**Real-based Polarity-preserving Asymmetric Fourier Imaging (RepAFI)**

Tokunori Kimura and Hiroshi Kusahara

We proposed and assessed a modified asymmetric Fourier imaging (AFI) technique named real-based polarity-preserving AFI (RepAFI), in which the low-pass filter kernel for background phase estimation in AFI is optimized to preserve the magnetization polarity information for blood vessels and cerebrospinal fluid (CSF) even for data obtained using phase-sensitive inversion-recovery spin-echo-based (PSIR-SE) sequences with asymmetrical sampling in the k-space. Our proposed RepAFI technique achieves a practical balance of image quality and simplicity to provide better performance than conventional AFI methods.

**Keywords:** asymmetric Fourier imaging, partial Fourier imaging, magnetization polarity, vessel wall imaging, FLAIR

**Introduction**

Phase-sensitive and real-part imaging techniques that use an inversion-recovery (IR) sequence (PSIR/Real-IR) in combination are useful for T₁-weighted (T₁W) imaging, fluid-attenuated inversion-recovery (FLAIR) imaging, and black-blood (BB) imaging, because they provide images in which the magnetization polarity is preserved. The presentation of the magnetization polarity is particularly vital when the longitudinal magnetization (Mₗ) polarities (positive and negative) are mixed as a result of the inversion time (TI), being set to a value that is smaller than the TI for nulling Mₗ (TIₙull). However, background phase correction is usually needed to produce correct PSIR images, even for spin-echo (SE) or fast-spin-echo (FSE) sequences that are free from the susceptibility-dependent phase artifacts that are seen in gradient-echo sequences. Therefore, other data that ensures positive Mₗ in whole tissue is used for phase correction in PSIR sequences. This data is obtained without the inversion pulse or with TI > TIₙull in PSIR sequences. In addition, the symmetric k-space sampling is required to prevent the introduction of phase errors in phase correction as will be shown later in theory section.

On the other hand, a standard asymmetric Fourier imaging (AFI) or a partial Fourier imaging (PFI) reconstruction technique for asymmetrically sampled k-space data in magnetic resonance (MR) imaging can produce images that are almost equivalent to the images obtained from symmetrically sampled full k-space data based on the Hermitian conjugate theory. These techniques have been widely used to reduce imaging time or shorten TE while minimizing blurring. Several AFI algorithms have been proposed and applied. The simplest algorithms include the Margosian and homodyne techniques, which are equivalent, in which the phase is estimated using symmetric portions of the low frequency parts of the k-space self-data. The projection onto convex sets (POCS) technique and the Cuppen technique, in which iteration is performed under the assumption that the real-space (r-space) image contains only the real component after phase correction, can reduce the artifacts induced by the Margosian and homodyne techniques at the cost of computing time. Xu et al. has extended the POCS algorithm to 2-dimensional (2D) partial sampling, and several approaches have been proposed combining AFI with parallel imaging (PI) techniques that allow acceleration using multichannel coil data. In a more recently proposed magnitude-based AFI technique, the phase information is not required and the phase-dependent errors are lower than in conventional methods.

However, none of the proposed AFI algorithms can be applied to data containing positive and negative signals, such as PSIR data, because MR signals are assumed to be all positive in standard AFI due to the phase estimation process. In standard AFI, the phase estimation is commonly performed using a low-pass filter kernel determined based only on the sampled data size in k-space without considering the spatial frequency components of the background phase, resulting in unstable signal polarities when the algorithm is applied to PSIR data.

In this study, we have proposed and assessed a modified AFI technique named real-based polarity-preserving AFI
(RepAFI), in which the magnetization polarity can be preserved even for PSIR sequences with asymmetric k-space sampling by optimizing the low-pass filter kernel used for phase correction in standard AFI algorithms.

