On the T1 of fat calculated from a segmented Look Locker scout scan and its implications in cardiac imaging

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Introduction: Recently, it has been shown that T1 mapping after gadolinium administration can differentiate between diffuse fibrosis and normal myocardium [1]. T1 change assumes gadolinium accumulation in fibrosis as the primary (only) histologic change but fat or iron deposition may also occur. Legacy data from several longitudinal studies such as MESA [2] and EDIC [3] are available for possible data mining to investigate correlations between T1 values and disease state. Such legacy data do not have a dedicated T1 mapping scan as part of the multi-center protocol. However, segmented Look-Locker with balanced SSFP (b-SSFP) acquisition is typically used (TI scout scan [4]) to determine the inversion time for delayed-enhanced imaging in such studies. The data from the scout scan can also be used to derive T1 values. The T1 values can be normalized for inter-patient comparison [5]. Certain diseases such as myotonic muscular dystrophy (MMD) or arrhythmogenic right ventricular dysplasia exhibit fatty infiltration as part of their etiology. Based on simulations and scanning results, we show that fat T1 quantification obtained from segmented LL scout scans can be highly erroneous depending on the scan parameters used. As a result, conclusions drawn from calculated cardiac T1 values in cases where fatty infiltration is substantial might be erroneous.

Materials and Methods: As is well-known, balanced SSFP acquisition exhibits periodic variation of the steady-state (s-s) signal with the signal being zero at frequencies $f = \pm 1/(2TR), \pm 3/(2TR)$ and so on. If the repetition time (TR) of the b-SSFP acquisition corresponds to the fat off-resonance frequency, the signal will deteriorate resulting in corresponding errors in T1 values determined by a segmented LL scan. For the sake of simplicity, we consider fat off-resonance as a single peak (at 220Hz for 1.5T and 440Hz at 3T). However, the effect of multiple peaks on T1 values can be explained although quantifying it accurately would be impossible. Figure 1 shows approach to s-s based on Bloch simulation for b-SSFP acquisition (with $\alpha/2$-TR/2 preparation) at two different TRs. At 3T, the fat peak (denoted "FP" in the figure) is close to the signal null (at steady-state) when TR=3.4ms but is away from the null at TR=3.9ms. Similarly, at 1.5T, the fat null corresponds approximately to TR=2.3ms. Note that signal at off-resonance frequencies close to the null will still exhibit depressed values and oscillations for initial excitation pulses (non s-s acquisition).

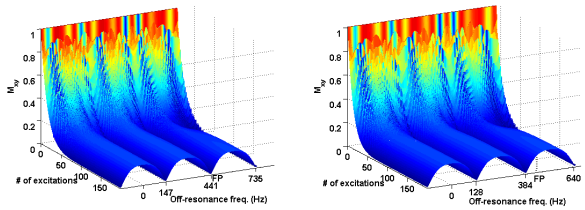

Figure 1: Transverse magnetization as a function of frequency for b-SSFP acquisition for TR=3.4ms and TR=3.9ms.

T1 Simulation: Next, the Look-Locker scout acquisition was simulated using Bloch equations. The T1/T2 values used for the simulations corresponded to values for fat at 1.5T and 3T. The longitudinal magnetization recovery curve obtained from the simulations was fit to a three parameter model (using the Nelder-Mead minimization algorithm in Matlab®) to obtain T1 values. This was done for a range of off-resonance frequencies (±50Hz) around the fat peak.

MRI experiments: Three agar-$NiCl_2$ tubes (different T1s) and a tube filled with vegetable oil were scanned on a Philips 3T Achieva scanner using a segmented LL scan with several TRs (for the b-SSFP acquisition) ranging from 2.9ms to 4.1ms in increments of 0.2ms. Other scan parameters were: etl = 7 (with two dummy acquisitions), $\Delta TI = 7*etl$, α=50°, TR_{seq} = 2s (sequence time corresponding to 2R-R intervals). Scanning for T1 values as a function of excitation angle at TR=3.5ms was also performed to further test the agreement between simulations and measurements. Similar scanning was performed on a 1.5T scanner with TRs in the range 1.9ms to 3.1ms. All simulations and T1 calculations were implemented in Matlab®.

