Reducing artefacts by inverting the effects of non-rigid motion during a free-breathing liver scan

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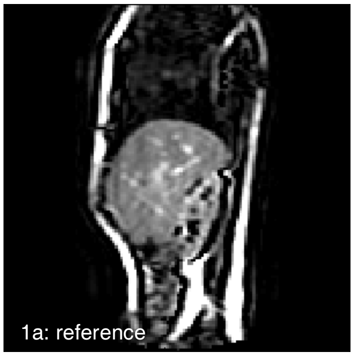
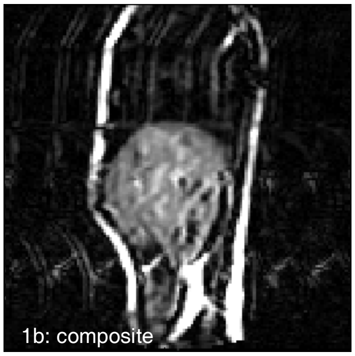
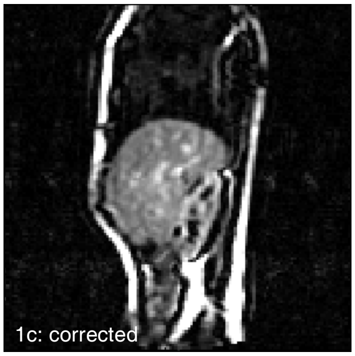
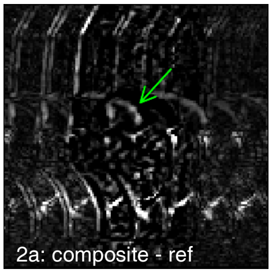
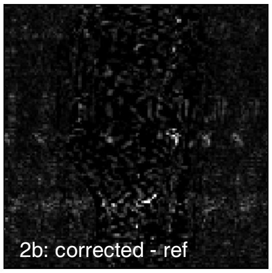
Introduction. A major challenge for MRI of the liver is reducing the artefacts caused by breathing motion. Many useful acquisitions exceed the length of a reasonable breath-hold, and even when breath-holds can be used they are often not maintained or not reproduced well. Navigator triggering is effective, but increases the acquisition time, fails in some patients, and is not appropriate to all sequences. Respiratory motion during multi-shot MRI causes both blurring and ghosting in the image when the liver is not aligned between shots. Batchelor et al (2005) describe a method for removing the effect of time-dependent motion on multi-shot images by inverting a matrix representing the motion and sampling [1], demonstrating it with simple examples. In this abstract we extend this approach to correct complex non-rigid motion over the whole field of view. Realistic motion-corrupted liver images were simulated by combining 'shots' from successive frames of a fast, low resolution dynamic free-breathing series. Fluid registration was used to estimate deformations.





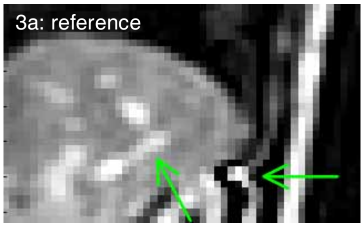


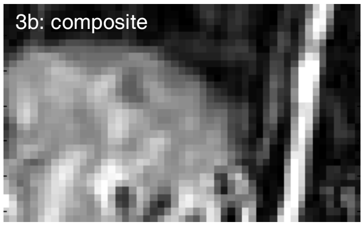


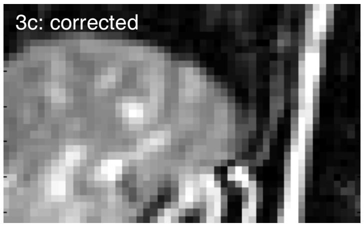


Methods and results. A series of volumes were acquired from a volunteer using a Philips 1.5T Achieva system during free breathing. A balanced 3D gradient echo sequence was used, with multi-shot EPI and a four-element body coil with SENSE reconstruction to achieve high temporal resolution: 58 sagittal slices covering the liver were acquired every 0.8s with a reconstructed in-plane resolution of 3.1 x 3.1mm. A reference volume (at exhale) was selected (Figure 1a), and all other volumes registered to this using a fluid algorithm [2]. A motion-corrupted 2D multi-shot image was simulated by interleaving lines of *k*-space from a chosen plane in eight successive volumes; the *k*-space 'lines' were formed by Fourier transforming the scanner's reconstructed modulus images. This composite image, which shows typical ghosting from motion corruption, is shown in Figure 1b.

This image was then corrected using the conjugate gradient iterative inversion technique; for a complete description of this approach see [1]. In brief, the motion corruption is described as a large matrix incorporating the Fourier transform, the multi-shot sampling scheme, and the actual time-varying deformations; inverting this matrix, if the correct motion is used, leads to an uncorrupted image. The conjugate gradient solver (`lsqr` from Matlab's standard library) uses only the product of this matrix with a search vector. The matrix need not be stored in full, as the multiplication can be approximated rapidly using the FFT and a standard non-rigid deformation with linear interpolation. The transpose must also be supplied, which requires an inverted deformation; this was computed by a simple iterative technique, in which an initial coarse estimate of the inverse at each point was refined by repeatedly transforming back into the target space and minimizing the residual between forward and reverse estimates. Computation of the matrix inverse was stopped after four iterations. Conjugate gradient inversion of poorly conditioned matrices may diverge after many iterations; this stopping point was determined by finding the low plateau in the RMS residual between corrected and reference images over several composite simulations. This 2D reconstruction took under a minute on a 2GHz P4. The corrected image is shown in Figure 1c. Corresponding differences to the reference image before and after correction are shown in Figures 2a and 2b.







Discussion. Several features of the reconstructed images are noteworthy. First, typical ghosting artefacts along the phase direction in the composite image (1b) are much reduced in the corrected image (1c). Second, blurring of the diaphragm is also reduced, as shown by the visible diaphragm in the composite difference image (2a; arrow). Third, a number of features of the liver are recovered following reconstruction. Zoomed views of the posterior part of the liver are shown in Figure 3; arrows on the reference image (3a) indicate a blood vessel within the liver and another structure posterior to it, both corrupted significantly in the composite image (3b) and largely restored in the corrected image (3c).

The composite simulation is realistic: the *k*-space 'shots' are genuinely taken from data acquired at different points in the breathing cycle, and the deformations (and approximate inverses) are also real, estimated from the data itself. If the shots are instead simulated by deforming a single reference image, reconstruction is near perfect; so errors in the images shown come from physical changes in the image during acquisition (flow artefacts, perhaps) which are not currently modelled in the general matrix description of varying deformation.

One major addition is needed to correct true multi-shot images with this approach. Deformation fields cannot be measured by direct registration of each 'shot', and must be estimated separately; White et al (2006) have shown a method for doing this based on a breathing model acquired with rapid MRI immediately before the ghosted acquisition, then associating a simple parameter (such as correlation of a repeatedly acquired central *k*-space profile [3]) associated with each shot [4]. The combined technique has the potential for ghost reduction in a variety of abdominal imaging applications, both to decrease imaging times by eliminating gating, and to improve images with time-critical components such as dynamic contrast-enhanced scans.

References.
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