Respiratory Reordered UNFOLD Perfusion Imaging

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Purpose: To propose a respiratory reordered UNFOLD (RR-UNFOLD) imaging sequence to significantly reduce the amount of k-space data required for first-pass MR myocardial perfusion imaging.

Materials and Methods: Rapid acquisition of high-resolution imaging data is essential to detailed quantitative analysis of first-pass myocardial perfusion. Existing MR sequences have explored the full capacity of the imaging hardware to reduce the acquisition window within each cardiac cycle while maintaining the desired spatial resolution. Further improvement in perfusion imaging will require a more efficient use of the information content of the k-space data. The method uses prospective diaphragmatic navigator echoes to ensure that temporal filtering of UNFOLD is carried out on a series of images that are spatially registered. An adaptive real-time rebinning algorithm is developed for the creation of static image subseries related to different levels of respiratory motion. Issues concerning the temporal smoothing of tracer kinetic signals are discussed, and a solution based on oversampling of the central k-space is provided. The method is assessed in 10 normal subjects without the administration of contrast agent, and further validated by administration of Gd-DTPA in 10 patients at rest.

Results: The results of this study show that RR-UNFOLD significantly extends the applicability of UNFOLD to perfusion imaging, which yields a 40% reduction in image artifact when the same amount of k-space information is used.

Conclusion: The scan efficiency achieved can be used in combination with MR hardware improvements for extending the three-dimensional spatial coverage and shortening the data acquisition window to provide detailed information on regional myocardial perfusion abnormalities.

Key Words: myocardial perfusion imaging; UNFOLD; navigator echoes; respiratory encode reordering; adaptive imaging; respiratory motion correction


EARLY DIAGNOSIS and localization of myocardial perfusion defects is an important step in the treatment of coronary artery disease. In recent years, the development of myocardial perfusion MR has extended the role of cardiovascular MR (CMR) in the evaluation of ischemic heart disease beyond situations in which gross myocardial changes, such as acute infarction or scarring, have already occurred. The ability to noninvasively evaluate cardiac perfusion abnormalities before pathologic effects occur, or as follow-up to therapy, is important for the management of patients with coronary artery disease. Early reperfusion of ischemic myocardium has been shown to have a positive reversal effect on the ischemic myocardium that reduces mortality and morbidity. The differentiation of ischemic but viable myocardium from infarcted regions requires a detailed global quantitative assessment and modeling of myocardial perfusion characteristics. CMR permits the acquisition of myocardial perfusion images with relatively high spatial resolution, and thus allows the transmural extent of myocardial ischemia to be determined. Thus far, the most common techniques used to assess myocardial perfusion based on first-pass imaging with CMR include turbo fast low-angle shot (turboFLASH) imaging (1–3), fast imaging with steady precession (trueFISP) (4) and echo-planar imaging (EPI) (5,6). Quantitative results have been achieved in animal studies with intravascular agents (polylysine-Gd-DTPA) as a macromolecular blood pool marker (7) and conventional extracellular agents (Gd-DTPA) for human studies (1.8–10). While limited multislice two-dimensional CMR perfusion studies are being increasingly used in a clinical setting to quantify gross ischemic burden, research is now directed toward complete three-dimensional coverage of the myocardium for accurate localization of the extent of possible defects. In three-dimensional myocardial perfusion imaging, one must acquire a complete volumetric data set for each cardiac cycle in order to study the first pass of the contrast bolus. This normally requires a relatively large acquisition window within each cardiac cycle to ensure a comprehensive coverage of the myocardium and reasonably high resolution of the images. With multislice imaging, long-axis cardiac motion during this large acquisition window can cause the myocardium, which is imaged in different cross-sections, to be misregistered (i.e., while some part of the myocardium may be imaged more than once, other parts may be missed completely). It is difficult to correct for this type of misregistration using postprocessing techniques. New imaging sequences, such as fast gradient echo with echo train readout...
(FGRE-ET) (11,12), have significantly reduced the acquisition window while maintaining the desired spatial resolution. Further improvements in perfusion imaging will require the application of parallel imaging techniques (13) or making full use of the information content of the \( k \)-space data. View-sharing is a common approach that involves the use of the similarity or redundancy in \( k \)-lines between images. Phase-encode lines, which through a Fourier transform represent image data that remain static across time, can be acquired once and shared between multiple images. Techniques such as block regional interpolation scheme for \( k \)-space (BRISK) (14) and broad-use linear acquisition speed-up technique (BLAST) (15) potentially can be adapted for this purpose.

