A Systematic Evaluation of an Auto Regressive Moving Average (ARMA) Model for Fat-water Quantification and Simultaneous T_2^* Mapping

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Introduction: Assessment of hepatic iron content is an emerging clinical application of quantitative T_2^* MRI [1,2]. In this context multi-echo gradient echo (mGRE) images are acquired in a single breath hold and the signal decay is evaluated. One of the major confounding factors in T_2^* quantification arises from lipids (e.g. in hepatic steatosis) which introduce additional modulations to the mGRE signal. Fortunately, these lipid modulations can be accounted for during the mGRE signal analysis [3]. Advanced techniques such as T_2^*-IDEAL [4,5] capitalize on these modulations to quantify the tissue's water and fat content and respective T_2^* times. Recently, an alternative approach for spectral parameter estimation based on mGRE acquisitions has been presented employing an autoregressive moving average (ARMA) model [6,7]. Here, we present a systematical analysis of ARMA for fat-water quantification and simultaneous T_2^* estimation, and compare ARMA modeling with conventional magnitude fitting techniques in phantom and volunteer scans.

Materials & Methods: Neglecting B_0 inhomogeneities and noise, the mGRE signal $S(TE_j)$ at the individual echo times (TE_j) can be expressed via Eq. A (see box) where C_k is the complex amplitude, $\Delta\omega_k$ the shift of the proton resonance frequency (PRF) relative to the PRF of water protons (i.e. $\Delta\omega_{water} = 0$ ppm), and $T_{2,k}^*$ the apparent spin-spin relaxation time of the k^{th} chemical specimen contributing to the MR signal (i.e. water, methylene, methyl etc.). This equation describes an ARMA model of the mGRE signal which can be used to determine the amplitudes, PRF shifts, and T_2^* times of each of the underlying chemical specimen via an iterative Stieglitz-McBride algorithm by representing the signal evolution as a rational polynomial in the z-domain [6,7].

$$(A)\quad S(TE_j) = \sum_{k=1}^{N} C_k \cdot e^{-\left(i\cdot 2\pi\cdot\Delta\omega_k + 1/T_{2,k}^*\right)TE_j}$$

$$(I)\quad S(t) = \left|\rho_W \cdot e^{-t/T_{2,W}^*} + \rho_F \cdot e^{-t/T_{2,F}^*} \cdot e^{-i\left(2\pi\cdot(\Delta\omega_F+\delta\omega)t+\varphi\right)}\right|$$

$$(II)\quad S(t) = \left|\rho_W \cdot e^{-t/T_{2,W}^*} + \sum_{p=1,2} \rho_{F,1} \cdot e^{-t/T_{2,F,p}^*} \cdot e^{-i\left(2\pi\cdot(\Delta\omega_{F,p}+\delta\omega)t+\varphi\right)}\right|$$

$$(III)\quad S(t) = \left|\rho_W \cdot e^{-t/T_{2,W}^*} + \rho_F \cdot e^{-t/T_{2,F}^*} \cdot \sum_{q} a_q \cdot e^{-i\left(2\pi\cdot(\Delta\omega_{F,q}+\delta\omega)t+\varphi\right)}\right|$$

Equation A can also be employed to directly fit the mGRE signal using appropriate fitting equations [3-5,8,10]. We compare 2-, 3-, and 4-peak ARMA models to three different fitting scenarios (implemented in MATLAB): Eq. (I) models the mGRE magnitude signal consisting of two separate chemical peaks – water and one fat specimen (i.e. bulk methylene, PRF shift $\Delta\omega_F = 3.4$ ppm) [8], (II) assumes three independent chemical peaks – water and two fat peaks (peak 1: bulk methylene, PRF shift $\Delta\omega_1 = 3.4$ ppm, peak 2: terminal methylene, PRF shift $\Delta\omega_2 = 2.6$ ppm), (III) accounts for a multi-peak fat spectrum (relative fat amplitudes a_q and PRF shifts $\Delta\omega_{F,q}$ according to [9]) and assumes the same T_2^* time for each fat specimen. This model has been considered as the "true" signal model [10]. All fitting equations account for a small frequency offset $\delta\omega$ due to potential temperature shifts of the PRFs (reference values in [9] reported for body temperature) and include an initial phase offset φ.

To study the ARMA model for fat-water T_2^* quantification, cylindrical phantoms (volume: 600 ml) were made from 1 % agar-water mixtures and peanut oil [11] with fat concentrations ranging from 0% up to about 50%. 2D mGRE images ($TR/TE_1/\Delta TE$ = 200/1.07/1.52 ms, 32 echoes, α = 10°, FOV =256×256 mm^2, matrix: 128×128, slice thickness: 10 mm) were acquired for each phantom at 1.5 T (Siemens Avanto) with the MR system's head coil. Finally, ARMA fat-water quantification was compared to fitting results via Eq. (III) in a healthy volunteer (2D mGRE acquisition at 1.5 T within one breath hold: $TR/TE_1/\Delta TE$ = 200/1.07/1.27 ms, 20 echoes, α = 35°, FOV =400×325 mm^2, matrix: 128×104, slice thickness: 10 mm).