**Theory**

First, the principles of standard AFI are reviewed. As can be seen in Fig. 1, an ideal MR signal \( V \) is assumed to be a vector summation of the complex conjugate signals \( V^+ \) and \( V^- \). In AFI, the unknown \( V^- \) (corresponding to data in the unsampled k-space region) is estimated from the known \( V^+ \) (corresponding to data in the sampled k-space region). However, the actual MR signals include the additional artifactual background phase \( \Phi_{\text{back}} \). For symmetrically sampled data for the full k-space with positive polarity, the ideal \( V \) is obtained simply by obtaining the magnitude even if \( \Phi_{\text{back}} \) is unknown. In contrast, for asymmetrically sampled data for the full k-space (\( V^- \) unknown), if \( \Phi_{\text{back}} \) can be estimated from the self-data and then corrected, \( V \) can be obtained by doubling the real part of \( V^+ \), and the polarity becomes correct. However, the correct \( V \) cannot be obtained regardless for the full or partial sampling if the polarity is negative, and the measured \( \Phi_{\text{back}} \) is incorrect. The purpose of RepAFI is to enable acquisition of the correct \( V \), including the polarity, by enabling the correct measurement of \( \Phi_{\text{back}} \).

Second, we consider the case where the positive and negative signals are mixed when there is no other signal whose phase is 0 or |\( \pi \)| at the ideal condition of \( \Phi_{\text{back}} = 0 \). This can happen, for example, when the TI of the PSIR sequence is shorter or longer than the \( T_{1\text{null}} \)S of the different tissues under the condition of mixing of several tissues with different \( T_1 \) values. The phases of the positive and negative signals are respectively \( \Phi_{\text{back}} \) and \( \Phi_{\text{back}} + |\pi| \). A basic assumption in the RepAFI technique is that the background phase \( \Phi_{\text{back}} \) can be separated from the measured total phase while preserving the polarity information in the r-space corresponding to the sampled self-data in the k-space. To preserve the magnetization polarity by eliminating only \( \Phi_{\text{back}} \) in the AFI algorithm, separation should be possible.

Does the use of spatial frequency differences, for example by windowing in the k-space, make separation possible? Fortunately, the background phase changes smoothly, and is concentrated in the low frequency part of the k-space, especially for SE- and FSE-based sequences (the high-frequency components in the background phase are significant for GRE-based sequences). The blood vessel and CSF sections have longer \( T_1 \) (thus longer \( T_{1\text{null}} \)) than those for the stationary tissues (gray matter, white matter, fat, muscle, etc.), and are also regarded to be relatively small spatially, concentrated in the high-frequency part of the k-space. If such conditions can be assumed, the background phase is expected to be separated in SE-based IR.

**Fig 1.** Principles of real-based polarity-preserving asymmetric Fourier imaging (RepAFI) for inversion-recovery (IR) signals with polarity. Here, it is assumed that the positive background signal is \( V^- \), and the negative blood vessel signal is \( V^+ \). The actual magnetic resonance (MR) signals are complex and include the additional artifactual background phase \( \Phi_{\text{back}} \). In AFI, the unknown signal \( V^- \) (corresponding to data in the unsampled k-space region) must be estimated from the known \( V^+ \) (corresponding to data in the sampled k-space region). If the pure background phase \( \Phi_{\text{back}} \) can be estimated and then corrected, the intensity of the ideal signal \( V = V^+ + V^- \), including the polarity, can be obtained by doubling the real part of \( V^+ \). However, the correct signal intensity, especially for negative polarities, cannot be obtained if the measured \( \Phi_{\text{back}} \) is incorrect. The purpose of RepAFI is to enable acquisition of the correct signal, including the polarity, by enabling correct measurement of \( \Phi_{\text{back}} \).
sequences even at TI > T1null for stationary tissues and TI < T1null for blood or CSF by using optimal low-pass windowing in the k-space in standard AFI algorithms. RepAFI is a modified AFI technique in which the low-pass filter for phase correction in standard AFI algorithms is optimally designed to correctly estimate the background phase even under the above conditions.

RepAFI is expected to be effective even for asymmetrically sampled data obtained with PSIR sequences. Alternatively, if Φback is estimated correctly using separate data (extra data) without using IR, the polarity and structure can be restored perfectly, in the same manner as for fully sampled data.