More recently, unaliasing by Fourier encoding the overlaps using the temporal dimension (UNFOLD) has been used for perfusion imaging (16,17). This technique attempts to encode spatial information into redundant regions of \( k \)-space. Initial experience has shown that this technique has promising practical value for breath-hold myocardial perfusion imaging because it doubles the scan efficiency, which can be used to either increase the spatial resolution/coverage or decrease the acquisition window. For perfusion imaging with free breathing, however, the technique suffers from significant motion artifacts and blurring due to respiratory-induced motion. It is generally not possible for patients to maintain a breath-hold for the duration of the perfusion scan, which typically lasts for about 50–60 heartbeats. In addition, prolonged breath-holding may alter the physiological response, which can affect the perfusion index quantification. Therefore, extensive improvement of the current UNFOLD framework is necessary before the technique can be of practical use for myocardial perfusion imaging. The purpose of this paper is to present a new prospective \( k \)-space reordering method for UNFOLD to eliminate respiratory-induced motion artifact. The method uses real-time diaphragm navigator echoes (18), similar to those used in CMR coronary angiography (19–21), to ensure that temporal filtering of UNFOLD is carried out on a series of images that are spatially registered. The method requires a prospective rebinning algorithm for the creation of multiple image subseries related to different levels of respiratory motion. Issues concerning the temporal smoothing of tracer kinetic signals are discussed, and a solution based on oversampling of the central \( k \)-space is provided. The strength of the technique is demonstrated with a detailed error analysis of 10 patients and 10 normal volunteers with UNFOLD and RR-UNFOLD simulated post-scan from the complete \( k \)-space data.

**MATERIALS AND METHODS**

**UNFOLD**

The principle of UNFOLD is based on temporal filtering to resolve spatial aliasing within the field of view (FOV) caused by a reduction in the density of \( k \)-space sampling. The method assumes that the dynamic structure under consideration is slowly varying throughout the imaging series, and therefore carries a low-temporal-frequency component (16). A reduction in the density of the \( k \)-space sampling reduces the distance between the central peaks of the point spread function (PSF), resulting in aliased reconstructions of the PSF image overlapping onto the central FOV. By shifting the sampling function in the phase-encode direction through time, we introduce a linear phase shift in the PSF. This has the effect of altering the phase through time of all but the central peak of the PSF, and introducing a temporal frequency phase modulation, effectively labeling the overlapping reconstructions. With this shift in the temporal-frequency spectrum, we are able to distinguish the central replica of the object from its overlapping replicas with the use of bandpass filters in the temporal-frequency domain. In the case in which the sampling function is shifted by half of its phase-encode resolution at each time-frame, we modulate the signal of the overlapping component by the Nyquist frequency while the central replica is unchanged. We achieve separation or “unfolding” by filtering out the extra information contained at each pixel location in the temporal Fourier domain before performing the inverse Fourier transform to reconstruct the image series with the overlapping component removed. A twofold reduction in the sampling function equates to a shift in the phase-encode direction by half a line for each image acquisition, which is tantamount to the shifting of one phase-encode line for a complete \( k \)-space acquisition in which alternate lines are obtained. We relate this to the full \( k \)-space acquisition by describing it as the acquisition of odd or even phase-encode lines.

The use of UNFOLD for myocardial perfusion imaging currently presents two major problems. First, the transit of the contrast bolus within the blood pool at the up-slope of the contrast intake is rapid, which can result in sharp signal intensity changes. Second, respiratory-induced cardiac deformation between cardiac cycles can be significant. Both of these introduce high-temporal-frequency components, and thus compromise the basic condition for UNFOLD to be effective. The associated artifact is normally manifested as an attenuation of the contrast bolus signal and aliased edges from the chest wall, as well as borders between the blood pool and myocardium. It is therefore essential to eliminate respiratory motion and restore tracer kinetics to perform UNFOLD for myocardial perfusion studies.

