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Line Profile Measure as a Stopping Criterion in CG-SENSE Algorithm

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Abstract Conjugate gradient SENSE (CG-SENSE) is a parallel magnetic resonance imaging reconstruction algorithm which solves the inversion problem of SENSE iteratively. One major limitation of CG-SENSE is the appropriate choice of the number of iterations required for good reconstruction results. Fewer iterations result in aliasing artifacts and too many iterations result in an increased noise level. This paper proposes a novel method to define the stopping criterion of CG-SENSE algorithm which is based on the use of correlation measure between the line profiles of the reconstructed images in the current and the previous iterations. The results are compared with Bregman distance-stopping criterion. Artifact power and peak signal-to-noise ratio are used to quantify the quality of the reconstructed images. The results demonstrate that the line profile correlation measure acts as an effective stopping criterion in CG-SENSE.

1 Introduction

Magnetic resonance imaging (MRI) [1] is a non-invasive and non-ionizing medical imaging modality with excellent contrast information in tissues. Its long data acquisition time is a curtailment in its strength. Parallel MRI (PMRI) [2] works well for reducing the MRI scan time by acquiring less data in k-space. PMRI acquires data from multiple receiver coils and uses dedicated reconstruction algorithms to reconstruct the MR image. PMRI can either use Cartesian or non-Cartesian trajectories to acquire the k-space data; however, non-Cartesian trajectories provide a faster way to acquire the MRI data efficiently as compared to Cartesian trajectories [3].

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Conjugate gradient SENSE (CG-SENSE) [4] is a PMRI algorithm that uses receiver coil sensitivity information in order to reconstruct an MR image from the acquired under-sampled data. It solves the inversion problem of SENSE iteratively by using the conjugate gradient method [4].

An appropriate choice for the right number of iterations is strenuous in CG-SENSE. A less number of iterations results in aliasing artifacts and too many iterations result in an increased noise level as the algorithm begins to reconstruct noise. Consequently, there is a requirement for an appropriate stopping criterion for CG-SENSE algorithm. In the past, some researchers have presented their work in this regard for CG-SENSE algorithm. Qu [5] proposed the stopping criterion for non-Cartesian SENSE by observing the residual norm along the iterations which were shown to converge where artifacts and signal-to-noise ratio (SNR) are well compromised. Bo Liu [6] proposed Bregman iterations for regularized SENSE and Bregman distance [6] was used as the stopping criterion for CG-SENSE.

This paper proposes the use of a correlation measure [7] between the line profiles of the reconstructed images in the current and the previous iterations, as a stopping criterion for the CG-SENSE algorithm. The reconstruction results of the proposed method are compared with the Bregman distance-stopping criterion [6], where Bregman distance between the current and the previous iterations was used as a stopping criterion. Artifact power (AP) [8], SNR [9] and peak SNR [9] are used as quantifying parameters to measure the reconstructed image quality.

The rest of the paper covers a brief description of CG-SENSE algorithm and Bregman distance in Sect. 2. Section 3 describes the materials and methods used in this work and Sect. 4 presents the "Results and Discussion". Finally, "Conclusion" is given in Sect. 5.

2 Theory

2.1 CG-SENSE

Conjugate gradient SENSE (CG-SENSE) [4] is a PMRI algorithm for non-Cartesian trajectories that uses receiver coil sensitivity maps to reconstruct MR images from the acquired under-sampled data. CG-SENSE is a powerful algorithm that has been used in many applications including coronary artery imaging, cardiac imaging, functional MRI etc. [3]. CG-SENSE works on the principle of SENSE algorithm, and is used to resolve the un-structured aliasing artifacts [3] appearing because of data under-sampling. Figure 1 shows the flow chart of the CG-SENSE algorithm. The main components of CG-SENSE algorithm are gridding, de-gridding, receiver coil sensitivity profiles, fast Fourier transform (FFT), inverse FFT and CG block.

