Dynamic Arterial Spin Labeling Perfusion Imaging at 4T Using Parallel Imaging: Effects on Parametric Mapping

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Introduction

Arterial spin labeling (ASL) is a noninvasive method for studying cerebral blood flow in various neurological disorders and injuries [1,2]. Recently it has been shown that array coil imaging in 3T and 7T can improve SNR and reduce imaging time (and spatial distortion) in ASL perfusion imaging with single-shot EPI [3,4,5]. In this study, we assessed parallel imaging at 4T using a 3D GRASE sequence for dynamic ASL, i.e., imaging a time series of 3-D perfusion images with varying delay time after spin labeling, based on the effects on parametric mapping of perfusion kinetics. It was found that in our study, GRAPPA with one-time calibration, though very efficient and with significant SNR degradation, was not sufficient for accurate parametric mapping. Frame-by-frame calibration (with acceleration factor 2 and 8-ch array) provided mapping results similar to those from the fully sampled data. With parallel imaging, it is expected to be feasible to image 22 slices with in-plane resolution of 2.4 x 8.8 mm in every 15 seconds. This will improve the quantitative perfusion study using ASL at high fields.

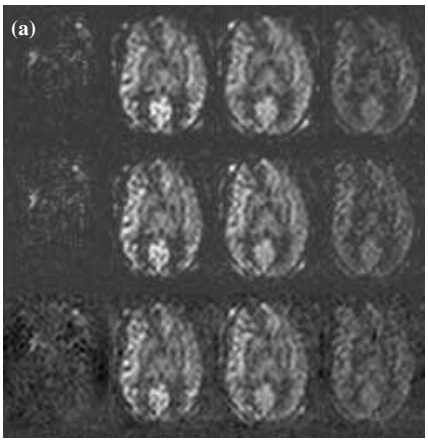
Methods

Five volunteers were scanned at a 4T MR unit (Bruker Medical Systems, Best, Erlangen) using an 8-channel head array coil. Interleaved tagged and control images were acquired using a fast 3D-GRASE sequence [6]. Three-dimensional images were collected at 13 different TI times (from 70 to 2600 ms) with TR=3000 ms and echo time of 23.28 ms. The data matrix was 128 x 34, with a field of view of 300 x 150 mm (in plane resolution, 2.34 x 8.82 mm), and slab thickness of 100 mm (slice thickness 4.7 mm). Twenty two axial slices were acquired to covers the entire hemispheric areas of brain. The total acquisition time per 3-D dataset is 24 seconds.

After acquisition, the raw datasets (tagged and control) were transferred to a PC workstation with 1.8 GHz CPU and 1 GB memory for processing. All image reconstruction and processing were performed off-line using the PULSAR program developed in MATLAB platform (Mathworks, Natick, MA) [7]. A perfusion model was implemented and adapted in IDL (ITT Industries Inc., Boulder, CO) to extract five kinetic parameters, cerebral blood flow (cbf) , bolus arriving time (t0), peak time (tp), scaled fit error (sfe), and exchange time (tex) [8]. Three reconstructions were performed: 1) *Reference:* Full datasets for all 8 channels, 22 slices, and 13 time frames were individually zero-padded to 128 x 64 and reconstructed using Fourier transform. Channels images were then combined using Sum-of-Squares (SoS) method and the corresponding tag and control images were subtracted. The perfusion model was fitted to the 13 time frames pixel-by-pixel. 2) *GRAPPA(I):* the full datasets were decimated by an acceleration factor of 2 to yield 128 x 17 data matrix. Six additional lines (total 12 lines) from each dataset in the central k-space were used as ACS lines in the GRAPPA reconstruction, making an effective acceleration factor of 1.5 (34/(17+6)). 3) *GRAPPA(II):* the model calibration was performed only once using the middle frame (TI 1400 ms) and then fitted model coefficients were used for all other frames. The reconstruction from full data set, the reference, were used as a gold standard and compared to those from accelerated data sets, GRAPPA (I) and GRAPPA (II), in terms of SNR (images) and deviations of the extracted maps.

