Accelerating Dynamic MRI with Efficient Multiple Acquisitions by SPEED Using Shared Information

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Introduction

Acquisition of multiple frames of high-resolution images is desirable in dynamic MRI. Unfortunately it is difficult to obtain both high spatial resolution and high temporal resolution. The fast MRI method of Skipped Phase Encoding and Edge Deghosting (SPEED) [1] can be used to accelerate multiple acquisitions more effectively by sharing redundant spatial information as previously demonstrated with two-point water-fat imaging [2]. In this work, this idea is further developed to accelerate dynamic MRI with efficient multiple acquisitions using shared information.

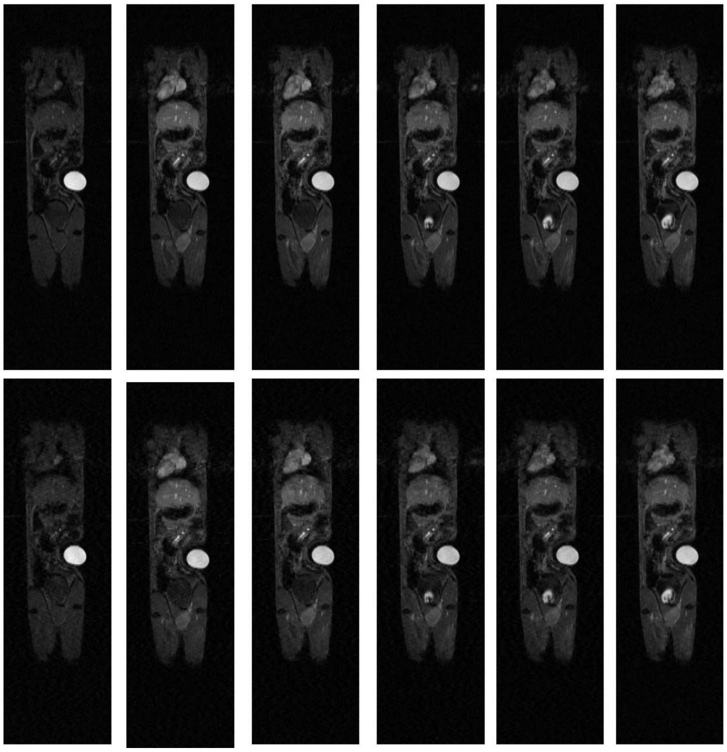
Methods

To understand the principle of efficient multiple acquisitions by SPEED, it is helpful to review the basics of SPEED. In SPEED, k-space is partially sampled with skipped phase encoding, while reducing the resulting aliasing ghosts by edge deghosting [1]. The principle of SPEED is illustrated below with an example, where k-space is undersampled by a factor of 3/5: 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 and high-pass filtered 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 $[\exp(i2\pi d/5)]^n$, where $n = 0,1\ldots4$ is the order of ghost depending on its relative location and d is a known relative sampling shift in PE. As defined in Ref.[2-4], 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. By minimizing least-square-error (LSE), a deghosted edge map is solved and subsequently inverse-filtered into a final deghosted image. Central k-space (*e.g.* 16 out of 128 lines) is fully sampled to avoid artifacts in the inverse filtering. In this way, a deghosted image is reconstructed by SPEED with an undersampling factor of 3/5.

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

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

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



The determination of the ghost order index pair (*n1,n2*) in the above process is a key. This is simply because the two ghost solutions (G_{n1} ,G_{n2}) are solved based on the ghost order index pair (*n1,n2*). 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 dynamic imaging, the similarities and redundancies in spatial information suggest a possibility to share the ghost order index pair (*n1,n2*) for different image frames. Based on the idea, only 2 interleaved data sets are needed to reconstruct a deghosted image for repeated acquisitions, enhancing its efficiency and reducing the total scan time for multiple acquisitions. In practice, 3 interleaved data sets are sampled for one acquisition, but only 2 interleaved data sets are sampled for other acquisitions. In this work, it is demonstrated below with a dynamic contrast enhanced (CE) mice tumor study.

Experiments

The proposed method was tested with *in vivo* dynamic CE mice tumor study. The dynamic CE scan was performed on a SISCO 4.7 T system using a rapid T1-weighted gradient echo sequence (matrix 512x128, FOV 24cm x 6cm, TR = 63 ms, TE = 4.3 ms, slice thickness = 2 mm, number of slices = 7, number of frames = 50).

Results

Figures in the top row are six representative temporal frames (1,3,5,7,9,10) of the middle fourth slice , all reconstructed from full k-space data. Figures in the bottom row show the corresponding reconstructed images of the figures in the top row, but from partial data, with undersampling factors of 3/5 for the last frame and 2/5 for all other frames, resulting in an acceleration factor of 2. In other words, the total scan time is [(3/5+2/5x16/128)+49x(2/5+3/5x16/128)] ~ 24 times that of a single acquisition after 16 fully sampled central k-space lines are taken into account. The images reconstructed from partial data by the proposed method show comparable quality as the images reconstructed from full k-space data.

Discussions

In this work, the technique of efficient multiple acquisitions by SPEED is further developed to accelerate dynamic MRI. By using shared spatial information, a dynamic CE mice tumor study is accelerated by SPEED with a factor of 2, which is greater than that achievable with a single acquisition. The key idea is to share the same ghost order index for multiple acquisitions. This saving can be used to double the image resolution, or to increase the frame rates of dynamic sequence. Furthermore, the new technique could be extended to other variations of SPEED such as the parallel imaging of SPEED-ACE [3] and Simplified SPEED [4].

References

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