

Accelerating MRA with Simplified Skipped Phase Encoding and Edge Deghosting (SPEED)

Z. Chang¹, Q-S. Xiang¹

¹Department of Physics & Astronomy, University of British Columbia, Vancouver, British Columbia, Canada

Introduction

Scan time reduction is desirable in MR angiography (MRA), which is often performed in 3D. Many fast imaging strategies such as undersampled projection reconstruction [1] have been proposed to accelerate MRA. In this work, we simplified Skipped Phase Encoding and Edge Deghosting (SPEED) [2] to reduce scan time of MRA. Simplified SPEED can also be combined with Half-Fourier [3] for improved performance.

Methods

To understand simplified SPEED, it is helpful to review the basics of the original SPEED. SPEED uses Skipped Phase Encoding and Edge Deghosting to accelerate MRI. For example, SPEED sparsely samples k-space into 3 data sets, each with a skip size of 5 and a different relative shift in phase encoding (PE). The sampled data are then Fourier transformed (FT) into 3 ghosted images with ghost overlapping up to 5 layers. To reduce the ghost overlapping, a differential filter is used to turn the ghosted images into 3 sparse ghosted edge maps. By modeling them with a bi-layer structure, a deghosted edge map is solved and subsequently inverse-filtered into a deghosted image. Central k-space (e.g. 32 out of 256 lines) is fully sampled to avoid artifacts in the inverse filtering. The key idea of SPEED is to reduce ghost overlapping by using sparseness of edge maps.

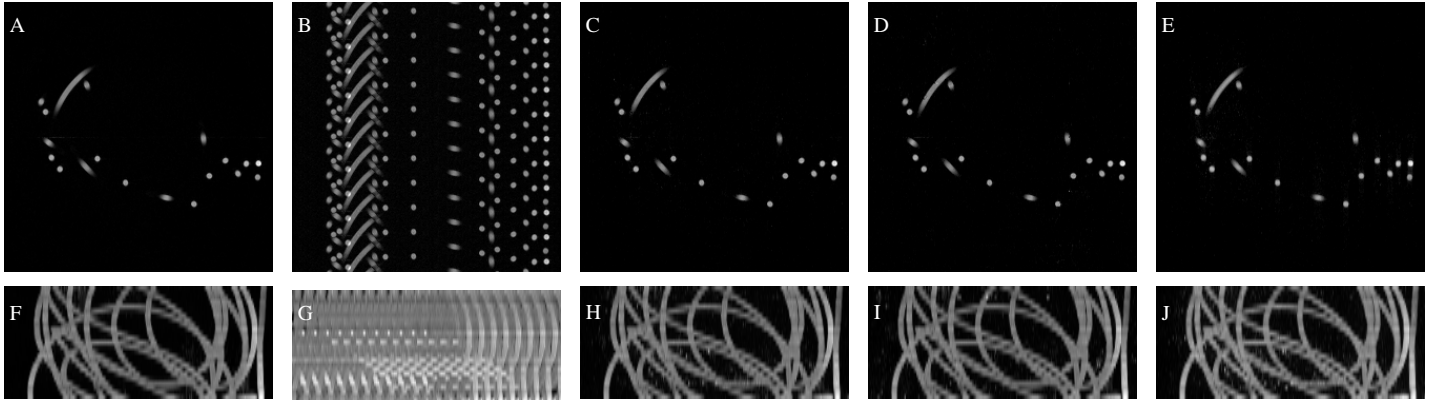
Similarly, simplified SPEED can accelerate MRA by taking advantage of sparseness of MRA images. Simplified SPEED does not use differential filtering and central k-space sampling as SPEED does and as such achieves more reduction of scan time. For example, to reconstruct a 2D MRA image, 3 interleaved data sets are obtained by sampling k-space at every $N=11^{\text{th}}$ PE step with 3 different relative shift sizes chosen from 0-10. The sampled data are then Fourier transformed separately into 3 ghosted images denoted as I_1 , I_2 , and I_3 . Since they are very sparse and have less overlapping, differential filtering is not used any more. If the ghosted images can be modeled with only 2 dominating layers, the three ghosted

images can be described by Eqns.(1-3). In Eqns.(1-3), G_{n1} and G_{n2} are the 2 dominating 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 PE. Although n is not completely known, it is known to be chosen from 0 to 10. By trying all possible pairs of $(n1, n2)$, the correct solutions of (G_{n1}, G_{n2}) and $(n1, n2)$ can be found when least-square-error (LSE) is minimized at each pixel. According to the resolved $(n1, n2)$, (G_{n1}, G_{n2}) can be sorted out to yield 11 separate deghosted MRA images. Finally, they are spatially registered and averaged to yield an improved

MRA image at an acceleration factor of 3.7. When 3D MRA data are sampled, 2 PEs are typically used. Thus, simplified SPEED can accelerate MRA in 2 PE directions and as such achieve more flexible reduction of scan time. Furthermore, simplified SPEED can be combined with Half-Fourier [3] to further accelerate MRA by a factor of nearly 2.

To test the proposed method, we built a vasculature phantom by mimicking blood vessels with a long wound plastic hose filled with water. The vasculature phantom was scanned on a clinical 1.5 T scanner with a spin-echo sequence (25 slices, slice thickness 5 mm, matrix 256x256, FOV 30cm, TR 1000 ms, TE 10ms, 2 averages). The full k-space data were saved and used to study the feasibility of the proposed method.

Results



A-E are 5 reconstructed images of the 10th slice. A is “gold standard” reconstructed from full k-space data. B is ghosted image reconstructed by direct 2DFT from one of the three k-space data sets each with a PE skip size of $N=11$ in vertical direction. C was reconstructed by simplified SPEED from 3 data sets sampled vertically with a skip size of $N=11$ and 3 different relative PE shifts, leading to a scan time reduction factor of 3/11. D was reconstructed by simplified SPEED applied in both vertical and horizontal directions. 3 relatively shifted data sets were sampled with a skip size of $N=5$ vertically and a skip size of $M=2$ horizontally. E was reconstructed by simplified SPEED from only 17% k-space data, which were similarly sampled as C except covering only half k-space including 64 central lines, with an acceleration factor of nearly 6. F-J are corresponding maximum-intensity-projections (MIPs) from 25 slices reconstructed similar to A-E. Compared with the gold standard F, H-J are all satisfactory.

Conclusion

Considering sparseness of MRA images, we simplified SPEED and demonstrated its feasibility to accelerate MRA data acquisition by a factor of up to nearly 6 with a single coil. When multiple receiver coils are available, simplified SPEED can be combined with SENSE [1] to accelerate MRA further.

References

[1] A.V. Barger, MRM 2002;48: 297-305. [2] Q.S. Xiang, 12th ISMRM p.2116, 2004. [3] P.Margosian, et al., 5th SMRM, p.834, 1986.