Correction for T1 Determined Using Rapid Look-Locker b-SSFP and a Simple Two Parameter Model Fit

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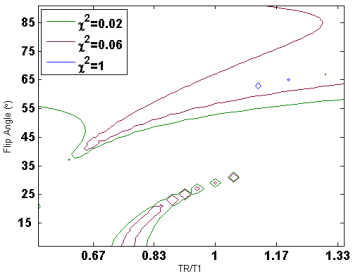
Introduction: Multiple acquisitions along the longitudinal magnetization curve as done with the Look-Locker (LL) technique perturbs the inversion recovery curve. The b-SSFP sequence perturbs magnetization minimally compared to other sequences [1]. However, when inversion recovery is incomplete (if $TR_{seq}<5T1_{max}$) or the flip angle is relatively large (>10° for GM/WM/CSF mapping), a three parameter model needs to be used to obtain correct T1 values [2]. A drawback though is that about six to ten LL phases are needed for a good fit. This compromises scan time or resolution. To improve temporal efficiency, ideally one would like to acquire the fewest number of phases allowed by the model. A scheme that corrects for modulated and/or incomplete inversion recovery using a simple two parameter model with three acquired phases is presented here. Factors affecting the accuracy of the proposed correction for T1 are also discussed here.

Materials and Methods: *Two parameter model:* When inversion recovery is incomplete or when the longitudinal magnetization is perturbed substantially as when the flip angle is relatively large for b-SSFP acquisition, simulations using Bloch equations [3] show that steady-state longitudinal magnetization has the form $M_z = M^*_o(1 - 2e^{-t/T1^*})$ where $1/T1^*=1/T1-\beta(T1^*)/TR_{seq}$; $\beta(T1^*) = mT1^*+c$ is a linear function of T1*. $\beta(T1^*)$ varies with sequence acquisition parameters (TR_{SSFP}/TE_{SSFP}, flip angle α, TR_{seq}, echo train length). *Correction:* The algorithm then consists of three steps: (a) Simulate the recovery curve using acquisition parameters from the imaging experiment and using two to four different values of T1 (say [800 1400]ms range). (b) Perform the two parameter fit from above to the recovery curve in (a) for each of the T1s used in the simulation. This gives us T1* for the corresponding T1 used. (c) Now find $\beta(T1^*) = TR_{seq}(1/T1^*-1/T1)$ for each of the two to four simulated T1s. A linear fit then provides the correction for any value of calculated T1*.



MRI Experiments: Phantoms with 2 different T1s and 6 healthy volunteers were imaged under an IRB approved protocol. A 3T Philips Achieva (release 2.5.3) scanner was used. For phantom scans, short TR_{seq} protocol parameters were: $TI_{1,2,3} \approx \{174, 548, 922\}$ms; TR_{seqt}=2s, b-SSFP acquisition TR/TE=3.2/1.18ms, α=10°, SENSE factor of 2 along phase (k_y) and slice encoding (k_z) direction. A IR-spin echo comparison scan was also done. For volunteers, scan parameters were: TR_{shot}=3s, 25 slices, $TI_{1,2,3} \approx \{300, 1000, 1700\}$ms; b-SSFP acquisition TR/TE=3.5/1.5ms, resolution=0.9×1×1mm. For comparison, accurate T1 mapping was also done with TR_{seq}=10s (WM/GM full recovery) [4] with other parameters similar to the short TR_{seq} scan. For a couple of volunteers, scans with a higher flip angle α=30° and with (k_y, k_z) SENSE factor=2 was done as were IR-SE gold standard scans. GM and WM T1 values were compared for the two scans.

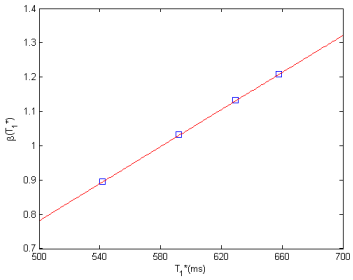


Figure 2: Linear fit at two to four T1* values (□) determines correction.

