Neural Networks in MR Image Estimation from Sparsely Sampled Scans

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Abstract. This paper concerns a novel application of machine learning to Magnetic Resonance Imaging (MRI) by considering Neural Network models for the problem of image estimation from sparsely sampled k-space. Effective solutions to this problem are indispensable especially when dealing with MRI of dynamic phenomena since then, rapid sampling in k-space is required. The goal in such a case is to reduce the measurement time by omitting as many scanning trajectories as possible. This approach, however, entails underdetermined equations and leads to poor image reconstruction. It is proposed here that significant improvements could be achieved concerning image reconstruction if a procedure, based on machine learning, for estimating the missing samples of complex k-space were introduced. To this end, the viability of involving Supervised and Unsupervised Neural Network algorithms for such a problem is considered and it is found that their image reconstruction results are very favorably compared to the ones obtained by the trivial zero-filled k-space approach or traditional more sophisticated interpolation approaches.

1. Introduction

MRI scans are sampled along trajectories in k-space [1]. Ideally, these trajectories are chosen to completely cover the k-space according to the Nyquist sampling criterion. The measurement time of a single trajectory can be made short. However, prior to initiating a trajectory, return to thermal equilibrium of the nuclear spins needs to be awaited. The latter is governed by an often slow natural relaxation process that is beyond control of the scanner and impedes fast scanning. Therefore, the only way to reduce scan time in MRI is to reduce the overall waiting time by using fewer trajectories, which in turn should individually cover more of k-space through added curvatures. This fast scanning approach in MRI is indispensable when dynamic phenomena are considered, as for instance in functional MRI. Although, however, such trajectory omissions achieve the primary goal, i.e. more rapid measurements,

P. Perner, M. Petrou (Eds.): MLDM'99, LNAI 1715, pp. 75-86, 1999.

they entail undersampling and violations of the Nyquist criterion thus, leading to concomitant problems for image reconstruction.

The above rapid scanning in MRI problem is highly related with two other ones. The first is the selection of the optimal scanning scheme in k-space, that is the problem of finding the shape of sampling trajectories that more fully cover the k-space using fewer number of trajectories. The second one is associated with image estimation from fewer samples in k-space, that is the problem of omitting as many trajectories as possible without attaining worse results concerning image reconstruction.

Regarding the former issue, mainly three alternative shapes of sampling trajectories have been considered in the literature and are used in actual scanners, namely, Cartesian, radial and spiral [2]. The last two of them are shown in fig. 1, presenting different advantages and disadvantages.

Both Cartesian and radial trajectories are straight lines. However, the former start at edge of k-space where the signal is weakest, whereas the latter start at the centre of k-space where the signal is strongest. An obvious advantage of Cartesian scanning is that all sample positions coincide with a uniform rectangular grid, allowing very fast image reconstruction simply using the Inverse 2D FFT. Advantages of radial scanning are: less sensitivity to motion of the patient and the ability to deal with possible very fast decays of signals. A disadvantage of radial scanning is that the data are not amenable to direct application of the Inverse 2D FFT, which significantly slows down the reconstruction process. In this case, the image can be obtained by using the Projection Reconstruction approach [2], the linogram method [2] or the SRS-FT [2] approach. Finally, spiral trajectories, being strongly curved, cover much more k-space than Cartesian and radial trajectories do. As a result, fewer spirals are needed to satisfy the Nyquist sampling criterion everywhere.

Concerning the second issue, the main result of the scan trajectories omissions is that we have fewer samples in k-space than needed for estimating all pixel intensities in image space. Therefore, there is an infinity of MRI images that satisfy the sparse k-space data and thus, the reconstruction problem becomes ill-posed. Additionally, omissions usually cause violation of the Nyquist sampling condition. Theses problems might be amended by using the so called Bayesian reconstruction approach recently proposed by two of the authors [2], through regularizing the problem invoking general prior knowledge in the context of Bayesian formalism. The algorithm amounts to minimizing the following objective function [2],

$$| \underline{\mathbf{S}} - T\, \underline{\mathbf{I}} |^2 / (2\sigma^2) + (3/2) \sum_{x,y} \log \{ \alpha^2 + ({}^{x}\Delta_{xy})^2 + ({}^{y}\Delta_{xy})^2 \} \tag{1}$$

