Image Deformation Recovery using Overlapping Partial Samples (iDROPS): model-based respiratory artefact correction in free-breathing liver MRI

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Introduction. Respiratory motion needs managing in most liver MRI protocols. It has been shown that, given a deformation field associated with each group of k-space samples (eg each shot in an interleaved sequence), artefacts in a free-breathing liver image may be corrected [1] using a general matrix model of motion and sampling scheme [2]. We introduce iDROPS, a model-based method for estimating the deformation fields associated with sub-sampled k-space.

Methods. The iDROPS process uses two sampling schemes. Considering a base image of N lines of k-space, the *training* data is acquired by repeatedly imaging the central N/T lines, giving a low-resolution cine series. The *imaging* data is acquired in an interleaved fashion: in each frame, every D^{th} line of k-space is acquired, such that the whole of k-space is acquired in D frames. An individual imaging frame, when zero-filled and Fourier-transformed, will exhibit N/D ghosting. Both series are acquired during free breathing.

The individual frames of the training series are registered to a chosen exhale reference using a non-rigid fluid algorithm [3]. A breathing model [4,5] is built by linear fit of each component of deformation at each spatial position to a *breathing parameter*: this can be any quantity (perhaps multi-dimensional) which describes the respiratory cycle, and here we use the mean displacement of the whole image (not just the liver) in the head-foot direction. Hence, given an estimate of the breathing parameter, a displacement field for the whole image may be derived.

A breathing parameter is then found for each imaging frame by minimizing a cost function (mutual information or sum of squared differences) between the imaging frame and the model-deformed exhale training frame. The images between which cost is calculated are formed from only those lines of k-space which occur in both: N/(TD) lines, every D^{th} line within the central N/T. Thus these images are low-resolution and ghosted. Deformations, however, must be applied to non-ghosted images: so a model-derived deformation is applied to the complex-valued, partially-reconstructed training frame, which is then returned to k-space, where lines not present in the imaging frame are zeroed. The imaging frame is also part-zeroed to leave only overlapping k-space lines, and both are then reconstructed to ghosted, low-resolution images for comparison. This process is repeated to find a parameter value minimizing the cost function, first by a coarse linear search to find an initial guess, followed by Brent (parabolic-interpolated golden-section) minimization [7]. Finally, the estimated parameters are used to generate deformation fields for each imaging frame. These, along with their iteratively-calculated inverses [6], are then used in an LSQR-based general matrix motion correction step [1,2]. This approach is readily adapted to handle repeated sampling of k-space and thus to give a corrected image averaged over several frames. The estimated deformations may also be used to reject the most-deformed frames in the imaging series.

