Fast and Accurate Two-Component Relaxometry with EPG Simulations and Dictionary Searching

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Target Audience

Researchers and clinicians interested in relaxometry

Purpose In the recent years, transverse relaxometry has been increasingly used as a biomarker to monitor tissue damage and abnormalities in many diseases. One of the most widespread approaches is to perform a mono-exponential regression on Multi-Slice Multi-Echo (MSME) data. Since it is known that the performance of this method is impeded by the presence of stimulated echoes in the signal, several authors have proposed more complex signal models to compensate for these effects with good results [1–4]. In these approaches, the effect of imperfect refocusing of the spins due to local deviations of the effective flip angle from the nominal value of 180° is simulated using the Bloch equations directly [3] or the Extended-Phase-Graph (EPG) formalism [1,4]. Fitting these models onto the acquired data is generally achieved using non-linear optimization techniques pixel-by-pixel at the cost of a prohibitive computing time. Some authors have proposed dictionary-based solving methods which greatly increase the speed without sacrificing the accuracy [3,4]. Nevertheless, single-component models are not reliable in cases where the MSME signal is a combination of several decays of different T2. For example, some neuromuscular disorders cause fatty infiltrations within the muscles, yielding a signal that is a mix of water and fat T2 components. The case of 2-component signals has been addressed by estimating the distribution of T2 via a pixel-wise non-negative least-square (NNLS) fitting of an EPG model, again at the cost of long processing times [2]. We propose a simpler and faster approach where a 2-component EPG model is explicitly fitted by dictionary searching, with one T2 fixed (e.g. the fat component), which should cover a large number of cases.

Material and methods

Acquisitions. Tests were performed on MSME data of twenty four patients' thighs with different degrees of fatty infiltration, acquired on a 3T whole-body scanner (Tim Trio, Siemens Healthcare). The following parameters were used: TR=3000 ms, nominal flip angles = 90 / 180°, 17-echo train, (TEs: from 9.5 to 161 ms, ES = 9.5 ms), FOV = 224x448 mm^2, pixel size = 1.4x1.4 mm^2, 10 slices (TH = 10mm, slice gap = 25 mm), Tacq = 3 min 41 s.

Processing. Using an in-house EPG simulation program written in Python, a dictionary of water and fat signal decays was generated for multiple water T2 and flip angle values. There were 10000 entries in the dictionary, with 200 T2 values between 20 ms and 60 ms and 50 values between 0.2 and 1, representing fractions of the nominal flip angle (e.g. fractions of 180° for refocusing pulses), and aim at taking into account the deviations from the nominal B1 perceived by the spins. The T2 of fat was first estimated on the subcutaneous fat using a single component EPG model and subsequently fixed at its average value of 135 ms (which is consistent with the literature [6]). The water and fat T1 were respectively set to 1400 ms and 365 ms using values from the literature [6]. The fat fraction in the muscle was estimated by solving the non-negative least square (NNLS) problem (Eq. 1) where the water and fat signal amplitude are respectively denoted as *w* and *f*, the observed signal decay as vector **y** and the simulated signal decays for water and fat from the i-th dictionary entry as vectors $\mathbf{d}_i^w$ and $\mathbf{d}_i^f$ respectively. The optimal pair (T2$_w$, B1) for each pixel was determined by minimizing the model of Eq. 1 over all dictionary entries. For comparison, the same model, with identical parameters, was fitted to the same data with a non-linear optimization using a modified version of the Lebel toolbox (modifications were necessary to allow setting a different T1 for each component). All results were computed on a 2.70GHz Intel CPU and 8Go RAM system.

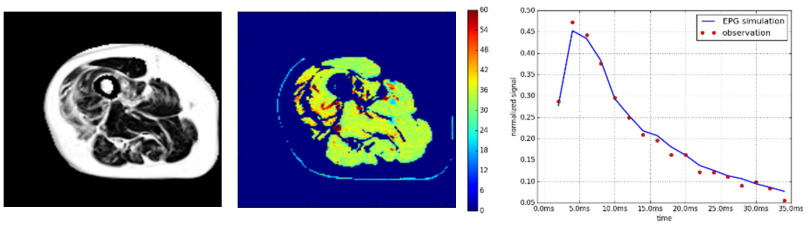

Fig 1. (left) fat fraction map and (middle) water T2 map (ms) obtained with our method on a fatty-infiltrated thigh; (right) observed and simulated signal decays in one pixel located in the Rectus Femoris muscle (red square) with FF=14%, T2=28.2ms, effective FA=65°.

$$\begin{bmatrix} w \\ f \end{bmatrix} = \arg\min_{w,f \geq 0} \left\| \mathbf{y} - \begin{bmatrix} \mathbf{d}_i^w & \mathbf{d}_i^f \end{bmatrix} \begin{bmatrix} w \\ f \end{bmatrix} \right\|_2 \quad \textbf{(Eq. 1)}$$

	Average difference ± 1.96*SD
T2 mapping (ms)	0.06 ± 0.73
Fat fraction (%)	1.46 ± 1.96

Table 1. Differences in T2 and FF between the non-linear optimization from [1] and the proposed method measured on 24 patients.

	1 pixel	All slices
Non-linear fit	24ms	5086s
Proposed method	1.29ms	273s

Table 2. Differences in processing time between the non-linear fitting and the proposed method for 1 pixel and one representative volume in our database.

Results Results obtained with the two methods on the same data were compared pixel-by-pixel in regions of interest (ROI) drawn inside the muscles. Differences in T2 and Fat fractions computed on all subjects are indicated in Table 1, showing significant ($p < 0.05$) but limited biases. Figure 1 shows fat fraction and T2 maps of the same slice, generated with the proposed method, and the comparison of the observed and simulated signal decays for one pixel of this slice. The given example shows the successful fitting of a signal comprised of a fat and a water component and affected by stimulated echoes. Differences in processing times between the two methods are displayed in table 2 and indicate a time gain of almost 20 using the proposed method.

Discussion and Conclusion The presented results demonstrate that an EPG-based two-component signal model associated with a dictionary-searching optimization can be used to provide accurate transverse relaxometry maps in a few minutes on a desktop computer. Although the tests were perform in the context of musculoskeletal studies and water/fat T2 components, we believe that the proposed approach could appeal to all researchers and clinicians interested in all types of multi-component T2-mapping. Another benefit is that only a very standard sequence is involved, easily available on clinical scanners. Future work includes increasing the number of components as well as additional efforts to reduce the computing time (e.g. through parallelization).

References

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