Results & Discussion: Fat fractions estimated from data fitting via Eqs. (II) and (III) are in excellent agreement to the theoretical values except for the phantoms with the lowest fat concentrations (Fig. 1a) which could be explained by instabilities of the non-optimized fitting routines due to the low fat signal for these phantoms. Nearly identical fat fractions were found with the 2-peak ARMA model and fitting via Eq. (I), but both methods systematically underestimate the fat content towards higher fat fractions. The 3-peak ARMA analysis fails for fat concentrations < 25% as the signal contributions from fat are too low to reliably identify two separate fat peaks. For fat fractions > 25%, 3-peak ARMA fat fractions are very consistent with the expected values. However even for the highest fat fractions, the 4-peak ARMA is not able to localize a third independent peak leading to completely erroneous fat content estimates. Water T_2^* times obtained from the three fitting models and the 2-peak ARMA are in excellent agreement showing a gradual decrease of water T_2^* with increasing fat content (Fig. 1b). Similar to the findings on the fat fraction, water T_2^* values from the 3-peak ARMA are consistent for fat fractions > 25%. Over the entire range of fat fractions, fat T_2^* seems to be almost independent of the water/fat composition, and the values from the fitting models (I) and (III) as well as the 2-peak ARMA appear in good agreement (Fig. 1c). The 3-peak fit model (Eq. (II)) indicates a fat component with a longer T_2^* (peak 1) and another short T_2^* component (peak 2) where the longer T_2^* component is consistent with the estimates from the other models. The fat T_2^* values from the 3-peak ARMA are in excellent agreement to the 3-peak fit for the phantoms with a fat content > 25%. *In vivo* fat fraction maps (Fig. 2) obtained from 2-peak ARMA and fitting via Eq. (III) appear very consistent with mean hepatic fat fractions of 10.5±1.4% and 11.0±1.6 %. With the fitting approach, ambiguities can occur when water and fat amplitudes are swapped due to non-optimized fitting routines leading to apparently low/high fat fractions (see arrows).

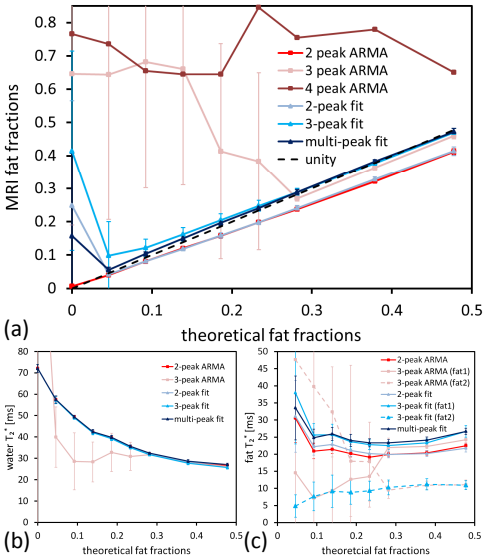

Fig. 1: (a) MRI fat fractions measured in fat-water phantoms. (b)/(c) Water/fat T_2^* times estimated from the different models.

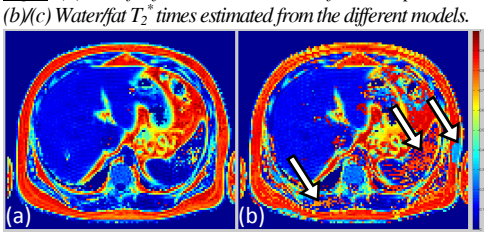

Fig. 2: Axial fat fraction maps in healthy volunteer from 2D mGRE acquisition for (a) 2-peak ARMA and (b) fit via Eq. (III).

Overall, our preliminary data suggest that ARMA can be used for a successful simultaneous fat and water T_2^* analysis. For correct fat-water quantification, an iterative approach should be pursued by step-wise incrementing the number of separate peaks as long as the peaks can be reliably localized. A quantitative criterion could be based on the standard deviations of the calculated $\Delta\omega_k$ values which were here below 10 Hz (≈ 0.1 ppm) for correctly detected peaks. As reported by previous studies [3-5,10], our analysis also demonstrates that correct fat-water T_2^* quantification is challenging due to the complexity of the fat spectrum. In contrast to existing techniques, e.g. [3-5,8], ARMA does not require any prior knowledge of the spectral location of the peaks and seems to be less sensitive to signal ambiguities as seen with our fitting methods. As discussed in prior work [6,7], ARMA needs minimal user interaction and allows for fast computation times (2-peak ARMA vs. *non-optimized* fit: 22 s vs. 71 s, Intel Xeon CPU @ 2.66 GHz). However, multi-peak ARMA modeling requires a sufficiently high fat signal, otherwise localization of the individual peaks and hence fat-water T_2^* estimation fails. Our future work will address a more detailed evaluation especially in scenarios with higher fat content and in the presence of iron. As noted previously [3], the increasing fat concentration shortens water T_2^* which should also be investigated further for purposes of reliable iron overload assessment in the presence of fat.

References: [1] Anderson LJ et al. Eur Heart J 2001;22:2171-9. [2] Wood JC et al. Blood 2005;106:1460-5. [3] Bydder M et al. MRI 2010;28:767-76. [4] Yu H et al. MRM 2008;60:1122-34. [5] Vasanawala SS et al. MRM 2012;67:183-90. [6] Taylor BA et al. MedPhys 2008;35:793-803. [7] Taylor BA et al MedPhys 2009;36:753-64. [8] O'Regan DP et al. Radiology 2008;247:550-7. [9] Hamilton G et al. NMR Biomed 2011;24:784-90. [10] Reeder SB et al. MRM 2012;67:389-404. [11] Hines CDG et al. JMRI 2009; 30:1215-22.