

Chemical shift-based water/fat separation: comparison of fitting models

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INTRODUCTION

Quantitative water/fat separation in MRI requires careful modeling of the acquired signal. Multiple signal models have been proposed in recent years, but their relative performance has not yet been established. This abstract presents a comparative study of 12 signal models for water/fat separation. The models were selected according to three criteria: magnitude or complex fitting [1-4], single-peak or multi-peak fat spectrum [2,5], and modeling of T2* (or R2*=1/T2*) decay [2,6]. The study uses theoretical Cramer-Rao Lower Bound (CRLB) results, simulation results, phantom and in vivo data. Comparisons are based on the bias and standard deviation of fat amplitude and fat fraction estimates.

METHODS

Phantom construction: A water fat phantom was built by mixing water and oil in separate vials, with fat fractions (%): 0, 10, 20,30,40,50,60,70,100 [1,7].

Data acquisition: Phantom data were acquired using a spoiled GRE sequence with monopolar readout (flip angle=25°/TR=2000ms/SNR≈90 and flip angle=8°/TR=500ms/SNR≈30), 8 TEs with initial TE=1.43ms and TE spacing=2.23ms (the same TEs used for CRLB and simulations). The acquisition was repeated 128 times to obtain “Monte-Carlo” phantom measurements. In vivo (liver) data were acquired with the same TEs using a segmented, cardiac triggered sequence. Simulations and CRLB used true R2* values of 42ms⁻¹ and 54ms⁻¹ for water and fat, respectively (means of R2*s measured in the phantom).

Processing: Data were fitted by nonlinear least-squares, according to the following models: magnitude and complex fitting (2 alternatives); single- and multi-peak fat (2 alternatives); no-R2*, one-R2* and two-R2* decay models (3 alternatives). Magnitude fitting was initialized with the estimates from complex fitting (as proposed in [4]), to avoid the ambiguities for fat fractions above 50%. Phantom multi-peak fat calibration was performed from an additional 32-point acquisition.

RESULTS AND DISCUSSION

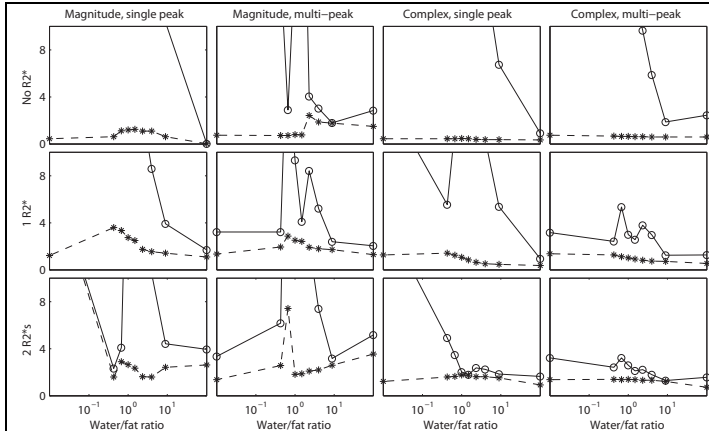


Figure 1. Phantom fat amplitude standard deviation (stars) and RMSE (circles).

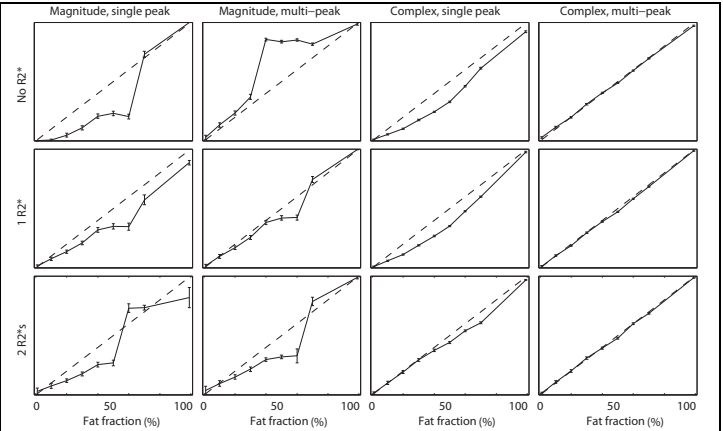


Figure 2. Phantom fat fraction estimates: means and standard deviations.

Figures 1 and 2 show phantom results for the high SNR dataset, comparing the 12 models. Figure 3 shows in vivo fat fraction results, which are qualitatively in good agreement with the phantom results.

From these results, we extract the following observations: 1) For the simpler models, the bias component of the RMSE often outweighs the standard deviation component. 2) Complex fitting is almost uniformly superior to magnitude fitting. This is in good agreement with CRLB analysis and simulations (not shown). Note that, in cases where significant phase distortions are present (e.g., due to eddy currents), magnitude fitting may be advantageous [4]. 3) Multi-peak fat modeling has significantly reduced bias with respect to single-peak [5]. 4) No-R2* models produce significant bias in fat amplitude estimation. However, in the complex-fitting, multi-peak case (with the present data) this bias is largely compensated by a similar bias in water amplitude estimation. 5) Among complex-fitting, multi-peak fat models, the choice between one-R2* and two-R2* depends on the true fat fraction and the SNR (SNR dependence not shown), in addition to the dependence on the R2* difference between water and fat [6].

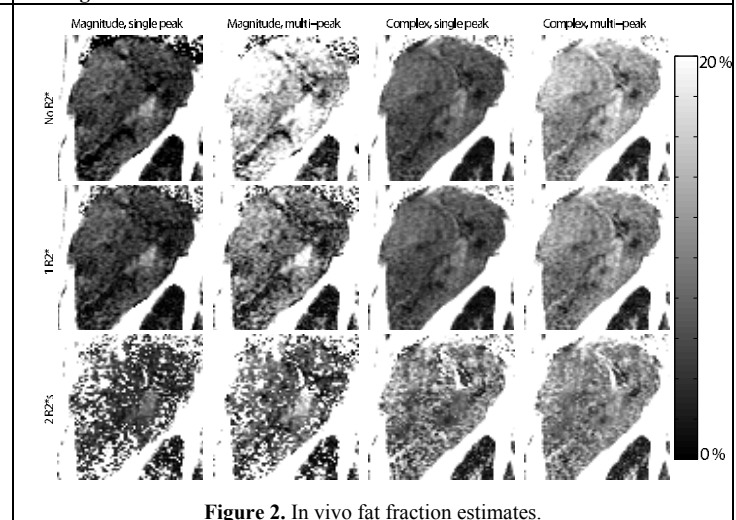


Figure 2. In vivo fat fraction estimates.

CONCLUSION: From the models considered in this work, complex-fitting, multi-peak fat models provide the best results for fat quantification. Among these, the one-R2* model is preferable over a wide range of fat fractions and SNRs that are clinically relevant.

REFERENCES: [1] Bernard CP *et al*, JMRI, 27, 192-197, 2008. [2] Yu H *et al*, MRM, 60:1122-1134, 2008. [3] Bydder M *et al*, MRI, 26:347-359, 2008. [4] Yu H *et al*, ISMRM 2009, p. 461. [5] Reeder SB *et al*, JMRI 29:1332-1339, 2009. [6] Chebrolu VV *et al*, ISMRM 2009, p. 2847. [7] Hines CD *et al*, MRM 30:1215-1222, 2009.