Accelerated Phase-Contrast MRI using Compressed Sensing and Parallel Imaging

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Introduction: Phase-contrast (PC) MRI is a promising modality for studying hemodynamics associated with pathophysiology. A major disadvantage of PC MRI for body applications, however, is its low data acquisition efficiency, which may limit the achievable spatial and temporal resolutions within a clinically acceptable breath-hold duration. One approach to accelerate PC MRI is to use compressed sensing [1] by exploiting image sparsity of the time-series data after applying an appropriate transform such as principal component analysis (PCA). We propose to accelerate PC MRI using compressed sensing and parallel imaging (CS-PI) to jointly exploit image sparsity and coil sensitivity encoding [2]. The motivation of this work is to study hepatic blood flow waveforms in liver diseases [3-5]. The purpose of this study was to develop an accelerated PC MRI pulse sequence and to validate it in vivo against PC MRI with GRAPPA [6].

Methods: An interleaved prospectively ECG-triggered PC MRI pulse sequence was used to acquire phase reference and velocity-encoded data within the same heart beat (see Fig. 1). We modified the PC MRI pulse sequence to use a variable density (i.e., higher at the center of k-space) random undersampling pattern along k_y (phase-encoding) for each t (time), and implemented it on a 3T MRI system (Tim Trio, Siemens) equipped with a 32-element cardiac coil array. The relevant imaging parameters included: FOV = 320mm x 320mm, matrix = 192x192, slice thickness = 7 mm, TE/TR = 4.1/6.4ms, flip angle = 20°, k-space segments = 3, temporal resolution = 38 ms, venc = 50 cm/s (through-plane), acceleration factor R = 6.3, and breath-hold duration = 11 cardiac cycles. In a preliminary experiment, we compared different R values 4, 6, 8, and 10, and our analysis showed that both R = 4 and 6 produced good results. As such, we selected R = 6 for accelerated PC MRI. The reference GRAPPA PC MRI acquisition was performed with identical imaging parameters, where R = 3.1, breath-hold duration = 23 cardiac cycles. We imaged 7 volunteers (1 female; 6 males; mean age = 28.0 ± 4.9 years). For each volunteer, after careful localization of hepatic and portal veins, both GRAPPA and accelerated PC MRI acquisitions were performed twice to assess inter-scan variability. Image reconstruction of the accelerated data was performed off-line using customized software developed in Matlab. Coil sensitivity maps were self calibrated by averaging undersampled data over time and computed using the adaptive array combination, as previously described [7,8]. We used PCA as the sparsifying transform. The interleaved accelerated phase reference and velocity-encoded data were reconstructed using two different approaches: separately and jointly (as shown in Fig. 1). To validate the resulting flow measurements, GRAPPA and reconstructed accelerated PC MRI data were randomized and blinded for flow quantification. For each data, the magnitude image was used to initially mask the background, and a region-of-interest was manually drawn to include the whole vessel. Mean flow was calculated for each time point. We performed both Pearson correlation and Bland-Altman analyses to compare flow results.

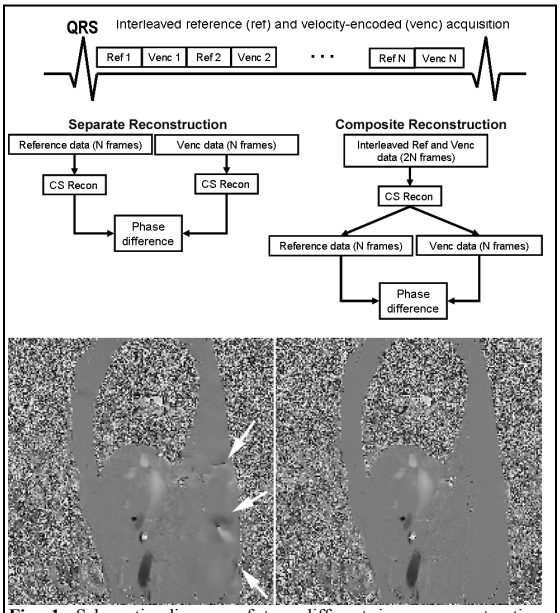

Fig. 1. Schematic diagram of two different image reconstruction approaches: (left) separate reconstruction of the reference and velocity-encoded data and (right) joint reconstruction of the reference and velocity-encoded data (interleaved as shown). Resulting phase difference images show residual errors (arrows) in the background for the separate case.

