# Comparison of T2* correction methods for vertebral bone marrow fat quantification using chemical shift encoding-based water-fat imaging

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**Target audience:** Scientists and clinicians interested in water-fat imaging and bone marrow fat quantification

**Purpose:** Chemical shift encoding-based water-fat imaging methods have been emerging for vertebral bone marrow fat quantification, as they can overcome the spatial resolution limitations of the single-voxel MRS and provide high-resolution fat fraction (FF) mapping across multiple vertebral bodies with growing applications in osteoporosis [1] and radiation therapy [2]. Vertebral bone marrow is embedded within the cavities of the trabecular bone matrix and it is therefore characterized by short $T_2$* relaxation times. Previous work in iron-loaded liver fat quantification has highlighted the importance of the correction of $T_2$* decay effects in water-fat imaging. Specifically, different signal models have been proposed correcting for common $T_2$* [3,4], dual $T_2$*[5] or common $T_2'$ [6] decay effects for the water and fat components. Previous work in bone marrow, sampling gradient-echo signal around a spin-echo, has suggested a common $T_2'$ for all spectral components, but focused in regions containing primarily fat [7]. Therefore, the purpose of the present study was to compare different approaches for $T_2$* correction in chemical shift encoding-based water-fat imaging of vertebral bone marrow using single-voxel MRS as a reference standard.

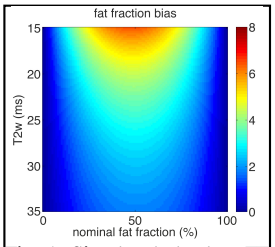

Fig. 1: Simulated absolute FF bias using a single $T_2$* correction approach on data generated assuming a common $T_2'$ for water and fat.

**Methods:** Simulations: Synthetic data was generated for an eight-echo experiment with $TE_{min}/\Delta TE$ = 1.47/1.05 ms. A water-fat signal model was used considering the presence of multiple fat peaks [8] and $T_2$* decay effects assuming a common $T_2'$=10 ms for the water and fat compartments, different $T_2$ relaxation times ($T_{2w}$ varying between 15 ms and 35 ms and $T_{2f}$ = 75 ms) and a nominal fat fraction in the range between 0% and 100%. Fat quantification was then performed using a single $T_2$* correction model.

*In vivo* measurements: The lumbar spine of 26 young, healthy subjects was scanned on a 3 T whole-body scanner (Ingenia, Philips Healthcare, Best, Netherlands) using the built-in-the-table posterior coil elements (12-channel array). The L3, L4 and L5 vertebral bodies were first scanned using a STEAM single-voxel MRS sequence (TR = 6000 ms, TM = 16 ms, VOI = 15x15x15 $mm^3$, 8 averages per TE) at four different echo times (TE = 11/15/20/25 ms). An eight-echo 3D spoiled gradient-echo sequence was then used for chemical shift encoding-based water-fat separation. The sequence acquired the eight echoes in two interleaves (4 echoes per TR) using flyback (monopolar) read-out gradients and the following imaging parameters: TR/TEmin/ΔTE = 15/1.47/1.05 ms, FOV = 220×220×80 $mm^3$, acquisition matrix = 124×122×4, receiver bandwidth = 1551 Hz/pixel, frequency direction = A/P (to minimize breathing artifacts), $N_{avg}$ = 2. A flip angle of 3° was used to minimize $T_1$-bias effects.

Fat quantification: MRS peak fitting was performed by constraining the areas of olefinic and glycerol fat peaks to the main fat methyl and methylene peaks [8]. Water and fat peak areas were corrected for $T_2$ effects assuming a common $T_{2f}$ for all fat peaks. Therefore, MRS quantification derived FF, $T_{2w}$ and $T_{2f}$. The gradient-echo imaging data was processed off-line using a region-growing algorithm to first initially estimate the fieldmap variation. A complex-based water-fat decomposition was then performed using the pre-calibrated fat spectrum previously measured in the red bone marrow of the proximal femur [8]. The gradient-echo signal values were averaged over the ROIs of the MRS and different approaches were evaluated for correction of $T_2$* effects: (a) single $T_2$* correction (assuming common $T_2$* for water and fat) [3,4], (b) dual $T_2$* correction (assuming different $T_2$* for water and fat) [5], (c) $T_2'$ correction using the a priori known $T_2$ from the MRS at each vertebral body (3 values per subject), (d) $T_2'$ correction using the a priori known $T_2$ from the MRS at the L4 vertebral body (single value per subject). Fat fraction maps were also generated using $T_2$* correction approaches (a), (b) and (d).

