The applicability of k-t GRAPPA for dynamic contrast enhanced MRI

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Introduction: Recently a *k-t* space based method *k-t* GRAPPA[1] was proposed to exploit local temporal and spatial correlations for dynamic cardiac parallel imaging. This method is not limited to imaging parts with quasi-periodic motion and is potentially applicable to dynamic contrast enhanced imaging. In this work, it is shown that *k-t* GRAPPA is suitable for dynamic contrast enhanced imaging to improve the spatiotemporal resolution. Theoretical analysis and simulated dynamic contrast enhanced breast magnetic resonance imaging (DCE-BMRI) data were applied to confirm the claims.

Method and Results : The missing data in *k*-space can be approximated by using convolution in *k*-space. GRAPPA [2] is a special case of the convolution in *k*-space. Similarly, *k-t* GRAPPA is a special case of convolution in *k-t* space that uses a truncated convolution kernel. If the multiplications of image ratios (between adajecnt time frames) and sensitivity maps are smooth enough at most of positions in the images' domain, such that the convolution matricis *Ms* are sparse and most of the energy of *Ms* is located in the elements used by *k-t* GRAPPA, then the truncation error is small and hence *k-t* GRAPPA is applicable. To show that *k-t* GRAPPA is applicable for dynamic contrast enhanced imaging, twenty-five time frames of BMRI data were collected on a SIEMENS 1.5T Avanto system (TR = 750ms, TE = 1.6 ms, FOV = 340mm x 340mm, slice thickness = 1mm, # of averages =1, matrix size 196 x 384) using turbo spin echo sequence with the prototype of the12-channel breast coil (Invivo, Gainesville, FL). The phase encoding direction was left-right. There was no contrast enhancement during the acquisition. The signal enhancement in DCE-BMRI was simulated by using a logistic model. (Eq. 1) described by Moate *et al* [3]. The values of the parameters P_1 to P_5 for different kinds of tumors were provided by Moate *et al*. With given parameters and location for tumor, a set of dynamic images can be generated by using Eq. 1. In simulations, the time resolution was 20 seconds. So the total simulated time interval was 500 seconds.

$$SI(t) = \frac{P_2 + (P_5 \cdot t)}{\{I + \exp(-P_4 \cdot (t - P_3))\}} + P_1 \qquad (1)$$

SI is the signal intensity and t is the time (in seconds). The bright regions in Fig 2a show the position of the tumor. The original intensity of the acquired image at these positions was used as the base intensity value P_1.

Without loss of generality, one channel data (10th channel among 12 channels) from time frame 5 to 11 are used to show an example of the convolution matrix *M* for one set of missing data at time frame 8 when acceleration factor is 4. The sensitivity maps were calculated by using the full average *k*-space along time direction [1]. Fig. 1a shows the convolution matrix *M*. Fig. 1b shows the correspondence of the convolution kernel and the data in *k-t* space. From Fig. 1, it can be seen that the convolution matrix *M* is very sparse, and to interpolate the missing data, *k-t* GRAPPA uses the acquired data that have the strongest correlation with the missing data. Therefore, *k-t* GRAPPA is applicable to DCE-BMRI. Figs 2c-g show the results by using *k-t* GRAPPA with acceleration factor 6 and 11 auto-calibrate signal (ACS) lines with 1, 4 and 12 channels. The true reduction factor is 4.67 (21.4% *k*-space). The precontrast image was used as the time invariant term to reduce the image support , 4 neighbors were used for reconstruction [1]. Reference images were generated by using sum of squares with full *k*-space. Fig. 2d shows the difference between the reference image and reconstruction of *k-t* GRAPPA with 21.4% *k*-space at time frame 4. Time frame 4 was used because the reconstruction of *k-t* GRAPPA has the highest error at this frame (Fig 2e). Fig. 2d was brightened 25 times for visibility. It confirms that *k-t* GRAPPA can generate very accurate reconstructions with high reduction factors for DCE-BMRI even with only one channel. As expected, *k-t* GRAPPA can generate better results with more channels. Figs. 2e to g show the improvement of signal intensity curve. It can be seen that the reconstructed signal intensity curves (blue) are very close to the intensity curves of the reference images(red) with reduction factors as high as 4.67. The relative errors are 2.55%, 2.08%, and 1.6% for the reconstructed images with 1, 4 and 12 channels.

