

Improved hybrid PRF-T₁ pulse sequence for accurate T₁ mapping in high field (3T)

M. Diakite¹, N. Todd², and D. Parker²

¹Physics, University of Utah, Salt Lake City, Utah, United States, ²Radiology, University of Utah, Salt Lake City, Utah, United States

Introduction: Accurate temperature mapping in tumor and surrounding tissue throughout the thermal therapy is essential to ensure the safety and efficacy of thermal treatment. Methods based on the temperature dependency of the water proton resonance frequency (PRF) shift have shown the best ability to quantify temperature rises in soft tissues. Unfortunately, the PRF shift with temperature does not apply to lipid protons, since there is no hydrogen bonding among the methylene protons that supply the bulk of fat signal. However, the temperature sensitivity of the spin-lattice relaxation time, T₁, has been measured for a number of fatty tissues and found to obey a linear relationship over a small temperature range [1]. We previously proposed the hybrid PRF-T₁ method to combine these two techniques to simultaneously monitor temperature in fat and soft tissues [2]. In this work, we show a sequence implementation and improve the accuracy of T₁ measurements for better temperature mapping.

Theory: A new hybrid PRF-T₁ sequence based on the variable flip angle (FA) DESPOT1 method [3] was implemented from the standard FLASH sequence by alternating two FAs from measurement to measurement. The two FAs were computed to minimize T₁ variance as described previously [4]. The complete temperature maps are acquired in either one or two measurements for PRF and T₁ methods respectively. The PRF temperature map uses the fact that temperature change is proportional to phase change:

$$\Delta\phi = \gamma \cdot \alpha \cdot B_0 \cdot TE \cdot \Delta T \quad (1)$$

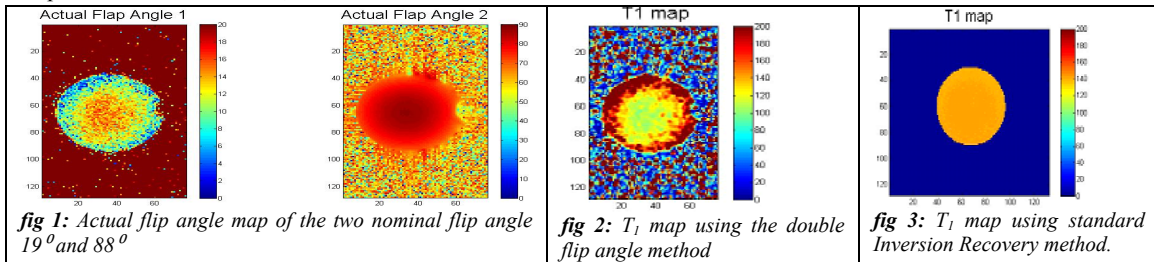
The T₁ map computed using the signals of both FAs, is based on the signal equation of an ideally spoiled steady state gradient echo (FLASH) sequence, which can be approximated as: $SI_{FLASH}(\alpha(r)) = \frac{M_0(1-E_1)}{(1-E_1\cos\alpha(r))} \sin\alpha(r)$, where $E_1 = \exp(-\frac{TR}{T_1})$ (2)

Rearranging equation 2 gives: $\frac{SI_{FLASH}(\alpha_{nominal})}{\sin(\alpha_{actual}(r))} = E_1 \frac{SI_{FLASH}(\alpha_{nominal})}{\tan(\alpha_{actual}(r))} + M_0(1-E_1)$, where T₁ can be extracted as: $T_1(r) = -TR / \ln(E_1(r))$. (3)

In practice, RF excitation is not uniform, and results in an imperfect slice profile and a spatial variation of the FA across the phantom. This variation becomes even more important in MRI scanners operating at 3T and higher. Therefore, measurement of the actual FA is necessary to obtain accurate T₁ mapping with the variable flip angle technique. The actual FA mapping requires two images which are acquired with a pair of FAs (α_1, α_2). Dividing the magnitude image of the two FA yields:

$$\alpha_{actual}(r) = \cos^{-1} \left| \frac{SI_{FLASH}(2\alpha)}{2 \cdot SI_{FLASH}(\alpha)} \right|. \quad (4)$$

Methods: All MR imaging was performed using a 12 channel phased array receive coil on the Siemens TIM Trio 3T MRI scanner (Siemens Medical Solutions, Erlangen, Germany). A conventional inversion recovery (IR) gradient echo pulse sequence (TR/TE = 2200/17 ms, 1.6X1.6X3 mm resolution, 128X132 image matrix, echo train = 5, TI = [50 200 400 800 2000]) was used for T₁ mapping of a homogeneous liquid phantom containing cupric sulfate, and this T₁ was used as a reference. Two scans were performed using our hybrid PRF-T₁ sequence with two pairs of nominal FAs ($\alpha_1, 2\alpha_1$) and ($\alpha_2, 2\alpha_2$) where α_1 and α_2 were set to be 19° and 88° respectively for TR = 45 ms and T₁ ≈ 140 ms [4]. The actual FA map of each nominal FA was acquired with TR/TE = 3000/10 ms, single slice, 1.6x1.6x3 mm resolution, 128x76 image matrix, and scan time was 7 min 36 s. Using the variable flip angle method, a T₁ map was derived from the images of the nominal FA α_1 and α_2 which were acquired with the same parameters sets except: TR/TE was 45/10 ms, and the scan time was 20 s for 4 measurements.



Results: Figure 1 shows the actual FA map of the nominal FAs α_1 and α_2 . From these FA maps, the average FA across the phantom for the two nominal angles were found to be $12 \pm 2^\circ$ and $84 \pm 3^\circ$. Figures 2 and 3 display the T₁ map of the phantom using double FA and the standard inversion recovery methods respectively. The mean T₁ of the phantom using the inversion recovery method was found to be 140 ± 0.5 ms which is relatively high compared to the mean T₁ = 126 ± 21 ms value obtained using the variable FA correction method.

Conclusion: Even though the proposed method is in an early investigation stage, we believe that this method can be used to map T₁. The accuracy of the T₁ map depends on a correct FA as well as a good spoiling of the transverse magnetization since equation 2 was derived under the assumption of a perfect spoiling of the transverse magnetization. We believed that the error in the T₁ map is caused by incomplete spoiling of the transverse magnetization. Investigation of this matter is under way, and the result will be presented in future work.

References: [1] Kullervo Hynymen et al. MRM 43:901-904(2000), [2] Todd N et al. ISMRM, 2008, Toronto, Canada, poster 1228, [3] Deoni et al. MRM 49:515-526, 2003 [4] Matthias C. Schabel et al. Phys. Med. Biol. 54 (2009) N1-N8.

Acknowledgements: This work was supported by The Ben B. and Iris M. Margolis Foundation, Siemens Medical Solutions, and NIH R01 CA134599.