Results

Figure 1(a) shows the difference images (between control and tag images) of the 8th slice from one subject. From left to right: the 2nd, 5th, 8th and 12th time frames; From top to bottom: *Reference*, *GRAPPA(I)*, and *GRAPPA(II)*. Figure 1(b) shows the SNR of the three reconstructions at different time frames (large signal null at 200 ms). As shown, the SNR decrease of the GRAPPA recons were less than the sqrt(2), which is normally expected for SENSE reconstruction. This result is consistent with the early report [4]. In addition, GRAPPA(I) always has better SNR than GRAPPA(II), indicating the significance of frame-by-frame calibration.



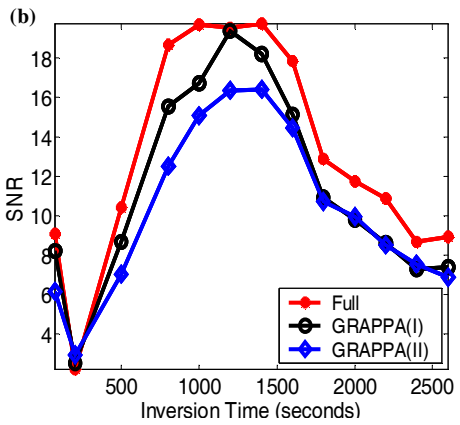
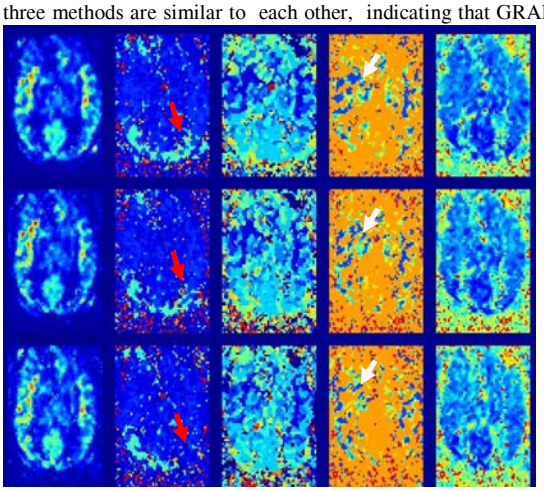


Figure 2 below shows the extracted kinetics parameter maps of the 8th slice in the same subject (all scaled for better visualization). From left to right: cbv, t0, tp, tex, and sfe; from top to bottom, *Reference*, *GRAPPA(I)*, and *GRAPPA(II)*. Note that there are very little differences between the GRAPPA (I) result and the gold standard, but perceivable difference was observed between the GRAPPA (II) and gold standard. This indicates frame-by-frame calibration is crucial if accurate parametric mapping if desired (using Reference as gold standard). In addition, the sfe maps, which represent spatial and temporal dependent SNR loss, of all three methods are similar to each other, indicating that GRAPPA with shared ACS lines for high acceleration does not introduce additional temporally instability of reconstruction in low-SNR regions.



Discussion

Using 3-D GRASE sequence, 22 ASL image slices with 2.4 x 8.8 mm in-plane resolution could be acquired in 24 seconds. Our simulation results indicates that parallel imaging using proper GRAPPA reconstruction can further reduce this time to be within 15 seconds, without significant degrading effect on either SNR or kinetic perfusion parameters extracted. Our study at 4 T highlighted the need for adequately frequent calibrations in parallel imaging. Though the single calibration did not lead to large SNR degradation and is more efficient, it has significant impact on parametric mapping. In practice, accelerated imaging can further reduce distortion at high fields, or be traded for high spatial resolution/coverage. Therefore, parallel imaging has potential to improve quantitative, dynamic ASL imaging.

References [1] Detre JA et al., *MRM* 1992; 23:37-45. [2] Kong KK et al. Proc Natl Acad Sci USA 1992; 89:5675-5679. [3] Duyn JH, et. al. JMRI 2005; 22:751–753. [4] Wang Z. et. al. MRM 2005; 54:732–737. [5] Gelderen P et. al. ISMRM 2005:1260. [6] Gunther M et al., MRM 2005; 54: 491-498. [7] Ji J et. al. MRE 2007 (in press). [8] Li KL et al., MRM 2005; 53: 511-518.