**RepAFI algorithm**

Here, as similarly as our proposed another AFI technique named MagAFI,13 we provide a simplified explanation of RepAFI using the case of 1D data with the negative part of the k-space truncated. The k-space data is denoted as S(k), the r-space data is denoted as V(r), and the real part of the image data is denoted as I(r). The original asymmetric k-space data is denoted as Sorig(k): −Kc ≤ k ≤ Kmax − 1 (Kc < Kmax), the truncated region (−Kmax ≤ k < −Kc) is filled with zeros and the Kc is truncation parameter. Initially, the following 1D k-space window functions for AFI are defined as:

\[ H_{\text{low.back}}(k) = \begin{cases} \exp((-\ln 2) \cdot (K_c / K_{r2})^2) : 0 < |k| \leq K_c, \\ 0 : \text{otherwise} \end{cases} \] (1)

where \( k \) is k in 1D data, or radial in polar coordinate in k-space in 2D or 3D data, and the \( K_{r2} \) is decided dependent only on the phase distribution in r-space and independent of \( K_c \) under \( K_{r2} \leq K_r / 2 \), because this window is used for background phase estimation, and thus that is different from the other windows, defined below. This window becomes circular symmetric shape for 2D or 3D data. The \( K_{r2} \) and the minimum \( K_r \) must be decided based on the phase distributions for the target sequence and subject. Appropriate setting of this window is one of the keys for ensuring the effectiveness of RepAFI.

\[ H_{\text{low}}(k) = \begin{cases} 1 : |k| \leq K_c - K_1, \\ \exp((-\ln 2) \cdot \left\{ k - 2(K_c - K_1) \right\} / K_1^2) : K_c - K_1 < |k| \leq K_c, \\ 0 : \text{otherwise} \end{cases} \] (2)

where \( K_1 (0 < K_1 \leq K_c) \) is a parameter that determines the range of the flat-top for gain = 1 for \(|k| \leq K_c - K_1\). This window is used for phase correction in the Margosian technique and other conventional AFI algorithms, but in the RepAFI technique, it is only used for creating the windows as described in c) and d) below.

\[ S(k < -K_c) = 0 : H_{\text{high.homo}}(k) = \begin{cases} H_{\text{low}}(k) : k < 0, \\ 2 - H_{\text{low}}(k) : k \geq 0 \end{cases} \] (3)

This window enhances the opposite side of the truncated high-frequency k-space region \((k > K_c)\) by a factor of 2 and is used to compensate for the truncated k-space region in the Margosian and homodyne techniques.

d) Asymmetric window:

\[ S(k < -K_c) = 0 : H_{\text{whole}}(k) = \begin{cases} H_{\text{low}}(k) : -K_{\text{max}} \leq k \leq 0, \\ 1 : \text{otherwise} \end{cases} \] (4)

This window is used to reduce truncation (ringing) artifacts for whole asymmetric data.

Next, we define the Fourier transform (\( FT[\cdot] \)), inverse Fourier transform (\( IFT[\cdot] \)), and real part (\( \text{Re}[\cdot] \)) operators. \( FT[\cdot] \) transforms the k-space in the range of \(-K_{\text{max}} \leq k \leq K_{\text{max}} - 1\) to the r-space in the range of \(-R_{\text{max}} \leq r \leq R_{\text{max}} - 1\); \( IFT[\cdot] \) is the inverse transformation of \( FT[\cdot] \), and \( \text{Re}[\cdot] \) extracts the real part of its argument. The RepAFI can be implemented in various ways as similar as the several standard AFI algorithms except for the following part of “low-pass windowing.”

### A. Margosian (Homodyne)-based RepAFI (Fig. 2a)

- **a1** Low-pass windowing:
  \[ S_{\text{low}}(k) = H_{\text{low.back}}(k) \cdot S_{\text{orig}}(k) \]

- **a2** FT:
  \[ V_{\text{low}}(r) = FT[S_{\text{low}}(k)] \]

- **a3** Homodyne windowing:
  \[ S_{\text{high.homo}}(k) = H_{\text{high.homo}}(k) \cdot S_{\text{orig}}(k) \]