Discussion: In this work, the convolution matrix of *k-t* GRAPPA for DCE-BMRI is calculated. From the sparseness of the convolution matrix, it can be seen that *k-t* GRAPPA is applicable to DCE-BMRI. The reconstructed images confirm the hypothesis. With a reduction factor 4.67 and only one channel, *k-t* GRAPPA can still generate results very similar to the results generated with full *k*-space. Increasing the size of convolution kernel (dotted arrows in Fig. 1b) can further improve the accuracy but may increase the reconstruction time. The application of *k-t* GRAPPA for other DCE-MRI exams will be further investigated.

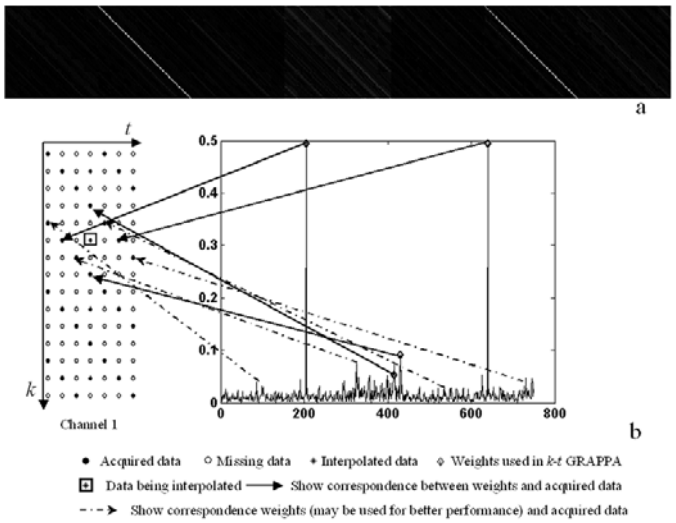

Fig 1. a) The convolution matrix *M* for time frame 4 with 1 channel data (channel 10) and 7 time frames (1 to 7). b) One row of a) and the correspondence with *k-t* space. It shows the convolution matrix is sparse (a) for DCE-BMRI and *k-t* GRAPPA uses the optimized convolution kernel (b).

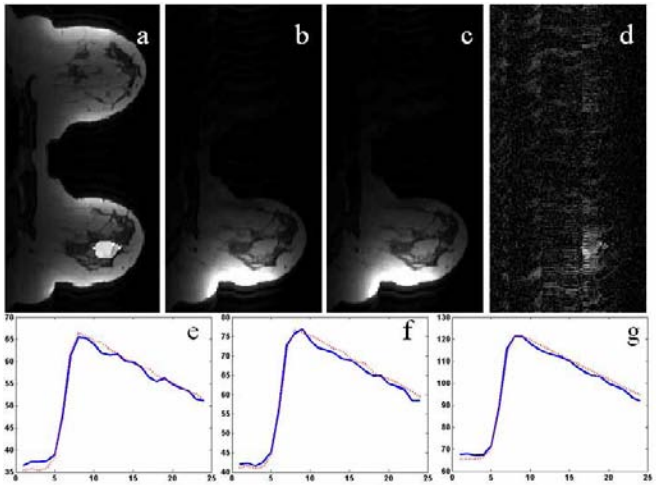

Fig 2. Results of *k-t* GRAPPA. a) the bright region shows the position of the simulated tumor; b) reference of the 10th channel at time frame 4; c) the reconstruction of the 10th channel with partial *k*-space at time frame 4; d) the difference between b) and c), brightened 25 times; e)-f) Blue curves show the signal intensity (at the tumor) curve of the images reconstructed by *k-t* GRAPPA with 1, 4 and 12 channels. Red curves show the reference signal intensity curves.

References: [1] Huang, F *et al*. Magn Reson Med; 54: 1172-1184, 2005 [2] Griswold M *et al*., MRM 2002, 47:p1202-1210
[3] Moate, PJ *et al*. Magn Reson Imag; 22: 467-473, 2004;