**Respiratory Reordered UNFOLD (RR-UNFOLD)**

The main steps of RR-UNFOLD involve the use of prospective diaphragmatic navigator echoes to split perfusion image series acquired for each cardiac cycle into different subseries (bins) so that within each bin the anatomical structures are spatially static. The method can be used for single- or multislice imaging, and images acquired within the same cardiac cycle are treated as a single \( k \)-space data set during the respiratory binning process. The only temporal change within the subseries is a varying contrast uptake among different anatomical regions. For each bin, a standard UNFOLD \( k \)-space acquisition is employed whereby, with twofold speed-up, alternating odd/even \( k \)-line coverage is used
for successive temporal frames. For the first acquisition cycle, odd lines are obtained and inserted into a respiratory bin. Subsequently, depending on the respiratory navigator position, the associated \( k \)-space data are assigned to an appropriate respiratory bin. As the data collection progresses, the proposed technique acquires data sets with odd/even \( k \)-space coverage dictated by the RR-UNFOLD algorithm, and assigns them to the appropriate respiratory bins. There is no limit on how many images should be acquired for each bin, as the data collection process is prospective. This process is illustrated in Fig. 1.

Figure 2 schematically illustrates how this algorithm is applied with the use of a diaphragm navigator trace in which five respiratory bins are used to cover the entire respiratory range. It also demonstrates how different bins are created as time progresses. One detail of note is that when a new bin is created, the first image is chosen to be in sequence (in terms of odd/even \( k \)-line coverage) with the previous image, regardless of respiratory position. For example, when bin 2 was first created, the first image used odd \( k \)-line coverage since the previous acquisition was for bin 1 and it used even \( k \)-line coverage. This is potentially useful for dealing with bins with orphan frames (single frame within bin) during subsequent reconstruction.

With the above data acquisition scheme, it is not always possible to guarantee that each bin will contain the same number of odd/even \( k \)-space pairs for UNFOLD reconstruction. Although it is possible to use prescan navigator echoes to obtain the general statistics of the respiratory pattern and the associated respiratory range so that the derived histogram can be used to equally distribute the raw \( k \)-space data among different bins, it is not practical in patient studies since the administration of Gd-DTPA and Adenosine for pharmacological stress can significantly alter the respiratory patterns of the patient during data acquisition. In this study, a fixed respiratory window size was used to dynamically create all the necessary bins used for RR-UNFOLD, as indicated in Fig. 1. A typical respiratory window size is in the range of 5 mm, and with this approach the method is immune to respiratory drifts since new bins are created on the fly when necessary.

Image Series Reconstruction After Rebinning

The image series created by the above rebinning process cannot be used directly for reconstruction because nonuniform breathing patterns can result in bins with too few images for UNFOLD reconstruction. The number of bins created depends on the respiratory range of the subject during acquisition, and the size of the window for each bin. Because of the way in which UNFOLD is implemented, certain restrictions are imposed on the contents of each bin (i.e., each bin must contain at least four images because fewer than this will make it impossible to separate the aliased image from the original image in the temporal-frequency domain, since we are

![Diagram](image-url)
In addition, because of the way in which Fourier temporal filtering is used, we must have an even number of images within each bin. To correct for these problems, we supplement each bin with additional frames before applying the UNFOLD method. Since all bins are created dynamically during acquisition, there are four possible cases that must be considered. The basic steps involved in the proposed method are shown in Fig. 3.

For example, when there is only one frame in the bin, images from the closest navigator position that are in odd/even sequence are appended to the bin. Further processing is then applied to ensure that the bin with padding has a minimum of four images with all of the odd/even acquisitions paired before conventional UNFOLD reconstruction is used. When there are only two images in the bin, the existing data in the bin are duplicated before reconstruction. The third case in Fig. 3 deals with situations in which there are an odd number of frames within the bin. In this case, the penultimate image is copied as the last image to complete the odd/even sequence. Finally, if none of the above applies, conventional UNFOLD reconstruction is applied directly.

