

# Convolution kernel decision scheme for reconstruction in k-t/k space

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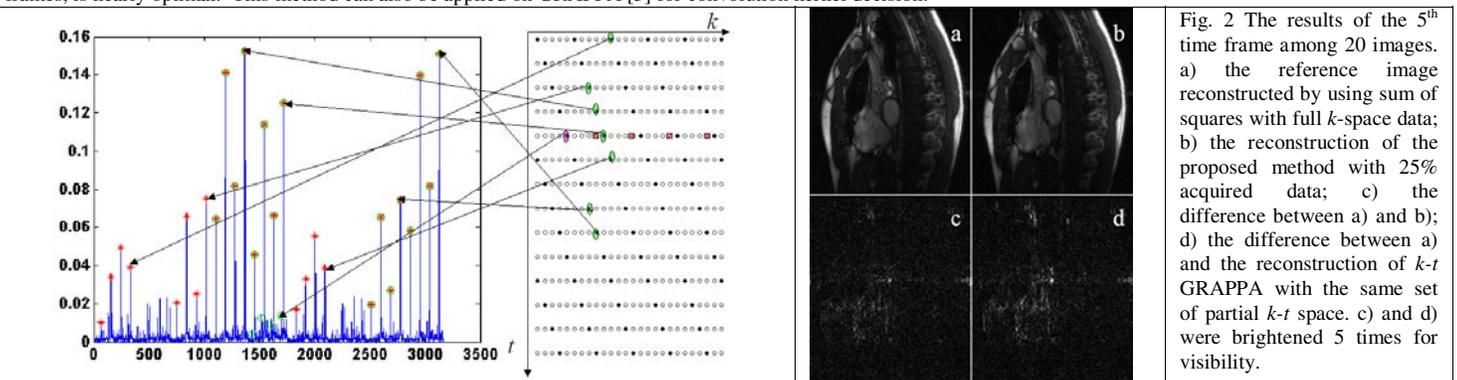
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**Introduction:** In this work, a novel reconstruction algorithm in  $k-t$  space is introduced. The method is based on allowing the convolution kernel to be selected on the basis of prior acquisitions or from ACS lines within the acquired data.  $k-t$  GRAPPA [1] is a special implementation of convolution in  $k-t$  space with a small convolution kernel. Because of the size of the convolution kernel, temporal resolution of the images reconstructed by  $k-t$  GRAPPA may be reduced. To improve the temporal resolution, it is proposed that the choice of the convolution kernel should be guided by the convolution matrix generated with acquired data. Dynamic cardiac MRI data were used in the experiments. The experiments showed that the proposed method could generate better results than  $k-t$  GRAPPA with a fixed, small kernel definition. For the size kernels previously reportedly used in  $k-t$  GRAPPA, significant error is due to inappropriate truncation of the convolution kernel.

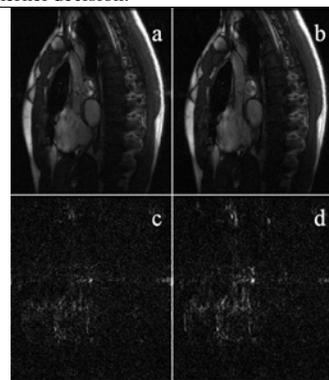
**Theory:** The missing  $k-t$  space data can be approximated by using convolution in  $k-t$  space. Given an acquisition trajectory, ratios between images along time direction and sensitivity maps, the true convolution matrix  $M$  can be calculated by using the equation  $M = C_m (C_a^H \Psi^{-1} C_a)^{-1} C_a^H \Psi^{-1}$ .  $C_m$  and  $C_a$  are the sub-blocks of the Fourier transform of the “scaled coil sensitivity matrix” corresponding to the missing and acquired phase encoding lines, the “scaled coil sensitivity matrix” is the pixel wise multiplication of image ratios and coil sensitivity maps;  $\Psi$  is the noise correlation matrix among channels;  $H$  is the conjugate operator.  $k-t$  GRAPPA is a special case of convolution in  $k-t$  space by using a truncated  $M$  with a small convolution kernel. Due to space limitations, the details of this theory are provided separately. Because of the huge size and the difficulty of computation, the convolution matrix has to be truncated for implementation. The value of any element in  $M$ , corresponding to an acquired data point, shows the correlation between that acquired data point and the missing data point that is being interpolated. To reduce the truncation error, the truncated convolution kernel should make use of acquired data points that are highly correlated to the missing data, *i.e.* with high values in  $M$ . A convolution matrix  $M$  can be approximated by using the acquired partial  $k$ -space and can be used as guidance for a truncation scheme. The proposed method, adaptive convolution in  $k-t$  space, first calculates  $M$ , and then uses the neighbors with large values in  $M$  for convolution.

