RR-UNFOLD: Respiratory Reordered UNFOLD for First Pass Myocardial Perfusion Imaging

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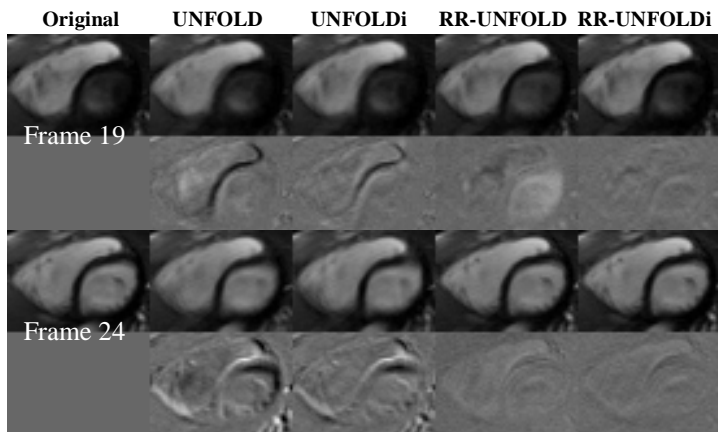
Introduction

Early diagnosis and localisation of myocardial perfusion defects is an important step in the treatment of coronary artery disease. The assessment of myocardial perfusion requires accurate quantification of the transmural extent of possible defects, which involves a complete multi-slice coverage of the ventricle at a given phase of the cardiac cycle. To this end, a number of rapid imaging sequences have been proposed in recent years [1] to minimise the data acquisition window so as to avoid mis-registration due to cardiac as well as respiratory motion. UNFOLD [2] is an image acquisition and reconstruction method which attempts to encode spatial information into redundant regions of k-t space. The sub sampling of k-space results in aliasing in the spatial domain and the success of the method is dependant on dynamic regions being uniquely represented in the spatial domain. Since myocardial perfusion imaging typically involves 50 cardiac cycles, respiratory induced cardiac deformation imposes a major limitation to the application of the UNFOLD method [3]. This paper presents a novel approach to the acquisition and reconstruction of MR myocardial perfusion images based on UNFOLD but with prospective respiratory phase encode reordering. It provides an adaptive real-time binning method that minimises the effect of respiration whilst maintaining the temporal tissue characteristics during the contrast up-take.

Method

A trueFISP sequence (FE=144, PE=288) with prospective diaphragmatic navigator echoes running on a Siemens Sonata 1.5T MR scanner was used for this study. For each acquisition, first-pass perfusion imaging was performed on 50 cardiac cycles. For each cardiac cycle, the navigator was timed after the imaging sequence to avoid cardiac filling motion, typically starting at about 400 to 500ms after the R-wave depending on the patient's R-R interval and R-R variability. This provided ample margin to avoid missing cardiac cycles. The total imaging duration was 260ms from start of non-selective saturation pulse to end of single-shot true-FISP sequence. Saturation recovery delay was 140ms, and 0.1mmol/kg Gd-GTPA dose was injected at approx 3ml/s followed by 10ml saline flush. Other imaging parameters were: 10mm slice thickness, 40-60 degrees flip angle (SAR limited), 370mm (FE) by 288mm (PE) FOV, 144 (FE) by 112 (PE) un-interpolated unfiltered pixels in the image. The k-space was filled with full ky coverage in linear order over ky versus time, and at 2.2ms repeat time between the FISP RF-pulses.

During data acquisition, a 90-180 respiratory navigator through the dome of the diaphragm was used to control the binning of each acquisition under different respiratory states. For UNFOLD with a factor of 2 in data reduction, it requires the alternation of acquiring odd and even k-lines between adjacent data sets within each bin. In practice, this cannot always be guaranteed as patient respiratory patterns are unpredictable. To ensure that within each bin there are at least 4 data sets and always paired with odd-even acquisitions, bins that do not fulfil this requirement involve a further processing step before reconstruction. This is achieved by copying the most recent odd or even frames from the same bin to the end of the sequence until the above condition is satisfied. For bins that had only one frame, alternating odd/even frames from neighbouring respiratory bins were copied. Traditional UNFOLD reconstruction was then applied to each bin, so that missing k-lines could be derived.

figure 1. Two frames from a perfusion sequence reconstructed with different methods and their corresponding artefacts introduced. It is evident that UNFOLD introduces significant motion artefact even with the addition of extra central k-lines (UNFOLDi), whereas RR-UNFOLD successfully eliminates motion artefact and with extra central k-lines (RR-UNFOLDi), an accurate reconstruction can be achieved.
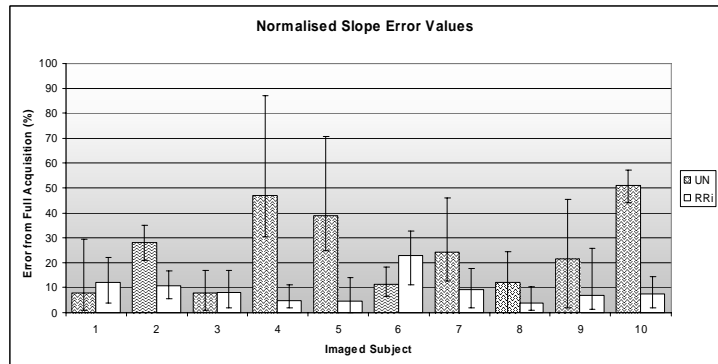
figure 2. The relative error in normalised slope measurement from the six segments of a mid-ventricular slice for the 10 patients studied. The difference is represented in % changes in normalised peak-contrast uptake derived with Fermi deconvolution.

With this approach, an imaging sequence that is free from motion artefact can be reconstructed.

The use of UNFOLD has a temporal smoothing effect on intensity changes within each bin. By prospectively adapting data acquisition according to respiratory reordered UNFOLD (RR-UNFOLD), sharp changes in signal intensity can be introduced when images from different bins are put back into temporal order. Through RR-UNFOLD we have effectively preserved the edges of the anatomical features while minimizing the aliased artefact. To restore intrinsic intensity variations due to contrast uptake, we ensured that for each odd/even frame the central k-space was completely covered. With this study, this entails additional acquisition of 6 extra k-space encoding steps.

Validation of the proposed technique was performed on 10 subjects undergoing myocardial viability study. For each subject a comparison was made between UNFOLD and RR-UNFOLD not only in image artefact but also differences in deriving perfusion indices as compared to conventional full acquisition. For assessing image artefact the sum of the squared subtraction error in pixel intensity was calculated, whereas for difference in perfusion index, changes in normalised slope in contrast uptake after Fermi deconvolution [4] for six myocardial segments was used (CMRtools, London).

Results

Figure 1 illustrates the effect of UNFOLD, and RR-UNFOLD with/without extra central k-space acquisition. The new method achieved an overall reduction in image artefact of 72% ±SD 8. By taking into account the extra central k-lines introduced, the overall reduction in imaging time achieved was 45%. The difference in the derived normalised slope for the two techniques is shown in Figure 2, where the overall deviation in normalised slops for all the segments measured was 25%, and 9%, respectively. The results indicate that the application of RR-UNFOLD is an effective method for reducing acquisition time of first-pass myocardial perfusion imaging in the presence of free respiratory motion.

References

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