

A Combination of Linear and Nonlinear GRAPPA with Variable Density Sampling

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Target audience: Scientists and clinicians interested in highly accelerated MRI

Purpose:

Partially parallel imaging (PPI) has been used routinely for many clinical MR applications. GRAPPA [1] is one of the most commonly used methods in PPI. With 2D data, although the outer reduction factor (ORF) could achieve 4 or 5, the net reduction factor (NRF) could hardly achieve 3 due to the use of auto calibration data (ACS). With higher ORF like 4 or 5, GRAPPA suffers a high level of noise. Recently a novel algorithm called nonlinear GRAPPA [2] is proposed to deal with the problem and it could significantly improve the SNR with high ORF compared with other GRAPPA's state-of-the-art derivatives like ILRS [3] and regularization [4]. However, nonlinear GRAPPA usually requires more ACS lines, which limits the NRF that can be achieved. In this abstract, we present a method that combines the advantage of GRAPPA and NL-GRAPPA to achieve even higher NRF than NL-GRAPPA.

Methods:

With a series of comparison, we have observed that GRAPPA is able to estimate the central k-space rather accurately with a small number of ACS lines but the SNR deteriorates with higher ORF. On the other hand, nonlinear GRAPPA is good at estimating the outer k-space signals with low SNRs, but when fewer ACS lines are available, the calibration process suffers from the ill-conditioning problem and the estimated k-space signals may have large errors especially at the central k space. Based on the above observations, we propose a new method called mix GRAPPA that takes advantage of the strengths of both GRAPPA and nonlinear GRAPPA. The proposed method uses a variable density sampling pattern with three different regions. The very central k-space is still fully sampled which provides a small number of ACS lines. The sub-central area is undersampled with a low ORF of 2, and the outer k-space is undersampled with an ORF of 5. This sampling pattern is illustrated in Fig. 1. To reconstruct the missing data, GRAPPA is firstly used to estimate the missing data in the sub-central area such that the sub-central k-space is fully sampled. Finally, both the acquired ACS and the estimated data in the sub-central k-space are combined as the new ACS data for nonlinear GRAPPA algorithm to predict the missing data in the rest of k-space.

To evaluate the performance of the proposed method, a set of human brain data was acquired on a GE 3T scanner (GE Healthcare, Waukesha, WI) with an 8-channel head coil. The dataset was an axial brain image acquired using a 2D spin echo sequence (TE/TR=11/700 ms, matrix size =256x256, FOV=220 mm²). Phase encoding direction was left-right. All k-space were fully acquired and then artificially down-sampled to simulate the partial acquisition. The proposed method, nonlinear GRAPPA and GRAPPA were used to reconstruct the image. Each method used its unique sampling pattern that best fits the method. For the proposed method, we used 12 ACS lines, an ORF of 2 for the sub-central region (38 lines in total) and an ORF of 5 for the outer k-space.

Results:

Fig. 2 and Fig. 3 show the experiment results. Fig. 2 compares the reconstructed images and the amplified difference images of the proposed method, nonlinear GRAPPA and GRAPPA with the reference obtained from full acquisition. Fig.3 compares the reconstruction RMSEs at different NRFs for all three methods.

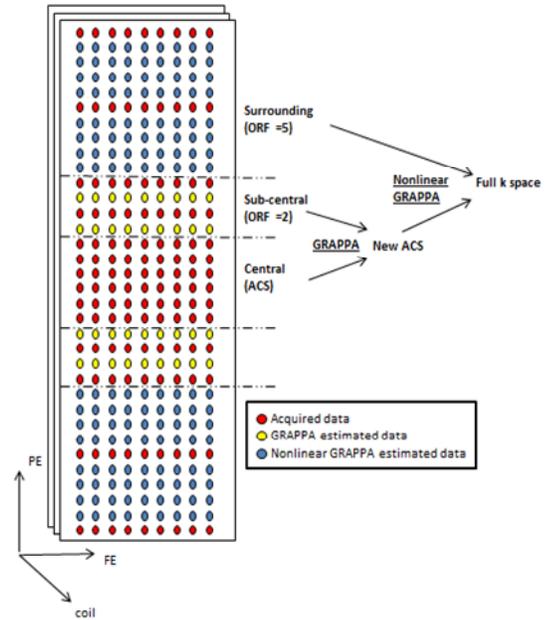
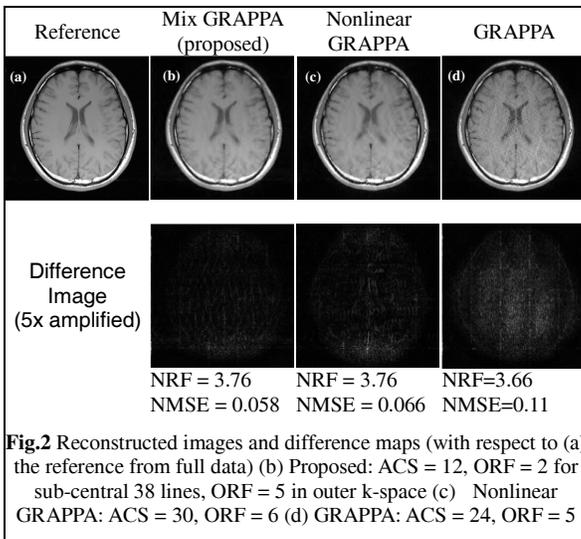


Fig.1 Illustration of the proposed mix GRAPPA method



Discussion:

Experimental results demonstrate that, compared with GRAPPA and nonlinear GRAPPA, the proposed method achieves lower RMSEs and more importantly, better SNR and fewer artifacts, especially at high net reduction factors, which could be clearly seen in the difference images in Fig.2. In addition, this method is promising in accelerating 3D and dynamic imaging with high factors.

Conclusion:

Our proposed method is able to achieve a much higher NRF than GRAPPA and nonlinear GRAPPA without significant SNR loss/artifacts.

References: [1] Mark A. G, et al, .MRM, 47, 2012: 1202-1210 [2] Yuchou C, et al., MRM, 68, 2012: 730-740 [3] Huo D, et al., MRI, 2008; 27:1412-1420 [4] Qu P, et al., MRI, 24, 2006: 248-255

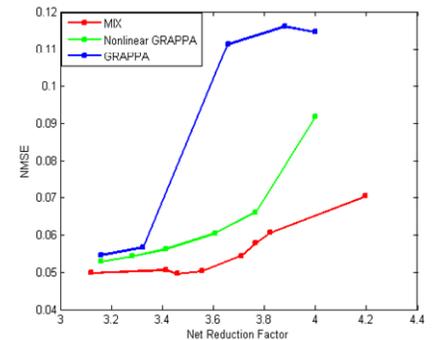


Fig.3 Reconstruction RMSEs at different acceleration factors.