The acquired under-sampled data are given as an input in CG-SENSE. FFT cannot be applied directly on the non-Cartesian k-space; therefore, the non-Cartesian data must be converted to Cartesian form (using gridding) before applying FFT. De-gridding is used to transform the Cartesian data back into non-Cartesian space as part of the algorithm. CG block iteratively calculates a progression of images, which converges towards the solution image [4].
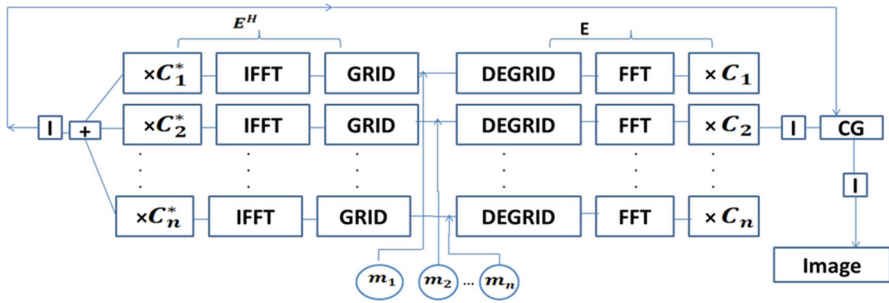
Fig. 1 Flow chart of CG-SENSE algorithm [4]

The algorithm starts with an under-sampled multi-coil k-space data. Gridding operation is performed on the under-sampled data and inverse FFT of the gridded data provides multi-coil images. The multi-coil images are multiplied with the conjugate of the receiver coil sensitivities. The individual multi-coil images are summed using sum-of-square (SOS) method [4], which provides a single image. Intensity correction on this single image is applied and the resulting image is fed into the CG algorithm, which will compute a new estimate of the solution image and checks whether the image converges towards the exact solution or not. If the resultant image converges then intensity correction is applied to get the desired image. If the solution has not converged, intensity correction is applied on the image and is multiplied with the receiver coil sensitivities. FFT of the multi-coil images obtained in the previous step provides the multiple-coil data in k-space. De-gridding is applied on the multiple-coil data which replaces the input of the previous iteration. This process continues until the reconstruction converges.

2.2 Bregman Distance Method

Bregman distance [6] is the distance between the reconstructed images in two consecutive iterations associated with the total variation (TV) norm. As the number of iterations increases, Bregman distance decreases until the system converges due to the convexity of TV norm [6]. The equation used to find Bregman distance is [6]:
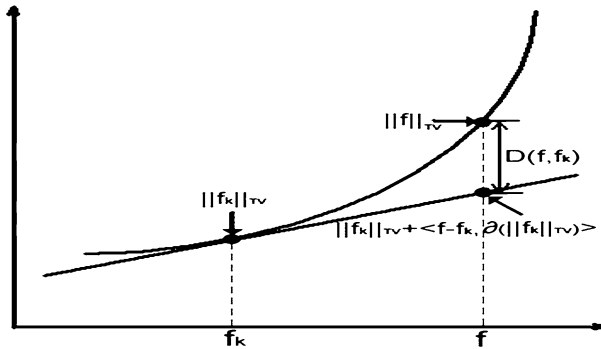
$$D(f, f_k) = f_{TV} - f_{kTV} - f - f_k, \partial(f_{kTV}), \qquad (1)$$

where f_{TV} denotes TV norm [6] at point f, f_{kTV} is the TV norm at point f_k, $\partial(f_{kTV})$ is the sub-gradient [6] of the TV norm at point f_k, $\langle .,. \rangle$ shows the inner product and D is the Bregman distance.

TV norm [6] is an edge preserving method, which is defined as:

$$f_{TV} = \sum \sqrt{|\nabla_x f|^2 + |\nabla_y f|^2}. \qquad (2)$$

TV norm is a function of the gradient of the image. In Eq. 2, f is the 2D image, ∇_x is the gradient along x-axis, ∇_y is the gradient along y-axis and |.| is the complex modulus. Figure 2 shows the graphical representation of Bregman distance:

Fig. 2 Graphical representation of Bregman distance. *x*-axis shows points of the reconstructed image and *y*-axis represents TV norm of these points [6]

Figure 2 shows the Bregman distance curve as a function of TV norm of the image. Tangent line is drawn at point f_k of the curve. Bregman distance is the distance between the tangent at point f_k and the curve. The slope of the curve is denoted by $f_{kTV} + f - f_k, \partial(f_{kTV})$ and it indicates an increase in f_{TV} over f_{kTV}.

