Average Correlation Orthogonal Matching Pursuit for Improved Relaxation Parameter Estimation

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Introduction: Orthogonal Matching Pursuit (OMP) has recently emerged as a powerful tool for the quantification of MRI relaxation parameters [1]. In using OMP for this purpose, a dictionary of possible signal evolution curves, or atoms, is generated for a specific range of possible T_1 and T_2 values. Each pixel in a set of time-resolved aliased images is compared with the dictionary, and the relaxation curve which most closely matches the undersampled data for that pixel is selected in order to create maps. For single parameter quantification, this method yields accurate results. However, fitting several parameters using OMP, different atoms can appear quite similar, and distinguishing between curves with different underlying parameters can be difficult, especially for fast relaxation curves near the acquisition rate. The dictionary entry with the highest correlation then does not correspond to the correct relaxation values. Here we propose to combat this quantification error using a simple average correlation OMP approach, where the average correlation across parameters is taken into account. This allows ambiguities between similar dictionary entries to be resolved and the appropriate dictionary entries selected. The benefits of this average correlation OMP over standard OMP for relaxation parameter determination are demonstrated using the IR-TrueFISP sequence [2], which allows the determination of M_0 and tissue relaxation parameters T_1 and T_2 in a single shot, in time scales of approximately 6 sec per slice [3,4].

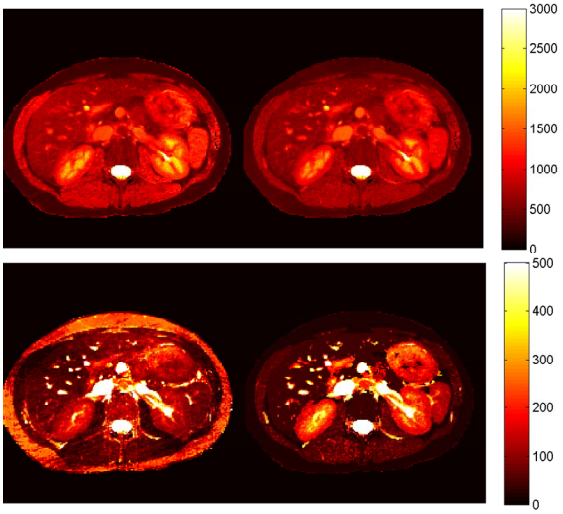

Fig 1: Example T_1 (top) and T_2 (bottom) maps generated using standard OMP (left) and average correlation OMP (right). Note the residual streaking and inaccurate estimation of the relaxation values when using standard OMP (especially in the T_2 values for fat) which is resolved when using average correlation OMP.

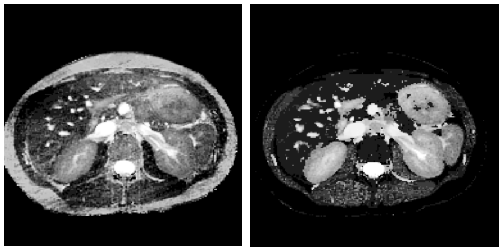

Figure 2: Synthetic T_2-weighted images corresponding to the maps in Figure 1; on the left is standard OMP and the right is average correlation OMP. Note the bright fat resulting from the misestimated T_2 value in the standard OMP image (left), which is not seen in the average correlation OMP image (right).

Methods: All data were collected using a 1.5 T Siemens Espree scanner in compliance with our institution's IRB. *In vivo* data were collected in abdomen, where a wide range of T_1 and T_2 values appear, with especially short relaxation values in the fat. IR-TrueFISP data were acquired in a radial fashion using the golden-angle trajectory as described in [2] with TR values ranging from 3.04 ms and an inversion time of 13.42 ms. Two averages were used with 1800 projections per average, resulting in a total acquisition time of 16 s for the complete dataset (including a 5 sec recovery period between the averages). The volunteers were instructed to hold their breath throughout the acquisition to avoid motion artifacts. These data were gridded using bunches of 2 projections and phase correction and coil combination operations were performed on the series of undersampled images. For the OMP reconstruction, a relaxation curve dictionary was generated using various T_1 and T_2 values (ranging from 0 ms to 2000 ms in increments of 20 ms) and the IR-TrueFISP relaxation equations [2]. T_1 and T_2 maps were derived by determining which curve in the dictionary was closest to the relaxation curve for each pixel using the standard approach (highest correlation value), as described in [1], as well as by selecting the T_1 and T_2 values with the highest *average* correlation over the dictionary.

Results: The T_1 and T_2 maps generated from the standard OMP method are shown in the left column of in Fig 1 (M_0 maps can also be generated but are not shown). In the standard OMP relaxation maps, residual streaking artifacts can be seen, especially in the T_2 maps. Most importantly, the standard OMP method yields quantitative inaccuracies. For example, T_2 values for the fat pixels with the standard OMP method range of 200-300 ms, which is significantly longer than reported in the literature [5]. When moving to the average correlation OMP fits (right column of Fig 1), the resulting maps are more homogeneous and accurately capture the T_1 and T_2 values (especially in short T2 species such as liver and fat). Fig 2 shows synthetic T_2-weighted images generate using the T_2 maps from Figure 1 and an echo time of 90ms. In the standard OMP image, the fat appears bright, which is not expected in a true T_2-weighted image (though fat is artifactually bright in a TSE image); in the average correlation OMP, fat has the proper appearance due to the lower fitted T_2 values..

Discussion: By using an average correlation over relaxation parameters, the proper dictionary entry in an OMP fit can found, leading to more accurate results than when using a standard OMP. This average correlation method is especially useful when quantifying very fast relaxation as the atoms in the dictionary appear similar to one another. By combining average correlation OMP and IR-TrueFISP, T_1, T_2, and M_0 values can be determined in less than 6 s / slice even in challenging areas such as the abdomen and pelvis which contain relaxation values which range from the high T_1 and T_2 values of water to the low T_1 and T_2 values in fat.

References: [1] Doneva M et al. Magn Reson Med. 2010 Oct;64(4):1114-20. [2] Schmitt P et al. Magn Reson Med. 2004 Apr;51(4):661-7. [3] Yutzy S et al, Proc ISMRM 17 (2009), Pg. 2765. [4] Ehses P et al, Proc ISMRM 18 (2010), Pg. 2969. [5] Tokoo et al. JCAT 2010 May/Jun;34(3):317-31.

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