Results: Figure 2 shows the simulated variation in T1 as a function of off-resonance around the fat peak (FP) for different values of TR at 3T. From the simulations one would expect T1 values to be significantly higher for TRs between 3.3ms and 3.5ms. Figure 3 shows the measured T1 values in the oil phantom and the predicted values from the Bloch simulations. Excellent agreement was found between the predicted and measured T1 values (Pearson r=0.872, p<0.003). T1 values in the three other phantoms did not show any significant variation for different values of TR (T1=516±3.6ms, 500±4.9ms and 355±6.2ms) as opposed to 399±177ms for the oil phantom indicating that the off-resonance response from oil results in large T1 variations. Figure 4 shows images obtained at two different TRs and clearly shows the variation in T1 for oil. Scanning on a 1.5T scanner showed a similar overestimation of T1 near TR values corresponding to s-s signal null for the fat peak. There was a slight mismatch in the peak values (as a function of TR) predicted by the simulation and measured values (~17Hz), mostly likely a result of frequency shift at the location of the oil phantom. After accounting for the shift, the model and measurements were in excellent agreement (Pearson r=0.9, p<0.003). Measured values for T1 of oil ranged from 222ms (at TR=3.1ms) to 1542ms (at TR=2.5ms). Fat signal at 1.5T was noisier around the null resulting in larger T1 estimation errors. Both Bloch simulations and scanning measurements showed an almost linear increase in T1 with increasing excitation angle for TR=3.5ms at 3T. T1 values (obtained from TI scout scan) of subcutaneous fat measured in a subset of MMD patients from a multi-center, multi-vendor study (at 1.5T) with TRs in the 1.9-2.2ms range showed values from 209ms to 511ms further supporting our claim.

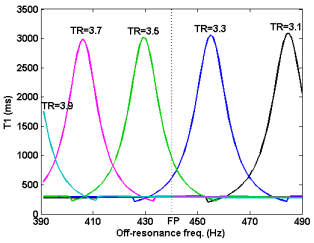

Figure 2: Simulated T1 as a function of frequency and TR.

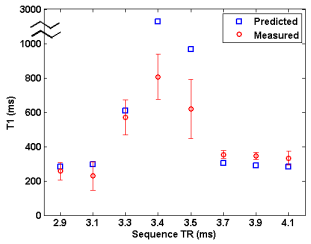

Figure 3: Predicted and measured T1 values in oil.

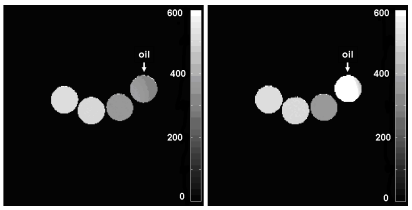

Figure 4: T1 maps of agar-$NiCl_2$ (three left) and oil phantoms at different TRs.

Discussion: Simulations and measurements show that fat T1 values can be grossly overvalued for certain TRs when TI scout LL with b-SSFP acquisition is used for T1 determination. There is also the possibility of slight undervaluation (Figure 2) though not as prominent as overvaluation. Although Bloch simulations cannot predict the exact value, the trend and correspondence between simulated and measured values is excellent. The exact value depends on the echo train length (therefore ΔTI), the local off-resonance frequency, the number of dummy pulses, the local excitation angle (B1 inhomogeneity), the SNR of the scan and the response from the exact fat spectrum. Predicted values typically were slightly higher where T1 overshoots as only a single fat peak is considered for simulations. The true T1 is a weighted mean of the entire fat spectrum resulting in a lower measured T1 value. The work presented here points to inherent pitfalls in using T1 values obtained from scout scans (at certain TRs) for deducing disease state where fatty infiltration is significant.

References: [1] Iles L et al. *J Am Coll Cardiol.* 2008; 52:1574-80. [2] Group ER. *Diabetes Care* 1999;22:99-111. [3] Bild DE et al. *Am J Epidemiol* 2002;156:871-881 [4] Huber A. *AJR* 2006; 186:627-636. [5] Gai N. et al. *MRM*; in print.