Bregman distance decreases as the system moves towards convergence. If the system diverges, Bregman distance starts increasing. The iterations in CG-SENSE algorithm continue until the Bregman Distance starts increasing. Bregman distance method can be used as a stopping criterion in CG-SENSE algorithm [6].
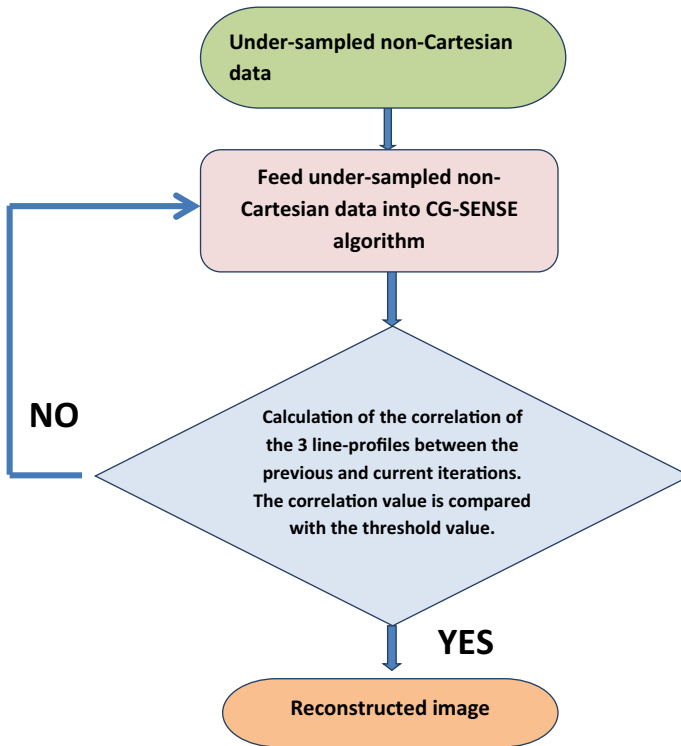
3 Methods

The human head and human cardiac MRI data sets are used in this work. The human head data are acquired using 1.5 Tesla GE scanner at St. Mary's Hospital in London, which contains eight channel head coil data of dimension $256 \times 256 \times 8$ at TE = 10 ms, TR = 500 ms, bandwidth = 31.25 kHz, FOV = 20 cm, flip angle = 50° and slice thickness = 3 mm.

Cardiac data (in radial k-space) are acquired using 3 Tesla Siemens Skyra scanner at Case Western Reserve University, USA, with 30-channel cardiac coils and 80 measurement frames (dimension $256 \times 144 \times 30 \times 80$) at TR = 2.94 ms with real-time, free-breathing and no ECG gating. The acquired data are undersampled retrospectively for different acceleration factors.

The reconstructions using the proposed method are performed for human head data set for the acceleration Factors 2, 3 and 4 and for human cardiac data set for the acceleration Factor 2, 4 and 8. Quality of the reconstructed images is evaluated using AP, SNR and central line-profiles.

In this work all the experiments and analysis have been performed using MATLAB (2013) at core i7 machine with 8 GB RAM.

Figure 3 shows a flow chart of the proposed method. The acquired undersampled radial data are fed into the CG-SENSE algorithm for the reconstruction of a fully-sampled MR image. To use correlation as a stopping criterion in CG-SENSE

Fig. 3 Flow-chart of the proposed method

algorithm, we find correlation between the three line-profiles of the images reconstructed in the last two iterations of CG-SENSE algorithm.

In each iteration of the CG-SENSE algorithm, a correlation [7] of the central horizontal line-profile and two other horizontal line-profiles (explained below) of the reconstructed image between the current and the previous iterations is computed. The lines other than central are chosen close to the center of the image.

The MATLAB script for the selection of first horizontal line i.e. [(total no. of rows in the image)/2.5] is taken as:

$x =$ abs(img(floor(end/2.5),:));

where "img" is the solution image using the proposed method. Here, the total no. of rows are divided by the "2.5" which provides a line that is close to central line. The MATLAB script for the selection of second horizontal line [i.e. (total no. of rows in the image)/1.5] is given as:

$x =$ abs(img(floor(end/1.5),:));

Here, the total no. of rows are divided by the number "1.5" which also results in a line that is close to central line of the reconstructed image.

The MATLAB script for the selection of the central horizontal line in the reconstructed image [i.e. (total no. of rows in the image)/2] is given as:

$x =$ abs(img(end/2,:));

The line profiles of all the three selected lines are taken. The value of the line profile correlation [7] between any two images determines the degree of similarity between the two images. A threshold value of correlation is set as 0.9985 in this paper.

Each line profile is correlated individually between the current and the previous iterations. Iterations of CG-SENSE method will continue until the correlation value becomes less than 0.9985 for all the three line profiles. Once the desired correlation value is achieved (i.e. 0.9985 in this paper) for all the three selected lines, CG-SENSE stops and the solution image is obtained. It has been observed in our experiments that a correlation value greater than 0.9985 increases the number of iterations of CG-SENSE algorithm with no significant improvement in the quality of the solution image.

