

Respiratory Artifact Reduction in MRI using Dynamic Deformation Modeling

H. Knutsson[†] M. Andersson[†] M. Borga[†] L. Wigström[‡]

[†]Medical Informatics
Dept. of Biomedical Engineering

[‡]Clinical Physiology
Dept. of Medicine And Care

Linköping University
<http://www.ami.imt.liu.se>

Abstract

This paper presents a novel magnetic resonance imaging (MRI) reconstruction method that will reconstruct an object correctly despite the presence of respiratory-type motions. The basis for the method is the observation that affine deformations of an object will correspond to a different but unique affine coordinate transform of the Fourier representation (k-space) of the object. The resulting sample points will be irregularly distributed prohibiting the use of standard IFFT to reconstruct the object. The object can however be reconstructed through the use of a weighted regularized pseudo inverse. Short computing times are obtained using a novel fast sequential pseudo inverse algorithm.

1 Introduction

Artifacts caused by respiratory motion during MRI scans is a well known unsolved problem when scanning the thorax. Since all data are not acquired simultaneously, the varying position of for example the chest wall and internal organs during the scan will produce artifacts in the reconstructed images. The k-space is usually scanned line by line. Due to the motion, each line will take samples from the Fourier transform of a slightly differently shaped object than the previous line. The Fourier domain sampling causes the distortion to spread out over the image in a non-trivial fashion. Figure 1 shows a typical example of ghosting in an axial 2D image of the thorax.¹ If not creating ghosting, respiratory motion will contribute to a considerable blurring of the image data.

¹This image is from G.A. Wright: *Magnetic Resonance Imaging: From Basic Physics to Imaging Principles* (www.sunnybrook.utoronto.ca:8080/~gawright/mrphys/icip_sep29.html)

1.1 Motion compensation

Several different methods for reducing respiratory motion artifacts have been proposed. Most of these are prospective methods that controls the acquisition directly on-line. The most straight-forward technique is to ask the patient to hold his/her breath. For relatively healthy patients this works when the scan time is less than 30 seconds. Another prospective method is respiratory gating, which allows data acquisition only in a predefined time window in the respiratory cycle. While this ensures that all image data is acquired in (almost) the same state, it will prolong the scan time. Especially in 3D imaging this is usually not acceptable, since the scan time is long as it is.



Figure 1: Example of severe ghosting effects in an MR image.

Available on most commercially available MRI systems are also respiratory motion compensation techniques based on on-line controlled ordering of the k-space acquisition. If the field-of-view (FOV) is made large, the ghosting can often be moved outside the region of interest. However, having to increase the FOV prolongs the

scan time, and since the respiratory motion pattern is not known in advance, an optimal choice of acquisition order can not be made.

Retrospective methods for compensation of respiratory motion have not been used to a large extent. Acquisition of all image data in every possible respiratory position makes it possible to retrospectively reconstruct an image in any desired respiratory phase [2]. This can be of interest for a better understanding of how respiration influences cardiovascular dynamics, but for clinical use the extremely long acquisition time is not acceptable.

A completely retrospective technique was developed by Manduca et al, at the Mayo clinic [4]. Their approach relies only on changing the phase values in the Fourier domain, and can in this way only handle translation. The geometric changes due to respiration is, however, a combination of translation, scaling (compression/expansion) and rotation. An affine transformation including these modes of motion is required in order to adequately model the motion.

Other methods with some relation to the present work are described in [1] and [5].

2 A method for retrospective motion insensitive reconstruction

In this section a method for retrospective motion artifact reduction based on an affine motion model is presented. The method handles a slightly limited affine motion case. However, it still captures the main deformations due to respiration and the gain is that computing times are kept comfortable, even for large images.