The purpose of this postprocessing step is to increase the contents of a bin to a suitable size for the successful application of UNFOLD. This is achieved either by reusing the current frames within the bin, or recruiting frames from neighboring bins. The frames recruited must adhere to the required phase-shifting pattern selected during the acquisition (in our case, odd and even phase-encode lines). From this, we keep the reconstructions for the frames originally contained within the bin and add them to the final series, while those from additional “borrowed” frames are discarded. In this way, we are able to optimize the result of the UNFOLD procedure for each bin by making use of the extra information we have from the full series.

**Image Acquisition**

To study in detail the effectiveness of the reordering scheme for motion artifact removal, and the robustness of the rebinning algorithm for free-breathing perfusion imaging, we applied a trueFISP perfusion sequence to 10 normal subjects (age = 24 ± 3 years) and 10 patients (age = 54 ± 18 years) with clinical referrals for late gadolinium myocardial viability assessment with written consent. In each cardiac cycle, the navigator column was formed immediately before the trueFISP image by the intersection of 90° and 180° 10-mm-thick slice-selective RF pulses, avoiding the heart, and posi-

**Figure 3.** A schematic diagram showing all the processing steps involved in preprocessing the k-space data within each bin before UNFOLD reconstruction is applied.

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**Restoration of the Tracer Kinetic Signal**

By splitting up the image series into spatially registered series, respiratory motion-induced artifact can be eliminated in the reconstructed images. However, UNFOLD works by eliminating temporal changes in pixel intensity at the Nyquist frequency, which has the effect of smoothing out sharp signal intensity changes between adjacent images within each bin. With respiratory reordering, this smoothing effect is amplified for each bin, since successive images are acquired with the same respiratory position but are not temporally immediately adjacent to each other. This is especially pronounced during contrast uptake, since by reordering we have effectively introduced sharper intensity changes. To reintroduce the correct intensities within the image, extra central phase-encode \( k \)-lines are acquired to reintroduce the low-frequency spatial intensity information. While the outer \( k \)-space lines contain the high-spatial-frequency information, such as edges and noise, the central lines predominantly determine the low-spatial-frequency information, such as regions of intensity, and are therefore highly significant in representing the contrast agent present in the blood pool and myocardium. During the acquisition, \( k \)-space is filled with alternate lines in the phase-encode direction for the outer region, and full coverage in the central region. This is equivalent to acquiring extra central phase-encode lines to complete the subsampled coverage in the central region. This additional sampling can be substituted into the \( k \)-space series after the application of RR-UNFOLD to correct for excessive temporal smoothing due to out-of-sequence UNFOLD reconstruction.
tioned along the head-foot direction through the dome of the diaphragm. For navigator echoes, a frequency-encoded readout of 256 points was used to cover a 400-mm range, which was then interpolated to 1-mm resolution during reconstruction for display and edge position measurement.

For each subject, images covering 50 cardiac cycles were acquired. For each cardiac cycle, the navigator was followed by complete k-space coverage of single-slice trueFISP imaging, which, to avoid cardiac motion, was run as late as possible in the cardiac cycle (typically starting about 400–500 msec after the R-wave, depending on the patient’s R-R interval and variability). The total image duration was 260 msec from the start of the nonselective saturation pulse to the end of the single-shot trueFISP sequence. Since Gd-DTPA was not used in the normal volunteers, the saturation pulse was turned off. Other imaging parameters included a 140-msec saturation recovery delay, 0.1 mmol/kg Gd-DTPA dose injected at ~3 mL/sec followed by a 10-mL saline flush, 10-mm slice, 40–60° flip angle (SAR limited), 370 mm (FE) × 288 mm (PE) FOV (both scaled up sometimes for bigger patients), 144 (FE) × 112 (PE) uninterpolated unfiltered pixels in the image, full k-space coverage in linear order over ky vs. time, and 2.2-msec repeat time between the trueFISP RF pulses. All images were acquired on a SIEMENS 1.5T Sonata scanner with a peak gradient strength of 40 mT/m and peak slew rate of 200 mT/m/msec. The full k-space data were stored, and subsequently phase-encode lines were zero-filled to simulate the UNFOLD and RR-UNFOLD acquisition.