Finally, performance comparison between the correlation method (proposed method) and the Bregman distance method [6] is performed on the basis of AP and mean SNR.

AP [8] of the reconstructed image has been computed using the following equation:

$$AP = \sum \frac{(I - G)^2}{I^2}, \tag{3}$$

where, I is the full FOV (Full Field-of-View) reference image and G is the reconstructed image.

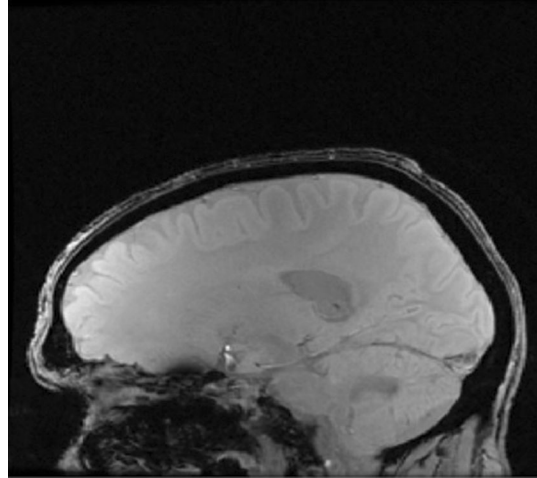SNR gives a measure of the image quality. It is calculated using Pseudo-Replica method [9].
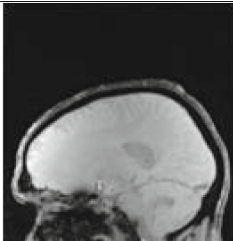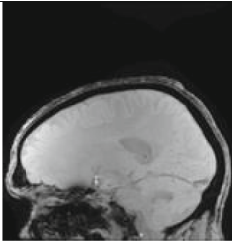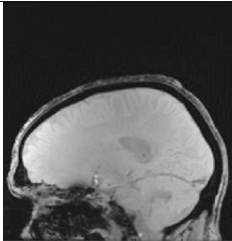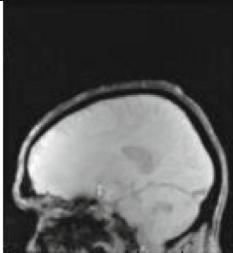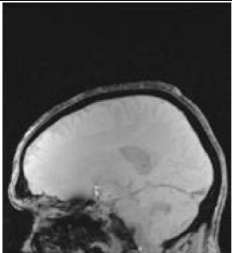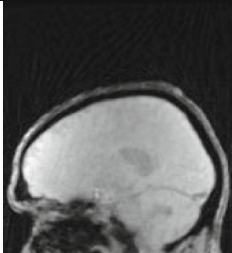
4 Results and Discussion

Figure 4 shows the fully-sampled 1.5T human head data. Figure 5 shows the results of the reconstructed human head images using both the correlation (proposed) and Bregman distance methods at different acceleration factors (AF), i.e. 2, 3 and 4. AP is mentioned at the bottom of each of the reconstructed human head images.

A comparison of the AP values show that at AF = 2, AP for the reconstructed images using correlation method is 0.0016, whereas AP for the Bregman distance method is 0.0024. At lower AF, the AP for Bregman distance method and correlation method is comparable. At AF = 3, AP for the correlation method is 0.0017, whereas AP for Bregman distance method is 0.0095. At AF = 4, AP for the correlation method is 0.0018, whereas AP for the Bregman distance method is 0.0186. Therefore, on the basis of AP values in our experiments it can be concluded that at higher acceleration factors the correlation method (proposed method) provides better results.

Table 1 shows the number of iterations of CG-SENSE algorithm performed to reconstruct the under-sampled 1.5T human head images at different acceleration factors. At AF = 2, the number of iterations taken by CG-SENSE with the line profile correlation stopping criterion (proposed method) is 24, whereas the number of iterations taken for the Bregman distance-stopping criterion is 16. At lower AF,

Fig. 4 Fully-sampled 1.5T
human head image

1.5T Human Head image	AF=2	AF=3	AF=4
Reconstructed image using Correlation Method	AP = 0.0016	AP=0.0017	AP= 0.0018
Reconstructed image using Bregman Distance Method	AP = 0.0024	AP=0.0095	AP = 0.0186

