

# K-space Inherited Parallel Acquisition (KIPA)

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**Introduction:** Parallel imaging is one of the most promising approaches for reducing scan time while maintaining field of view (FOV) and spatial resolution. GRAPPA [1] is a widely used technique for auto-calibrating reconstruction operating in the k-space domain. The technique gives good quality results for low reduction factors but it is less applicable for high reduction factors due to residual aliasing artifacts and substantial noise amplification in the reconstructed images. A novel method for dynamic parallel imaging called K-space Inherited Parallel Acquisition (KIPA) has been developed to overcome the limitations of GRAPPA. The application to dynamic temperature imaging is presented.

**Theory:** GRAPPA reconstruction coefficients found from the central (fully sampled) k-space region may not be optimal for the outer (undersampled) regions because of the substantial difference in SNR between these regions. In KIPA, to find reconstruction coefficients adapted to local SNR characteristics of k-space data, the complete dataset for the first time frame(s) in a dynamic series is acquired and the subsequent frames are highly undersampled. Then, the k-space is segmented in the phase-encoding (PE) and frequency-encoding (FE) direction as shown in Fig. 1 (thick solid band: the central k-space lines which are acquired for all frames; thin solid (dashed) lines: the outer k-space measured (missing) lines) The k-space segmentation is demarcated by the shading in the PE direction and by the vertical lines in the FE direction. The number of segments is arbitrary. The KIPA reconstruction coefficients for each segment are calculated using the full k-space data of the first (reference) frame. For all subsequent frames, the unmeasured k-space lines in every segment are predicted by directly using the coefficients determined from the same segment in the reference k-space dataset. Like GRAPPA, some central k-space lines are completely acquired in every time frame to minimize image artifacts due to errors in the prediction.

KIPA reconstruction coefficients are calculated for each k-space segment by using a small number of points with offsets in  $k_x$  and  $k_y$  in a manner similar to GARSE [2]:

$$S_j^{n_s}(k_x, k_y + m\Delta k_y) = \sum_{l=1}^{N_c} \sum_{q=1}^{N_b} w(n_s, j, l, m, q) S_l(k_x + a_q \Delta k_x, k_y + b_q \Delta k_y) \quad (1)$$

where  $S_j^{n_s}(k_x, k_y + m\Delta k_y)$  is the predicted k-space signal at the point  $(k_x, k_y + m\Delta k_y)$  in segment  $n_s$  of coil  $j$ , and  $m$  is the offset of the missing lines from the actually acquired data in the under-sampled frames. Index  $l$  counts through the coils and  $N_c$  is the number of coils. The index  $q$  counts through the individual reconstruction blocks ("block" is defined as in the original paper on GRAPPA [1]) in the  $k_x$  and  $k_y$  direction and  $a_q$  and  $b_q$  are the offsets of the blocks in the  $k_x$  and  $k_y$  directions respectively.  $N_b$  is the number of blocks.

The temperature map is obtained from the phase difference image between two adjacent time frames [3]:

$$\Delta T = \frac{\Delta\phi}{2\pi \cdot \gamma \cdot \alpha \cdot B_0 \cdot TE} \quad (2)$$

where  $\Delta\phi$  is the phase change in radians,  $\Delta T$  is the temperature change in °C,  $TE$  is the echo time in seconds,  $\gamma$  is the proton gyromagnetic ratio (42.58 MHz/T), and  $\alpha$  is the thermal coefficient of the proton resonance frequency shift (-0.01 ppm/°C) [4].

