

# Accelerating Phase Contrast MR Angiography by Simplified Skipped Phase Encoding and Edge Deghosting with Array Coil Enhancement (S-SPEED-ACE)

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## Introduction

It is desirable to reduce scan time to improve the performance of MRI and to increase patient comfort level. In the past few years, various fast imaging techniques have been proposed. Some of these methods make use of the unique nature of the data[1-4] such as sparsity. The parallel imaging method of Skipped Phase Encoding and Edge Deghosting with Array Coil Enhancement (SPEED-ACE) [3] can be both simplified and further accelerated when the signal distribution is sparse. This idea has been previously demonstrated with a computer simulated study [5] and is termed simplified SPEED-ACE (S-SPEED-ACE); however, it has not been tested with any real human MRI scan. In this work, this technique is further developed to accelerate 3D head phase-contrast (PC) MR angiography (MRA).

## Methods

To understand the proposed method, it is helpful to review the basic principle of SPEED-ACE. In a fashion similar to SENSE [6] and SMASH [7], k-space is sampled with a skip size of N along phase encoding (PE) using multiple coils in parallel. The sampled data are first reconstructed by inverse Fourier transform (FT) into a set of ghosted images, each with N-fold aliasing ghosts due to undersampling. To reduce ghost overlapping, a differential filter is used to turn the ghosted images into ghosted edge maps, which are typically sparse and thus can be adequately modeled with a double-layer structure. This is analogous to the sparsification operation used in compressed sensing [8]. A deghosted edge map is solved and inverse-filtered into a deghosted image. A central part of k-space (e.g. 32 out of 256 lines) is fully sampled to avoid artifacts in the inverse filtering.

For sparse data, SPEED-ACE can be simplified by omitting the differential filter for sparsification. The simplified method named S-SPEED-ACE does not fully sample the central k-space and thus achieves further acceleration. As shown in the workflow on the left, the principle of S-SPEED-ACE can be illustrated by the following example: four sets of data are obtained with four coils in parallel simultaneously, each sampled at every Nth PE step with a relative shift size of k. The acquired data are then reconstructed by inverse FT into four sensitivity-weighted and ghosted images:  $I_1(r)$ ,  $I_2(r)$ ,  $I_3(r)$ , and  $I_4(r)$ , each associated with N-fold aliasing ghosts. Given the sparsity of the data,  $I_{1,k}$  to  $I_{4,k}$  are modeled with a single-layer structure. Specifically, the most dominant ghost within the potentially overlapped ghosts at each pixel is selected to represent the signal of that pixel, analogous to the Maximum-Intensity-Projection (MIP) algorithm that selects only the brightest signal even when there are overlapped vessels. In this way,  $I_{1,k}$  to  $I_{4,k}$  can be described by equations (1-4), where  $G_n$  is the dominant ghost;  $P_k^n$  is a ghost phasor known to take the form of  $[\exp(i2\pi k/N)]^n$ , and  $n = 0, 1, \dots, N-1$  is the order of ghost depending on its relative location; and  $S_k^n$  are separately measured coil sensitivities for the ghost of the  $n$ th order. The four ghosted images can be deghosted into a ghost-free image  $I_0(r)$  through an analytical algorithm based on least-square-error minimization, along with a residual map used to monitor the quality of the deghosted image. An acceleration factor of N can be achieved. In this way, S-SPEED-ACE has more efficient data acquisition and more straightforward image reconstruction than SPEED-ACE[3]. Although the simple single-layer ghost model is often adequate, more layers can be added to improve the solution, without cost of additional scan time but with potential noise amplification.

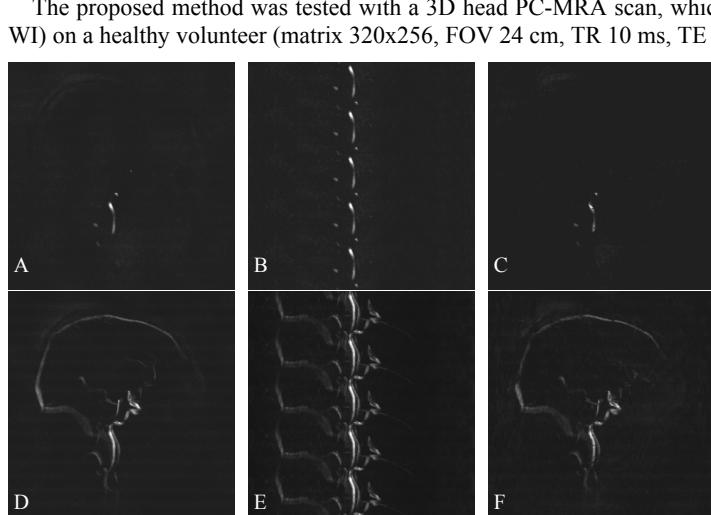
$$I_{1,k} = S_1^n P_k^n G_n \quad (1)$$

$$I_{2,k} = S_2^n P_k^n G_n \quad (2)$$

$$I_{3,k} = S_3^n P_k^n G_n \quad (3)$$

$$I_{4,k} = S_4^n P_k^n G_n \quad (4)$$

The proposed method was tested with a 3D head PC-MRA scan, which was acquired using a clinical 1.5T scanner (GE Health Care, Milwaukee, WI) on a healthy volunteer (matrix 320x256, FOV 24 cm, TR 10 ms, TE 4 ms, slice thickness 2.4 mm, single acquisition, 140 slices).



## Results

A is a reference image of one slice obtained from full k-space data. B is one of the 4 ghosted images from 4 coils with a PE skip size  $N=5$ . C is reconstructed by S-SPEED-ACE from the 4 ghosted images, each sampled with a skip size of 5 within 60% k-space asymmetrically, achieving an acceleration factor of 8.3. D, E and F are the corresponding MIP images of A, B and C from a side view. C and F show comparable results to the reference images A and D.

## Conclusion

By taking advantage of signal sparsity naturally existing in the data, SPEED-ACE was simplified and its efficiency was improved. In this work, the previously proposed parallel imaging method named S-SPEED-ACE has been further developed to accelerate a 3D head PC-MRA scan.

## References

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