with regards to $\underline{\mathbf{I}}$, which is the unknown image to be reconstructed that fits to the sparse k-space data given in $\underline{\mathbf{S}}$. The first term comes from the likelihood term and the second one from the prior knowledge term of the well known Bayesian formulation [2]. In the above formula, $T((k_x, k_y),(x,y)) = e^{-2\pi i(xk_x + yk_y)}$ represents the transformation from image to k-space data (through 2-D FFT). The second term symbols arise from the imposed 2D Lorentzian prior knowledge. ${}^{x}\Delta_{xy}$ and ${}^{y}\Delta_{xy}$ are the pixel intensity differences in the x- and y- directions respectively and α is a Lorentz distribution-width parameter.

Although the Bayesian reconstruction approach tackles the problem of handling missing samples in k-space, it exhibits, however, some disadvantages. First, the validity of the assumption that the gaussian probability distributions involved in this method are adequate for formulating the probability distributions occurred in any MRI image is an issue under question. Second, the fact that Bayesian formulation of the problem treats it as being an optimization problem could lead to inferior reconstruction results. Indeed, as it was discussed above, after the Bayesian formulation of the reconstruction task in MRI, the conjugate gradient method is applied to the corresponding objective function in order to find its optima. Conjugate gradients, which is a local optimization technique, has been invoked here as the optimization procedure of preference since a huge number of variables is actually involved (all N X N image pixels). It is well known, however, that local optimization procedures can usually get stack to some local optima of the objective function, been unable to find the desired global optimum. Their performance depends on the initial values of the design variables. On the other hand, even if global optimization techniques were invoked there would be no guarantee, in the general case, that the global optimum could be reached. Therefore, the optimization formulation of the MRI reconstruction from missing samples cannot ensure the quality of the resulted image by its own, but it depends, instead, on the quality of the initial conditions for the design variables. Third, the fact, again, that the Bayesian reconstruction approach leads to a formulation in terms of an extremely huge optimization problem has as another consequence the need for immense computing power and storage requirements. The above disadvantages worsen things when 3-D Bayesian MRI reconstruction is considered, especially in the case of functional MRI. In this case a lot of slices should be acquired in order to have a 3-D reconstruction and the problem of reducing scan time by omitting scanning trajectories becomes of primary importance.

The previous discussion makes obvious that another more effective methodology for handling the reconstruction problem in the sparse sampled k-space is needed and this is exactly the motivation for the research presented here. The methodology herein suggested is based on the attempt to fill in the missing complex values in k-space from their neighboring complex values. This approach transforms the original problem into an interpolation one in the complex domain. While linear interpolators have already been used in the literature [3-5], the novelty of this paper lies on the fact that it deals with nonlinear interpolation in k-space. The obvious advantages of the interpolation approach compared to the Bayesian formalism are the capability for faster reconstruction since it avoids optimization procedures during reconstruction, the need for less computing power and fewer storage requirements as well as the avoidance of any model assumption about the probability distributions. This last point is ensured because of the application of Artificial Neural Network (ANN) models in the complex domain interpolation task herein involved. The reconstruction results achieved by both supervised architectures of the MLP type and unsupervised ones of the Kohonen type are very promising and very favorably compared to the reconstruction results obtained by traditional interpolation techniques as well as by the simplest "interpolation" procedure, that is by zero-filling the missing samples in k-space.

The organization of this paper is as follows. In section 2 the proposed methodology is illustrated. In section 3 the experimental study exhibiting the comparisons of the various interpolation techniques herein involved in MRI reconstruction is presented and the results obtained are discussed. Finally, section 4 concludes the paper.

2. The Neural Network Approach for Estimating the Missing Samples in K-Space

The proposed interpolation procedure for predicting missing complex values in the k-space from their surroundings is outlined in the following steps.