Results: Figure 1 shows results using two different reconstruction approaches: separate reference and velocity-encoded data reconstruction vs. joint reconstruction of both at once. The separate reconstruction method yielded visible residual phase errors in the background, whereas the joint reconstruction did not. The separate reconstruction result is consistent with previously reported separate reconstruction results using k-t GRAPPA and k-t SENSE [9]. Based on this preliminary experiment, we elected to use the joint reconstruction scheme for all data. Figure 2 shows representative magnitude, phase difference, and flow vs. time curves for the GRAPPA and accelerated data sets. Compared with GRAPPA PC MRI, accelerated PC MRI exhibited less noise and better visualization of smaller blood vessels. For pooled data (n=14; 7 hepatic and 7 portal veins), the flow measurements by GRAPPA and accelerated acquisitions were strongly correlated ($R=0.93$; $p < 0.05$) and in good agreement (mean difference = 0.69 mL/s; upper and lower 95% limits of agreement = 6.09 and -4.72 mL/s, respectively). As summarized in Table 1, the inter-scan repeatability was similar between GRAPPA and accelerated acquisitions.

Discussion: We developed a six-fold accelerated PC MRI pulse sequence using CS and parallel imaging that resulted in an acquisition time of 11 s for images with true temporal resolution (no view sharing) of 38 msec. The use of joint reconstruction of interleaved reference and velocity-encoded data produced less phase errors in the background than the separate reconstruction approach (Fig. 1), likely due to signal correlation of interleaved phase reference and velocity-encoded data (i.e., increased sparsity in the combined space). We note that the difference in breath-hold duration between the GRAPPA (23 s) and accelerated (11 s) acquisitions could have contributed to differences in flows for each acquisition. Further studies in a larger number of patients are necessary to fully evaluate the clinical utility of the accelerated PC MRI pulse sequence and to establish the intra- and inter-instrumental and study variability of the pulse sequence.

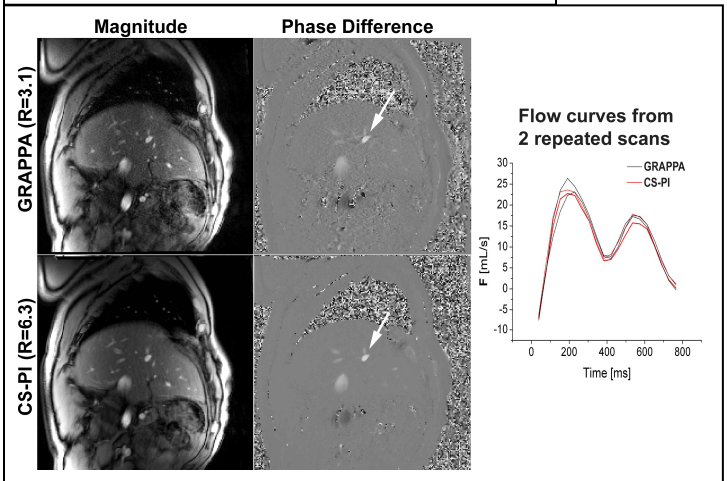

Fig. 2. Representative (left) magnitude and (middle) phase difference images, and the corresponding (right) flow curves in the right hepatic vein from two repeated scans: (top row) GRAPPA and (bottom row) accelerated using CS-PI.

References: [1] Lustig, M, et al. MRM 2007;58:1182-1195. [2] Otazo, R et al. MRM 2010;64:767-776. [3] Lebrec, D. Gastroent Clin North Am 1992; 21:41-59. [4] Ohnishi, K, et al. Radiology 1985;155:757-761. [5] Baik, SK, et al. Radiology 2006;240:574-580. [6] Griswold, MA, et al. MRM 2002;47:1202-1240. [7] Walsh, DO, et al. MRM 2000;43:682-90. [8]. Griswold, MA, et al. ISMRM 2002: 2410. [9] Jung, BA, et al. ISMRM 2009; 4559.

Table 1. Bland-Altman and Pearson correlation statistics (n =14).

Agreement type	Difference (mL/s)	Upper 95% limit (mL/s)	Lower 95% limit (mL/s)	Pearson's coefficient R
GRAPPA vs CS-PI	0.69	6.09	-4.72	0.93
GRAPPA 1 vs. GRAPPA 2	0.05	4.01	-3.90	0.97
CS-PI 1 vs. CS-PI 2	0.57	5.19	-4.06	0.96

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