Generalized Conjugate Gradient Image Reconstruction – Combination of SENSE/SPIRiT, Chemical Shift Imaging and Multi-Frequency Interpolation

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Introduction

Image Reconstruction in MRI is addressed by a variety of techniques depending on the specific data acquisition scheme and the information one wants to resolve. For parallel imaging, SENSE [1] and SPIRiT [2] can be used. For chemical shift imaging (CSI), such as metabolic imaging using hyperpolarized ^{13}C [3], one may acquire data with different echo times repeatedly and subsequently separate the metabolites' data using IDEAL [4]. To correct for B_0-artefacts, Multi-Frequency Interpolation (MFI) has been applied successfully [5,6]. Goal of this work is the combination of all the above mentioned methods in a single generalized encoding formula which can be solved using Conjugate Gradient (CG) methods.

Theory

The MRI signal of an image $I_m(r)$ of a metabolite m with chemical shift f_m, defined on a domain Ω, acquired with a k-space trajectory $k(t)$, echo times T_o and a set of coils with sensitivities $s_n(r)$, given the B_0-field inhomogeneity $\nu(r)$, reads

$$(EI)_{no}(t) = \sum_m \int_\Omega I_m(r) s_n(r) e\left(-k(t)^T r - (\nu(r) + f_m)(t + T_o)\right) dr.$$

whereas $e(x) = \exp(2\pi i x)$. To separate temporal (t) and spatial coordinates (r) in the exponential term, MFI samples the range of values $\nu(r)$ at supporting points ν_l defining basis functions $b_{lo}(t)$ and determines coefficients $c_{lo}(r)$ (e.g. using least squares fitting) such that

$$e(-\nu(r)(t + T_o)) \approx \sum_l c_{lo}(r) \bar{b}_{lo}(t).$$

Hence the approximate encoding reads

$$(EI)_{no}(t) \approx \sum_{m,l} \int_\Omega I_m(r) s_n(r) c_{lo}(r) e\,(-k(t)^T r) b_{lo}(t) p_{mo}(t)\, dr = (BGCSI)_{no}(t)$$

Definitions:

$p_{mo}(t) = e(-f_m(t + T_o))$
$b_{lo}(t) = e(-\nu_l(t + T_o))$
$(SI)_{mn}(r) = I_m(r) s_n(r)$
$(CJ)_{mnol}(r) = J_{mn}(r) c_{ol}(r)$
$(GI)(t) = \int_\Omega I(r) e(-k(t)^T r)\, dr$
$(Bd)_{no}(t) = \sum_{m,l} d_{mnol}(t) p_{mo}(t) b_{ol}(t)$

The operator G thereby describes the mapping from the potentially non-cartesian k-space data to image space and can be implemented using gridding [7] or nuFFT [8]. Given measured data $d_{no}(t)$, the task of reconstructing $I_m(r)$ in a least squares sense reads $\min_I \|BGCSI - d\|$. Solving this task using CG methods means a generalization of CG SENSE to MFI and CSI is called *genCG*$_{SENSE}$.

Alternatively, in particular if no sensitivity maps are available, a SPIRiT based approach can be used, i.e. coil images $J_{mn}(r) = I_m(r)s_n(r)$ are reconstructed by finding the minimum of a linear combination of $\|BGCJ - d\|$ (data consistency) and $\|KJ - J\|$ (calibration consistency) with a standard SPIRiT-kernel K. Again, the task can be solved via CG methods and is referred to as *genCG*$_{SPIRiT}$.

Methods

The *ISMRM MRI Unbound Double Vision* (DV) spiral trajectory data [9] was reconstructed using standard CG SENSE and the proposed *genCG*$_{SENSE}$ using the provided sensitivities and B_0-map. Note that since no CSI is involved and only a single echo time is acquired, the method is similar to the one presented in [6].

Additionally, a water phantom containing 4 tubes of different ^{13}C-sensitive chemical substances (acetate, lactate, alanine and glycine) was imaged on a 3T GE HDx scanner (*GE Healthcare, Waukesha, MI*) using a dual-tuned 4-channel rat coil (Rapid Biomedical, Würzburg, Germany). Data was acquired at ^{13}C resonance frequency using a single shot spiral trajectory (FOV=80 mm, nom. resolution 32x32) and 7 echo times (ΔTE=1.1 ms). A ^1H-B_0-map was acquired using a Cartesian gradient echo sequence at two echo times (ΔTE=1.0 ms) and scaled by the gyromagnetic ratios of ^1H and ^{13}C. The data was reconstructed to a 128x128 matrix using IDEAL and standard SPIRiT [10] as well as by applying *genCG*$_{SPIRiT}$ with and without MFI.