- The k-space data of an N X N MRI image is raster scanned by a (2M+1) X (2M+1) sliding window containing the associated complex k-space values. The estimation of the complex number in the center of this window from the rest of the complex numbers comprising the sliding window is the goal of the proposed interpolation procedure. Each position of the previously defined sliding window in k-space is, therefore, associated with a desired output pattern comprised of the complex number in k-space corresponding to the window position, and an input pattern comprised of the complex numbers in k-space corresponding to the rest (2M+1) X (2M+1) -1 window points. This scheme is used in the MLP case, while in the Kohonen's Self Organizing Feature Map (SOFM) case there is only an input pattern with (2M+1) X (2M+1) complex number components.
- Each such pattern is then, normalized according to the following procedure. First, the absolute values of the complex numbers in the input pattern are calculated and then, their average absolute value $|z_{aver}|$ is used to normalize all the complex numbers belonging both in the input and the desired output patterns. That is, if z_1 is such a number then this normalization procedure transforms it into the $z_1/|z_{aver}|$. This pair of normalized input and desired output patterns of complex k-space values can be next used in the training procedure of the ANN interpolation architecture. On the other hand, in the case of test patterns we apply the same procedure. That is, the average absolute value $|z_{aver}|$ for the complex numbers of the test input pattern is first calculated and used to normalize them. Afterwards, these normalized complex values $z_i/|z_{aver}|$ feed the ANN interpolation technique to predict the sliding window central normalized complex number $z^{norm}{}_{centre}$. The corresponding unnormalized complex number is simply $z^{norm}{}_{centre} * |z_{aver}|$.
- The next step is the production of training patterns for the ANN interpolators. To this end, we compile a set of representative MRI images as training pictures and their corresponding k-space data. Then, by randomly selecting sliding windows from the associated k-spaces and producing the corresponding input and desired output training pairs of patterns as previously defined, we construct the set of training patterns. The assumption that underlies such an approach of training ANN interpolators is that there are regularities in every sliding window associated k-space data, the same for any MRI image, which can be captured by the ANNs.

Unlike Bayesian reconstruction, however, this can be achieved without any prior assumption for the model of their probability distributions.

- In the sequel, the ANN interpolators are trained using the previously defined learning sets. In the case of the MLP based complex interpolator both input and desired output patterns are involved. Each complex number, component of either an input or an output pattern, is associated with two adjacent neurons of the MLP input or output layer respectively, having its real part assigned to the left neuron of the pair and its imaginary part to the right one. The same assignments for the complex numbers belonging to the input training patterns are met in the case of the Kohonen's SOFM. However, since this is an unsupervised architecture there is no desired output response employed in its training phase. Instead, the SOFM is comprised of a L X P array of output neurons that map the probability distribution of the (2M+1) X (2M+1) complex numbers of any input pattern, preserving the topological conditions of the input pattern space. That is, the training phase of the SOFM attempts to assign every input pattern to a neuron of the map so that the quantization error becomes as small as possible.
- After completion of the above defined training procedure both ANN interpolators can be evaluated by applying them to the sparse k-space data corresponding to a completely unknown set of MRI images. This application involves the following procedure.

1. The (2M+1) X (2M+1) sliding window raster scans the sparse k-space data starting from the center. Its central point position moves along the perimeter of rectangles covering completely the k-space, having as center of gravity the center of the k-space array and having distance from their two adjacent ones of 1 pixel. It can move clockwise or counterclockwise or in both directions. For every position of the sliding window, the corresponding input pattern of (2M+1) X (2M+1) – 1 or (2M+1) X (2M+1) complex numbers is derived following the above described normalization procedure.
2. Subsequently, this normalized pattern feeds the ANN interpolator, either MLP or SOFM. In the case of MLP, the wanted complex number corresponding to the sliding window center is found as $z_{centre} = z_{MLP}^{out} * |z_{aver}|$, where z_{MLP}^{out} is the MLP output and $|z_{aver}|$ the average absolute value of the complex numbers comprising the unnormalized input pattern. In the case of SOFM, for the winning neuron corresponding to the test input pattern, its associated weight vector $\underline{\mathbf{W}}^{win}$ might be considered as a good representative of the cluster of input patterns that correspond to it. Then, the wanted complex number z_{centre} is equal to $z_{centre} = (W^{win}_{x0}, W^{win}_{y0})$, where W^{win}_{x0}, W^{win}_{y0} are the weights corresponding to the central values of the input pattern and the associated central point (x0, y0) of the sliding window. Following this procedure, the unknown complex number that corresponds to the current sliding window position can be interpolated from its neighboring points values.
3. For each rectangle covering the k-space, the previously defined filling in process takes place so that it completely covers its perimeter, only once, in both clockwise and counterclockwise directions. The final missing complex values are estimated as the average of their clockwise and counterclockwise obtained counterparts.