Affine transformations

Let $F(\mathbf{u})$ be the Fourier transform of $f(\mathbf{x})$. If $f(\mathbf{x})$ is subject to an affine transform, defined by a matrix \mathbf{A} and a translation vector \mathbf{b} , such that:

$$g(\mathbf{x}) = f(\mathbf{A}\mathbf{x} + \mathbf{b}) \quad (1)$$

then the the Fourier transform of $g(\mathbf{x})$ is given by (see for example [3]):

$$G(\mathbf{u}) = \det(\mathbf{A})^{-1} F\left([\mathbf{A}^{-1}]^T \mathbf{u}\right) e^{i\mathbf{u}^T \mathbf{b}} \quad (2)$$

This implies that, as long as a large part of the object deformation can be modeled as an affine transformation, it is possible to make a reasonable estimate of the k-space displacement and phase change for a k-space sample at any given time instant. An example of a true sample distribution is shown in the upper part of fig. 2. Assuming a uniform distribution as is indirectly

done when inverse FFT is used for reconstruction, will naturally lead to the introduction of various types of disturbances.

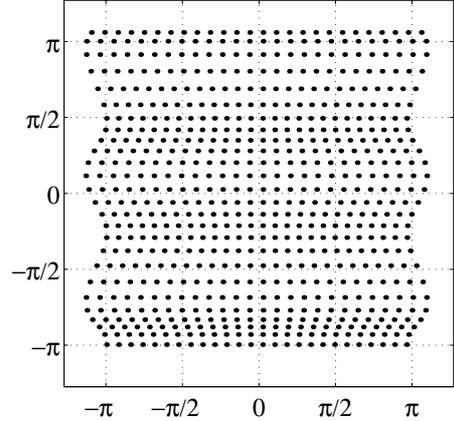


Figure 2: True location of the samples in the Fourier domain due to patient motion.

Pseudo-inverse reconstruction

A much more reasonable reconstruction approach is to use a regularized and weighted pseudo inverse. The principle of the method is described by:

$$f = [\mathbf{B}^T \mathbf{W} \mathbf{B} + \varepsilon \mathbf{I}]^{-1} \mathbf{B}^T \mathbf{W} F \quad (3)$$

Where: \mathbf{B} is the transform matrix between the image/volume and the obtained displaced k-space samples, see figure 3. \mathbf{W} is a diagonal weighting matrix that contain a Fourier weighting function $w(\mathbf{u})$ designed to give a suitable transform space metric (normally tapering off towards higher frequencies). ε corresponds to an estimated k-space noise level.

The size of the transform matrix \mathbf{B} is equal to the number of samples in k-space \times the number of samples in the reconstructed body, $f(\mathbf{x})$.

Efficient algorithm

A drawback with the direct approach in eq. 3 is the high computational effort required, rapidly increasing with matrix size. However, restricting the deformation model to a subset of affine transformation will allow a *sequential* approach that is orders of magnitude more efficient. This model assumes that: a) The deformation in the first direction attended to is independent of the other dimensions and varies only with time. and b) The deformation in the second dimension attended to is assumed to be independent of the remaining dimension.

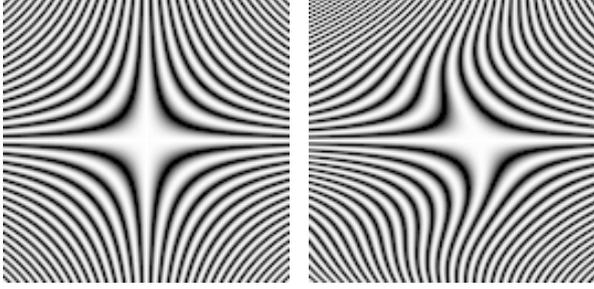


Figure 3: Real part of transform matrices. Left: the conventional \mathbf{B} matrix. Right: The motion compensated \mathbf{B} matrix.

It is felt that this model will be sufficient to capture the main deformations occurring in many cases, e.g. respiration induced deformations. The preliminary studies in section 3 indicate the potential of this method. In the 2D case the sequential reconstruction is obtained using the following algorithm.

1. The method is here first applied in the x -dimension. Calculate an intermediate result $F_f(u_y, x)$ by performing a row by row adaptively scaled inverse Fourier transform along the x -axis.

$$F_f(u_y, x) = \sum_{u_x} F(u_x, u_y) e^{i s(t) u_x (x - b_x(t))} \quad (4)$$

Where: $s(t)$ is the estimated x -scale factor at x -scan time t .

