Calibrationless Chemical Shift Encoded Imaging Using a Time-Segmented k-Space Reconstruction

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Target Audience: Researchers who are interested in advanced techniques for chemical shift encoded imaging.

Purpose: Chemical shift encoding (e.g. IDEAL[1]) techniques have proven to be a valuable tool in the research and clinical settings. However, conventional image-domain-based methods are limited both by their long scan time, which can restrict spatial resolution and/or volume coverage, and their sensitivity to intraecho off-resonance, which can cause geometric distortions in the image. Previous works have proposed either accelerating image-domain-based methods[2,3] or using a k-space-based formulation[4] to mitigate the effects of intraecho off-resonance. In this work, we develop and demonstrate a framework for accelerated k-space-based chemical shift encoding. We employ a time-segmented approximation[5] of the multispecies MR signal equation to implement the k-space-based iterative reconstruction and we exploit prior information on the local low-rank structure of multicoil data[6] and image sparsity to achieve acceleration. We demonstrate accelerated water-fat separation with reduced geometric distortions as compared to a conventional image-domain-based method.

Methods: <u>Modeling & Estimation</u>: The k-space signal, g, that is generated by an object composed of M species and observed using a C-channel phased array receiver is modeled in Eq. 1, where f represents the pixel value, n is an index over pixels, α and Δ represent, respectively, the relative amplitude and frequency of the pth peak of the mth species, ψ is the B0 field map, x is the spatial position, and ω represents the spectral location of the sample. To avoid working with dense matrices, we invoke a time-segmented approximation of the exponential function, which yields an approximation of the k-space signal model (Eq. 2), where a are the coefficients of the interpolation window, l is an index over time segments, and τ is the length of each

$$g^c[k] = \sum_m \sum_n f_m^c[n] \sum_p \alpha_m^p e^{-j2\pi \Delta_m^p t_k} e^{-j2\pi \psi[n] t_k} e^{-j\bar{x}[n]\bar{\omega}[k]} \quad (1)$$

$$\tilde{g}^c[k] = \sum_l a_l[k] \sum_m \sum_n f_m^c[n] \sum_p \alpha_m^p e^{-j2\pi \Delta_m^p \tau l} e^{-j2\pi \psi[n]\tau l} e^{-j\bar{x}[n]\bar{\omega}[k]} \quad (2)$$

$$\min_{\mathbf{f}} \left\| g - \hat{\tilde{g}} \right\|_2^2 + \lambda_1 P_1(\mathbf{f}) + \lambda_2 P_2(\mathbf{f}) \quad (3)$$

$$\min_{\psi} \left\| \mathbf{r} - \mathrm{u}(\psi) \right\|_2^2 \ s.t. \ \psi \in B_s \quad (4)$$

segment. The signals of interest (i.e. chemical species & B0 field map) are estimated via a two-step alternating minimization, as follows: 1) the species are estimated using penalized weighted least squares regression (Eq. 3); and 2) the B0 field map estimate is updated (Eq. 4). Specifically, in Eq. 3, P_1 promotes local low-rankedness (CLEAR[6]) and P_2 promotes wavelet sparsity (compressed sensing (CS)). Both penalties operate jointly across coils and species. This minimization is performed using FISTA[7]. In Eq. 4, r is the current residual, u is the update function, and B_s represents cubic B-splines[3] of successively finer scale that are used to provide a compact representation of the B0 field map while avoiding local minima that cause swaps of species. <u>Experiments</u>: Fully-sampled k-space data (256x256x20) of the thigh were acquired at three echo times (TEs = [9.14 10.728 12.316 ms]) on a GE 1.5T Signa scanner (GE Healthcare, Waukesha, WI) using a 3DFT-SPGR sequence and an eight-channel cardiac array. A readout bandwidth of 15.6 KHz was used to highlight the effects of intraecho off-resonance. The fully-sampled data were reconstructed using both a conventional image-domain-based method[1] and the proposed k-space-based method without CLEAR and CS. The data were also retrospectively undersampled along the phase encode axis using a Poisson disk sampling pattern to simulate 3x acceleration, and were reconstructed using the proposed method with CLEAR and CS. Note that undersampling was only possible in 1D because scan time restrictions limited the number of acquired slices.

Results: Figure 1 shows the estimated water and fat images as well as the synthesized in-phase (IP) image (water + fat) for each of the three methods. Using the image-domain-based method, the estimated fat image is spatially shifted relative to the water image (left column). The proposed k-space-based method (without CLEAR & CS) estimates the water and fat images with reduced geometric distortion (center column). In addition, by exploiting intercoil structure via CLEAR and image sparsity via CS, the proposed framework maintains high quality estimation of the water and fat images from a retrospectively undersampled acquisition (right column).

Discussion: By both formulating the multispecies signal in the k-space domain and exploiting prior information, we have demonstrated accelerated k-space-based chemical shift encoding with reduced geometric distortion. The proposed framework has potential for significant impact in non-Cartesian multispecies acquisitions, which is an item of future work.

Conclusion: We have developed and demonstrated an accelerated k-space-based chemical shift encoding framework that employs time-segmentation and exploits intercoil structure and image sparsity.

References: [1]Reeder et al. MRM 2004 51:35-34; [2]Doneva et al. MRM 2010 64:1749-59; [3]Sharma et al. MRM doi:10.1002/mrm24270; [4]Honorato et al. MRM 2012 68:400-408; [5]Sutton et al. TMI 2003 22:178-188; [6]Trzasko et al. ISMRM 2012 p. 517; [7]Huang et al. MIA 2011 15:670-679;

water

fat

IP (W+F)

image-domain (1x)   k-space (1x)   k-space w/CLEAR & CS (3x)
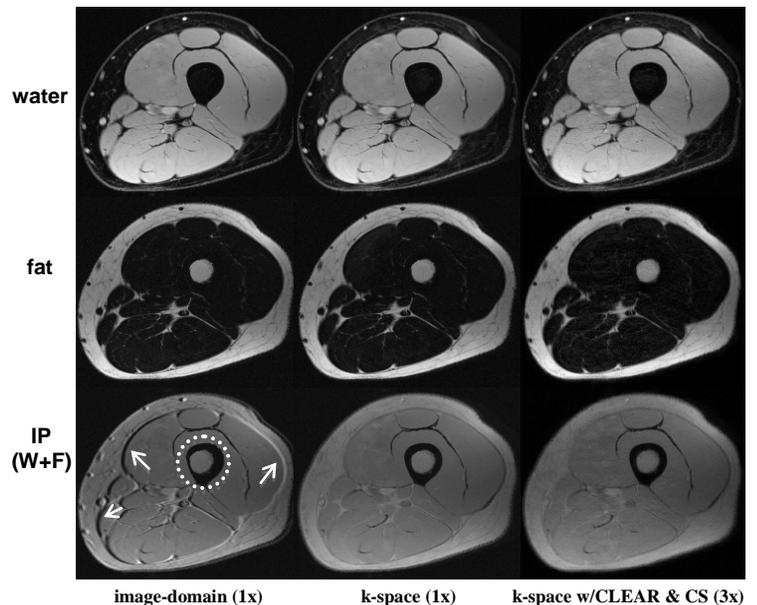
Fig. 1: In the image-domain method, the water & fat estimates are spatially shifted (dashed circle), which causes signal pileup and dropout in IP image (white arrows). Using a k-space formulation, the water & fat estimates are aligned. Adding CLEAR and CS, the aligned water & fat estimates are recovered from a 3x retrospectively-accelerated acquisition.