A preliminary investigation into the use of joint Entropy for correction of fold over artefacts

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Introduction: Incorrect choice of the field of view or foldover direction in clinical MRI examinations can lead to aliasing artefacts that compromise the diagnostic power of the images. This kind of error can be made by even the most experienced personnel and generally leads to wasted time as further images are reacquired. In this study we make some preliminary tests of a method to correct such aliased images using a reference image that may be already available. The principle behind the method also has potential for speed up of imaging by deliberately allowing aliasing and then correcting the image post acquisition. This has clear similarities to the data acquired for subsequent processing by the SENSE[1] version of partially parallel imaging (PPI). In this method array coils are not required, however, the power to unfold multiply aliased pixels may be limited.

Theory: For two images A and B, the joint probability p(a,b) of intensities a in image A and b in image B occurring together can be used to define a joint entropy (E_j) as the sum over all p(a,b) of p(a,b).log p(a,b). E_j is a measure of the degree to which image B predicts the intensity in image A and vice versa[2]. In this application we take image A to be the aliased image and image B to be a reference image that may have different contrast, but covers the full intended field of view (FoV). We note that aliased pixels in A are simple sums of the signals at the locations X_1 and X_2 , that have been folded in. Initially A is extended to a full FoV image by simply dividing the aliased signal into equal parts located at X_1 and X_2. We now adjust the intensity at X_1 and X_2 by adding equal and opposite complex signals, ds and –ds, with ds adjusted to minimise E_j. This optimisation is achieved separately for each pixel pair by a simple search in ds. The function E_j in general remains constant for large ranges of ds due to the sparseness of the joint histogram hence gradient dependent optimisation schemes are not useful and the search strategy was chosen.

Method: T2 weighted aliased images of the brain were generated from the MNI brain atlas[3] by Fourier Transformation and decimation, in the extreme example shown a reduction of the field of view by half was simulated. A full field of view T2 weighted reference image was used. The aliased regions were identified by an automated comparison with the reference image and non-aliased regions were excluded from the processing. A starting estimate of half the original signal was applied in these regions. The restored images produced using the proposed algorithm were then compared to the original images by subtraction from a gold standard reference image to look for unfolding errors. The aliased images were corrected by minimising E_j using code written in IDL and run on a Compaq Alpha station.

Results: Successful unfolding of aliased images was achieved. Figure 1 shows an example. Subtraction of the gold-standard full FoV data in the test examples (e.g. figure 1e) showed that errors were less than 0.5% of the signal amplitude in the brain. Larger residuals are located at the edges of regions that have been identified using an intensity threshold however we believe this is a methodological problem which can be solved. The threshold is required to ensure reasonable starting estimates are applied to each pixel pair. Processing took approximately 120mins for this 120x120 pixel image.

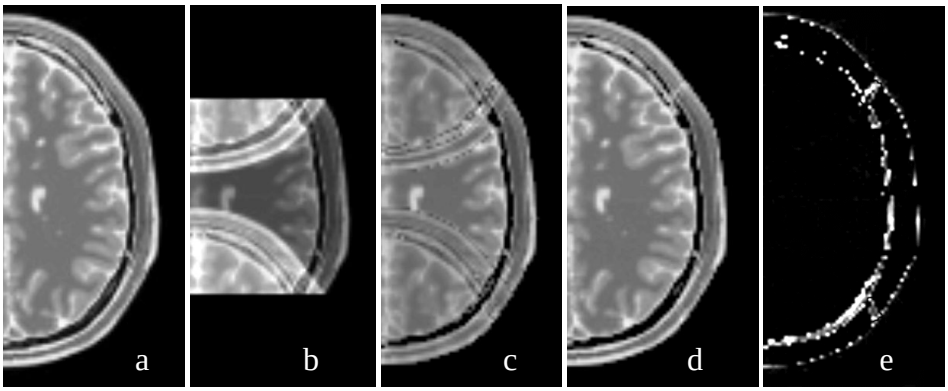

Figure 1: a) original full FoV gold standard reference image, b) aliased image produced from (a), c) starting estimate applied d) regenerated image, e) subtraction of a-d. In e the correction within the brain is excellent but the boundaries of the brain are less well corrected.

Discussion: The method has potential to provide a way of recovering from a common error. The reference image could be already available from previous images (scouts, PPI ref scans etc) or could be acquired quickly. In principle the reference scan does not have to have the same contrast as the image to be corrected just the same tissue classes allowing rapid T1 weighted images to correct slow T2 weighted images for example. Joint entropy and related similarity measures have proven to be very powerful tools in image registration between images of different contrasts and even between modalities, and for this reason we speculate that the method described should be robust for different contrasts and resolutions. However we have yet to test this thoroughly. Artefacts in either the target or the reference image, such as caused by motion can be a problem and lead to incorrect unfolding. This is a somewhat fundamental limit, but must be weighed against the likelihood of success with a full repeat examination. Since correction is only applied to aliased regions, which are already compromised the method has produced improvement in all cases so far. It is necessary for the reference and target images to be spatially aligned, but this can be achieved to the required accuracy by standard image registration methods. At present the processing is prohibitively slow and the correction procedure flounders in regions where the starting estimate is far from the solution due to the finite size of the search space. This is not an intrinsic limit. The method holds promise for situations where a reduced FoV image is deliberately acquired, such as for speeding acquisition or for reducing artefacts in single shot imaging. Further testing is required to assess robustness and scope of application.

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References:
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