Equation 4 assumes, in addition, that the time it takes to perform one x -scan is short, i.e. the deformation of the object during that time is insignificant. This condition normally holds and is in practise no restriction.

2. Perform a regularized weighted pseudo inverse for each column.

$$f = [\mathbf{B}_y^T \mathbf{W} \mathbf{B}_y + \varepsilon \mathbf{I}]^{-1} \mathbf{B}_y^T \mathbf{W} F_f \quad (5)$$

Where: F_f is a matrix containing all entries of $F_f(u_y, x)$. \mathbf{B}_y is a transform matrix obtained from the y -positions of the obtained k -space samples. The size of \mathbf{B}_y is equal to the number of y -positions in k -space \times the height of the reconstructed image.

The limited size of the equation system implies that the algorithm can be used interactively on a conventional desktop computer, even for large images. The results were computed on a Sun ultra10, 440Mhz with 768Mb of memory installed using Matlab. The time to compute the sequential reconstruction on a 255×255 image from an equal amount of samples in the k -space is in this experimental environment 36 seconds.

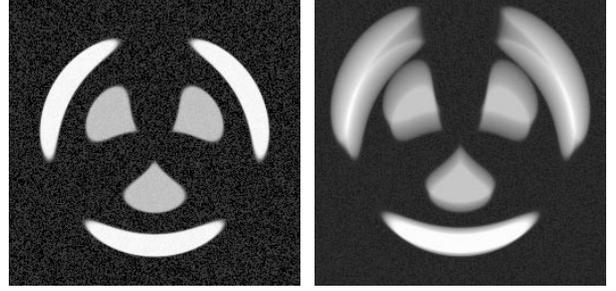


Figure 4: Left: Two samples of the 255 frames long sequence. Image size 255×255 pixels. Right: A projection of all frames to illustrate the magnitude of the motion.

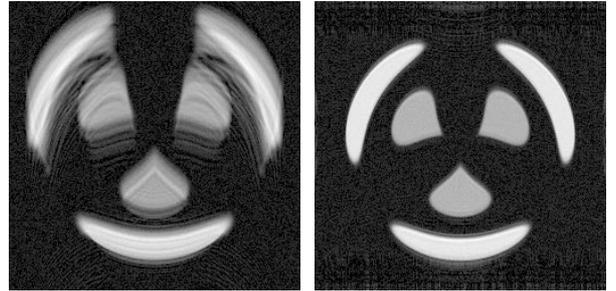


Figure 5: Left: Reconstruction by using conventional IFFT. Right: Reconstruction using motion adaptive pseudo-inverse.

3 Preliminary results

For the initial tests a synthetic image sequence was created. The purpose is to simulate the motion of the chest when the patient breaths during the image acquisition. Two (non consecutive) frames of the sequence are shown in the upper part of fig. 4. The 255 frames contain some (uncorrelated) noise and the size is 255×255 pixels. The lower part of fig. 4 contains a projection of all frames over time and illustrates the motion magnitude in the sequence. The synthetic patient breaths 2.7 times during the image acquisition. The motion present in the x -direction (horizontal) is a scaling that depends of time and y -position. The motion in the y -direction (vertical) consists of a time dependent scaling (around the image center) and a (time dependent) translation which makes the bottom of the image to be fix.

From each frame in the image sequence a 255 samples long x -line in the k -space $F(u_x, u_y)$ is computed. The efficient sequential approach described in the previous section was then used to reconstruct the original image ($\mathbf{W}_{diag} \propto (u_x^2 + u_y^2)^{-1/2}$). Figure 5 (left) shows a conventional reconstruction and figure 5 (right) shows the result using the algorithm in section 2. The ghosting in the y -direction is removed and the resolution and detail is increased.

Error measures

In a simulated environment it is straight forward to estimate an error measure for the reconstructed object. An objective error E based on the correlation between the reconstruction f and a reference frame, of the original sequence f_{ref} , see fig. 4, can be calculated as:

$$E = \sqrt{1 - (\text{corr}[f, f_{ref}])^2} \quad (6)$$

Figure 6 shows the correlation error E computed using different scale-factors $s(t)$ in eq. 4. The true scale change is multiplied by a factor in the range of $[0.5-1.5]$ and the corresponding error is plotted as the dashed line.