3. Experimental Study

An extensive experimental study has been conducted in order to evaluate the above described ANN interpolation methodology. All the interpolation methods involved have been applied to a large MRI image database which has been downloaded from the Internet, namely, the Whole Brain Atlas http://www.med.harvard.edu/ AANLIB/home.html (copyright © 1995-1999 Keith A. Johnson and J. Alex Becker). There exists the permission that portions of that database might be individually downloaded, copied, and cited for the personal and educational purposes of individuals and organizations in their work, provided that proper attribution and context are given. We have used 3 images, shown in figure 2, for training the ANN interpolators, and 4 images, shown in figures 3-8, for testing them. All these images have 256 by 256 dimensions. The k-space data for these images have been produced by applying the 2D FFT to them. Radial and spiral trajectories have been used to scan the resulted 256 X 256 complex array of k-space data. In the case of radial scanning 4 X 256 = 1024 radial trajectories are needed to completely cover k-space. On the other hand, in the case of spiral scanning 60 spirals are enough for attaining a good image reconstruction. In order to apply the interpolation techniques involved in this study, the k-space has been sparsely sampled using 128 only radial trajectories in the former case and 30 only spiral trajectories in the latter. Regarding the sliding window raster scanning the k-space, the best results were obtained using a 5 X 5 window for the MLP case and a 3 X 3 in the SOFM case.

Concerning ANN architectures, the best results for the MLP based interpolator have been achieved using an architecture of 48 input neurons, 10 hidden ones and 2 output neurons. On the other hand, concerning the SOFM interpolator the best results have been obtained using an architecture of 18 input neurons and 25 X 10 output neurons in the map. These ANN interpolators have been trained using 3600 training patterns. Apart from the neural interpolators there was experimentation using two traditional interpolation techniques, namely, the linear and the cubic one. Moreover, the simplest “interpolation” approach, namely filling in the missing samples in k-space with zeroes and then reconstructing the image, has been invoked. All these methods (2 neural, 2 traditional and the zero-filling based reconstruction) have been implemented in the MATLAB programming language and all simulations have been carried out using the MATLAB programming platform.

Concerning the measures involved to quantitatively compare the performance of the various interpolation techniques, we have employed the usually used Sum of Squared Errors (SSE) between the original MRI image pixel intensities and the corresponding pixel intensities of the reconstructed image. Additionally, another quantitative measure has been used, which expresses performance differences in terms of the RMS error in dB. This is outlined in the following MATLAB code and has been proposed in [5]

```
lambda=(image_recon(:)’*image_orig(:))/(image_recon(:)’
*image_recon(:));
```

```
residu=image_orig-lambda*image_recon;

dB=10*log10((image_orig(:)’*image_orig(:))/(residu(:)’*
residu(:)));
```

The quantitative results obtained by the different interpolation methods involved are outlined in table 1, except for the results of the two traditional interpolation techniques. These latter methods have always given worse results than the zero-filling reconstruction. For instance, for the test image of figure 5 the cubic interpolation gives 2.7E3 for the SSE and 15.02 dB for the comparison with the original image, which are obviously worse than the ones obtained by zero-filling reconstruction. Concerning reconstruction performance qualitative results, they are all shown in figures 3-8. Both quantitative and qualitative results clearly demonstrate the superiority of the proposed ANN interpolation approach in terms of MRI image reconstruction performance.

Test	sampled	zero-filled		Kohonen network		MLP	
Picture	trajectories	SSE	dB	SSE	dB	SSE	dB
tc1 (Fig. 3)	128 radial	3.71E3	15.26	3.57E3	15.55	3.02E3	16.69
tc1 (Fig. 4)	30 spiral	1.61E4	3.76	1.48E4	4.57	9.62E3	8.17
tl4 (Fig. 5)	128 radial	2.49E3	15.51	2.19E3	16.54	1.62E3	18.73
tl4 (Fig. 6)	30 spiral	1.03E4	4.11	9.19E3	5.34	5.72E3	8.6
dg1 (Fig. 7)	128 radial	3.38E3	10.04	2.99E3	10.99	2.24E3	12.94
038 (Fig. 8)	128 radial	2.47E3	14.32	2.1E3	15.65	1.49E3	17.95

Table 1. The quantitative results with regards to reconstruction performance of the various methodologies involved

