Performance comparison of two signal decay models in assessment of T2-star (T2*) for diagnosis of myocardial iron overload by multiecho cardiovascular magnetic resonance

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Introduction: Magnetic resonance imaging (MRI) is able to measure the iron overload in myocardial tissue, exploiting the fact that paramagnetic iron compounds produce susceptibility variability shortening the T2-star (T2*) relaxation time. In order to evaluate the T2* value, the MR signal is monitored at several echo times (TEs), a mathematical model of the signal decay dependence from T2* is introduced, and T2* is estimated as the value that realizes the best fitting of the MR signal with the decay model. In this study, effectiveness of two decay models is compared by exploiting both software simulation and real data analysis.

<u>Materials and methods</u>: The dependence of the MR signal from TE can be modelled as a multi-exponential decay, where each exponential represents the signal decay related to a particular tissue. Although bi-exponential signal decay model was successfully used in human liver studies, the most popular decay models in heart studies are the single exponential decay model [1,2] (S-EXP, Eq. 1) and a simplified bi-exponential model [3] (C-EXP, Eq 2) that uses a constant value instead of the second, slowly varying, exponential.

$$S = S_0 e^{\frac{TE}{T2^*}} (1) \qquad S = S_0 e^{\frac{TE}{T2^*}} + C (2) \qquad S = (1 - \lambda) S_0 e^{\frac{TE}{T2^*}} + \lambda S_0 e^{\frac{TE}{T2^*}} + n_R (3)$$

Synthetic decay curves were randomly generated using the Eq. 3 with parameters assessed from the observation of real MR multiecho heart images. Hence, S₀ is the signal value at the lower TE (gaussian distributed, mean=174, SD=65), $n_{\rm R}$ represents simulated Rician distributed noise with σ =5.1, T2_b* was assumed to be 200 ms, similar to oxygenated blood, and λ was assumed to be 0.1. Random T2* values were generated from an uniform distribution in the range 1:60 ms. Synthetic curves were sampled at ten echo times (2.0, 4.2, 6.4, 8.6, 10.8, 13.0, 15.2, 17.4, 19.6 21.8), mimicking the TEs used in clinical studies.

Synthetic decay curves were fitted by the S-EXP and the C-EXP models, using the Levenberg-Marquardt algorithm. Test on real data was performed on decay curves corresponding to one-pixel ROIs, evaluated on the myocardium of thalassemia intermedia/major patients with assessed global T2* ranging from 1.0 to 60 ms. Informed consent was obtained from all subjects.

<u>Results</u>: Results of the simulation performed on 10,000 synthetic curves are shown in figure (A). The error in assessment of T2* is plotted vs. the simulated T2* value for C-EXP and S-EXP models. About five-thousands curves extracted from real multi-echo images were also analyzed. The fitting error (i.e. the mean square error between the curve and the best fitting model) in synthetic and real data analysis was plotted in (B) vs. the estimated T2* value for both models.

Discussion and Conclusions: The proposed simulation correctly predicts the fitting error in both models. As expected, for low T2* values (T2*<25 ms), the C-EXP model is able to estimate T2* with good precision, while the S-EXP model introduces a noticeable error [3]. Although the problem can be solved excluding higher TEs from the analysis [1,2], C-EXP model may be preferable for assessing relaxation time values in the range 0:25 ms (that is the range of clinical interest) for the chosen TEs. Both models provide good fitting performances at high T2* values (T2* \geq 25 ms). However, the C-EXP model progressively underestimates T2*. The reason of this phenomena is likely the overestimation of the *C* value in the C-EXP model for high T2* values, due the fact that the fitting algorithm may be trapped in local minima. Figure C shows two good-fitting realizations of the C-EXP model realizations with underestimated (27 ms) and correct (40 ms) T2* values provide almost the same fitting algorithm. The S-EXP model doesn't suffer this problem and should be preferred when precise assessment of T2* values in the normal range is important.

<u>References:</u> [1] Pepe A et al. JMRI 2006;23(5):662-668. [2] Westwood M et al. JMRI 2003;18(1):33-39. [3] Ghugre NR et al. JMRI 2006;23(1):9-16.

