

## Evaluation of Sensitivity of Fat Fraction Measurement to Fat Spectral Model Precalibration

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**Target audience:** Researchers and clinical scientists working on liver fat quantification

**Purpose:** Multi-echo chemical shift encoded (CSE) fat water imaging can quantify liver fat accurately over the entire liver in a single 20s acquisition. It has been shown that multi-peak spectral modeling of fat, compared with single peak model of fat, is necessary for accurate fat quantification<sup>1</sup>. Different groups have reported different spectral models of fat (triglycerides) in the liver<sup>2-5</sup>, and it is unknown how these differences will impact the technical accuracy and reproducibility of fat quantification if different spectral models of fat are used. The purpose of this work is to evaluate the sensitivity of chemical shift encoded fat quantification to different spectral models of fat.

**Theory:** In multi-echo CSE imaging, the complex signal acquired in each voxel can be written as:  $s_{t_e} = (\rho_w + \rho_f \sum_m a_m e^{-j\Delta\omega_{f,m}}) e^{-j\Delta\omega_0} e^{-r_2^2 t_e}$ .  $t_e$  denotes the echo time,  $\rho_w$ ,  $\rho_f$  are proportional to proton density of fat and water.  $\Delta\omega_0$  refers to static field shift while  $\Delta\omega_{f,m}$  and  $a_m$  refer to the frequency shift and relative amplitude of the m-th peak in a fat spectral model. Fat and water proton density can be recovered with a non-linear least-squares fit of variables  $(\rho_w, \rho_f, \Delta\omega_0, r_2^2)$ . Due to eddy current induced phase error, a mixed fitting scheme is applied. In mixed fitting, the phase of the first echo is discarded leaving a magnitude signal for the first echo and complex signal for the rest. Fat is quantified by calculating proton density fat fraction as  $\rho_f / (\rho_w + \rho_f)$ . In addition to a basic single-peak model, six different fat models were examined in this study: 6- and 9-peak models calibrated by Hamilton et al, 7-peak model calibrated by Ren et al, 4- and 5-peak fat models derived by Wokke by merging peaks that are close together in the 6 peak model, and 3- peak model calibrated by Yu et al using 16-echo SPGR signal.

**Methods: Simulation:** In simulation study, MR signal is generated using the equation shown above assuming one of the fat models to be the true fat MR spectrum. Generated signal is processed with the mixed fitting algorithm using another fat model (“estimation” model) to render a fat fraction estimate. In simulation, proton density fat-fraction was assumed to be 30%,  $TE_{min}=1.2ms$ ,  $\Delta TE=2.0ms$ , 6 echoes were generated. For each combination of true fat model and estimating model, a fat-fraction estimate error is calculated.

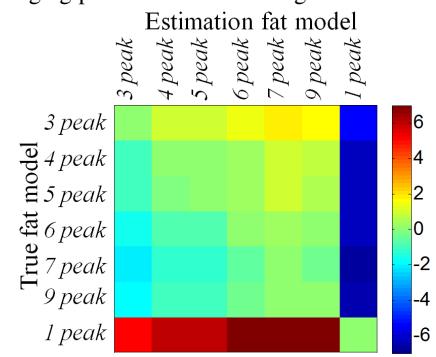
**In vivo liver study:** In vivo liver datasets from a study of 38 patients were analyzed. These datasets were acquired using a whole-liver 3D SPGR scan,  $TE_{min}=1.2ms$ ,  $\Delta TE=2.0ms$ , 6 echoes. A single-voxel STEAM-MRS was acquired in every subject to provide a reference fat-fraction (measured from STEAM data using AMARES fitting in jMRUI, including correction for T2 decay). A fat-fraction map was generated from SPGR data using the mixed fitting algorithm with each fat model listed above respectively. For each fat model, a mixed fitting fat-fraction was measured from the fat-fraction maps, co-localized with the STEAM voxel. A linear regression was subsequently performed between mixed fitting fat fraction using each model and spectroscopy measured fat fraction to investigate the impact of fat model on the accuracy of CSE fat quantification.

**Results:** Figure 1 shows the estimation error for each combination of true fat model and estimation fat model. These results demonstrate that differences between multi-peak spectral models lead to small errors in fat quantification, typically under 2% at a true fat fraction of 30%. However, the differences between single peak fat model and multi-peak fat models introduce errors up to 7% in fat fraction. Spectroscopy fat fraction of all patients average 8.26, with a median of 3.63. Linear regression results from in vivo liver data are shown in Table 1. A slope near 1.0 and intercept near 0.0 indicate accurate fat quantification compared with the spectroscopy reference. Single peak model in the statistical analysis results in a slope significantly different from 1 ( $P=9.8\times10^{-15}$ ). All multi-peak models result in a slope not significantly different from 1 ( $p>0.05$ ) with the exception of 3 peak model ( $p=0.004$ ). Nevertheless, the error with a 3 peak model is significantly smaller than that with a single peak model.

**Conclusions:** The use of spectral modeling of fat is needed for accurate CSE fat quantification. However, the specific choice of spectral model (among recently proposed choices) has a much smaller impact on fat quantification accuracy.

**References:** [1]Hernando et,al. MRM 2010;64:812-822.[2]Hamilton et,al. NMR Biomed 2010;24(7):784:790. [3]Ren et,al. JLR 2005;49:2055-2062. [4]Wokke et al. JMRI 2012;38(3):619-624. [5]Yu et al.MRM 2008;60(5):1122-1134.

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**Figure 1.** Fat fraction estimate % error in simulation. Signal is generated using true fat model at 30% fat fraction, fat fraction is estimated using estimation model. the difference between single peak and multi peak has a much bigger impact on estimate error than the differences between multi peak models

fat model	3 peak	4 peak	5 peak	6 peak	7 peak	9 peak	1 peak
slope	0.93 ±0.05	0.97±0.06	0.97±0.06	1.00±0.05	1.04±0.05	1.03±0.05	0.75±0.04
intercept	-0.31±0.63	-0.30±0.66	-0.30±0.67	-0.31±0.62	-0.25±0.64	-0.30±0.63	-0.38±0.45
R <sup>2</sup>	0.975	0.976	0.976	0.979	0.980	0.980	0.974

**Table 1.** Linear regression between mixed fitting fat fraction using each model and spectroscopy fat fraction. A slope close to 1.0 was observed for each multi-peak model but not with the single peak model. Spectroscopy fat fraction of all patients average 8.26, with a median of 3.63. Linear regression results from in vivo liver data are shown in Table 1. A slope near 1.0 and intercept near 0.0 indicate accurate fat quantification compared with the spectroscopy reference. Single peak model in the statistical analysis results in a slope significantly different from 1 ( $P=9.8\times10^{-15}$ ). All multi-peak models result in a slope not significantly different from 1 ( $p>0.05$ ) with the exception of 3 peak model ( $p=0.004$ ). Nevertheless, the error with a 3 peak model is significantly smaller than that with a single peak model.