Fig. 5 CG-SENSE reconstruction of 1.5T human head images using the correlation method (proposed) and Bregman distance method for radial trajectory with different AF

the numbers of iterations for Bregman distance method and correlation method are comparable; however, at AF = 3, the number of iterations taken for the correlation method is 46, whereas for the Bregman distance method, 21 iterations are performed. At AF = 4, the number of iterations taken for the correlation method is

Table 1 Number of iterations used for the 1.5T human head images using the correlation and Bregman distance-stopping criteria for radial trajectory with different AF

Acceleration factor	Number of iterations using correlation method	Number of iterations using Bregman distance method
2	24	16
3	46	21
4	90	25

Table 2 mSNR of the reconstructed images of 1.5 T human head using correlation and Bregman distance methods for radial trajectory with different AF

Acceleration factor	mSNR using correlation method	mSNR using Bregman distance method
2	34.3836	34.3206
3	34.3839	34.3134
4	34.3628	34.2931

90, whereas the Bregman distance method takes 25. Therefore, by comparing the number of iterations, it can be concluded that the correlation method takes more iterations as compared to the Bregman method for high acceleration factors, but the quality of the reconstructed image is significantly improved by using the proposed method.
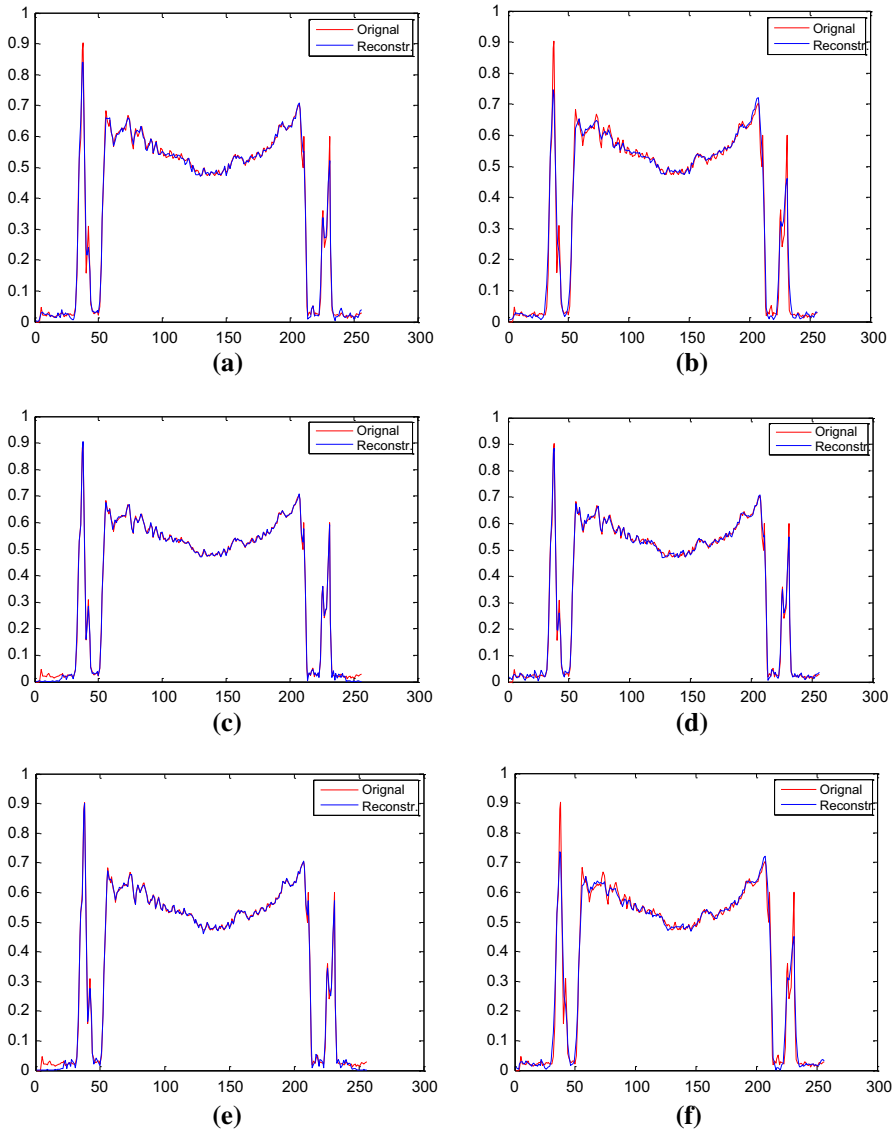
Table 2 shows mean SNR (mSNR) of the reconstructed images of 1.5 Tesla human head data with different AFs (i.e. 2, 3 and 4). The results from Table 2 show that the mSNR values achieved in both the methods are almost similar.