**Method and Results:** Axial cardiac images were collected on 1.5T GE system (GE Healthcare, Milwaukee, WI) (FOV 240 mm, matrix 192x256, TR 4530 ms, TE 1704 ms, flip angle 45°, Slice thickness 5 mm, number of averages 1) through FIESTA with a GE 4-channel cardiac coil. There are 20 images per heartbeat. Simulated time interleaved  $k-t$  space data with acceleration factor 5 (Fig. 1) were used for reconstruction. Central 12 lines were used as auto-calibration signal (ACS) lines. Hence the true reduction factor was 4. The sensitivity maps were generated by using the average  $k$ -space (along time direction) of the partial  $k-t$  space [1]. The raw sensitivity maps were then inpainted [2] to fill in the holes and remove noise. This filtering step is important because a noisy sensitivity maps makes the reconstruction matrix less sparse and difficult to find the pattern. Low-resolution image sequence can be reconstructed using the ACS lines and some lines from adjacent time frames. The low-resolution image sequence was used to calculate the ratios between images. The width of the window along time direction for reconstruction is  $2 \times R - 1$ , where  $R$  is the acceleration factor, and the window is centered at the time frame that is being interpolated. This means only the local time frames are used for interpolation. Fig.1 shows one example of the convolution matrix and its correspondence in the  $k-t$  space. It can be seen that the convolution matrix is sparse; hence it is reasonable to use a truncated convolution kernel.  $k-t$  GRAPPA uses a convolution kernel that includes the acquired neighbors that have the highest correlation with the missing data. However, there are still other acquired data points (stars without circles in Fig. 1) that have high correlation with the missing data. Therefore, 4 more neighbors with highest correlation with the missing data in each channel were added to the convolution kernel in this example. One neighbor used by  $k-t$  GRAPPA was deleted because of low value in  $M$ . Similar to  $k-t$  GRAPPA, ACS lines were used to calculate the values of the elements in the convolution kernel. Fig.2 shows the results of time frame 5. The root of relative square error (RRSE) is defined as Eq. 1 (under Fig. 2). The means (along time direction) of RRSE of the images reconstructed by the proposed method and  $k-t$  GRAPPA are 15.16% and 13.57% in the cardiac region. By comparing Figs. 2c and 2d, it can be seen again that the image reconstructed by using the proposed method has lower artifact power than that by  $k-t$  GRAPPA.

**Discussion:** The proposed method uses the convolution kernel decided by the acquired data for reconstruction. Hence this method guarantees less truncation error than  $k-t$  GRAPPA. High quality images were generated when reduction factor was as high as 4 for CMRI in the experiment. The choice of convolution kernel can be made only once for one application on a fixed system. Notice, increasing the size of convolution kernel increases the number of unknowns to solve when calculating weights with ACS lines. Therefore, only the neighbors with high correlation with the missing data should be chosen, otherwise the error caused by more unknowns may exceed the reduced truncation error. Although this post acquisition method always results in minimal truncation error for a given kernel size, it has been observed experimentally that using a fixed kernel, consisting of weights from all of the acquired data with distance less than 2 in PE direction in the adjacent  $2 \times R - 1$  time frames, is nearly optimal. This method can also be applied on GRAPPA [3] for convolution kernel decision.



**Fig. 1** The right side shows the time interleaved  $k-t$  space of one channel. The red boxes show the positions of the missing data that are being interpolated. The left side shows one row of the convolution matrix  $M$  for that set of missing data; other rows of  $M$  are rotations of this row. The green ellipses (right) and the stars (left) show the neighbors used by adaptive convolution for one missing data point in  $k-t$  space. The solid lines show the correspondence between elements in  $M$  and the acquired data in  $k-t$  space. The green circles (left) show the neighbors used by  $k-t$  GRAPPA. The pink ellipse shows one neighbor used by  $k-t$  GRAPPA but not by the proposed method because of the low correlation with the missing data point (the green circles without stars in it on the left side).



**Fig. 2** The results of the 5<sup>th</sup> time frame among 20 images. a) the reference image reconstructed by using sum of squares with full  $k$ -space data; b) the reconstruction of the proposed method with 25% acquired data; c) the difference between a) and b); d) the difference between a) and the reconstruction of  $k-t$  GRAPPA with the same set of partial  $k-t$  space. c) and d) were brightened 5 times for visibility.

$$RRSE = \sqrt{\frac{\sum_{\text{domain}} (\text{recon} - \text{reference})^2}{\sum_{\text{domain}} (\text{reference})^2}} \quad (\text{Eq. 1})$$

**References:**

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- [2] Huang, F *et al.* Magn Reson Med; 53: 388-397,2005
- [3] Griswold, M.A., *et al.* Magn Reson Med 47:1202-1210, 2002