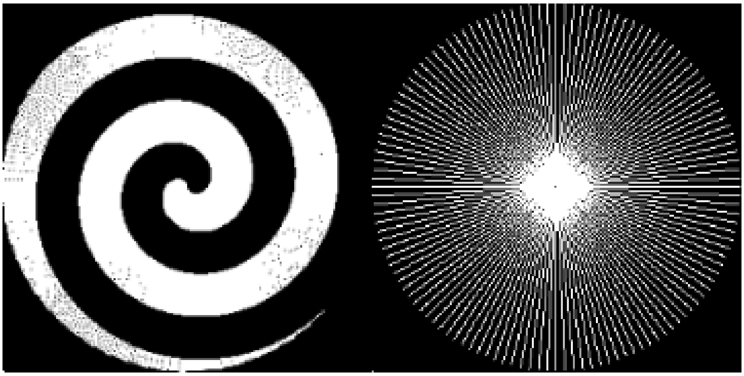

Fig. 1. Spiral (left) and radial (right) scanning trajectories in k-space (white area). For the spiral sampling, out of 60 trajectories covering the complete k-space, the first 30 trajectories are omitted, while for the radial 128 trajectories have been sampled.

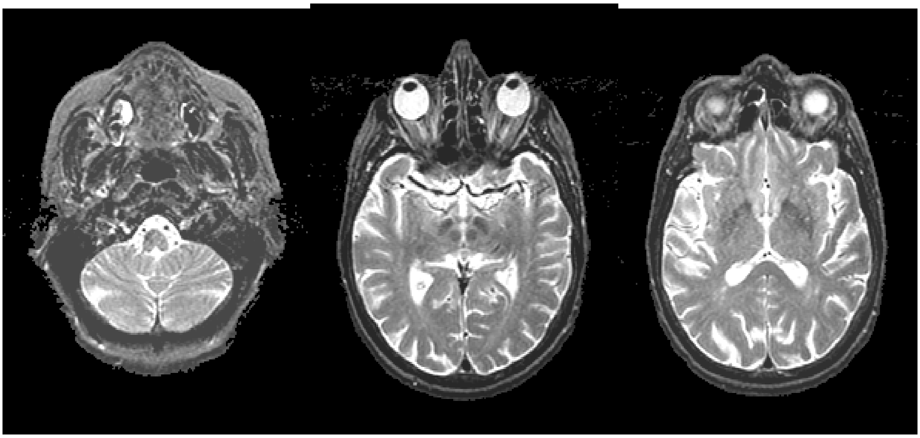

Fig. 2. Training images, normal brain, 3 slices out of the complete database (http://www.med.harvard.edu/AANLIB/cases/caseM/mr1/008.html, 024.html, 028.html)

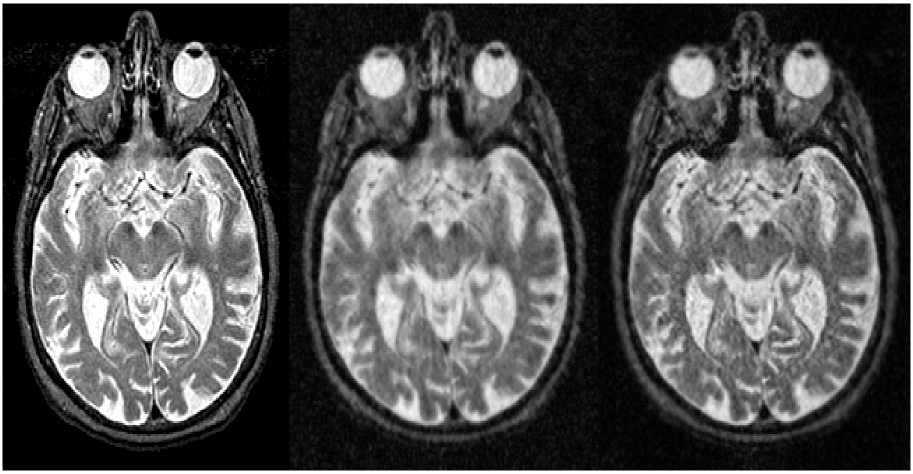

Fig. 3. A Test Image illustrating a brain slice with Alzheimer's disease (http://www.med.harvard.edu/AANLIB/cases/case3/mr1-tc1/020.html), the sparse-sampled k-space (nr=128) –zerofilled image reconstruction and the BP-interpolated image