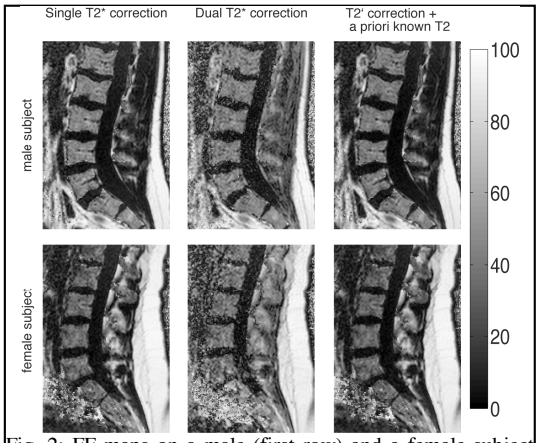

Fig. 2: FF maps on a male (first row) and a female subject (second row) using single $T_2$* correction, dual $T_2$* correction and common $T_2'$ correction + a priori knowledge of $T_2$. Notice the noisy FF maps with the dual $T_2$* correction.

**Results:** When a single $T_2$* correction approach is used on synthetic data generated assuming a common $T_2'$ for water and fat but different $T_2$, the FF bias is maximized at nominal FF values close to 50% and for maximal difference between the water and fat $T_2$ relaxation times (Fig. 1). Fig. 2 shows typical FF maps in two subjects using different $T_2$* correction approaches. The dual $T_2$* correction approach leads to noisy fat fraction maps, especially in the female subject with lower vertebral FF values (Fig. 2). Fig. 3 shows the linear regression analysis of the imaging FF results using the different $T_2$* correction approaches with the results from the single-voxel MRS. The linear regression intercept is significantly different from 0 ($p < 0.05$) for all $T_2$* correction methods. The linear regression slope is significantly different from 1 ($p < 0.05$) for the single $T_2$* (Fig. 3a) and dual $T_2$* (Fig. 3b) correction methods, but non-significantly different from 1 for the $T_2'$ correction methods using either the a priori known $T_2$ from the MRS at each vertebral body ($p = 0.39$, Fig. 3c) or the a priori known $T_2$ from the MRS at L4 ($p = 0.45$, Fig. 3d).

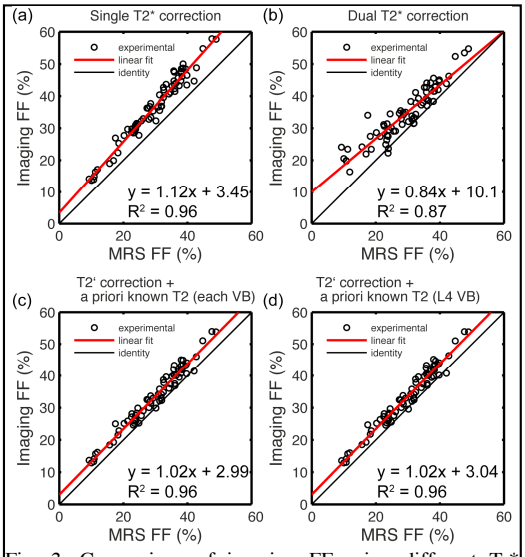

Fig. 3: Comparison of imaging FF using different $T_2$* correction approaches with the MRS FF. The best agreement between imaging and MRS is shown for the $T_2'$ correction methods using a priori known $T_2$.

**Discussion & Conclusion:** The reported results show that $T_2$* correction effects are important in vertebral bone marrow fat quantification. Bone marrow contains water and fat components with a similar $T_2'$ but different $T_2$. Therefore, a single $T_2$* correction introduces a bias in the FF, especially for moderate nominal FF values close to 50% (Fig. 3a). A dual $T_2$* correction can correct for this FF bias at nominal FF close to 50%, but shows poor noise performance at low FF (Fig. 3b) [9]. A $T_2'$ correction using a priori known $T_2$ relaxation times can remove the FF bias with good noise performance (Fig. 2). $T_2$ of fat shows in general little variation across subjects, but $T_2$ of water shows much larger variations and it has to be measured. The present results show that using the $T_2$ from an MRS measurement at a single vertebral body location is adequate for $T_2$* correction of the imaging data in the lumbar spine (Fig. 3d). A small bias of the order of 3% remains between imaging FF and MRS FF, which could be related to the presence of short $T_2$* water components in the MRS [8]. In conclusion, a $T_2'$ correction using a priori known $T_2$ can remove $T_2$* bias without degrading noise performance in FF mapping of the spine.

**References:** [1] Kuhn, Eur Radiol 23:3432 2013, [2] Bolan, J Magn Reson Imag 38:1578 2013, [3] Yu, J Magn Reson Imag 26:1153 2007, [4] Bydder, Magn Reson Imag 26:347 2008, [5] Chebrolu, Magn Reson Med 63:849 2010, [6] Mansson, Magn Reson Imag 30:1461 2011, [7] Wehrli, J Magn Reson 131:61 1998, [8] Karampinos, Magn Reson Med 71:1158 2014, [9] Reeder, Magn Reson Med, 67:389 2012.

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