

Efficient Multiple Acquisitions by SPEED with Shared Spatial Information

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Introduction

Multiple acquisitions are used in many MRI applications, such as PC MRA with double-acquisitions, multi-point water-fat imaging and diffusion imaging. They are in general quite time consuming. For example, at least seven acquisitions are required for diffusion tensor imaging. The strong structural similarities in multiple acquisitions imply redundancy and suggest opportunity for scan time reduction. In this work, the efficiency of Skipped Phase Encoding and Edge Deghosting (SPEED) [1] is further improved in multiple acquisitions, which is successfully demonstrated in two-point water-fat imaging with *in vivo* data.

Methods

It is helpful to review the basic principle of SPEED. SPEED partially samples k-space with skipped phase encoding and suppresses the associated aliasing ghosts with edge deghosting [1]. SPEED can be illustrated by the following example with a scan undersampling factor of 3/5: k-space is partially sampled into 3 interleaved data sets, each with a skip size of $N = 5$ and a different relative shift size chosen from 0 to 4. The 3 data sets are then reconstructed by 2DFT and high-pass filtered into 3 ghosted edge maps. By modeling the ghosts 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 known to have a form of $[\exp(i2\pi d/N)]^n$, where $n = 0, 1 \dots N-1$ is the order of ghost depending on its relative location and d is a known relative sampling shift in phase encoding. For convenience, the integer $n1$ or $n2$ in the unique ghost order pair $(n1, n2)$ is named "ghost order index", which must be an integer chosen from 0 to 4. Based on a least-square-error (LSE) solution, a deghosted edge map can be solved and subsequently inverse-filtered into a final deghosted image. Few central k-space lines (eg. 32 out of 256) are sampled to avoid artifacts in the inverse filtering. In this case, SPEED reconstructs a deghosted image with 3 skipped and relatively shifted partial k-space data sets, resulting in a total undersampling factor of 3/5.

In the above process, the determination of the ghost order index pair $(n1, n2)$ is very crucial because (G_{n1}, G_{n2}) are solved based on $(n1, n2)$. Once $(n1, n2)$ are determined, (G_{n1}, G_{n2}) can be solved and be sorted out according to $(n1, n2)$, yielding N separate edge ghosts. To determine the ghost order index pair $(n1, n2)$, SPEED needs 3 equations by acquiring 3 interleaved data sets which allows a LSE solution; however, after $(n1, n2)$ are determined, only 2 equations are sufficient to solve (G_{n1}, G_{n2}) , leading to a deghosted image. It appears that 1/3 of the acquired data is used to determine only $(n1, n2)$. This is surely quite expensive and implies potential for further efficiency improvement. In multiple acquisitions, the strong similarities in structures suggest a possibility to share the ghost order index pair $(n1, n2)$ for different acquisitions. This is the key idea of this work. In this way, reconstructing a deghosted image may need only 2 rather than 3 interleaved data sets as required by the original SPEED, further reducing the total scan time. More specifically, 3 interleaved data sets are sampled for the first acquisition, but only 2 interleaved data sets are sampled for the following acquisitions. Efficient multiple acquisitions with SPEED is demonstrated in this work by its application to 2-point water-fat imaging.

A new method for 2-point water-fat imaging method is recently proposed, which samples water and fat vectors at "partially-opposed-phase" (POP) in addition to the conventional in-phase acquisition [2]. Since 2 images are required, SPEED can be used to reduce scan time with more efficiency. The procedure can be divided into 2 steps: First, 3 interleaved data sets are used to reconstruct one of the 2 images and in addition output the ghost order index maps of $(n1, n2)$. Second, using the $(n1, n2)$ maps from the first step, the other image can be reconstructed with only 2 interleaved data sets.

The total fractional scan time is therefore $3/N + 2/N = 5/N$, where N is the skip size. At $N = 5$, separate water and fat images can be obtained within a scan time close to a single acquisition of conventional MRI after taking account of the additional central k-space lines.

Experiments

The technique was tested with existing *in vivo* data obtained from a clinical spin-echo transverse head scan on a 1.5 T scanner (matrix 256x256, FOV 24 cm, TR 800 ms, TE 24 ms, slice thickness 4 mm, no average). Two interleaved complex images were acquired with water and fat vectors at $(0^\circ, 135^\circ)$.

Results

(a) and (b) show respectively water and fat images reconstructed from full k-space data and are considered as the "gold standard". (c) and (d) show respectively water and fat images reconstructed from partial data, with fractional scan times of 3/5 and 2/5 for the in-phase and POP acquisitions respectively, reducing total scan time by almost half as compared to that needed to acquire the "gold standard". More specifically, the total scan time is $[(3/5+2/5)+(32/256 \times 2) \times (1-3/5+1-2/5)/(1+1)] \times 100\% = 112.5\%$ of a single acquisition after the central 32 k-space lines are taken into account. The water and fat images shown in (c) and (d) are comparable the gold standard shown in (a) and (b).

Discussions

In this work, the efficiency of SPEED is further enhanced in multiple acquisitions. The key idea is to share the same ghost order index $(n1, n2)$ for different acquisitions. Moreover, the idea could be extended to other extensions of SPEED such as SEN-SPEED [3]. Although the principle is only demonstrated by water-fat imaging with double acquisitions in this work, it can be useful in other application with multiple acquisitions.

References

- [1] Q.S. Xiang, MRM 2005; 53:1112-1117. [2] Q.S. Xiang, 11th ISMRM p.1130, 2003.
- [3] Z. Chang, *et al.*, 13th ISMRM, p.2448, 2005.

