k-t GRAPPA

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INTRODUCTION:

k-t BLAST utilizes the correlations among dynamic images in both *k*-space and in time [1]. GRAPPA [2], linearly interpolates the missing data in *k*-space. Based on these approaches, a novel method that takes advantage of correlations and interpolates the missing data in *k-t* space is proposed. For this method, neither training data nor sensitivity maps are necessary. This method can work for either multi-channel data or single channel data. Examples for 4-channel cardiac imaging with fourfold acceleration are provided as well as functional MRI examples for single channel data with threefold acceleration.

METHODS:

Dynamic MRI acquires sets of raw *k*-space data at various points in time. Fig. 1 shows the sampling pattern for *k-t* GRAPPA when the reduction factor is 4. In *k-t* GRAPPA, uncombined images are generated for each coil in the array by applying multiple block wise reconstruction to generate the missing lines for each coil. Unlike conventional GRAPPA, *k-t* GRAPPA utilizes data from nearby time slices as well as the same time slice to interpolate the missing data. Fig. 1 illustrates three examples of interpolation for the case of single channel data. For the case of reduction factor *r*, to interpolate the data at a line $k_y - m\Delta k_y$ at time *t*, where *m* is the offset from the actual acquired data at line k_y, data at lines k_y and $k_y - r\Delta k_y$ at the same time *t* as well as data from the same line $k_y - m\Delta k_y$ but in different *k*-spaces at time slices *t-m* and *t+r-m* are utilized. In the case of multiple channels, data from multiple lines at the same positions as described above in *k-t* space but from each coil in the array are used to interpolate a missing line in any given single coil. We first use the accquired data in the manner described above to linearly fit the ACS lines. This fit gives us a different set of weights for each coil at each different time step. These are then used to generate the missing lines for a given coil at a given time.Once all of the lines are reconstructed for a particular coil (at a given time), a Fourier transform can be used to generate the uncombined image for that coil. Once this process is repeated for each coil of the array, the full set of uncombined images can be obtained, which can then be reconstructed using a normal sum-of-squares.

RESULTS:

Oblique cardiac images were collected by a 1.5T GE system (FOV 280 mm, matrix 160×120, TR 4510 ms, TE 2204 ms, flip angle 45°, Slice thickness 6 mm, number of averages 2) through fast imaging employing steady-state acquisition (FIESTA) with a GE 4-channel cardiac coil. Breath-holds ranged from 10 - 20 seconds. There are 20 images per heartbeat. Table 1 compares the relative errors of GRAPPA and *k-t* GRAPPA when the reduction factor is 4 (along with the reconstriction times for all 20 images). It can be seen from Table 1 that *k-t* GRAPPA is not very sensitive to the number of ACS lines and hence allows reduction in the acquisition time with little loss of image quality. Even when conventional GRAPPA does not work, *k-t* GRAPPA can still generate very accurate results. Furthermore, *k-t* GRAPPA requires less reconstruction time.
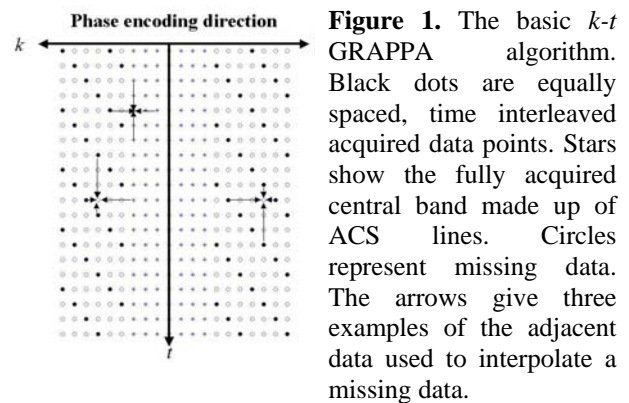
Figure 1. The basic *k-t* GRAPPA algorithm. Black dots are equally spaced, time interleaved acquired data points. Stars show the fully acquired central band made up of ACS lines. Circles represent missing data. The arrows give three examples of the adjacent data used to interpolate a missing data.

Table 1. Comparsion using cardiac MRI data.

# of ACS lines	GRAPPA	*k-t* GRAPPA
31	6.67%/9.39s	3.20%/7.25s
21	13.51%/7.42s	3.48%/5.75s
11	Does not work	3.80%/3.95s
6	Does not work	4.11%/3.79s
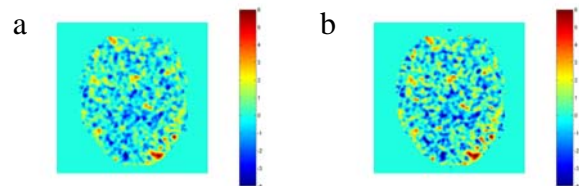
Figure 2. T-test maps for single channel fMRI data (sample data of BrainVoyager). a) T-test map of fully acquired reference images. b) T-test map of images reconstructed with *k-t* GRAPPA with threefold acceleration.

DISCUSSION:

k-t GRAPPA does not require sensitivity maps or training data, both of which are required by *k-t* SENSE. It produces more accurate results than GRAPPA with fewer ACS lines and less reconstruction time. It also works for single channel data (with reduced *k*-space) in contrast to ordinary GRAPPA.

REFERENCES:

[1] J. Tsao et al., MRM 2003; 50(5):p1031-1042
[2] M.Griswold et al, MRM 2002, 47:p1202-1210