**Results:** The temperature curve from the data acquired while heating the agar phantom by ultrasound is shown in Fig.2. The improved consistency of the result of KIPA with  $R=6$  and  $N_{ref}=24$  over that of conventional GRAPPA with  $R=4$  and  $N_{ref}=24$  can be observed clearly. The difference of the KIPA results from the reference temperature measurement is less than 1°C which is within the range of accuracy of the PRF method. The results from the human volunteer study are shown in Fig. 3. The reference image from the complete data is shown in Fig. 3a. The images reconstructed from the undersampled data ( $R=4$  and  $N_{ref}=24$ ) using KIPA, our GRAPPA implementation, and product GRAPPA (Siemens, IDEA VA25) are shown in Figs. 3b-d, respectively. The image reconstructed by KIPA has improved quality (reduced noise and no obvious aliasing) relatively to the images reconstructed using either GRAPPA implementation. Vessel visibility in the KIPA image (Fig. 3b) while lower than in the image from the complete data (Fig. 3a) is much better than vessel visibility in the GRAPPA images reconstructed from the same undersampled data (Fig. 3c-d) due to the excessive noise amplification and residual aliasing artifacts in the GRAPPA images.

**Discussion:** GRAPPA reconstruction coefficients found from the central k-space region may not be optimal for the undersampled regions because of the substantial difference in SNR of the central region and the outer k-space regions. Non-optimality of the reconstruction coefficients may cause strong noise amplification in the resulting images. Whereas, KIPA reconstruction coefficients are adapted to local SNR characteristics of k-space data. From these results, for large reduction factors, the image quality is largely improved using the KIPA method relative to the conventional GRAPPA method. Specifically, noise amplification and unresolved aliasing are substantially reduced by using KIPA. The strength of KIPA comes mainly from two sources: the use of localized reconstruction coefficients (segmentation) and incorporation of all relevant data dimensions into the reconstruction process.

**Conclusion:** A novel technique for parallel image acquisition and reconstruction for dynamic MRI has been developed. In KIPA, unique reconstruction coefficients are calculated for different segments of k-space using the complete data of the first frame(s). In this way, the reconstruction coefficients are adapted to the local SNR characteristics of the k-space data allowing reliable image reconstruction from highly undersampled data of the subsequent time frames.

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**References:** [1] Griswold MA, et al. MRM 2002;47:1202-10. [2] Kholmovski EG, et al. ISMRM, 2005, p. 2672. [3] Chung AH, et al. MRM 1996;36:745-52. [4] Peters RD, et al. MRM 1998;40:454-9.

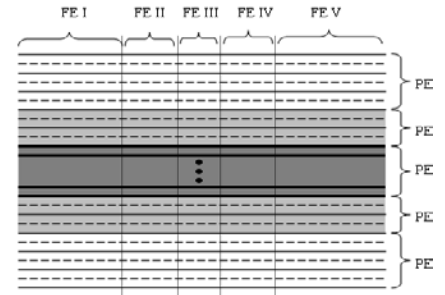


Fig. 1. The k-space diagram for the KIPA method in the case of 2D imaging with reduction factor 2 and k-space segmentation in 25 regions.

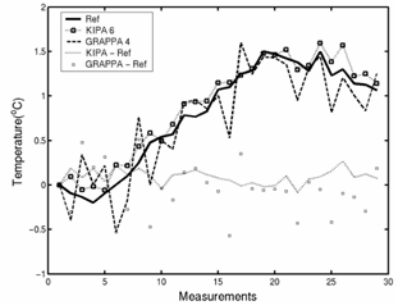


Fig. 2. The temperature curves from the image time series reconstructed by KIPA and GRAPPA.

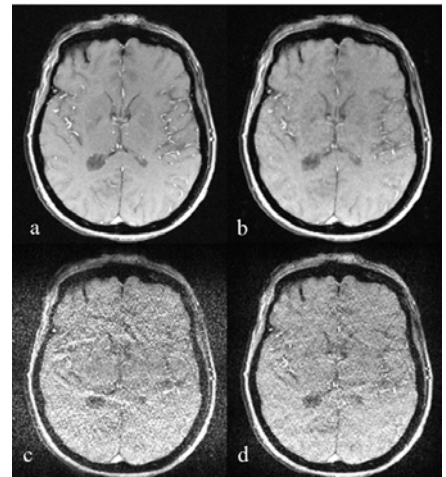


Fig. 3. Images from the human volunteer study: (a) reference; (b) KIPA image; (c) our own GRAPPA image, and (d) GRAPPA image from scanner.  $R=4$  and  $N_{ref}=24$  for (b-d).