B1 Correction using Dual Tau Look-Locker (DrLL)

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Introduction: Transmit B1 inhomogeneity has become an increasingly obvious problem in high field human MRI. As higher field main magnets are used, wavelength effects distort the RF field, leading to image intensity gradients and incorrect values in quantitative maps, in particular in fast T1 and T2 mapping methods such as DESPOT1 and DESPOT2 \cite{1}, which require accurate knowledge of the flip angle. Unlike other double angle method (DAM) based B1 mapping techniques \cite{2,3}, a double angle implementation of the accelerated 3D Look-Locker (DALL) sequence introduced last year \cite{4}, rapidly and efficiently produces a B1 map using low flip angle pulses and additionally yields a corrected T1 map; however, the DALL method still relies on accuracy of the double angle assumption. We present here a novel alternative that avoids this assumption, which we term dual $\tau$ Look-Locker (DrLL). This sequence is run twice using two different values for the timing between identical low angle pulses ($\tau$) in the Look-Locker sequence. This produces a B1 map efficiently and avoids the double angle assumption inherent in other methods.

Methods: The Look-Locker sequence utilizes an inversion pulse followed by a low flip angle, spoiled gradient echo read out train \cite{5}, which can be further accelerated and integrated into a fast 3D imaging acquisition \cite{6}. The sampled recovery curve is similar to a standard inversion recovery curve, but it approaches steady state following a modified time constant, T1*, that depends on the separation between low angle pulses ($\tau$), flip angle ($\alpha$) and T1 value (eq 1). By performing the same experiment and extracting T1* a second time with a different value for $\tau$ ($\tau_1 = \tau_2$), and increasing the time between inversions, TR, to keep the number of $\alpha$ pulses between inversions, N$\alpha$, constant, simple analytical solutions for both $\alpha$ (and hence B1), and corrected T1 can be derived (eq 2 & 3). Increased flexibility in the pulse sequence was also achieved by implementing centric ordering in the slice and phase encoding directions, allowing TR to be fully decoupled from the imaging matrix, the number of reconstructed Look-Locker recovery points, and $\tau$, allowing easier optimization of the sequence.

\[
\frac{1}{T1*} = \frac{1}{T1} + \frac{\ln(\cos(\hat{\alpha}))}{\tau} \quad [1] \quad \hat{\alpha} = \arccos(E^{1/(r-(\tau))}) \quad [2] \quad E1 = \exp\left(\frac{\tau}{T1_{rr}^1} - \frac{\tau}{T1_{rr}^2}\right) \quad [3] \quad \text{efficiency} = \frac{\hat{\alpha}}{\sigma_\alpha/\text{scantime}} \quad [4]
\]

Experiments were performed on a spherical 0.5%-NaCl, 21.8mM-NiCl2 doped agarose-filled phantom (17.5 cm diameter) with a known T1 of 520 ms and on a volunteer head. Optimum imaging parameters were chosen by using a propagation of error analysis based on \cite{7} to optimize the efficiency (eq 4) for a given T1 (assumed to be 520 ms in the phantom and 1200 ms in the head). Based on this analysis, phantom imaging was performed using a 64x64x48 matrix with 5mm slices, 8 Look-Locker recovery points and N$\alpha$ = 384 for both DrlL and DALL, other parameters were chosen to be DrLL = ($\sigma_{\alpha\text{nom}}$ = 11°, $\tau_1$ = 2.8 ms, $\tau_2$ = 10.4 ms, scantime = 5:40 min), DALL = ($\sigma_{\alpha\text{nom}}$ = 6°, $\tau$ = 2.8 ms, scantime = 2:20 min), DAM = (2D GRE,$\alpha_{\text{nom}}$ = 30°, TR = 3s, resolution = 128x128x1, 10mm slice, scan time = 12:48 min) and in vivo imaging was performed using a 64x64x20 matrix with 10mm slices, 8 Look-Locker recovery points and N$\alpha$ = 640 with other parameters: DrLL = ($\sigma_{\alpha\text{nom}}$ = 7° deg, $\tau_1$ = 2.8 ms, $\tau_2$ = 10 ms, scantime = 3:12 min), DALL = ($\sigma_{\alpha\text{nom}}$ = 4° deg, $\tau$ = 3.3 ms, scantime = 1:20 min).

Results: The flip angle map in degrees in figure 1a shows the optimized DrLL image for a central axial slice of the acquisition. A 1D profile through the image is presented in figure 1b showing good agreement between the three different B1 mapping techniques. The in vivo results (figure 2a) show minimal bleed through of the underlying tissue into the flip angle map. A 1D L/R profile is compared to the DALL and DrLL technique is that they also provide B1 maps resolved in the z-direction (not shown) allowing for slab profile correction. The additional benefit of the DrLL technique is that it does not require accurate linearity of the RF system, which is a fundamental requirement for all double angle methods. With a reduced resolution or number of Look-Locker recovery points, DrLL could be implemented as a two breath hold acquisition, important if B1 correction is to be performed in the abdomen.

Discussion and Conclusion: The DrLL method produces a full 3D B1 flip angle map in a short time period that shows good agreement with the existing DALL and DAM methods. This novel 3D B1 mapping method can use the identical RF pulse used in the imaging sequence (such as the fast T1 and T2 mapping techniques for which we require B1 correction) and thus will correct for not only wavelength effects, but also any slab profile based variation in the flip angle, all in several minutes and without relying on the double angle approximation.