Error Analysis

Validation of the proposed technique was performed in two stages. A detailed study of the technique on 10 normal subjects without the administration of contrast agent allowed for the assessment of RR-UNFOLD in the removal of motion artifact. Following this, the method was applied to 10 patients for further assessment of the quantitative errors associated with perfusion index calculation under normal CMR perfusion settings. The aim of the patient study was to determine the effects of the changing image intensity through time on the success of RR-UNFOLD. By using full k-space coverage in the acquisition stage, we were also able to determine the optimum number of extra central k-lines required to maintain the contrast agent intensity through time. For quantifying image artifact, the image series reconstructed with full k-space encoding was used as a gold standard, and the sum of the squared subtraction error was calculated for the different reconstruction methods used.

RESULTS

Figure 4 illustrates the image artifact introduced by applying the original UNFOLD and the proposed RR-UNFOLD methods (with and without intensity correction) to a perfusion sequence. It is evident that with UNFOLD, significant motion blurring and movement artifacts are present. Before the restoration of the tracer kinetic signal, the proposed RR-UNFOLD method eliminates motion artifact and restricts the difference between the reconstructed images and those with fully encoded data to temporal intensity attenuation only. This attenuation can be corrected for by the use of extra central k-lines. This is demonstrated in Fig. 5, where signal intensity curves from regions within the blood pool and myocardium are provided to illustrate the effectiveness of the proposed intensity correction method. It is evident that by using extra central k-lines with RR-UNFOLD, the reconstructed perfusion image series is very close to the result obtained with full k-space encoding. In the examples shown in Fig. 5, only six extra central k-lines were used, which represents a 45% reduction in imaging acquisition time.

To obtain a more quantitative assessment of the errors introduced by the proposed RR-UNFOLD technique, we conducted the following experiments to analyze the effect of the window width of each bin and the number of extra k-lines used for RR-UNFOLD reconstruction: Figure 6 illustrates the amount of reduction in image artifact with RR-UNFOLD compared to UNFOLD when different window sizes (bin width) were used during data acquisition. To make the comparison fair, the extra central k-lines were also used for UNFOLD reconstruction, and the ratio of image artifact between the two was used for Fig. 6a and b. For normal volunteers with no Gd-DTPA injection, the amount of image artifact mainly reflects the effectiveness of the binning algorithm for respiratory motion correction, whereas for patients, this is associated with the combined effect of motion and contrast uptake restoration. As expected, smaller respiratory windows are advantageous for motion correction, whereas for normal perfusion sequences in the presence of Gd-DTPA bolus, a window size of 5 mm is optimal. Overall, the average image artifact was reduced to 60% of the UNFOLD technique when the same number of k-space encoding lines were used. This reduction is significant for quantifying subtle perfusion defects in clinical applications.

The graph in Fig. 7 illustrates the reduction in image artifact with RR-UNFOLD when different numbers of central k-lines, ranging from 1 to 20, were used to reconstruct the data sets for the 10 patients studied. For this analysis, the navigator window size used for each bin was fixed at 5 mm. As before, all values provided are represented as the amount of artifact reduction achieved with RR-UNFOLD compared to normal UNFOLD. It is evident that the error reduces rapidly with the first five extra lines, and after this point the reduction in image artifact is marginal. A good compromise between image quality and scan efficiency is to use six extra central lines for the present imaging sequence, with which the artifact is reduced to 30% of the normal UNFOLD method.

To help relate the above image artifact ratio to the actual improvement in the visual quality of the reconstructed images, Fig. 4 provides an example image series obtained by using the optimum parameter settings determined above (i.e., the navigator window size and the number of extra central k-lines were set to be 5 mm and six, respectively). Four frames from a perfusion
image series are shown for one of the patients studied. Each frame was reconstructed using five different methods, with the respective subtraction images demonstrating the difference between the original image and the reconstruction results. It can be seen that UNFOLD introduces a large amount of spatial motion artifact even with the addition of the six extra central k-lines. While RR-UNFOLD almost entirely eliminates this edge artifact, it suffers from low-frequency image intensity artifact. With the use of RR-UNFOLD with the additional six extra central k-lines, we are able to eliminate both types of artifact from the final reduced k-space reconstruction. This acquisition gives a 45% saving in k-space coverage, with an average reduction in artifact of 72% ± 8% over the UNFOLD method.

