

Fast and Robust Separation of Multiple Chemical Species from Arbitrary Echo Times with Complete Immunity to Phase Wrapping

Yun Jiang¹, Mark Griswold^{1,2}, and Jeffrey Tsao³

¹Department of Biomedical Engineering, Case Western Reserve University, Cleveland, Ohio, United States, ²Department of Radiology, Case Center for Imaging Research, University Hospitals of Cleveland and Case Western Reserve University, Cleveland, Ohio, United States, ³McKinsey & Company, Boston, Massachusetts, United States

INTRODUCTION: We present an extremely fast and robust method, called hierarchical IDEAL (1), which has been extended to separate multiple chemical species from images acquired at three or more arbitrary echo times, while retaining complete immunity to phase wrapping issues. This method combines three key features. First, direct phase estimation completely avoids the phase wrapping problem. Second, the optimized algebraic formulation allows for high computational efficiency. Third, a multi-resolution, hierarchical optimization improves robustness against local optima. Data from human ankle and knee with three or more echo times are shown to demonstrate its performance in fat-water separation.

THEORY: We re-arrange the multi-peak signal model (2,3) for multiple chemical species at arbitrary echo times TE_m as follows:

$$\text{diag}(\mathbf{s}) \mathbf{d} = \mathbf{A} \tilde{\mathbf{p}} \quad [1]$$

where $\text{diag}(\cdot)$ denotes an operator that forms a diagonal matrix from a vector. The left side of Eq. [1] represents the MRI signal at M echo times $\mathbf{s} = [s_1 \ s_2 \ \dots]^T$, after correcting for the T_2^* decay and off-resonant dephasing since the first echo time, TE_1 , $\mathbf{d} = [1 \ e^{(R_2^* + i2\pi\Psi)(TE_2 - TE_1)} \ \dots]^T$. On the right side, \mathbf{A} is an $M \times N$ matrix representing the multi-peak signal model with matrix elements $a_{m,n} = \sum_{p \in \text{peaks}} \alpha_{n,p} e^{-i2\pi\Delta f_p TE_m}$, relative amplitudes $\alpha_{n,p}$, and chemical shifts Δf_p . $\tilde{\mathbf{p}}$ represents the intensities of the chemical species to be separated (ρ_1, ρ_2, \dots), modulated by the signal evolution up to TE_1 , $\tilde{\mathbf{p}} = [\rho_1 e^{-(R_2^* + i2\pi\Psi)TE_1} \ \rho_2 e^{-(R_2^* + i2\pi\Psi)TE_1} \ \dots]$. With this formulation, the sum-of-square fitting error can be expressed as:

$$\text{Sum-of-square fitting error} = \sum \{ (\text{diag}(\mathbf{s})^H (\mathbf{I} - \mathbf{A}\mathbf{A}^+) \text{diag}(\mathbf{s}))^\circ \text{conj}(\mathbf{d}\mathbf{d}^H) \} \quad [2]$$

where $\sum\{\cdot\}$ denotes summation over matrix elements, $^\circ$ denotes element-wise multiplication, and $\text{conj}(\cdot)$ denotes complex conjugation.

We define a time resolution ΔTE , such that all the inter-echo spacings are multiples of ΔTE . Eq. [2] is minimized by directly determining a complex-valued scaling factor that accounts for the T_2^* decay and dephasing during ΔTE . As a result, all elements of \mathbf{d} in Eq. [2] are simply integer multiples of this scaling factor, which eliminates phase wrapping issues entirely. We call this approach direct phase estimation. With the algebraic formulation in Eq. [2], each iteration of the optimization is extremely efficient, since the first factor on the right side of Eq. [2] can be pre-calculated, and only the $\mathbf{d}\mathbf{d}^H$ factor needs to be adjusted at each iteration of the optimization. Finally, the optimization process is guided by a multi-resolution, hierarchical coarse-to-fine approach to improve robustness against local minima.

