Efficient Non-Contrast-Enhanced MRA with Inflow Inversion Recovery by Skipped Phase Encoding and Edge Deghosting (SPEED)

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Introduction

Non-contrast-enhanced MR angigraphy (MRA) has always been a valuable clinical tool to study vasculatural diseases. The recently arising concerns of constrast agents in contrast-enhanced MRA encouraged more use of non-contrast-enhanced MRA. In this work, the fast imaging method of Skipped Phase Encoding and Edge Deghosting (SPEED) [1] is further developed to enhance efficiency of non-contrast-enhanced MRA with inflow inversion recovery (IFIR), in which vasculature is more visible on tissue background [2]. By taking advantages of sparsity of vasculature, a single-layer-model can be used in SPEED to achieve more scan time reduction and higher computational efficiency than that achievable with a double-layer-model. This approach is similar to a previously proposed method of S-SPEED [3], and is demonstrated with a 3D renal IFIR study.

Methods

To understand the principle of the work, it is helpful to review the basics of SPEED. In SPEED, k-space is partially sampled with N-step skipped phase encoding [1]. The sampled data are first reconstructed by inverse Fourier transform (FT) into a set of ghosted images, each with N-fold aliasing ghosts. To reduce ghost overlap, a differential filter is used to turn the ghosted images into sparse ghosted edge maps, which can be adequately described by a double-layer-model. A deghosted edge map is solved and subsequently inverse-filtered into a deghosted image. The central part of k-space (e.g. 32 out of 256 lines) is fully sampled to avoid artifacts in the inverse filtering. SPEED is proposed to accelerate typical MRI, and can be further developed to achieve better efficiency where signal distribution becomes sparser.

Non-contrast-enhanced MRA with inflow inversion recovery (IFIR) is a very promising MRA technique. In IFIR imaging, a preparatory inversion recovery pulse is used to modestly suppress signals from static tissue, while leaving inflow arterial blood unaffected. As a result, sparse arterial vasculature is clearly visible on modest tissue background. By taking advantages of sparsity of vasculature, SPEED can be simplified to use a single-

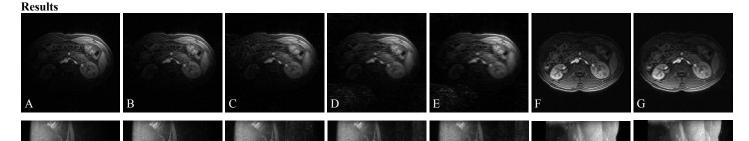
$$E_1 = P_1^n G_n \quad (1)$$

 $E_1 = P_1 G_n$ (1) proposed technique is illustrated below with an example, where k-space is sparsely sampled into 2 interleaved data sets, each with a skip size of N and a different relative shift in phase encoding (PE), corresponding to an undersampling factor of 2/N. The sampled data are then inverse Fourier transformed and high-pass filtered into 2 sparse ghosted edge maps. By modeling them

layer-model to reduce more scan time and achieve higher computational efficiency than SPEED with a double-layer-model. The

with a single-layer structure, the 2 ghosted edge maps can be described by Eqns.(1-2) where G_n is the dominating ghost layer and P_d^n is a ghost phasor expressed as $[\exp(i2 \pi d/N)]^n$, where n = 0,1...4 is the order of ghost depending on its relative location and d is a known relative sampling shift in PE. By minimizing least-square-error (LSE), a deghosted edge map is solved and subsequently inverse-filtered into a final deghosted image. In a 3D scan, the single-layer-model SPEED can be generalized to further reduce scan time by applying undersampling along two PE directions. When multiple coils are available, the proposed method can achieve even higher efficiency, in a similar manner as a previously described technique of SPEED with Array Coil Enhancement (SPEED-ACE) [4].

In this work, SPEED was tested with a 3D renal non-contrast-enhanced IFIR MRA study. The MRA scan was performed on a 3.0 T scanner (GE Healthcare, WI, USA) with a Respiratory Triggered IR-Prepared Fiesta (SSFP) sequence (matrix 256x256, FOV 36 cm, TI 200ms, TR 4.2 ms, TE 2.1 ms, slice thickness 2 mm, space between slices 1mm, flip angle 70°, single acquisition, slices 116).



(A) is a reference image of one slice obtained from full k-space data of one coil. (B) is reconstructed by SPEED from three skipped phase encoded data sets with a skip size of 5 along vertical direction, achieving an undersampling factor of 5/3 = 1.7. (C) is reconstructed by SPEED using a single-layer-model with an undersampling factor of 5/2 = 2.5. (D) is reconstructed by SPEED applied in two orthogonal directions, from three skipped phase encoded data sets with a skip size of 5 along vertical direction and a skip size of 2 along horizontal direction, achieving a total undersampling factor of (2x5)/3 = 3.3. Similarly, (E) is reconstructed by SPEED using a single-layer-model with an undersampling factor of (2x5)/2 = 5. (F) is a reference image formed as root-mean-square of the four individual magnitude images, each reconstructed from full k-space data of the corresponding receiver coil. (G) is the deghosted image reconstructed by SPEED-ACE based on a single-layer model, with an undersampling factor of 5.0. (H-N) are the corresponding MIP images of (A-E). The reconstructed images are generally comparable to the reference images (A) and (F).

Conclusion

In this work, we applied SPEED with a single-layer model to accelerate non-contrast-enhanced IFIR MRA. By taking advantage of signal sparsity naturally existing in the data, SPEED with a single-layer-model can reduce more scan time and achieve higher computational efficiency than those achievable with a double-layer-model. The technique is demonstrated in a 3D renal IFIR study with an undersampling factor of up to 5. The technique can also be combined with half-Fourier k-space coverage to further reduce scan time by another factor of ~60%.

References

[1] Q.S. Xiang, MRM 2005; 53:1112–1117 [2] M. Braendli, et al. AJR 2003; 180:725-728 [3] Z. Chang, et al. Med. Phys. 2007;34:3173-3182 [4] Z. Chang, et al. Med. Phys. 2006:33: 3758–3766