Figure 6 shows the central line-profiles of the reconstructed human head images. Figure 6a, c, e shows the line-profiles of the reconstructed images with the proposed method for AF = 2, AF = 3 and AF = 4, respectively. Figure 6b, d and f shows the line-profiles of the reconstructed images using the Bregman distance method for AF = 2, AF = 3 and AF = 4, respectively. Visual inspection of the results shows that the line profiles of the reconstructed images using the proposed method are closer to the original image as compared to the Bregman distance method which shows effectiveness of the proposed method.

Figure 7 shows the fully-sampled human cardiac data. Figure 8 shows the reconstructed cardiac images using both the correlation and Bregman distance methods at different AFs, i.e. 2, 4 and 8. AP is mentioned at the bottom of the reconstructed images in Fig. 8.
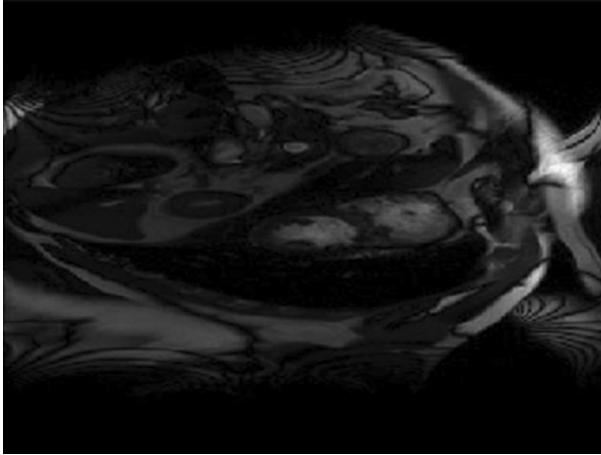
Figure 8 shows that for AF = 2, AP for the proposed method is 0.0034, whereas AP for Bregman distance method is 0.0037. At lower AF, the AP for Bregman distance method and correlation method is comparable. At AF = 4, AP for the correlation method is 0.0035, whereas AP for Bregman distance method is 0.0052, and at AF = 8, AP for the correlation method is 0.0038, whereas AP for Bregman distance method is 0.0112. This shows that at higher acceleration factors, the correlation method gives better results as compared to the Bregman distance method.
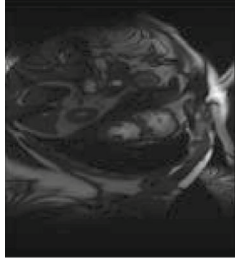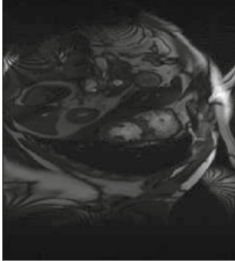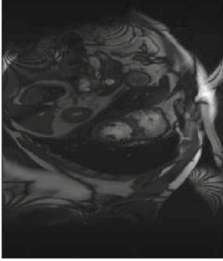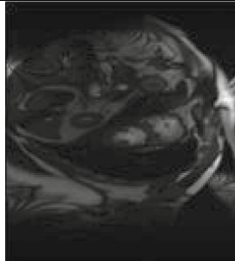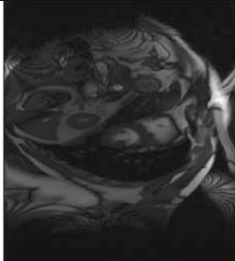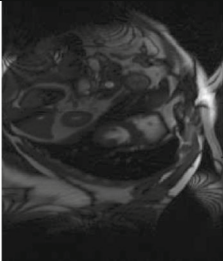
Fig. 6 Central line-profiles of the reconstructed human head images (1.5T), **a** and **b** give the line-profiles at AF = 2 using correlation and Bregman distance methods, respectively, compared with the original image, **c** and **d** give the line-profiles at AF = 3 using correlation and Bregman distance methods, **e** and **f** give the line-profiles at AF = 4 using correlation and Bregman distance methods, respectively

Table 3 shows the number of iterations performed to reconstruct the human cardiac images at different acceleration factors. At AF = 2, the number of iterations taken by the correlation method is 31, whereas the number of iterations taken for the Bregman distance method is 18. Similarly, the number of iterations for Bregman distance method and correlation method are comparable for low AF (Table 1). At