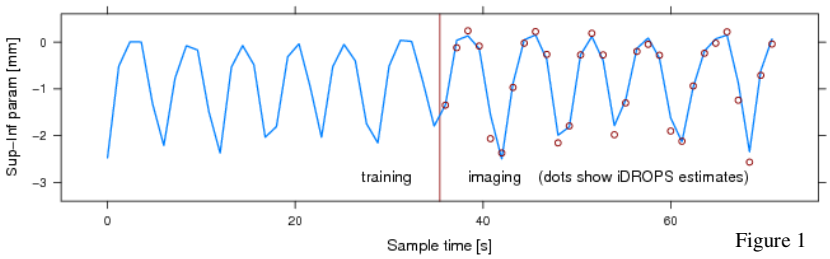

Figure 1

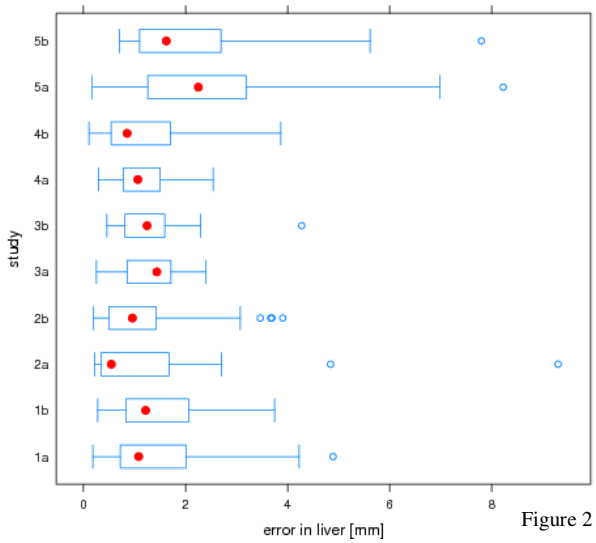

Figure 2

Results. Optimisation was tested by deriving both the training and imaging data from a single longer dataset, acquired using multi-shot EPI on a 1.5T Philips Intera with 128x128x45 voxels covering the liver every 1.2s during free breathing. The first 30 frames were centrally reduced in the AP direction by factor T=4 to provide training data; the remaining 30 reduced by retaining only every D=4^{th} line to provide imaging data. The estimated imaging parameters could thus be compared to their true values estimated from the original data, and the error in derived deformation fields found (the resulting images are, however, lower resolution than possible in a true imaging context). **Figure 1** shows the breathing parameter (mean displacement) for one such dataset. The line shows the 'true' parameter measured from the original data. The graph is divided into training and imaging data, with iDROPS-estimated points shown for the imaging data. **Figure 2** shows the distribution of error (modulus difference, in mm, between true and estimated displacement) measured at a point in the liver just below the diaphragm, with data from five volunteers (1-5) each visiting for two scans (a-b). Outliers are shown above 2 sd for each study; the overall mean error is 1.5 mm. Finally, **Figure 3** shows reconstructions from real (unsimulated) data, acquired during free breathing using a 2D gradient echo sequence, with 256x180 voxels in an 8mm slice. The training data comprised 80 frames, each of 45 central lines acquired in 1.1s. The imaging dataset (shown) is 72 frames, each including every 4^{th} line (ie 18 acquisitions of each k-space sample) and also acquired in 1.1s. The corrected image was created with LSQR and the iDROPS-derived deformation fields, calculated in groups of 4 frames and summed. An uncorrected sum of the same data is also shown.

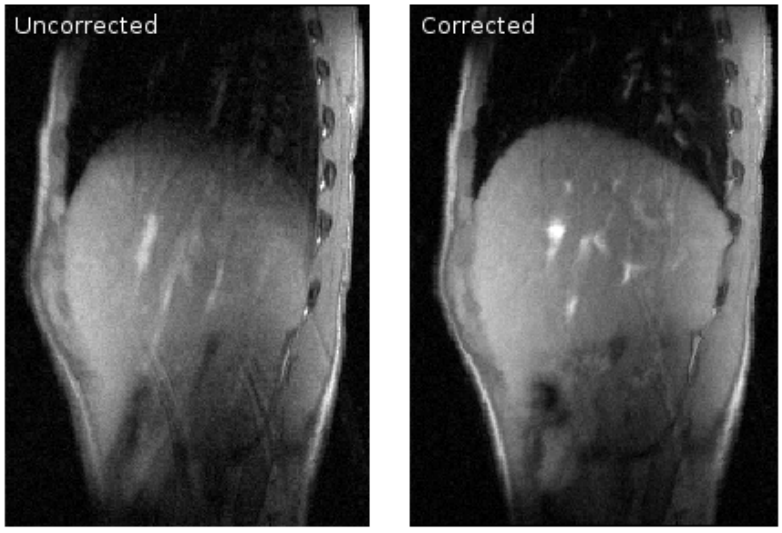

Figure 3

Conclusion. The iDROPS approach, given suitable training and imaging data, allows deformations to be recovered with an error of a few mm in the region of the liver. These can be used to remove ghosting and blurring from data acquired continuously during free breathing. This method has clinical applications both in dynamic and morphological MRI where acquisition times exceed the duration of practical breath-holds.

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