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 13C [3], one may acquire data with different echo times repeatedly and subsequently separate the metabolites' data using IDEAL [4]. To correct for B₀-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 \( I(t) \) of a metabolite \( m \) with chemical shift \( f_m \), defined on a domain \( \Omega \), acquired with a k-space trajectory \( k(t) \), echo times \( T \), and a set of coils with sensitivities \( s_i(r) \), given the B₀-field inhomogeneity \( \nu(r) \), reads

\[
(EI)_{\nu}(t) = \sum_{i} \int I_{m}(r) s_i(r) e^{-j(k(r) T + f_m) (t + T)} dr,
\]

whereas \( \Omega = \{ r : \exp(2\pi i \nu) \} \). To separate temporal \( t \) and spatial coordinates \( r \) in the exponential term, MRI samples the range of values \( \nu(r) \) at supporting points \( \nu \) defining basis functions \( b_i(t) \) and determines coefficients \( c_i(r) \) (e.g. using least squares fitting) such that

\[
E(-\nu(t)(t + T)) = \sum_{i} c_i(r) b_i(t).
\]

Hence the approximate encoding reads

\[
(EI)_{\nu}(t) = \sum_{i} \int I_{m}(r) s_i(r) e^{-j(k(r) T)r} b_i(t) p_{nu}(t) dt = (BGCSI)_{\nu}(t)
\]

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 \( d_i(t) \), the task of reconstructing \( I_{m}(r) \) in a least squares sense reads \( \min_{\nu} \| BGC - d \| \). Solving this task using CG methods means a generalization of CG SENSE to MFI and CSI is called genCGSENSE.

Alternatively, in particular if no sensitivity maps are available, a SPIRiT based approach can be used, i.e. coil images \( I_{m}(r) = I_{m}(r)s_i(r) \) are reconstructed by finding the minimum of a linear combination of \( \| BGC - d \| \) (data consistency) and \( \| K \| \) (calibration consistency) with a standard SPIRiT-kernel \( K \). Again, the task can be solved via CG methods and is referred to as genCGSPIRiT

Methods

The ISMRM MRI Unbound Double Vision (DV) spiral trajectory data [9] was reconstructed using standard CG SENSE and the proposed genCGSENSE using the provided sensitivities and B₀-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 13C-sensitive chemical substances (acetate, lactate, alanine and glycine) was imaged on a 3T GE HDx sequence at two echo times (\( \Delta T = 1.0 \text{ ms} \)) and scaled by the gyromagnetic ratios of 1H and 13C. The data was acquired at 13C resonance frequency using a single shot spiral trajectory (FOV=80 mm, nom. resolution 32x32) and 7 echo times (\( \Delta T_{E}=1.1 \text{ ms} \)). A 1H-B₀-map was acquired using a Cartesian gradient echo sequence at two echo times (\( \Delta T_{E}=1.0 \text{ ms} \)) and scaled by the gyromagnetic ratios of 1H and 13C. The data was reconstructed to a 128x128 matrix using IDEAL and standard SPIRiT [10] as well as by applying genCGSPIRiT with and without MFI.

Results

The genCGSENSE reconstruction (elapsed time (per slice): 33.6 sec for computing MFI coefficients \( c_i(r) \) + 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 B₀-artefacts could be removed completely or at least reduced significantly. The few remaining circular distortions correspond to very steep slopes in the B₀-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 genCGSPIRiT reconstructions of the 13C 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 genCGSPIRiT 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 genCGSENSE and genCGSPIRiT have been successfully applied to reduce B₀-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

[1] Pruessman et al., MRM 1999
[2] Lustig et al., MRM 2010
[6] Barret et al., ISMRM 2005

Fig. 1: Reconstructions of slice 5 of the DV data.
Fig. 2: Phantom experiment. Left: 1H image and B₀ map (Hz).