Fig. 7 Fully-sampled 3T human cardiac image

Human Cardiac Images (3T)	AF=2	AF=4	AF=8
Reconstructed images using Correlation Method	AP = 0.0034	AP=0.0035	AP= 0.0038
Reconstructed images using Bregman Distance Method	AP = 0.0037	AP = 0.0052	AP= 0.0112

Fig. 8 CG-SENSE reconstruction of 3T human cardiac images using correlation and Bregman distance-stopping criteria for radial trajectory with different AF

$AF = 4$, the number of iterations taken for the correlation method is 74, whereas the number of iterations taken for Bregman distance method is 25. At $AF = 8$, the number of iterations taken for the correlation method is 286, whereas for the

Table 3 Number of iterations performed for the reconstruction of 3T human cardiac images using correlation and Bregman distance-stopping criteria for radial trajectory with different AF

Acceleration factor	Number of iterations using correlation method	Number of iterations using Bregman distance method
2	31	13
4	74	25
8	286	34

Table 4 mSNR of the reconstructed 3T human cardiac images using correlation and Bregman distance-stopping criteria for radial trajectory with different AF

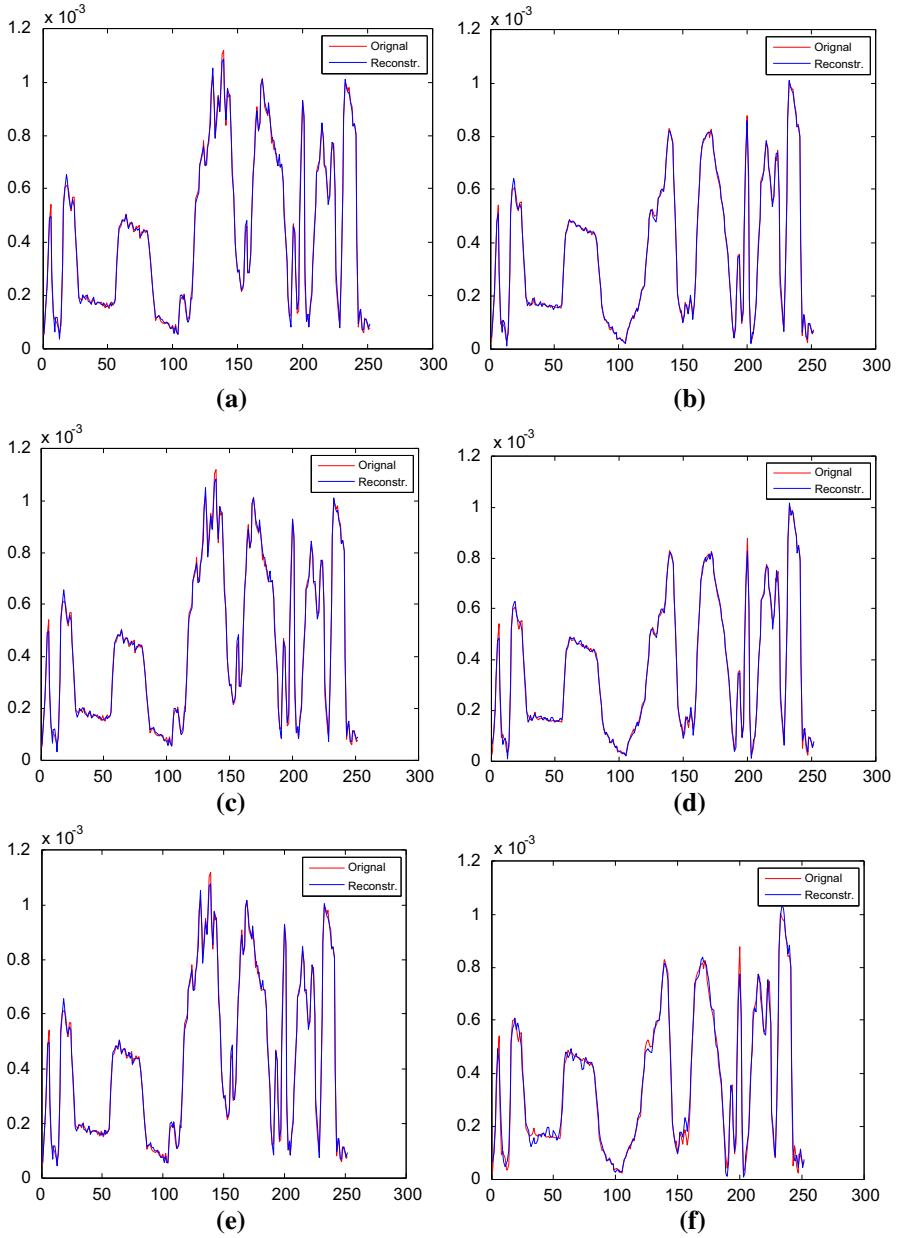| Acceleration factor	mSNR using correlation method	mSNR using Bregman distance method
2	20.8623	14.9056
4	20.8613	14.9016
8	20.8617	14.9048