- **a4** FT:
  \[ V_{\text{high.homo}}(r) = FT[S_{\text{high.homo}}(k)] \]
a5) Phase correction:
\[ V_{\text{AFI}}(r) = V_{\text{high.homo}}(r) \cdot \overline{V}_{\text{low}}(r) / |V_{\text{low}}(r)| \]

a6) Extraction of the real part in the r-space:
\[ I_{\text{AFI}}(r) = \text{Re}[V_{\text{AFI}}(r)] \]

B. RepAFI with POCS Combination (Fig. 2b)
The initial data \((n = 0)\) produced by the Margosian-based RepAFI technique \((A)\) is defined as \(I_{\text{AFI}}(r, 0) = I_{\text{AFI}}(r).\) \(N\) iterations \((n = 1 \text{ to } N)\) of steps b1) to b5) given below, where the \(N\) is decided experimentally, are performed.

b1) Phase restoration:
\[ V_{\text{AFIrest}}(r, n) = V_{\text{AFIrest}}(r, n - 1) \cdot V_{\text{low}}(r) / |V_{\text{low}}(r)| \]

b2) IFT: \(V_{\text{AFIrest}}(r, n) = \text{IFT} [V_{\text{AFIrest}}(r, n)]\)

b3) Merging of the original and estimated k-space data:
\[ S_{\text{merge}}(k, n) = \{1 - H_{\text{merge}}(k)\} \cdot S_{\text{AFIrest}}(k, n) + H_{\text{merge}}(k) \cdot S_{\text{orig}}(k) \]

Here, it is defined that \(H_{\text{merge}} = H_{\text{whole}}\)

b4) FT: \(V_{\text{merge}}(r, n) = \text{FT} [S_{\text{merge}}(k, n)]\)

b5) Phase correction:
\[ V_{\text{AFI}}(r, n) = V_{\text{merge}}(r, n) \cdot \overline{V}_{\text{low}}(r) / |V_{\text{low}}(r)| \]

b6) Extraction of the real part in the r-space:
\[ I_{\text{AFI}}(r, n) = \text{Re}[V_{\text{AFI}}(r, n)] \]

Note that the main difference between the RepAFI technique and the standard Margosian (Homodyne) technique is the shape of the low-pass filter used for phase estimation. Instead of \(H_{\text{low}}\) which is used in the standard Margosian technique in step a1), \(H_{\text{low.back}}\) is used in the RepAFI technique.

In addition, it is not supposed to contain negative signals in a standard AFI algorithm, final images are usually displayed after taken absolute as \(|I_{\text{AFI}}(r)|\) to suppress negative signals.

Materials and Methods

Simulations
Numerical 1D phantom was assumed as shown in Fig. 3, where the background phase of 2nd order \(\Phi_{\text{back}} = a \cdot r^2 \text{[rad]}, \) \(-N_{\text{max}} = < r \leq N_{\text{max}}, (N_{\text{max}} = 128),\) and three sizes of blood
vessels of width = 10, 8, 5 pixels with the constant phase $\Phi_{\text{vessel}}$ were included in the stationary tissue with rectangular magnitude. The number of data points of full k-space data was 256 ($-128 \leq k \leq 127$) and truncated k-space data ($-K_c \leq k \leq 127$) were made after FT of r-space data. The standard parameters were: $\Phi_{\text{vessel}} = 180^\circ$ (ideally inverted); $\alpha = 0.0002$, $K_{\text{max}} = 128$, $K_c = 16$, $K_1 = 8$, and $K_2 = K_1/2$. Evaluation items were as follows: a) vessel phase dependency as a parameter of $\Phi_{\text{vessel}} = 90^\circ$, $120^\circ$, $150^\circ$, and $180^\circ$ (ideal); b) $K_c$ dependency as a parameter of $K_c = 8, 16, 24, \text{ and } 32$; and c) background phase dependency as a parameter of $\alpha = 0.0001, 0.0002, 0.0003, \text{ and } 0.0004$. In this study, the RepAFI with POCS of $N = 4$ was commonly used.

MRI experiments
Imaging was performed on 3T whole-body imager (Vantage Titan, Toshiba Medical Systems, Tochigi, Japan) using a 14-ch brain coil for PI. Normal volunteer brain data was obtained according to the regulations of our institution’s internal review board after receiving written informed consent.