METHODS: Images were acquired from volunteers after informed consent with a 3D spoiled-gradient-echo sequence. Ankle images were acquired on a GE 3T Signa EXCITE HDx (GE Healthcare, Waukesha, WI) with three echo times (2.184, 2.978, and 3.772 ms), one echo per TR, a 125kHz bandwidth, a 256x256 matrix, and a flip angle of 5° with field of view of 18cm, a voxel size of 5mm along the z direction, and a single-channel coil. Knee images were acquired on a Siemens Magnetom Espree 1.5T (Siemens AG Medical Solution, Erlangen, Germany) with a 15-channel coil, with six echoes (2.36 ms initial, and echo spacing of 3.57 ms), 6 echoes per TR, a BW = 520 Hz/pixel, a 256x256x24 matrix, a flip angle of 8° , a field of view of 20 cm, and a voxel size of 4 mm along the z direction. A multi-peak fat spectrum (3) was used in the signal model, with spectral peaks at 0.9, 1.3, 2.1, 2.76, 4.31, and 5.3ppm (water peak at 4.7ppm), and relative amplitudes of 0.087, 0.694, 0.128, 0.004, 0.039, and 0.048, respectively.

RESULTS: Fig. 1 shows the result from one slice of the ankle images. The top row shows the phase map and the R_2^* map. The phase map shows a variation in the superior-to-inferior direction, indicating a B_0 inhomogeneity gradient. The phase map and R_2^* map have a lower spatial resolution compared to the full images. The resolution is controlled by the number of decomposition levels. Finer resolution can be achieved with more levels, albeit at an exponentially increasing computation time due to the hierarchical nature of the decomposition. The bottom row of Fig. 1 shows the corresponding water and fat components of the ankle image. Fig. 2 shows one slice of water and fat images of the knee. In both examples, water-only and fat-only images show that a clean and correct water-fat separation was achieved throughout the field of view. Our algorithm took less than 5 seconds for the ankle data set with 4 slices of 256 x 256 images at three echo times, and less than 60 seconds for the knee data with 24 slices of 256 x 256 images at six echo times in Matlab (The Mathworks, Natick, MA) on a 64-bit Mac OS laptop with a 2.4GHz Intel dual-core i5 processor and 8Gb of memory.

CONCLUSION: Our algorithm is a fast and robust reconstruction method for separating multiple chemical species from images acquired at three or more arbitrary echo times. It will be available in Matlab as part of the water-fat toolbox initiative for ISMRM workshop on fat-water separation in 2012.

ACKNOWLEDGEMENTS: We would like to thank Houchun H. Hu and Samir Sharma for the ankle images used in this abstract. YJ and MG acknowledge support from Siemens Medical Solutions, Erlangen, Germany.

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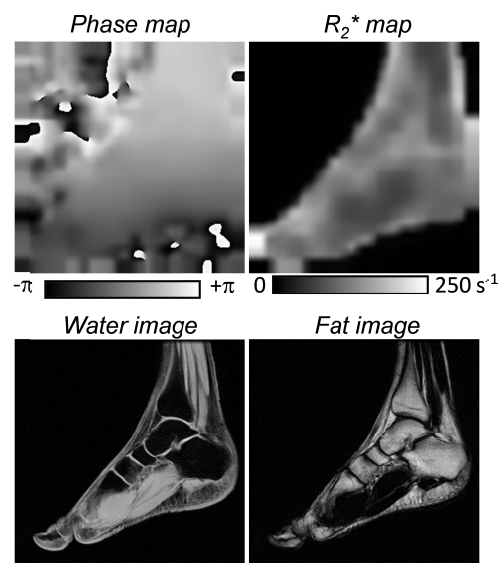


Fig. 1. Phase map, R_2^* map and corresponding water and fat images from one slice of a 256x256x4 three-echo ankle data set. Reconstruction took <5 seconds in Matlab.

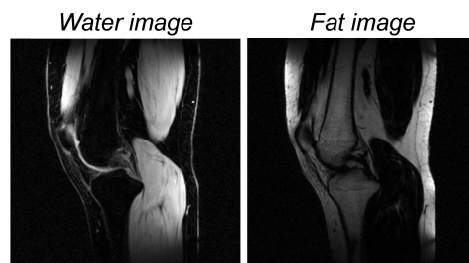


Fig. 2. Water and fat images from a 256x256x24 six-echo knee data set. Reconstruction took <60 seconds in Matlab.