T1 corrected fat quantification using a dual flip angle acquisition and joint fit reconstruction

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Target audience: Researchers and clinicians interested in liver fat quantification

Purpose: Chemical shift-encoded (CSE) fat quantification methods can provide accurate quantification of the proton density fat-fraction (PDFF) over the entire liver, showing great promise for detection and treatment monitoring of non-alcoholic fatty liver disease (NAFLD). However, the estimation of PDFF may be biased by confounding factors such as B_0 inhomogeneity, R_2^* ($=1/T_2^*$), and T_1 relaxation[1], if they are not accounted for. T_1 related bias in spoiled gradient echo (SGRE) acquisitions can be minimized by using a small flip angle (SFA) approach[1,2,3]. Unfortunately, the SFA method results in reduced SNR and has some residual bias. In this study, we propose a joint fitting of T_1, B_0, R2* and PDFF based on multi-echo dual-flip-angle SGRE acquisition to perform T_1-corrected fat quantification, with the aim of improving SNR relative to existing methods.

Theory: T_1 bias can also be corrected using a dual flip angle method[4] (DFA), where two acquisitions at different flip angles are performed. In prior DFA methods (standard DFA), T_1, B_0, R2*, fat and water are estimated for each flip angle, before the two sets of measured water, fat signals are used to eliminate the T1 weighting, inherently correcting the PDFF estimate for T_1 effects. The standard method introduces two redundant parameters by estimating R2* and B_0 twice, for each flip angle, respectively, without imposing the constraint that R2* and B_0 should be equal for both flip angles.

A general signal model in CSE fat quantification in the context of an SGRE acquisition can be written as:

$$s_{n,q} = e^{i(2\pi\Delta B_0 \cdot TE_n)} \cdot e^{-R2^* \cdot TE_n} \cdot \left(We^{i\phi}\frac{(1-\sin(\beta_q))e^{-TR/T_{1w}}}{(1-\cos(\beta_q)e^{-TR/T_{1w}})} + Fe^{i\phi}\frac{(1-\sin(\beta_q))e^{-TR/T_{1f}}}{(1-\cos(\beta_q)e^{-TR/T_{1f}})} \cdot \sum_{p=1}^{P} \alpha_p e^{i2\pi \cdot f_p \cdot TE_n} \right)$$

where $s_{n,q}$ is the signal acquired at echo time TE_n, flip angle β_q. The unbiased signals of water and fat are denoted as W and F. The common initial phase is ϕ. Spectral modeling of fat was used, where α_p, ω_p denote the relative amplitude and chemical shift, respectively, of each spectral peak of fat. In our proposed method (joint DFA), signals are acquired at 6 echo times and 2 different flip angles, and subsequently fit into the signal model above to estimate the parameters (W, F, ϕ B_0, R2*, T_{1w}, T_{1f}) using least-squares fitting. PDFF is calculated as F/(W+F) including noise bias correction[4].

Methods: The noise performance of the proposed method was compared with SFA and standard DFA using Cramer-Rao lower bound (CRLB) and Monte-Carlo simulation. The simulated environment is a voxel with PDFF ranging from 0% to 100%. T_1 of water and fat are assumed to be a pair of typical values[5] at 1.5T: T_{1w}=583ms, T_{1f}=343ms. R2*= 40^{-1}, ΔB_0=2ppm, ϕ=0. Simulated signals in a 1.5T system using 6 echo SGRE acquisition with TR = 15ms, TE_{min} =1.2ms, ΔTE=2.0ms were generated. Flip angle of 3° was used for SFA. Flip angle pair (8°,49°) was chosen for standard DFA and joint DFA to minimize the lower bound of the variance of the PDFF estimate predicted by the CRLB.

Monte-Carlo simulation of SFA, standard DFA and joint DFA was also performed to validate the CRLB predictions. This simulation used 1000 trials for 24 PDFF values between 0% and 100%. Gaussian noise was added such that SNR=25 at a flip angle of 3°, also adjusted to compensate for difference in scan times. For both standard and joint DFA, T_1 constraints (0ms<T_{1w},T_{1f}<2000ms) were applied to prevent unstable water or fat estimates for very low or high fat fraction[4]. Variances of the estimators of PDFF and R2* were calculated from this simulation. The corresponding CRLBs were calculated with the same parameters for SFA, standard DFA and joint DFA.

Results: Excellent agreement between Monte-Carlo simulations and the CRLB was observed in Figure 1, indicating that our least-squares estimator is efficient, and that the CRLB accurately predicts the noise performance of the 3 methods. For both DFA methods, the agreement breaks down when PDFF is near 0% or 100%, due to signal model instability and the effects of T_1 constraints.

Lower variances in PDFF estimate for both standard and joint DFA relative to SFA were observed for PDFF values below 60%. Standard and joint DFA both showed significantly lower noise in R2* estimate compared with SFA. Joint DFA results in a slightly lower variance in PDFF estimate and R2* estimate than standard DFA.

Conclusions: CRLB analysis and Monte-Carlo simulations both demonstrate an SNR advantage for the proposed joint DFA method, compared with standard DFA and SFA methods.

References: [1] Meisamy, et al, Radiology 2011; 258:767-775. [2] Hines, et al, JMRI 2011;33:873-881. [3] Hines, et al, Radiology 2011;258:767-775.[4] Liu, et al, MRM 2007;58:354-364. [5] de Bazelaire, et al, Radiology 2004;230:652-659.
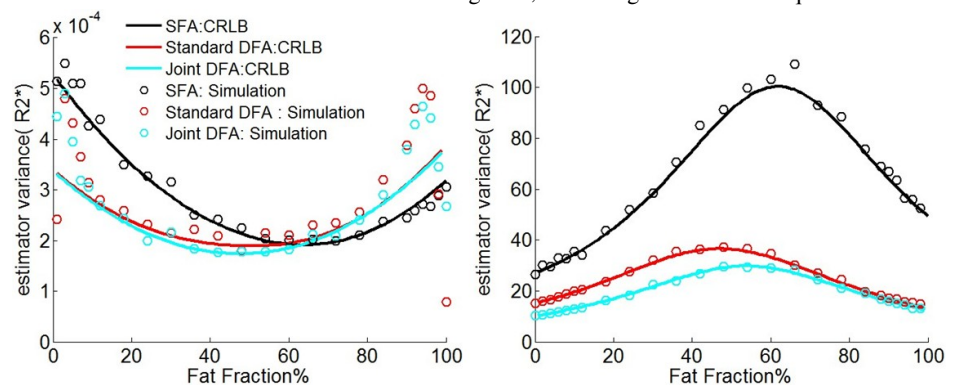
Figure 1. Joint DFA (proposed method) has slightly better noise performance compared with standard DFA in both PDFF and R2* estimate as shown in variance of PDFF and R2* estimate predicted by Cramer-Rao lower bound (CRLB) and Monte-Carlo simulation. Excellent agreement between CRLB and simulations was observed. Both standard and joint DFA reduced noise in R2* estimate compared with SFA method. Joint and standard DFA have lower noise in PDFF estimate than SFA at low PDFF values (PDFF<60%).