Bregman distance method the iterations are 34. The results show that for the correlation method (proposed method), higher acceleration factors required more iterations than lower acceleration factors to provide better results.

Table 4 shows the mSNR of the reconstructed images of 3T human cardiac images using the correlation and Bregman distance-stopping criteria for radial trajectory with different AF i.e. 2, 4 and 8. By comparing mSNR values, we can see that the correlation method provides images with higher SNR.
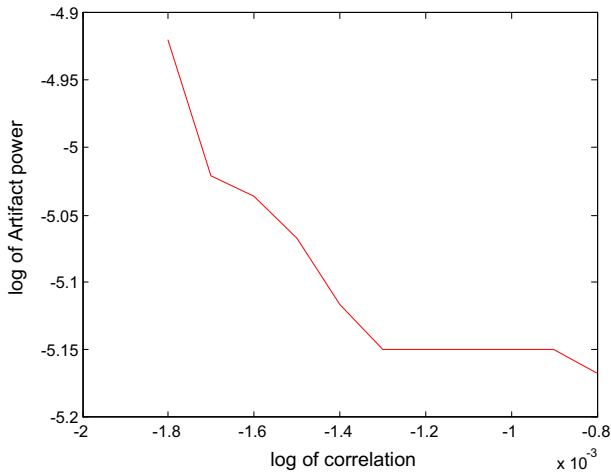
Figure 9a, c and e show the central line-profiles of the reconstructed images with the correlation method for AF = 2, AF = 4 and AF = 8, respectively. Figure 9b, d and f show the line-profiles of the reconstructed images using the Bregman distance method for AF = 2, AF = 4 and AF = 8, respectively. It can be seen that the central line-profiles using the correlation method are closer to the reference image.

Figure 10 shows a plot of AP versus correlation in log scale. These values are obtained for human cardiac data set at AF = 8. Similar plots can be obtained for other AFs for human cardiac data sets and also for the human head data sets. Figure 10 shows that the AP decreases as the correlation value increases. At a specific value of correlation (i.e. 0.9985 in this paper), AP does not decrease further and the solution image is produced as an output.

In this paper we have tried to work on one of the major limitations of CG-SENSE algorithm, i.e. the stopping criterion. We propose the use of line profile correlation measure as a stopping criterion in CG-SENSE algorithm and compared the results with Bregman distance-stopping criterion. The proposed method is tested on different data sets. The results show that Bregman distance method takes lesser number of iterations to converge to the solution image as compared to our proposed method (Tables 1, 3) but the reconstructed image quality is compromised. The proposed method can be used as an effective stopping criterion in CG-SENSE algorithm and provides better reconstructed images with minimal aliasing artifacts as compared to Bregman stopping criterion.

Fig. 9 Central line-profiles of the reconstructed 3T Cardiac images, **a** and **b** show the line-profiles at AF = 2 using the correlation and Bregman distance methods, **c** and **d** show the line-profiles at AF = 4 using correlation and Bregman distance methods, **e** and **f** give the line profiles at AF = 8 using correlation and Bregman distance methods, respectively

Fig. 10 Graph shows *L-curve* between the log of correlation values and log of artifacts power for successive nos. of iterations for the 3T human cardiac data set

5 Conclusion

One of the limitations of CG-SENSE algorithm is an appropriate stopping criterion, too few iterations or too many iterations result in the reconstructed image with severe artifacts. A method using the line profile correlation stopping criterion in CG-SENSE is presented in this research work. The results are compared with the Bregman distance-stopping criterion. The results show that the proposed method can be used as effective stopping criteria in the CG-SENSE algorithm and produces a reconstructed image with minimal aliasing artifacts. The results show that the Bregman distance method takes lesser number of iterations for higher AFs as compared to the proposed method but the reconstructed image quality is compromised. Therefore, the correlation method demonstrates better AP in all the simulations, e.g. 33% performance improvement in terms of AP for AF = 3 for human cardiac data set.

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