Finally, the effect of RR-UNFOLD on the accuracy of the derived perfusion index was analyzed for the 10 patients studied. We analyzed the image series using CMRtools (Imperial College, London, UK), and a model-based approach based on Fermi deconvolution (9) was used to fit the signal time course curves. Six transmural regions of interest (ROIs) were selected in addition to the blood pool from the short-axis slice of the myocardium. The image series full k-space acquisition was then automatically aligned with image registration to correct for rigid body motion. Manual adjustment was applied when necessary if the automatic registration was suboptimal. We analyzed the resulting time series curves by deconvolving the myocardial signal with that of the blood pool. The same analysis, including the same motion correction parameters, was applied to RR-UNFOLD reconstructed data. We used the normalized slope as the perfusion index for the 10 patients studied (Fig. 8 gives regional values for one of the patients studied). It is evident that the error from normal UNFOLD ranges from 25% to 71%, whereas with RR-UNFOLD the maximum error is only 14%. Figure 9 illustrates the mean absolute error of the perfusion index obtained with conventional UNFOLD and the proposed RR-UNFOLD technique with a 5-mm bin width and six extra central lines for all of the 10 patients studied. The average error of the two techniques was 25% and 9%, respectively.

DISCUSSION

In this study, we have presented a new RR-UNFOLD technique for myocardial perfusion imaging. The relative strength and potential pitfalls of the techniques were assessed in detail, and the results demonstrate the potential clinical value of the technique. The method achieved an overall 45% reduction in image acquisition time, and significantly reduced image artifacts compared to UNFOLD, based on the trueFISP per-
fusion sequence used. One of the major advantages of the proposed method is its simplicity, in terms of both respiratory motion correction and data reconstruction. The method involves only minor changes to the sequence design if prospective navigator echoes are available on the CMR system. The rebinning algorithm proposed is straightforward to implement, and our study involving both normal subjects and patients demonstrates the robustness of the technique in dealing with different respiratory patterns.

For this study, the bin used for each image subseries was created dynamically, which made the technique resilient to changes in respiratory patterns. It is worth noting that for the results presented here, a fixed respiratory window was used for all of the bins. This introduced a non-equal distribution of the number of images in each bin, since for normal respiratory patterns the dwell time at end-expiration and -inspiration can be extensive. Although the rebinning algorithm proposed can effectively deal with this issue, certain optimizations, such as using variable window sizes at different phases of the respiratory cycle, can be introduced. Furthermore, it is also important to consider the respiration speed during data acquisition given that in perfusion imaging the acquisition window is long compared to that in conventional imaging, due to the complete spatial coverage required for every cardiac cycle. This effect is most pronounced at mid-respiration, when the speed of the diaphragm movement is at its maximum.

An optimized solution to these issues, however, is not trivial and will require prior knowledge of subject-specific respiratory patterns. Although one can acquire this information, to some extent, by using prescans so that the respiratory patterns are monitored for a short period of time before actual perfusion imaging is performed, it is difficult to put this into practice because respiratory patterns change during the course of image acquisition, especially when pharmacological stress is used to assess the perfusion reserve.

It is worth noting that although all results shown in this paper are based on a trueFISP perfusion sequence, the method is applicable to general perfusion sequences. Our results show that RR-UNFOLD significantly extends the applicability of UNFOLD to perfusion imaging, and yields a 40% reduction in image artifact (or a 70% reduction if the extra central k-lines are not used for UNFOLD reconstruction). The scan efficiency achieved can be used to extend the three-dimensional spatial coverage or to shorten the acquisition window of the perfusion sequence, both of which are fundamental to the accuracy of the CMR technique in providing detailed information on regional myocardial perfusion ab-

Figure 5. ROI signal intensity curves showing the effectiveness of signal intensity correction by the introduction of extra central k-space encoding lines for RR-UNFOLD. The three intensity curves of each figure show the signal derived from images with and without central k-space encoding measured within the blood pool and myocardium, respectively, compared to those from the original fully encoded perfusion image sequence.

