Relaxometry Using Sequence SimuLation (RUSSL): Application to myocardial T1-mapping using MOLLI

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Introduction: Myocardial T1 mapping has recently been used for detecting and quantifying myocardial diffuse fibrosis [1] after the administration of contrast. It has also been shown to detect edema in the pre-contrast setting [2]. Therefore it is important to measure myocardial T1 with good accuracy over a wide-range of T1 values [250ms to 2000ms]. Currently, MOLLI is the favoured method for T1 mapping [3]. It uses 3-parameter exponential fitting [4] and three pausing heart cycles. It has been shown to depend on heart-rate and underestimate T1 for longer T1 values for higher heart-rates [5]. The exponential fitting approach, though it seems to work well in practice, was derived only for gradient-echo (FLASH) sequences [4]. Here, we propose an alternative fitting method, Relaxometry Using Sequence Simulation (RUSSL), based on Bloch-simulation for improving the heart-rate dependency of MOLLI and for proposing a physical explanation for the validity of the exponential fit.

Methods: In general, the signal evolution from MOLLI depends on a number of sequence parameters (flip-angle, TR, TE, TI for each RR etc.), physiological parameters (heartrate, trigger delay), system parameters (B0, B1 offsets) and tissue parameters (T1, T2 and M0). From the actual sequence played-out, all the sequence and physiological parameters are known. If we also know the B0 and B1 offsets, we can then fit the acquired data for tissue parameters by simulating the whole sequence as it was played out using Bloch-equation simulation. We can expect that the fitted tissue parameters become more accurate if the simulated sequence is more faithful to the actual sequence played-out. For fitting MOLLI, the B0-offset was assumed to be zero. Two fits were done using 3 and 4 model parameters. The 4-parameter fit model used T1, T2, M0 and B1-offset of the imaging RF pulse (FA). The 3-parameter fit model used only T1, T2 and M0 assuming B1-offset to zero.

A set of phantoms were prepared with different T1s and T2s using varying concentrations of manganese chloride, copper sulphate and agar. Their T1s were measured accurately using an IR Spin-Echo sequence (TR=15 sec, TI=50 to 3200 ms). The MOLLI sequence was implemented with two additions. A realtime timer [6] was added which records the heart-cycle duration to get correct timings for simulation. A crusher was also introduced along the slice-direction at the end of acquisition in each RR, to reduce T2 dependency. Different heart-rates (60, 75 and 100 bpm) were tested using an ECG-simulator. Four healthy volunteers were also scanned to compare the T1 values.

Results: The phantom T1 values measured using the standard IR Spin-Echo sequence were compared against MOLLI images with different reconstruction methods. The standard T1 measurement values varied from 235 ms to 1600 ms. All methods showed a reduction in measured T1 compared to the standard, especially for T1 greater than 1000ms. However, the standard MOLLI reconstruction showed the highest variation with higher heart-rates. The RUSSL reconstruction also showed dependence with heart-rate; however it was less compared to MOLLI reconstruction. The max error in T1 was 255 ms for the MOLLI fit and 199 ms for the RUSSL fit. Both 3 and 4 parameter models showed very similar results. In Fig-1, only the 4-parameter model is shown.

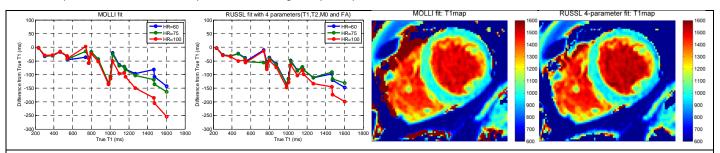


Fig.1: The first two plots show the variation of measured T1 with heart-rate for different methods. The T1-value from the IR-SpinEcho sequence (True-T1) is plotted against the difference between the measured and the standard T1. Both the MOLLI fit and the RUSSL fit show dependence on heart-rates. However for the RUSSL fit the dependence is less and the T1 values for higher heart-rate are much closer to the values for lower heart-rate. The right two images show the resulting T1 maps from one volunteer with a heart rate of 75 bpm. Both the MOLLI fit and RUSSL fit seem to show very similar T1 values for the myocardium. Also, the right ventricular wall seems to have been better visualized in the RUSSL fit.

Discussion: We have demonstrated the feasibility of using Bloch-simulation (RUSSL) to fit T1 values for images acquired from the MOLLI sequence. RUSSL also supports the validity of the exponential MOLLI fit. The T1 values were dependent on heart-rates but less so compared to MOLLI fits. In addition, the RUSSL fit also provides M0 and T2 values. Though we could distinguish large variations in T2, the values were noisy and of limited accuracy. This is due to weak dependence of MOLLI signal on T2. RUSSL is also flexible with respect to sequence parameters. For example, the type and number of SSFP catalyzing pulses, heart-rate variation during acquisition and the actual k-space order are easily incorporated in to the fit. However the fit did not yet incorporate other effects such as magnetization transfer, which has been reported to have a small but detectable effect at the applied flip-angle of 35 deg and TR of 3.6 ms. RUSSL can also be applied to sequences other than MOLLI and in general, to any sequence where the signal can be numerically calculated.

References

- 1. Quantification of Diffuse Myocardial Fibrosis and Its Association With Myocardial Dysfunction in Congenital Heart Disease: Broberg et. al: CIRCIMAGING.108.842096
- 2. Non-contrast T1-mapping detects acute myocardial edema with high diagnostic accuracy: Ferreira et.al: JCMR 2012, 14:42
- 3. Optimization and Validation of a Fully-Integrated Pulse Sequence for MOLLI T1 Mapping of the Heart: Messroghli et.al: JMRI 26:1081–1086 (2007)
- 4. Quantification of TI Values by SNAPSHOT-FLASH NMR Imaging: Deichmann et.al: JMR,96, 608-612 (1992)
- 5. Shortened Modified Look-Locker Inversion recovery (ShMOLLI) for clinical myocardial T1-mapping at 1.5 and 3 T within a 9 heartbeat breathhold: Piechnik et.al: 2010, 12:69
- 6. The Effect of Heart Rate in Look-Locker Cardiac T1 Mapping: Slavin et.al: ISMRM 2010