The purpose of computing an error measure is twofold. First it enables a quality estimate of the reconstructed image and secondly it provide the means for further tuning of the motion parameters. For clinical use the correlation error can obviously not be used but a useful error measure can be attained in the following way. First segment the volume in one object region, f_1 , and one non-object region, f_2 . Then calculate the errors inside and outside the object and add them. The estimated error inside the object relies on the fact that all image values should be real (implying a full k-space scan). The contribution to the error of a given voxel inside the object will be proportional to the magnitude with a multiplicative factor given by $\sin(\alpha/2)$, where α is the complex angle. This means that the worst case is a negative value giving a factor of unity. An imaginary value yields a factor of 0.707. The error outside the object is simply estimated as the sum of all volume magnitudes as the correct value is known to be zero. Adding the two errors gives the estimated total error, H .

$$H = \sum_{inside} | \text{im}(\sqrt{|f_1|} f_1) | + \sum_{outside} |f_2| \quad (7)$$

The similarity between the two error estimates, displayed in fig. 6 shows that minimizing H will correspond to an approximate minimization of the objective measure E . It is reasonable to assume that, after making an initial estimation of object deformation based on, for example, respiratory indicators, a simple gradient descent type optimization algorithm can be used to find an approximate minimum. Further, this error estimation principle makes it possible to interactively increase the quality in regions of the image that is of special interest to the physician.

4 Summary and Conclusions

We have presented a novel technique that retrospectively compensates for the induced corruption of the

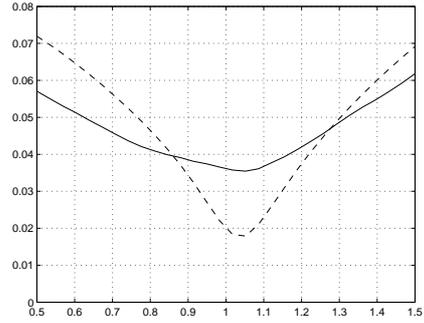


Figure 6: The correlation based error E (dashed) and estimated error H (solid)

raw MR data caused by respiratory motion. The method is based on the fact that affine deformations of an object correspond to a different but unique affine coordinate transform and phase shift of the object. By estimating the deformation at each time instant and calculating the induced Fourier space sample displacements a much more accurate Fourier representation is found. The samples will be irregularly distributed prohibiting the use of a standard IFFT and a weighted regularized pseudo inverse is used to reconstruct the object.

The results show that the proposed method produces results that are superior to standard techniques and is robust with respect to errors in the estimated motion. Computing times have been brought to a comfortable level due to the development of a new fast sequential pseudo inverse algorithm.

References

- [1] R. Van de Walle, H. H. Barrett, K. J. Myers, M. I. Altbach, B. Desplanques, A. F. Gmitro, J. Cornelis, and I. Lemahieu. Reconstruction of MR images from data acquired on a general nonregular grid by pseudoinverse calculation. *IEEE Transactions on Medical Imaging*, 19(12):1160–1166, December 2000.
- [2] J. O. Fredrickson, H. Wegmuller, R. J. Herfkens, and N. J. Pelc. Simultaneous temporal resolution of cardiac and respiratory motion in MR imaging. *Radiology*, 195(1), 1995.
- [3] G. H. Granlund and H. Knutsson. *Signal Processing for Computer Vision*. Kluwer Academic Publishers, 1995. ISBN 0-7923-9530-1.
- [4] A. Manduca, K. P. McGee, E. B. Welch, J.P. Felmlee, R. C. Grimm, and R. L. Ehman. Autocorrection in MR imaging: adaptive motion correction without navigator echoes. *Radiology*, 215(3):904–9, 2000.
- [5] P. Munger, G. R. Crelier, T. M. Peters, and G. B. Pike. An inverse approach to the correction of distortion in EPI images. *IEEE Transactions on Medical Imaging*, 19(7):681–689, July 2000.