Accelerating Phase Contrast MRA by SPEED Using Efficient Multiple Acquisitions and Shared Information

Z. Chang[1], Q-S. Xiang[2,3], and J. Ji[4]

[1]Radiation Oncology, Duke University, Durham, North Carolina, United States, [2]Department of Physics and Astronomy, University of British Columbia, Vancouver, BC, Canada, [3]Department of Radiology, University of British Columbia, Vancouver, BC, Canada, [4]Department of Electrical and Computer Engineering, Texas A&M University, College Station, TX, United States

Introduction

Multiple acquisitions are often used in many MRI applications, such as multi-point water-fat imaging, phase-contrast (PC) MR Angiography (MRA) and diffusion tensor imaging (DTI). These applications are usually time consuming, and have relatively longer scan times than other applications with single acquisition. Given the fact that multiple acquisitions are spatially registered and share similar spatial information, the fast imaging method of Skipped Phase Encoding and Edge Deghosting (SPEED) [1] can be used to accelerate multiple acquisitions more effectively by using efficient sampling and shared spatial information, which has been demonstrated previously with two-point water-fat imaging [2]. In this work, the technique is further developed to accelerate PC-MRA.

Methods

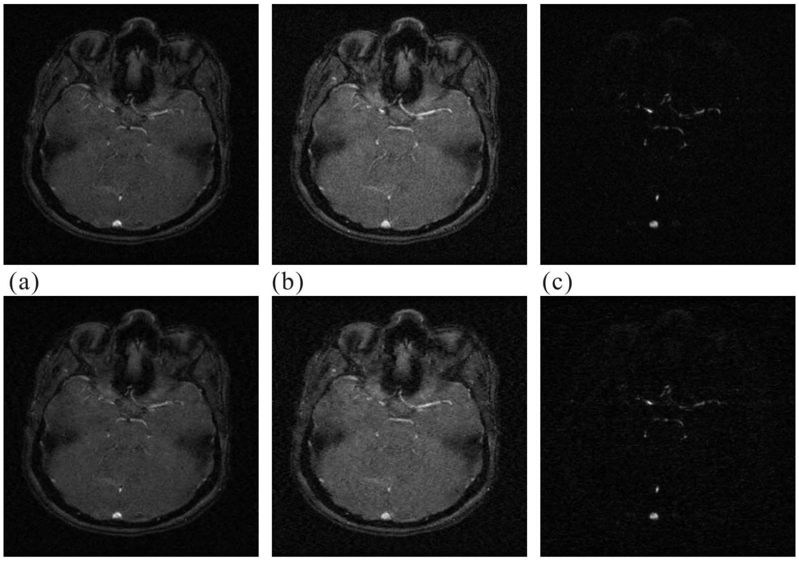
To understand the technique of efficient multiple acquisitions by SPEED, it is helpful to review the basic principle of SPEED. In SPEED, k-space is partially sampled with skipped phase encoding, while suppressing the aliasing ghosts with edge deghosting [1]. The principle of SPEED is illustrated below with a specific example: k-space is sparsely sampled into 3 interleaved data sets, each with a skip size of N = 5 and a different relative shift in phase encoding (PE). The sampled data are then Fourier transformed into 3 ghosted images with ghost overlapping up to 5 layers. To suppress the ghost overlapping, a high-pass differential filter is used to turn the ghosted images into 3 sparse ghosted edge maps. By modeling them with a double-layer structure, the 3 ghosted edge maps can be described by Eqns.(1-3) where G_{n1} and G_{n2} are the two dominating ghost layers; P_d^n a ghost phasor expressed as $[\exp(i2\pi d/N)]^n$, where $n = 0,1\ldots N-1$ is the order of ghost depending on its relative location and d is a known relative sampling shift in PE. As described in Ref. [2, 3], the integer $n1$ or $n2$ in the unique ghost order pair ($n1, n2$) is named "ghost order index". In this case, $n1$ or $n2$ must be an integer chosen from 0 to 4. By minimizing least-square-error (LSE), the ghost order index pair ($n1,n2$) are first determined through a multiple, but limited number of trials. With the ($n1,n2$) determined, the two ghost solutions (G_{n1},G_{n2}) are then solved. Finally, (G_{n1},G_{n2}) are sorted and spatially registered according to ($n1,n2$) to yield a deghosted edge map, which is inverse-filtered into a final deghosted image. Central k-space (*e.g.* 32 out of 256 lines) is fully sampled to aid the inverse filtering by avoiding artifacts. As illustrated by the example, a deghosted image is reconstructed by SPEED with an undersampling factor of 3/5.

$$E_1 = P_1^{n1}G_{n1} + P_1^{n2}G_{n2} \quad (1)$$

$$E_2 = P_2^{n1}G_{n1} + P_2^{n2}G_{n2} \quad (2)$$

$$E_3 = P_3^{n1}G_{n1} + P_3^{n2}G_{n2} \quad (3)$$

It has been shown that the determination of the ghost order index pair ($n1,n2$) is a key step in SPEED. This is simply because the two ghost solutions (G_{n1} ,G_{n2}) are solved, sorted and spatially registered based on the ghost order index pair ($n1,n2$). Please note that, for a single acquisition, three equations are needed to determine the ghost order index pair ($n1,n2$), while only two equations are required to solve the two ghost solutions (G_{n1},G_{n2}). This shows both inefficiency and potential. In multiple acquisitions, the ghost order index pair ($n1,n2$) may possibly be shared for different acquisitions because of the similarities and redundancies in spatial information. Based on the idea, it needs only 2 interleaved data sets to reconstruct a deghosted image rather than 3 data sets as required by the original SPEED, reducing the scan time more effectively and thus enhancing its efficiency. In practice, 3 interleaved data sets are sampled for the first acquisition, but only 2 interleaved data sets are sampled for the following acquisitions. In this work, it is demonstrated in a PC-MRA study with two acquisitions.


(a) (b) (c)
(d) (e) (f)

Experiments

The technique was tested with *in vivo* PC-MRA data obtained from a gradient-echo scan on a 1.5 T clinical scanner (matrix 256x256, FOV 24 cm, TR 34 ms, TE 6.4 ms, slice thickness 5 mm, single acquisition, 25 slices, VENC = 8.6 cm/s, velocity sensitivity direction is S/I).

Results

(a) and (b) are respectively the original phase contrast images with velocity compensation and velocity sensitization, both reconstructed from fully sampled data. (c) is the PC-MRA image, obtained by subtracting (a) from (b). (d-f) are the corresponding reconstructed images of (a-c) with about 55% of the total scan time. More specifically, the total scan time is [(3/5+2/5) + (32/256x2)x(1-3/5+1-2/5)/(1+1)]x100% = 112.5% of a single acquisition after the central 32 k-space lines are taken into account. The images reconstructed from partial data by the proposed method are comparable to the images reconstructed from full k-space data.

Discussions

In this work, the efficient multiple acquisition method by SPEED is further developed to accelerate PC-MRA. By sharing the same ghost order index between two acquisitions, the scan time of a PC-MRA study is roughly reduced to that of a single acquisition. The total scan time reduction rate is more than that achievable for a single acquisition. Moreover, the principle could be extended to accelerate dynamic studies, and could be combined with other extensions of SPEED such as SPEED-ACE [3] for more efficient performance.

References

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