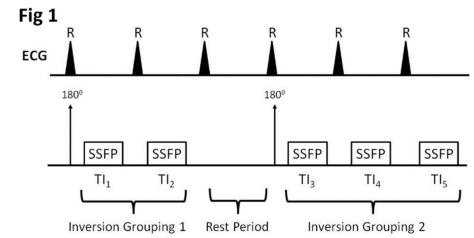


Inversion Group (IG) Fitting: A New Fitting Algorithm for Modified Look-Locker Inversion Recovery (MOLLI) that allows for Arbitrary Inversion Groupings

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Introduction: Modified Look-Locker Inversion Recovery (MOLLI)¹ is commonly applied for myocardial T₁ mapping. Following a 180° pulse, SSFP readouts are performed on consecutive cardiac cycles to acquire multiple TI's (inversion groups) (Fig1). To improve the quality of the subsequent T₁ fit, additional inversion group(s), separated by quiescent “rest periods” are typically acquired. Rest periods are needed for magnetization recovery to equilibrium, otherwise data combined from different inversion groups will not follow a MOLLI-like recovery curve. The requirement of rest periods can significantly reduce the scan efficiency and/or increase scan time (by up to ~30-40%)². In this study, we present a new technique, Inversion Group (IG) fitting, which allows accurate T₁ fitting without requiring rest periods.



Theory: In conventional MOLLI, data is fitted with a three parameter model³: $S(TI) = A - Be^{-\frac{TI}{T_1}}$. In the proposed IG fitting technique, a more general model with a separate B_i parameter for each inversion group is used:

$$S(TI) = A - B_i e^{-\frac{TI}{T_1}} \quad (1)$$

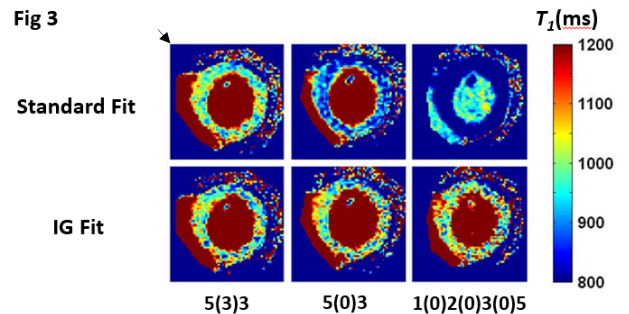
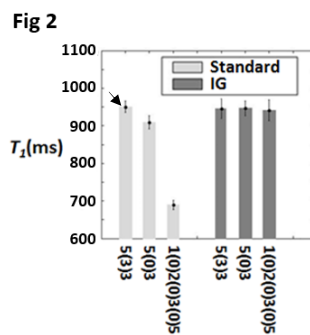
The additional B_i parameters account for incomplete magnetization recovery between groupings. As a result, Eq.1 may be used regardless of the presence or absence of rest periods. T₁ can be calculated from T₁^{*} as⁴:

$$T_1 = T_1^* \cdot \left(\frac{B_i}{A} - 1 \right) / \delta_i \quad (2)$$

δ_i denotes the fraction of magnetization inverted on inversion group i . For simplicity, we calculate T₁ from the first inversion group where it is known that $\delta_i=1$.

Methods: Phantom and in vivo experiments were performed on a 1.5T scanner (Magnetom Avanto fit). T₁ maps were calculated with both 3-parameter and IG fits. Phantom experiments were performed on MnCl₂ doped water ($T_1 \approx 1000$ ms). In vivo experiments were performed on 5 patients. In all experiments, three different MOLLI inversion groupings were acquired: 5(3)3, 5(0)3, and 1(0)2(0)3(0)5 (non-bracketed numbers indicate number of readouts within inversion group and bracketed numbers denote number of heartbeats in rest period).

Results: The phantom results (Fig 2) demonstrate that T₁ values for the IG fits are consistent across all inversion groupings and not statistically different ($P=0.25$) from the 5(3)3 acquisition-the reference standard (arrows), while the 3-parameter 5(0)3 and 1(0)2(0)3(0)5 showed substantial deviations ($p \approx 0$). On the other hand, precision of the IG fits was found to be slightly poorer than the 3-parameter fits, likely due to the larger number of free parameters in the fit. Fig 3 shows T₁ maps from one patient. For 3-parameter fits, a dramatic decrease in T₁ value is observed across different inversion groupings while IG fits remained consistent. Quantitatively, the reduced χ^2 values were very similar across all IG fits and the 3-parameter 5(3)3, while the reduced χ^2 of other inversion groupings of the 3-parameter fit were much larger (Table 1). However, all IG cases aside from the 1(0)2(0)3(0)5 showed slightly poorer precision compared to the 3-parameter fits, as indicated by the coefficients of variation listed in Table 1.



Conclusion: The IG fitting technique provides accurate T₁ fitting for any inversion grouping /rest period combination at the cost of a slight loss of precision relative to the conventional 3-parameter method. Further improvements will likely allow overcoming this current limitation.

References:

1. Messroghli et al. *Magn Reson Med* 2004. **52**(1)
2. Reiter et al. *Radiology* 2014. **271**(2)
3. Deichmann et al. *JMRI* 1992. **96**(3)
4. Kellman et al. *Magn Reson Med* 2014. **71**(4)

Table 1: Reduced χ^2 and coefficient of variation over all patients

	3-Parameter Fit			IG-Fit		
	5(3)3	5(0)3	1(0)2(0)3(0)5	5(3)3	5(0)3	1(0)2(0)3(0)5
Reduced χ^2	17 +/- 6	41 +/- 13	137 +/- 68	18 +/- 7	16 +/- 5	25 +/- 12
COV	0.06 +/- 0.005	0.07 +/- 0.007	0.06 +/- 0.004	0.08 +/- 0.004	0.08 +/- 0.005	0.1 +/- 0.08