First, for comparison among different $K_c$, two types of 2D IR–FSE with fully sampled data of (A) brain axial $T_2$-weighted ($T_2$W) FLAIR and (B) neck axial proton-density weighted (PDW) double IR (DIR) were used. The standard AFI (with POCS) and the RepAFI (with POCS) were also compared for both the data as a parameter of $K_c$. The low-pass filters for phase estimation in the standard AFI and the RepAFI were respectively “a) Low-pass symmetric window #1” and “b) Low-pass symmetric window #2” as shown in theory section.

A) $T_2$W-FLAIR 2D-FSE selecting $T_1 < T_{\text{null}}$ of CSF:
TR/TE/TI = 10000 ms/120 ms/2200 ms, ETI = 13, 24 slices, slice thickness = 5 mm, FOV = 24 cm, acquisition matrix = 224 (phase encode: $x$) $\times$ 272 (readout: $y$) (voxel size = 1.1 mm $\times$ 0.88 mm), display matrix = 320 $\times$ 320 after sinc interpolation, and PI of $R = 2$. For AFI parameters, $K_c$ was varied and k-space data was truncated the front of phase-encode direction (anterior–posterior for A right-to-left for B), $K_2 = 4, K_1 = 8, \text{ and } K_2 = 4$, POCS ($N = 4$) were commonly used.

B) PDW DIR BB-2D-FSE selecting $T_1 < T_{\text{null}}$ of blood:
TR/TE/TI = 13000 ms/10 ms/40 ms, ETI = 8, slice thickness = 5 mm, FOV = 20 cm, acquisition matrix = 224 (phase encode: $y$) $\times$ 384 (readout: $x$) (voxel size = 0.89 mm $\times$ 0.52 mm), display matrix = 384 $\times$ 384 after sinc interpolation, no cardiac gating, and the other parameters were same as A).
Second, three reconstruction methods of 0-filling, magnitude-based standard AFI, and RepAFI were compared among several TIs (300–600 ms). Although the RepAFI is originally a method that self-data is used for the phase correction, it was not succeeded when the inverted regions were relatively spatially greater than the non-inverted region especially for short TI. Therefore, the phase data of TI = 500 ms was used when TI ≤ 400 ms. The following imaging data was used.

C) T₁W IR–3D-FSE with variable flip angle (3D IR-VFA-FSE):
TR/TE/TI = 1200 ms/16.5 ms/300–1000 ms, ETL = 32, FOV = 25.6 cm, acquisition matrix = 256 × 256 (voxel size = 1 mm × 1 mm), display matrix = 512 × 512 after sinc interpolation, slice thickness = 3 mm, # of slices = 52, NAQ = 1, PI of reduction-factor (R) = 2 and acquisition time = 4:29. The k-space sampled data, \( S(k_e, k_r, k_s) \) was truncated to \(-12 \leq k_e \leq 128\) in the front of phase-encode direction (A-P).

**Evaluation**

The AFI algorithms of RepAFI with POCS, respectively, between full sampling and partial sampling were compared visually and quantitatively using a root-mean-square-error (RMSE) ratio, defined for 1D data as:

\[
RMSE = \sqrt{\sum_{r=1}^{R} \left[ I_{\text{AFI}}(r) - I_{\text{full}}(r) \right]^2 / R}
\]

where \( R \) is a r-space data size, \( I_{\text{AFI}}(r) \) and \( I_{\text{full}}(r) \) are respectively the signal intensities for AFI and fully sampled images at the position, \( r \). For 2D image data, those were similarly obtained for whole pixels in each 2D image data.

**Results**

**Simulations**

The results for vessel phase dependency, \( K_c \) dependency, and background phase dependency are shown in Figs. 3, 4, and 5, respectively. Errors (RMSE) in the RepAFI profiles were negligible at vessel phase = 180° but were increased with increasing the vessel phase difference from 180° (Fig. 3). Errors in resultant profiles even at vessel phase = 180° were negligible for the ideal phase but not negligible for the phase estimation with low-pass filter particularly around the vessel portions where the phase changes rapidly; and those were decreased with increasing \( K_c \) (Fig. 4) or with decreasing background phase distribution range (Fig. 5).