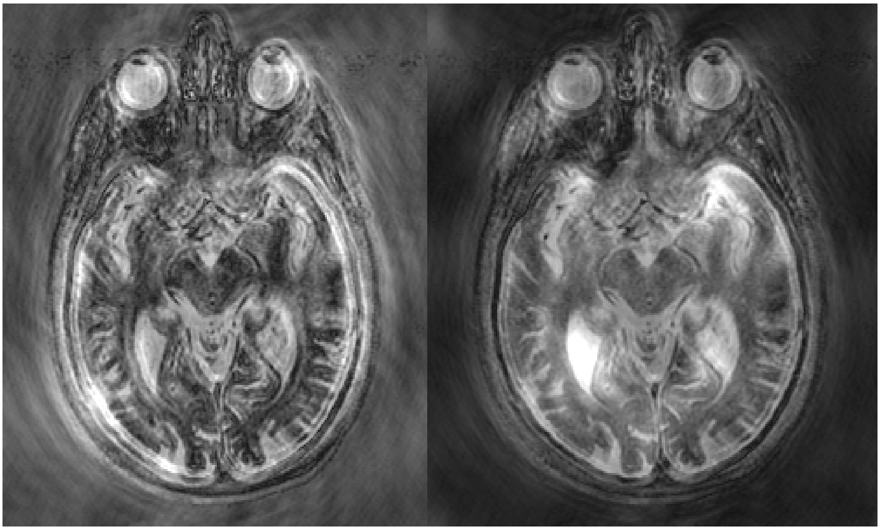

Fig. 4. Same test image, the sparse-sampled on 30 spiral trajectories-zerofilled image reconstruction and the BP-interpolated image

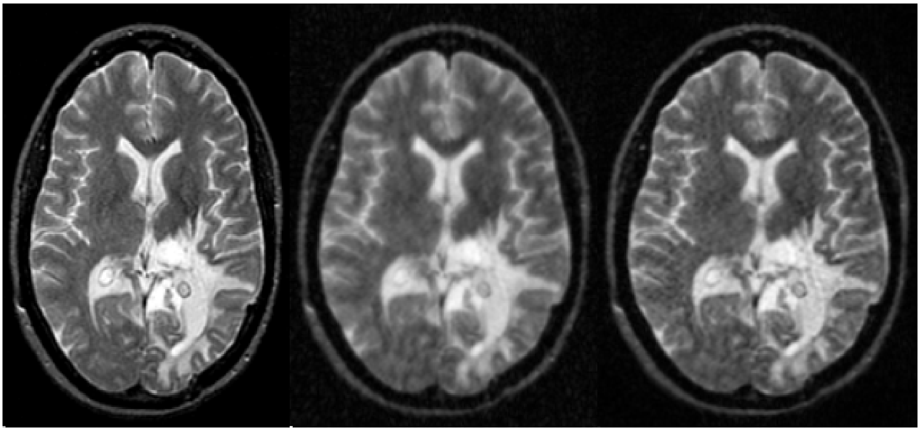

Fig. 5. A Test Image showing a brain with Glioma (brain-tumor)-TlTc-SPECT (http://www.med.harvard.edu/AANLIB/cases/case1/mr1-tl4/029.html), the zerofilled image reconstruction and the BP-interpolated image