Figure 6. The ratio of subtraction errors between RR-UNFOLD and conventional UNFOLD for normal subjects (a) and patients (b) studied when different respiratory window sizes are used for each bin. In both figures, the same k-space data with extra central lines were used for RR-UNFOLD and conventional UNFOLD techniques. An error ratio of less than 1.0 indicates an improved artifact suppression of the RR-UNFOLD technique. The solid curve demonstrates the mean error ratio, and the vertical bars indicate the standard deviation (SD).
normality. The reduction in the acquisition window is particularly important for three-dimensional perfusion imaging with multislice coverage, since misregistration due to materials moving in or out of the imaging plane caused by cardiac- and respiratory-induced long-axis motion is particularly difficult to rectify, and it cannot be restored by postprocessing techniques. The proposed technique is therefore valuable for accurately quantifying perfusion so as to extend the role of CMR in managing patients with suspected coronary artery disease, and following up patients with known ischemic defects.

The reduction in k-space coverage can be used in different ways. The 45% reduction in k-space coverage required may allow an almost twofold increase in myocardial coverage. This, paired with the latest imaging sequences (13), would allow the possibility of several short-axis myocardial slices and the acquisition of long-axis slices for greater apical coverage. With a multislice image acquisition, the navigator would be acquired prior to image data acquisition for each cardiac cycle as with single-slice imaging. Binning would then be applied in a similar manner to single-slice imaging.

It is important to note that for this study the prescribed dose of contrast agent (0.1 mmol/kg of Gd-DTPA) is likely to result in signal-clipping of the arterial input function. For this study, we concentrated mainly on the measurement errors by using the same experiment setting but with a different reconstruction (i.e., full acquisition, traditional UNFOLD, and RR-UNFOLD imaging techniques). The study of the arterial input function under high-dose Gd-DTPA imaging and its impact on perfusion index quantification, as well the avoidance of nonlinear response-induced errors are active fields of research in MR myocardial perfusion (22).

While the results for RR-UNFOLD show marked improvements in accuracy for the perfusion index measured by the normalized slope in comparison with UNFOLD, in two instances RR-UNFOLD actually produced greater error in the measured perfusion index value (patient 1 increased from 8% to 12%, and patient 6 increased from 12% to 23%, as shown in Fig. 9). In the case of patient 1, both UNFOLD and RR-UNFOLD provided acceptable error of around 10%. For patient 6, however, the error is significant. This is attributed to the poor navigator trace from the patient, which when used with RR-UNFOLD degrades the consistency of the k-space data and actually increases the image artifact.

In summary, we have developed an effective way to extend the UNFOLD framework for myocardial perfusion imaging. We demonstrated the strength of the technique with in vivo data acquired from both normal subjects and patients referred for myocardial viability assessment. The method provides a near twofold increase in imaging efficiency, with only minor deterioration in image quality compared to full k-space coverage. Furthermore, the method is relatively simple to imple-

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Figure 7. The reduction in error (mean and SD of the 10 patients studied) represented as a ratio of RR-UNFOLD against normal UNFOLD when different numbers of extra central k-lines are used.

Figure 8. Perfusion index calculated for six midventricular segments of a patient, demonstrating the effect of RR-UNFOLD and conventional UNFOLD for myocardial perfusion quantification. Relative values between reduced k-space reconstructions and the original data are shown for UNFOLD and RR-UNFOLD, where 1.0 indicates no change in perfusion index. With UNFOLD, the derived perfusion index has an error range of 25–71%, whereas for RR-UNFOLD the error range is kept within 14%.
ment and can be applied to most of the current state-of-the-art CMR scanners.

REFERENCES


\begin{figure}
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\caption{The relative error in the perfusion index after the same processing steps as in Fig. 8 are applied to the 10 patients studied with the UNFOLD and RR-UNFOLD techniques. The mean absolute error of the perfusion index, and minimum/maximum absolute error of the perfusion index are shown for each patient.}
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