**MR imaging experiments**

The results of dependency on \( K_c \) for A) T₂-W-FLAIR and for B) DIR–BB–FSE are shown in Figs. 6 and 7, respectively. The standard AFI did not provide correct magnetization polarity with increasing \( K_c \) due to the effects that positive signal regions
became wider in CSF regions (Fig. 6) or blood vessel regions (Fig. 7). In contrast, the RepAFI provided similar images as the real images obtained from the fully sampled data, almost independent of $K_c$ when $K_c$ was selected greater than the twice of 2D low-pass window size ($2K_{r2} = 8$ for seq-A, and $= 32$ for seq-B) for background phase estimation. For seq-A, it was regarded as the $M_z$ in CSF sections were almost perfectly inverted to $180^\circ$ and the background phase was almost correctly estimated in this data; however, for seq-B, the vessel phase might not be perfectly $180^\circ$. This could be due to the
motion (flow)-induced phase after inversion, because the blood vessel phase becomes $|\phi_{\text{vessel}}| < 180^\circ$ even in the fully sampled data in spite of the background phase being estimated relatively well by the 2D low-pass filter.

Regarding the results for brain 3D IR–VFA–FSE imaging with TI as a parameter (Fig. 8a: images, b: graph), it can be seen that the blurring in the 0-filling images was corrected in the RepAFI images. Also, the $M_z$ polarity wraparound in the standard AFI images was corrected in the RepAFI images. In addition, the RepAFI provided correct T1W contrasts while preserving the signal polarity. The relationships among the signal intensities of different tissues were not preserved with the standard AFI, but they were preserved for all TI values with RepAFI, irrespective of whether the signal intensities were positive or negative (TI = 300 ms: CSF < GM < WM < 0, TI = 400 ms: CSF < GM < 0 < WM, TI = 500 ms: CSF < 0 < GM < WM, and TI = 600 ms: 0 < CSF < GM < WM).

Discussion

We proposed a modified AFI technique named RepAFI, in which the background phase is estimated using an optimal low-pass window in the standard AFI algorithm, and assessed thorough simulations and volunteer MR study. It was confirmed that our RepAFI provided $M_z$-polarity-preserved data nearly equivalent to fully sampled data even when asymmetrically sampled k-space data is used, and in addition, the main requirements for RepAFI are that the background phase estimation should be correct and the inverted portions should be close to $180^\circ$ as far as possible. Next, we discussed about the limitations and the solutions on RepAFI technique.

**TI dependency in phase estimation**

We found that, for actual MR imaging data acquired using IR–FSE sequences, the TI range for successful phase correction was limited to the range where the tissue signals were positive as shown in Fig. 8. This limitation for RepAFI applies when the background phase map is estimated from the self-data with low-pass filter. The limitations related to the TI range and the spatial extent of the negative signal sections in the current low-pass filter-based method used for IR self-data in RepAFI will be reduced by utilizing a better phase estimation technique, such as measurement of the background phase after elimination of the blood vessel and CSF regions.

**Sequence type for RepAFI**

It is known that VFA–FSE sequence enables to well suppress the blood vessel signals due to the dephasing effects of variable FA pulses but it is not sufficient alone. To further enhance BB effects on VFA–FSE, a combination with motion-sensitizing driven equilibrium (MSDE) prepared technique was proposed; however, its minimum signal is zero and sometimes introduces motion artifacts or SNR reduction. Wang’s gradient echo-based PSIR method requires another data for phase correction. In contrast, the RepAFI with IR–VFA–FSE...
could enhance vessel-to-background contrasts by keeping blood signal negative by itself if the global signals are positive, without introducing artifacts or SNR reduction.

When our RepAFI is applied to highly asymmetric data (data with smaller $K_c$) obtained under unignorable motion-induced phase errors such as in neck arteries, as shown in Fig. 7, the use of a shorter TE or a flow-refocusing sequence will further improve the results, because the vessel phase is expected to become closer to 180°.

