

Retrospective rigid motion correction of undersampled MRI data

Alexander Loktyushin¹, Maryna Babayeva^{2,3}, Daniel Gallichan⁴, Gunnar Krueger^{2,3}, Klaus Scheffler^{5,6}, and Tobias Kober^{2,3}

¹Empirical Inference, Max Planck Institute for Intelligent Systems, Tübingen, Germany, ²Siemens ACIT - CHUV Radiology, Siemens Healthcare IM BM PI, & Department of Radiology, University Hospital (CHUV), Lausanne, Switzerland, ³LTS5, École Polytechnique Fédérale de Lausanne, Lausanne, Switzerland, ⁴CIBM, École Polytechnique Fédérale de Lausanne, Lausanne, Switzerland, ⁵High-Field Magnetic Resonance Center, Max Planck Institute for Biological Cybernetics, Tübingen, Germany, ⁶Department for Biomedical Magnetic Resonance, University of Tübingen, Tübingen, Germany

Introduction

Subject head motion during long scans is one of the major sources of image artifacts in MR brain imaging. Although advances in parallel imaging techniques allow reducing the scan time significantly, it still remains in the order of minutes, increasing the probability of head motion to occur. Motion during the acquisition leads to inconsistent k-space data and thus impedes parallel imaging reconstruction techniques, such as GRAPPA [1]. On the other hand, Fourier domain-based retrospective motion correction techniques typically require a fully acquired k-space as input, and thus necessitate the GRAPPA reconstruction to be performed first. This couples the problems of motion correction and GRAPPA reconstruction, yielding a complex problem to solve.

Here, we propose a prototype motion correction algorithm that operates on multi-channel undersampled data acquired with a Cartesian sequence which was augmented by a free induction decay navigator (FIDnav, [3]) motion monitoring module. The algorithm is based on iterating the application of the GRAPPA reconstruction, motion estimation and motion correction. The acquired FIDnavs which were recently shown to be beneficial for retrospective motion correction [2] were used to aid the motion correction process.

Materials & Methods

After obtaining written consent, three healthy volunteers were scanned at 3T (MAGNETOM Skyra, Siemens AG, Erlangen, Germany) with a prototype MP-RAGE sequence (TI/TR/ α /TA = 900ms/2300ms/9°/5:12min, matrix 240x256x176, 1.2 mm³ isotropic) with 2x acceleration (32 ACS lines) using a commercial 32-channel head coil. The subject's head was rested on an inflatable air cushion. During the course of the scan, air was manually pumped in and out of this cushion, inducing slow periodic head displacements with a frequency of ~0.5 Hz.

The employed reconstruction pipeline is presented in Figure 1: Since ACS lines are likely to be corrupted by motion while their consistency is essential for the GRAPPA interpolation, they are corrected in a first step by employing the method reported in [4]. Subsequently, GRAPPA kernels are computed and kept fixed for all following processing steps. Then, a GRAPPA reconstruction of the uncorrected, undersampled part of k-space data is performed. These data may be inconsistent due to motion, inducing artifacts both directly from the motion and from the application of GRAPPA on the inconsistent spectral data. Subsequently, motion parameters are estimated (as proposed in [4]) for every k-space line using the full GRAPPA-reconstructed k-space data. This step is based on an optimization-based search of a linear operator that inverts the effects of motion so that an image metric applied in the spatial domain is minimized. We use a total variation image metric (L1 norm on the image gradients), which promotes image sparsity in the gradient transform domain. This optimization procedure is prone to be trapped in undesirable local minima due to the highly non-convex nature of the optimized function. To address this problem, FIDnavs are used as an additional source of information on the occurred motion. In the present study, FIDnavs acquisitions were included in each repetition of a prototype MP-RAGE sequence. The known sensitivity to motion of the FIDnavs [3] is exploited to generate a good initialization of the motion trajectory used in the optimization. After the motion parameters are estimated, the linear operator that inverts the effects of motion is constructed and applied to the k-space data. The motion-corrected k-space data is then used as an input to the subsequent GRAPPA step, and the entire loop is iterated N times. This results in a gradual improvement in image quality over several loop iterations. For comparison, the motion-corrupted data was also reconstructed with a standard GRAPPA algorithm without motion correction ("naïve GRAPPA").

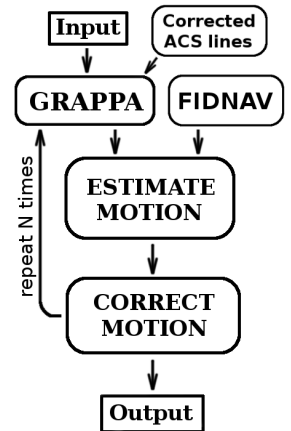


Fig. 1: Reconstruction and motion correction pipeline.

Results

Figure 2 shows an exemplary slice of the motion corrupted volume reconstructed with naïve GRAPPA and using the proposed algorithm. An improvement in image quality was consistently observed in all datasets with only a negligible residual ringing remaining after correction. The reconstruction time for one image volume was approximately 30 min (typically 6 iterations), the runtime being dominated by the convolutions with GRAPPA kernels to solve for missing data.

Discussion

We have proposed a retrospective motion correction algorithm that is applicable to data acquired with parallel imaging. The FIDnavs used to guide the motion correction algorithm can be added to a great variety of sequences "for free", i.e. with no or negligible impact on sequence. Using our method, clinical data could hence be motion-corrected without any impact on the clinical workflow. The algorithm currently exhibits a long computational time, which may be improved by a GPU implementation of both GRAPPA and the motion correction. Future work will focus on expanding the method to other image contrasts as well as address the computational efficiency of the algorithm.

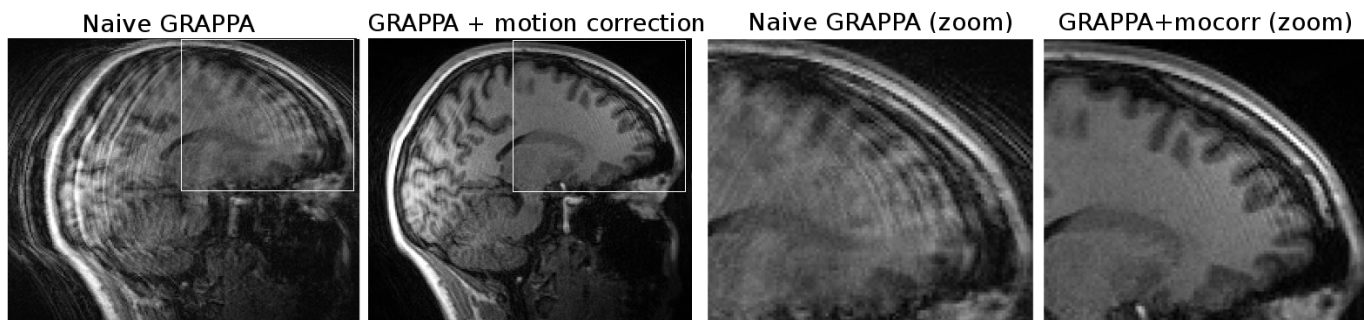


Fig. 2: Representative example of acquired data showing a slice of the uncorrected image volume (naïve GRAPPA) and using the proposed algorithm.

References: [1] Griswold et al., 2002, Magn. Reson. Med., 47(6):1202-1210; [2] Babayeva et al., ISMRM, 22:2227; [3] Kober et al., 2011, Magn. Reson. Med.66(1):135-43; [4] Loktyushin et al., 2013, Magn. Reson. Med. 70(6):1608-18.