Optimization and acceleration of Multi-band EPI reconstruction using the reduced reference k-space window

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Target audience: MR physicists and MR reconstruction engineers

Purpose

While two dimensional (2D) single-shot echo planar imaging (EPI) has been popularly used to monitor brain functionality due to its fast acquisition paradigm, various methods have been proposed to increase the speed of 2D EPI. One such promising method, simultaneous excitation of multiple slices using multi-band (MB) radio-frequency (RF) excitation has shown the potential to accelerate the spatial and temporal resolution of EPI [1-2]. The Slice-GRAPPA method calculates the linear interpolation kernel for each slice of MB accelerated k-space and de-aliases images using the estimated kernel [2]. It is known that the interpolation kernel size, acceleration factor (R value) and the number of reference lines (ACS line number) determine the reconstructed image quality in in-plane parallel imaging (PI). Since Slice-GRAPPA employs the same basic principles as in-plane GRAPPA [3], we hypothesize that the sizes of the interpolation kernel and data used to estimate the kernel could affect the performance of MB de-aliasing. In this study, we evaluate MB de-aliasing performance in simulated data while varying the kernel and fitted data sizes and show considerable reductions in compute time are possible with no apparent loss in data quality.

Methods

We collected raw data in a 3T scanner (Siemens, Enlangen) with a 32 ch head coil using a conventional EPI acquisition under an IRB-approved protocol. The following MR parameters were used; FOV=240×240mm^2, matrix=96×96, voxel size 2.5×2.5×2.5mm^3, TR/TE=3.37s/29 ms, 48 slices, partial Fourier = 7/8, 133 repetitions, scan acquisition time 7:32. The full data was reconstructed in a conventional manner to generate baseline EPI data. By combining the raw k-space data from multiple slices prior to reconstruction, MB acceleration acquisition was simulated from the conventional EPI dataset with MB factor = 4 (gap between adjacent summed slices = 3 cm). An additional phase shift was added in the readout (RO) direction to the raw EPI data to create a simulation of blipped-CAIPI acquisition with FOV/2 shift [2]. Slice-GRAPPA was used to de-alias these simulated MB accelerated acquisitions, varying the interpolation kernel size and the size of the fitted data (see Fig1.). Finally, in-plane (i.e., non-MB) GRAPPA acceleration was also simulated for an additional comparison (R=2 and ACS lines = 24).

To determine the temporal precision of MB de-aliasing, we introduced the normalized temporal standard deviation of the difference (NTSDD) map between a baseline and the simulated image, which indicates the temporal variation of the MB simulated signal from the truth. To present the spatial accuracy of MB de-aliasing, a simple normalized difference map between the temporally averaged reference and MB reconstructed images was calculated. NTSDD and difference maps were calculated for a range of kernel sizes (3×3, 5×5 and 7×7 in RO and PE), and fitted data sizes (1/4 increase both in RO and PE; 24×24, 48×48 and 72×72)

$$NTSDD\ (i, j, k) = std\ (ref\ (i, j, k, t) - recon\ (i, j, k, t)) / \overline{ref}\ (i, j, k)$$

Results

The 3×3 kernel fitted to full k-space data (96×84) generates the smallest average and standard deviation of NTSDD (2.36±1.44%) in whole brain. However, 5×5 with full k-space produces comparable metrics (2.42±1.60%) but also the smallest standard deviation of the difference in whole brain (2.15%), indicating the smallest spatial inhomogeniety of difference between MB reconstructed and reference images, as shown in Table 1. This result is also shown in Fig 1. The NSTDD map with 5×5 kernel size and full k-space demonstrates the smallest local variation of NTSDD and normalized difference. In-plane GRAPPA simulation produces 1.21±1.15 % of NTSDD and -0.41±2.68% of normalized difference in whole brain.