Results: Figure 1 shows a contour plot indicating goodness of fit of the two parameter model to simulated values of $T1/TR_{seq}$ and flip angle. (χ^2 = 11.07 for a significance level of 0.05). As can be seen, an excellent fit is obtained over the entire parameter space with accuracy somewhat compromised only when T1/TR~0.8 in conjunction with low flip angles. T1 values obtained in two phantoms is shown in Table 1. A typical linear fit used for correction in a volunteer scan is shown in Figure 2. Figure 3 shows images obtained with (A) full recovery (accurate T1 mapping) and those obtained with partial inversion recovery before (B) and after correction (C). T1 values obtained with the two acquisition schemes are shown in the form of a bar plot in Figure 4. When compared with the accurate full recovery scheme, average error across six volunteers was 4.5% for WM and 2.6% for GM while it is 11.9% and 20.1% before correction. With the scan using higher flip angle and SENSE, error was 6.7% for WM and 1.6% for GM after correction while it was 34.7% and 49.5% prior to correction. For two volunteers, corrected T1 values (obtained with partial recovery TR_{seq}=3s) were found to differ by 0.7% in WM and 0.6% in GM when compared with IR-SE T1 values.

Table 1. Measured T1 values in phantoms in ms

	Full TR	Uncorrected	Corrected
Short T1 phantom	871±12.5	735.5±9.1	861±16.5
Long T1 phantom	2705±67	1167 ±26	2676 ±242

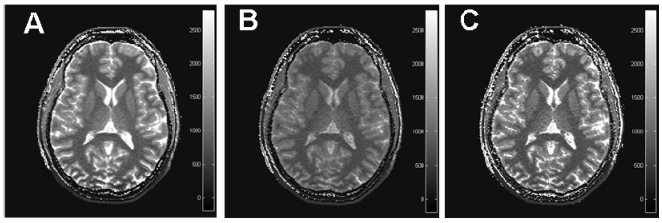
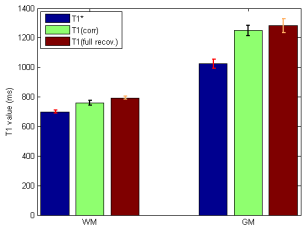


Figure 3: T1 maps obtained with (A) complete T1 recovery (B) T1* (uncorrected) map and (C) corrected map.



Discussion: The algorithm described here is accurate for T2 values that do not show much variation between tissues of interest. For example, T2 was assumed to be 60ms for all simulations. The error resulting from a different T2 (since GM/WM T2 values reported in literature vary between 50-90ms) of say 100ms results in an error in T1 of 1.25% for WM and 1.12% for GM. No correction for B1 inhomogeneity is needed since RF inhomogeneity gets reflected as a multiplicative field in M_0* [5]. This can be seen from Figure 5 which shows the M_0* map corresponding to the T1 maps in Figure 3 (B,C). The resulting correction is only a function of the nominal flip angle used to derive β(T1*). Accordingly, if the gross flip angle (which is assumed to be the nominal flip angle for correction) is 5° instead of 10°, values for WM would be higher by 2.5% and GM by 2.96%. In short, the sources of error discussed above result in only minor variations in T1 values for WM/GM mapping. The correction does increase signal variation in the image as it can be seen as a stretching function.

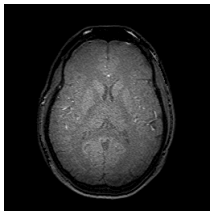


Figure 5: M_0* image

References: [1] K. Scheffler et al. *MRM* 2001:45:720-723. [2] P. Schmitt et al. *MRM* 2004:51:661-667. [3] B. Hargreaves et al. *MRM* 2001:46:149-158. [4] N. Gai et al. *JMRI* 2009 :30(3):640-648. [5] O. Noterdaeme et al. *Phys. Med. Biol.* 2009 :54 : 3473-3489.