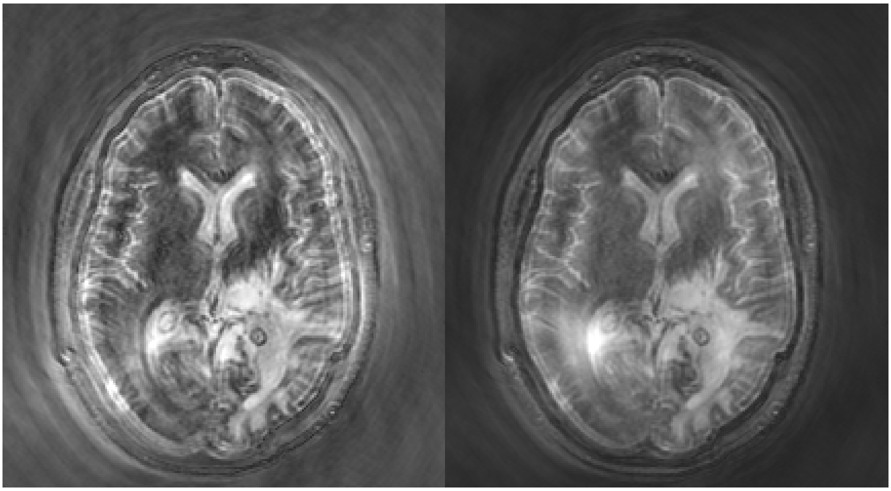

Fig. 6. Same test image-sparse-sampled on 30 spiral trajectories, zerofilled image reconstruction and the BP-interpolated image

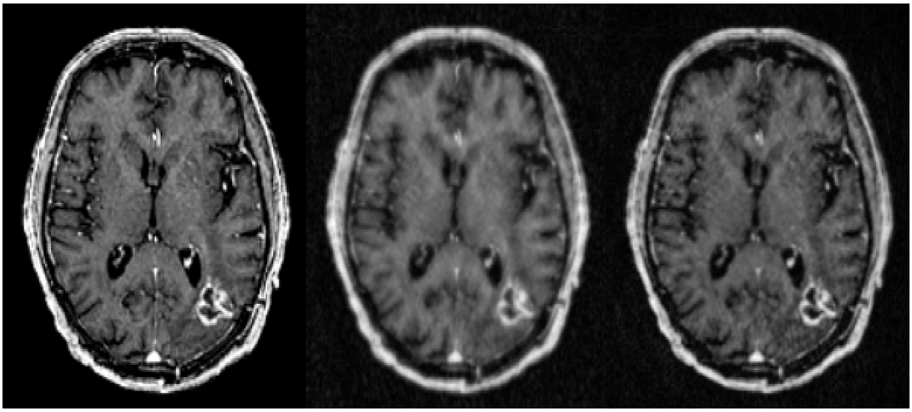

Fig. 7. A Test Image-Glioma (brain-tumor)-FDG-PET (http://www.med.harvard.edu/AANLIB cases/caseSLU/mr1-dg1/060.html, the zerofilled image reconstruction and the BP-interpolated image

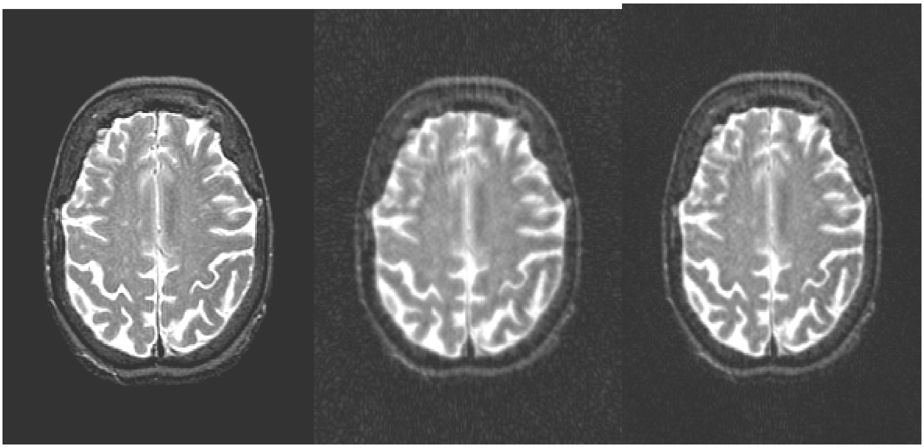

Fig. 8. A Test image showing a normal brain slice 38- (http://www.med.harvard.edu/ AANLIB/cases/caseM/mr1/038.html), the zerofilled image reconstruction and the BP-interpolated image

4. Conclusions and Future Trends

A new methodology has been developed for reconstructing MRI images from sparsely sampled k-space data using MLP and SOFM interpolation for estimating the missing samples. A detailed experimental study on a well organized MRI image database demonstrates that the proposed approach gives very promising results concerning reconstruction performance compared to some traditional interpolation techniques. A comparison with Bayesian MRI reconstruction is under development and the results will be presented in another occasion. What is more interesting, however, is to achieve a combination of these two approaches since ANN interpolation can supply Bayesian reconstruction with a better starting point for the optimization process.

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