Correction of Motion Artifacts using a Genetic Algorithm

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Introduction

Subject motion during MRI scans can severely affect the acquired images and render them unsuitable for further post-processing or diagnosis. There exist a number of techniques that reduce motion artifacts by either faster acquisition (e.g. parallel imaging) or oversampling portions of k-space (e.g. PROPELLER [1]) or a combination of both. Also navigator techniques can be used to detect and correct motion. However, in many MR applications cartesian sampling of k-space is used. High resolution techniques, such as susceptibility weighted imaging (SWI), have acquisition times in the order of minutes even if parallel imaging is used. This increases the chance of motion artifacts.

Because of the Fourier shift theorem, translations that occur in between the acquisition of two k-space lines can be represented using a phase gradient and offset. Methods to correct the phase of k-space lines by minimizing a quality measure have been proposed in the past [2,3]. We propose to address the optimization problem using a genetic algorithm. Since genetic algorithms are inherently parallelizable, such an approach could benefit greatly from advances of modern computer technology.

Methods

Algorithm: Two genetic algorithms were developed and implemented in Matlab (Mathworks, USA). The set of phase gradients and phase offsets for all k-space lines represented a genome. Both algorithms were based on the following principle:

- 1. Initialization of *p* genomes.
- 2. Repeating the following steps until the maximum number of *N* iterations was reached:
 - a. Multiplication of the *p* genomes to a total number of *P* genomes.
 - b. Evaluation of each of the *P* genomes by: applying the respective phase shifts to k-space, computing the Fourier transform and image metric.
 - c. Selecting the *p* best solutions.

The two algorithms differed in the multiplication step. The first algorithm mimicked non-sexual reproduction. A random number of mutations was applied to each genome at every multiplication. Mutation rates between 0.25% and 25% were investigated. In case of a mutation a Gaussian distributed random number was added to (or subtracted from) the value representing the shift.

The second algorithm used following strategy for multiplication: for each pair of the p best solutions, a number children were generated by exchanging a random number of genes. After this cross over phase, mutations were applied in the same manner as in the first algorithm.



Fig. 1: Original magnitude (a) and phase (d) image; with artificial motion artifacts (b,e); corrected images (c,f). Note that also motion present in the original image was corrected. This is especially apparent in the phase images (d,f).

Four different quality measures were tested: entropy [2], normalized gradient squared (NGS) [3], signal in the background and local coherence (LC) [4] in the background.

Data: The performance was evaluated on simulated data as well as on slices of an SWI data-set to which artificial motion (random with a Gaussian distribution as well as periodic) was applied. The SWI [5] data-set was acquired on 1.5 T Siemens Vision (Siemens, Germany) scanner. The parameters were TE=40ms, TR=65ms, α =25°, matrix=256x192x48, FoV=256x192x96 mm³.

Results

Using the same parameter sets (number of iterations, population size etc.) the first algorithm led to significantly better images (less ghosting and blurring) than the algorithm allowing cross-overs. The best results were achieved using NGS and entropy. Artifacts were corrected best if the mutation rate was low ($\leq 1\%$). However, modifying only one k-space line at a time did not lead to a substantial reduction of artifacts. Comparing the number of iteration versus population size, showed that a stronger dependency on the number of iterations than on population size.

Fig. 1 shows an exemplary data-set. Artificial motion is added to the original image (fig. 1(a,d)) resulting in a corrupted image (fig. 1(b,e)). The corrected image is shown in fig. 1(c,f). The mutation rate was 0.5%. The displacements were drawn from a Gaussian distribution with σ =0.5 voxels.

Discussion

The better performance of the first algorithm can probably be attributed to the larger changes in k-space between two solution vectors that can be caused by the cross over. This hypothesis is supported by the fact that increasing the mutation rate does not lead to improved images.

Although LC was shown to be very sensitive to ghosting artifacts, it was the least usable minimization criterion. Furthermore LC and the signal in the background criterion suffered from requiring a definition of the background. This would make them less robust in practical applications.

Conclusions

Using a genetic algorithm for correction of motion artifacts was shown to be feasible. We think that it is a promising approach because of its inherent parallelizability. Using implementations of the FFT on GPUs might allow implementations that are sufficiently fast for every day applications. Further studies to optimize the parameters such as mutation rate, population and minimum number of iterations are still required. However, first results indicate that a significant increase in computation speed can be expected.

References

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