

Comparison of three partial k-space reconstruction techniques for dynamic myocardial perfusion MR imaging

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Introduction:

Partial k-space acquisition and reconstruction techniques have been used for the study of cardiac wall-motion and viability for the past few years in the field of cardiac MRI, two of the more popular ones being GRAPPA[1] and SENSE[2]. Dynamic contrast enhanced myocardial perfusion MRI is becoming an increasingly popular technique to detect and assess coronary artery disease. However, more rapid acquisitions are needed to obtain good volume coverage for clinical use. In this work, we apply three partial k-space reconstruction techniques for myocardial perfusion MRI studies. We compare a standard GRAPPA reconstruction, an improvised k-t-GRAPPA[3] technique and the sliding-window[4] technique as applied to dynamic perfusion MRI data acquired from a 3Tesla scanner. The reconstructed data is analyzed with a modified 2-compartment model [5] for comparisons of regional blood flow.

Methods:

Full k-space rest data was acquired on a 3 Tesla Trio scanner (Siemens Medical Systems, Erlangen, Germany) using a perfusion - turbo flash saturation recovery sequence (TR 2; TI 100; TE 1.27; FOV 251x189; Flip Angle 12; Slice thickness 8mm; matrix 192x89) with a Siemens 8-channel cardiac coil. Contrast agent Gd-DTPA (Omniscan) was injected at a rate of 6cc/sec with a dose of ~0.06mmol/kg. The raw data was reconstructed using each of the three mentioned methods and the standard square root of sum of squares (SoS) images from full k-space data were also reconstructed for reference. Reconstruction was performed for reduction factors 2 and 4 using 14 auto calibration signal (ACS) lines. The relative error was defined as the relative difference in energy between the reference image (SoS) and the reconstructed image as a percentage of the energy of the reference image. All reconstructions and processing were performed on a 3.2 GHz, 2GB machine using MATLAB 7.0 (The Mathworks Inc. Natick, MA). The time taken and relative errors are reported in Table 1. The value of reduction factor in parenthesis indicates the computed reduction factor taking into account the ACS lines. Figure (1) illustrates time frame 15 of slice 4 for all the 4 reconstructions performed. The images were then registered to minimize respiratory motion artifacts and the myocardium was manually segmented into 6 regions of interest. The same contours used for segmenting the images were applied to all of the reconstructions. The signal intensities obtained were corrected for non-uniformity due to coil sensitivity and fit to the modified 2-compartment model to estimate the contrast washin and washout parameters to determine blood flow [5]. Table 2 details the values of blood flow obtained for each of these reconstructions (mean \pm sd from 4 slices and six regions) and the relative error with respect to those estimated from the standard SoS images.

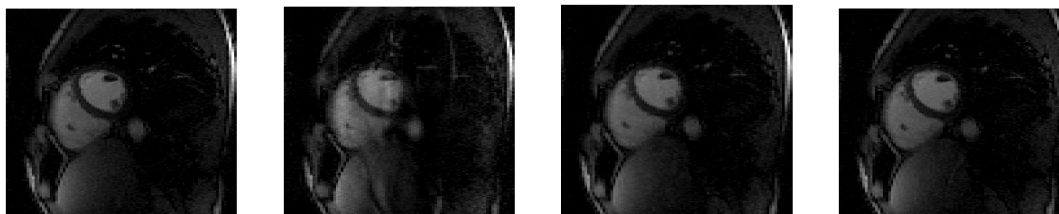


Figure 1. Figure illustrating the images reconstructed using (a) SoS, (b) GRAPPA, (c) k-tGRAPPA, (d) Sliding Window, all at (R=4)

Table1. The time taken and relative errors for the different reconstruction techniques (mean \pm sd) for 4 slices.

	GRAPPA		k-tGRAPPA		Sliding Window	
Reduction Factor	2 (1.68)	4 (2.55)	2(1.68)	4(2.55)	2(1.68)	4(2.55)
Time (sec)	49.93 \pm 0.20	109.1 \pm 3.19	27.74 \pm 0.32	42.81 \pm 0.23	2.23 \pm 0.1	9.23 \pm 0.15
Relative Error (%)	13.84 \pm 1.02	25.12 \pm 2.46	10.74 \pm 0.56	13.57 \pm 0.72	11.4 \pm 0.56	13.53 \pm 0.66

Table2. Estimated flows (ml/min/g) from images reconstructed using each of the 3 methods (4 slices, 6 regions each) at R=2 & 4

	SoS	GRAPPA		k-tGRAPPA		Sliding Window	
Reduction Factor	-	2	4	2	4	2	4
Flow	1.23 \pm 0.5	1.37 \pm 0.87	1.03 \pm 0.34	1.23 \pm 0.85	1.12 \pm 0.49	1.11 \pm 0.36	1.12 \pm 0.38
Relative Error (%)	-	11.4%	16.26%	0%	8.9%	9.8%	8.9%

Results/Discussion:

This study simulated the downsampling by acquiring full k-space data and then using the required reduction factor partial k-space was obtained. This offers an ideal way to provide a reference standard for comparison. It is interesting to note that the sliding window technique offers reduced variance in the estimates at the cost of increased bias. From Tables (1) and (2), we infer that it is better to apply k-t techniques for dynamic imaging as compared to regular parallel imaging techniques since the k-tGRAPPA and sliding window techniques significantly outperform the conventional GRAPPA technique with regard to the flow estimation, image quality and time required for reconstruction.

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References:

[1] Griswold M.A, et al. MRM 47:1202-1210 (2002). [2] Pruessmann K.P, et al. MRM 42:952-962 (1999). [3] Huang F, et al the 2nd Parallel Imaging Workshop, Zurich, P 53 (2004). [4] J.A. d'Arcy et al. NMR Biomed, 15:174-183 (2002). [5] Vijayakumar S, et al. Proc. ISMRM 2004, p1847.