**Data spatial dimension**

Regarding the spatial dimension for RepAFI, the higher the better (3D than 2D) results will be obtained. Our simulation was performed using 1D data and MR imaging were performed using 2D data. The higher dimensional data that RepAFI is actually applied will provide further better estimation for background phase even using the self-data with low-pass filter, since the multi-dimensional low-pass filter enable to effectively suppress the negative-polarity regions such as CSF, which become relatively smaller in higher dimensional image, i.e., 3D will be better than 2D. For 2D partial sampling in 2D data, low-pass filter shape becomes similar to $H_{\text{low,back}}$, however, it depends on $K_c$.

**Background phase estimation using extra data**

If it is not easy to correctly and robustly estimate the background phase using the only self-data obtained by IR sequence regardless for full or partial sampling, it is alternative to use separately acquired data of including only background phase such as no IR sequence instead of using self-data; though extra acquisition time is required. In addition, it is desirable to use the same readout conditions including motion correction might become necessary between the main data and the extra data for phase estimation. This will decrease the dependence on the TI and the readout sequence type (SE or GRE), because the background phase can be eliminated without using the spatial frequency differences in the self-data. In addition, even if the high-frequency components in the background phase are significant, such as in the case of GRE sequences, the background phase and negative signal components can be separated out independently, thus enabling perfect correction.

**Conclusion**

Although the main limitations are that our proposed RepAFI technique is only applicable to spin-echo-based PSIR sequences and the negative signal structures must be confined to relatively small parts in imaging volume, it achieves a practical balance of image quality and simplicity to provide better performance than conventional AFI methods. It is expected to be especially useful in 3D black-blood vessel wall imaging, although further optimization of parameters for pulse-sequence or clinical evaluation are required.
References

1. Hou P, Hasan KM, Sitton CW, Wolinsky JS, Narayana PA. Phase-sensitive T$_1$ inversion recovery imaging: a time-efficient interleaved technique for improved tissue contrast in neuroimaging. Am J Neuroradiol 2005; 26:1432–1438.
2. Wang J, Ferguson MS, Balu N, Yuan C, Hatsukami TS, Börnert P. Improved carotid intraplaque hemorrhage imaging using a slab-selective phase-sensitive inversion-recovery (SPI) sequence. Magn Reson Med 2010; 64:1332–1340.
3. Kimura T, Sueoka K. A real-IR 3D T$_1$-weighted black-blood imaging technique combining with white-blood. Proceedings of 21st ISMRM, Milan, 2014; 3912.
4. Feinberg DA, Hale JD, Watts JC, L. Kaufman L, Mark A. Halving MR imaging time by conjugation: demonstration at 3.5 kg. Radiology 1986; 161:527–531.
5. Margosian P. Faster MR imaging: imaging with half the data. In: Proceedings, 4th SMRM Conference Abstracts 1985; 1024–1025.
6. Margosian P, Schmidt DE, Purdy DE. Faster MR imaging: imaging with half the data. Health Care Instrum 1986; 1:195.
7. Noll DC, Nishimura GD, Macoviski A. Homodyne detection in magnetic resonance imaging. IEEE Trans Med Imaging 1991; 10:154–163.
8. Haacke EM, Lindskog ED, Lin W. A fast, iterative, partial-Fourier technique capable of local phase recovery. J Magn Reson 1991; 92:126–145.
9. Cuppen J, van Est A. Reducing MR imaging time by one-sided reconstruction. Magn Reson Imaging 1987; 5:516–527.
10. McGibney C, Smith MR, Nichols ST, Crawley A. Quantitative evaluation of several partial Fourier reconstruction algorithms used in MRI. Magn Reson Med 1993; 30:51–59.
11. Xu Y, Haacke EM. Partial Fourier imaging in multidimensions: a means to save a full factor of two in time. J Magn Reson 2001; 14:628–635.
12. Bydder M, Robson MD. Partial Fourier partially parallel imaging. Magn Reson Imaging 2005; 53:1393–1401.
13. Kimura T, Shigeta T. Magnitude-based asymmetric Fourier imaging (MagAFI). Magn Reson Med Sci 2016; 15:94–104.