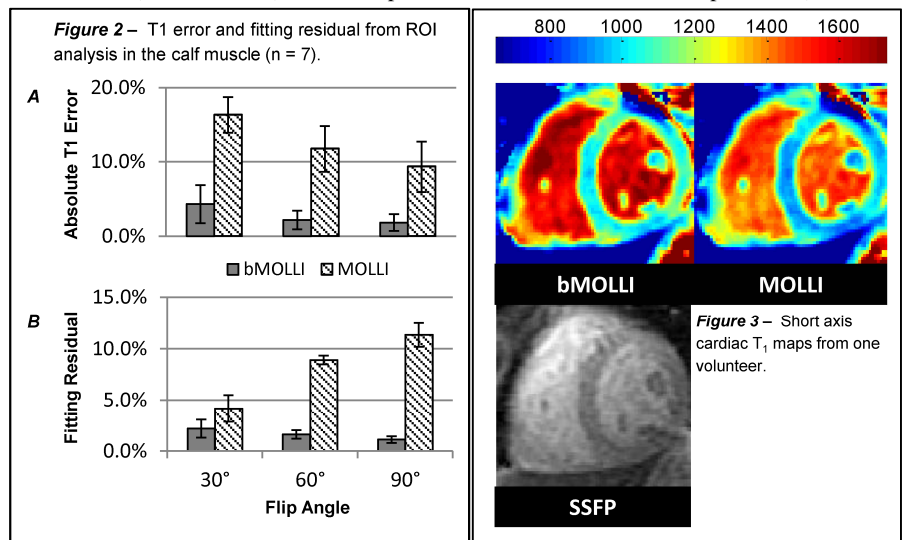


Figure 3 – Short axis cardiac T<sub>1</sub> maps from one volunteer.