An Efficient and General GRAPPA Reconstruction Method For Non-Cartesian Parallel Imaging

T. Zhao[1], R. Nana[1], and X. Hu[1]
[1]Biomedical Engineering, Emory University, Atlanta, GA, United States

Introduction

The Cartesian GRAPPA reconstruction algorithm assumes that the GRAPPA fitting kernel is shift-invariance. That is, the GRAPPA kernel depends only on the relative distance and orientations of the acquired datum relative to the missed data to be filled. For non-Cartesian data sampling scheme, such as spiral and radial imaging, a rigorous GRAPPA reconstruction requires different fitting kernels for each missing data [1] because an invariant kernel is not applicable. Consequently, the reconstruction process can be very time consuming, and the use of GRAPPA is limited in non-Cartesian sampling. To overcome this difficulty, various schemes were introduced based on dividing the data into many sectors and assuming the kernel within each sector to be approximately the same [2-4]. In this paper, we describe a method in which GRAPPA fitting is carried out directly on the gridded data to obtain artifacts free images.

Methods

All data were acquired on Siemens Tim 3.0T system with a 12-channel head coil. Full four-segment spiral data with identical acquisition parameters were acquired twice. The first measurement served as an external reference scan to derive the GRAPPA kernels. The second measurement was subsampled to simulate parallel imaging with acceleration factors of 2 and 4, respectively. The acquisition parameters were, matrix size: 128×128, FOV: 256 mm×256 mm, slice thickness: 5.0 mm and TR/TE: 2000/30 ms. Maximum slew rate and gradient amplitude for the spiral trajectory were 150 T/m/s and 23 mT/m, respectively.

Images were reconstructed offline with the algorithm schematically shown in Fig. 1 and implemented in Matlab. For each coil, missing spiral segments in the parallel imaging data are zero-filled, and the zero-filled data are subsequently gridded to a Cartesian grid (aliased grid) using the Kaiser-Bessel function with a window width of 6. For each coil, a fully sampled reference data set is also gridded to form the reference grid. Next, we assume that each data point in the reference grid for each coil can be calculated by a simple weighted average (defined by a kernel) of the corresponding point and its neighbors in the aliased grids of all the coils as shown in Fig.1. For segmented spiral trajectory, different segments have different contribution to a given Cartesian point, depending on the distance between the Cartesian point and the segment trajectory. Consequently, different Cartesian points require different kernels in general although the support of kernels is invariant. As it turns out, the number of different kernels needed for high-quality reconstruction can be reduced to the number of segments. Specifically, the grid points are divided into as many groups as the number of segments and each group of points are assumed to have the same kernel. Operationally, each grid point is assigned to the group defined by the segment that makes the most contribution in terms of energy in the standard gridding process. For the four-shot spiral acquisition in this study, four different kernels were employed. The GRAPPA kernel size for the fitting was chosen to be 11 × 11, larger than a normal GRAPPA kernel to account for the two-dimensional nature of spiral acquisition. In the reconstruction, the reference data were used to derive the kernels for each group of grid points, which were subsequently used in deriving the image from the data with missing segments.

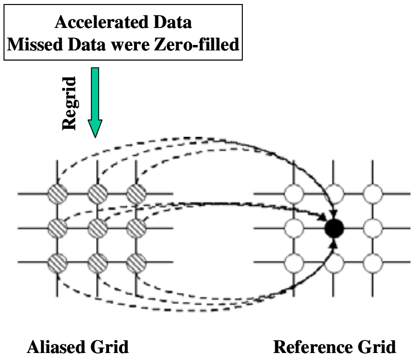

Fig. 1 Scheme of the new parallel imaging reconstruction method.

Results and Discussion

Fig. 2 shows the 128×128 reference images, accelerated (2 and 4-fold) under-sampled images and their corresponding reconstructed images using the new method for the phantom and one healthy volunteer. The aliased artifacts apparent in the under-sampled images are removed in reconstructed images. All calculations were carried out in MATLAB programming environment on a Pentium 3.0 GHz computer with 2 G RAM. The total calculation for determining GRAPPA weights took less than 2 min. Once GRAPPA weights and regridding table were determined, subsequent imaging reconstruction including regridding took approximately 10 s per image, making online imaging reconstruction possible for fMRI studies using this method.

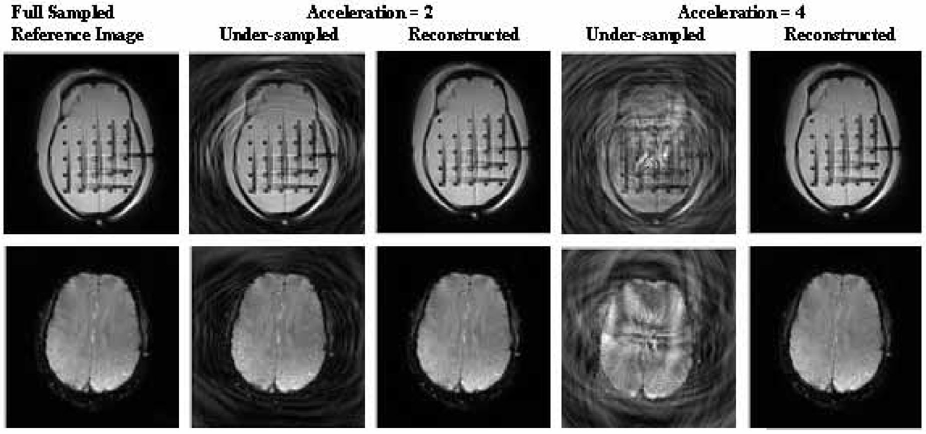

Fig. 2 The phantom (top) and *in vivo* (bottom) results of spiral imaging.

Conclusions

A new parallel imaging reconstruction method for spiral sampling was demonstrated in phantom and *in vivo*. Compared to the previous methods, the new method works directly on the regridded data. Consequently, the new method is faster and more general. Extending the new reconstruction method to other non-symmetric, non-Cartesian applications is straightforward.

Acknowledgements: This work was supported in part by the National Institutes of Health (RO1EB002009) and Georgia Research Alliance. The authors would like to thank Dr. Keith Heberlein for providing the initial IDEA codes for multi-segment spiral sequence.

References

[1] Samsonov A. A., *et al.*, Magn Reson Med 2006; **55**:431-436. [2] Heberlein K., *et al.*, Magn Reson Med 2006; **55**:619-625.
[3] Heidemann R. M., *et al.*, Magn Reson Med 2006; **56**:317-326. [4] Seiberlich1 N. et al., Proc. ISMRM 2006; **14**: 2463.