Results

The *genCG*$_{SENSE}$ reconstruction [*elapsed time (per slice)*: 33.6 sec (for computing MFI coefficients $c_{lo}(r)$) + 101.5 sec (for 15 CG iter.) using Matlab (*The Mathworks, Natick, MA*) and a 3 GHz processor] of the DV data (Fig. 1) shows reduced blurring as compared to standard CG SENSE [6.0 sec for 15 CG iter.]. The typical B_0-artefacts could be removed completely or at least reduced significantly. The few remaining circular distortions correspond to very steep slopes in the B_0-map, whereas the Gibbs-ringing observed at these artefacts indicates that this error is due to the limited bandwidth of the acquisition and not due to the reconstruction technique.

The *genCG*$_{SPIRiT}$ reconstructions of the ^{13}C phantom [10 CG iter., 4.4 sec w/o MFI, 6.3 sec+16.4 sec w/ MFI] show improved SNR as compared to IDEAL [0.2 sec (for spectral decomposition) + 4*0.5 sec (for 10 CG iter. of 4 metabolites)] for two of the metabolites (acetate and lactate) even without MFI. Since also signal from other metabolites is visible in the reconstructions, e.g. alanine in the glycine image, the spectral domain might not have been sampled sufficiently by the applied echo times and this undersampling might affect IDEAL and *genCG*$_{SPIRiT}$ in a different way. By including MFI, the SNR is significantly improved for all metabolites. Furthermore, the signal peaks – in particular for acetate and lactate – appear more centered within the tubes indicating reduced blurring.

Discussion and Conclusion

The proposed generalized reconstruction techniques *genCG*$_{SENSE}$ and *genCG*$_{SPIRiT}$ have been successfully applied to reduce B_0-artefacts and/or to resolve multiple chemical shifts. In particular their general formulation makes them a powerful reconstruction framework for various MRI reconstruction purposes, i.e. they can handle MRI data independently of a particular acquisition protocol. In contrast to IDEAL, no additional data processing is required. Furthermore, the proposed methods make use of the superior convergence properties of the CG algorithm, i.e. they are linear, very robust and can be regularized in case of ill-posed, i.e. low-SNR, data.

References

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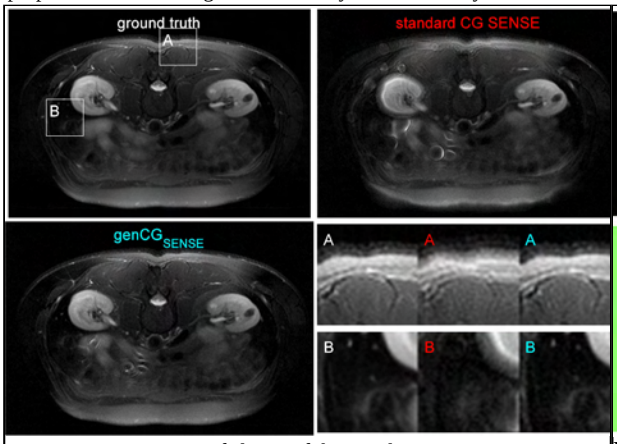

Fig. 1: Reconstructions of slice 5 of the DV data.

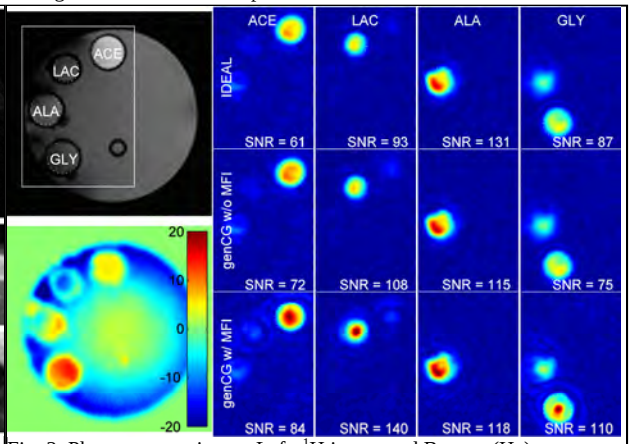

Fig. 2: Phantom experiment. Left: ^1H image and B_0 map (Hz).