Clearly, reducing the size of fitted data for estimation of the kernel increases NTSDD and the local variation of signal intensity. Fig 2 demonstrates the difference between images reconstructed with 5×5 kernel and different sizes of fitted data (72×72 vs the full k-space).
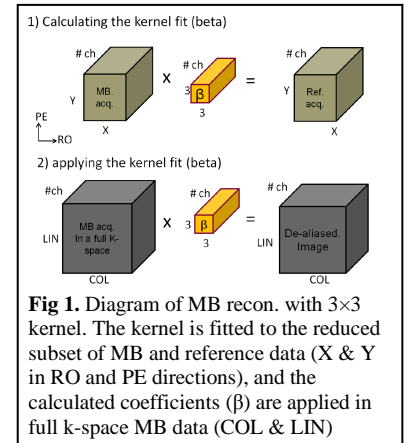
Conclusion & Discussion

In the MB CAIPRININHA simulation using the empirical conventional EPI data set, a kernel size of 5×5 fitted to the full k-space data provides the best MB de-aliasing performance as measured by temporal precision/accuracy and local variation. However, it is still possible to get good performance with modest reductions in the amount of data used for fitting the kernel. We observe here that a reduction to ¾ full data in both RO and PE directions produce equivalent images with a time savings of 264 % for kernel fitting (from 301 to 114 secs on 2.4GHz Xeon quad-core workstation using home-built matlab scripts).
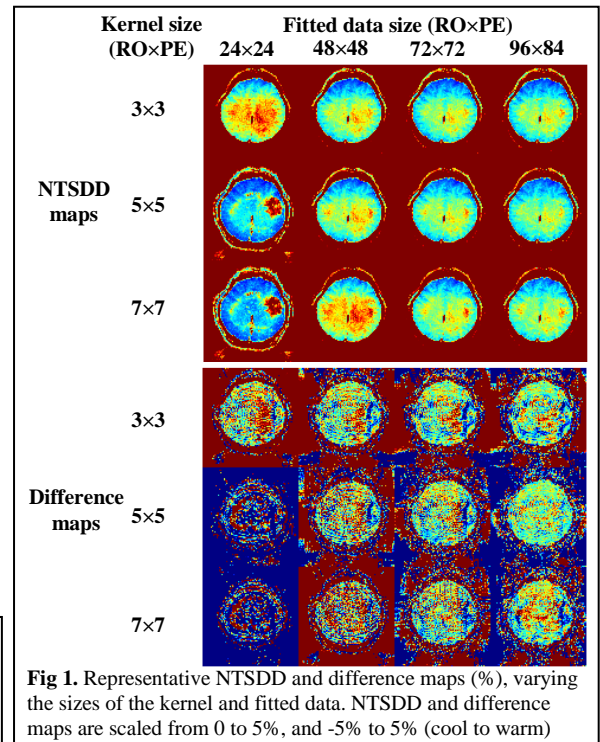
Reference: 1. Moeller et al., MRM, 2010;63(5):1144-53. 2. Setsompop et al., MRM, 2012;67(5):1210-24. 3. Griswold et al., MRM,2002;47(6):1202-10

Fig 1. Diagram of MB recon. with 3×3 kernel. The kernel is fitted to the reduced subset of MB and reference data (X & Y in RO and PE directions), and the calculated coefficients (β) are applied in full k-space MB data (COL & LIN)

Fig 1. Representative NTSDD and difference maps (%), varying the sizes of the kernel and fitted data. NTSDD and difference maps are scaled from 0 to 5%, and -5% to 5% (cool to warm)

Fig 2. Representative reconstructed images with commonly 5×5 kernel and different sizes of fitted data (left: 72×72, and right 96×84)

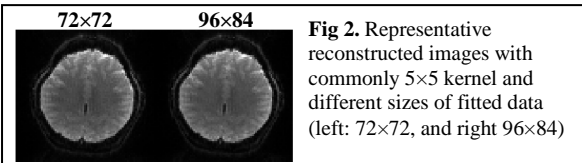| Whole brain	Kernel size RO × PE	Data window (RO × PE) 24×24	48×48	72×72	96×84
Average NTSDD	3×3	3.01±1.75	2.47±1.50	2.40±1.48	2.36±1.44
	5×5	2.15±1.87	2.63±1.71	2.54±1.76	2.42±1.60
	7×7	2.17±2.00	3.22±2.03	2.75±2.01	2.72±1.93
Average Normalized Difference	3×3	0.81±4.66	0.20±3.93	0.00±3.60	-0.25±3.31
	5×5	-7.31±12.9	0.24±4.80	-0.01±4.17	-0.19±2.15
	7×7	-9.97±16.6	0.90±6.34	0.16±4.94	0.04±4.57

Tab1. Whole brain normalized average and standard deviation of the difference between MB reconstructed and a baseline (reference) images (%). Note that simulated in-plane GRAPPA (R=2 and 3×3 kernel) shows average 1.21±1.15 % of NTSDD and -0.41±2.68% of difference