

Motion correction of magnetic resonance imaging data by using adaptive moving least squares method

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ABSTRACT

Image artifacts caused by subject motion during the imaging sequence are one of the most common problems in magnetic resonance imaging (MRI) and often degrade the image quality. In this study, we develop a motion correction algorithm for the interleaved-MR acquisition. An advantage of the proposed method is that it does not require either additional equipment or redundant over-sampling. The general framework of this study is similar to that of Rohlfing et al. [1], except for the introduction of the following fundamental modification. The three-dimensional (3-D) scattered data approximation method is used to correct the artifacted data as a post-processing step. In order to obtain a better match to the local structures of the given image, we use the data-adapted moving least squares (MLS) method that can improve the performance of the classical method. Numerical results are provided to demonstrate the advantages of the proposed algorithm.

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1. Introduction

Motion artifacts in MRI are one of the most common problems that reduce the quality of the images. In the interleaved MRI acquisition technique, 3-D image volumes can be acquired in sequence simultaneously across all slices. For instance, in two-packet MRI, all the even slices (termed ‘even volume’) are acquired first before the odd slices (termed ‘odd volume’) are obtained. Then the reconstructed MR images are vulnerable to motion artifacts due to subject movements during interleaved sequences [2]. This may result in mis-alignments among the acquired packets, which can be easily detected in sagittal and coronal views.

To prevent motion artifacts, short acquisition time is preferred. Although current technology allows taking an MR image in short time for basic MR-scans (e.g., T1-MRI), specialized MR-scans like diffusion-weighted MRI (DWI) and functional magnetic resonance imaging (fMRI) require longer acquisition time. Diffusion tensor imaging (DTI), an extension of the DWI method that enables in vivo investigation of molecular diffusion in biological tissues, has been used not only to assess various neuropsychological disorders but also to understand the connectivity of the human brain. However, due to

the long acquisition time required, DWI also suffers from motion artifacts. In DWI, a volume image is acquired using a single shot echo-planar imaging (EPI) sequence, which is composed of a series of MR slices. EPI is commonly achieved using interleaved MR sequences. Since most sporadic movements occur in a short time period during a volume scan, motion artifacts may affect only a portion of the volume rather than the whole one. For example, a volume scan of DWI in a conventional scanner takes approximately 8 s for $b = 600 \text{ s/mm}^2$ and 1 s for $b = 3000 \text{ s/mm}^2$. Each slice scan takes about 110–220 ms. Most sporadic movements appear during a period of less than 1 s. Another MR acquisition, Fluid-Attenuated Inversion Recovery (FLAIR) requires long TR (repetition time) and short TI (inversion time) to enhance white matter with suppressing CSF effects [12]. It has a greater chance to generate a motion artifact between passes because the interleaving acquisition factor increases the thickness of the inversion pulse [27].

Various methods have been suggested to help solve this problem, such as using physical restraint or sedation to prevent the subject's motion. Although physical restraint is partially effective, its limitation is evident. Also, sedation increases the medical risk (e.g. hypoxia) and adds complication to the scan. Methods for detecting the position of an object in the scanner using an external apparatus have also been proposed. Navigator echo techniques have been developed to acquire data selectively at only a particular point. Navigator data are used to update the scanner gradients (and thus the position of the imaging volume) prior to each spin

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excitation [3–5]. However, this requires acquisition of extra data and errors in the navigator information also result in residual errors in each k-space line. Some techniques have been developed to track subject motion by using ultrasound and other devices [6,8–10]. These techniques offer the advantage of compensating for the patients' motion in real time by adjusting scanner gradients, but additional hardware devices are required.

As an alternative approach, the data are corrected by a post-processing once the motion is detected. The advantage of this method is that no additional equipment is needed. The motion correction in post-processing can be separated into two categories depending on the processing domain: the k-space and the image space. PROPELLER [11] and TRELLIS [13] MRI methods obtain extra k-space data to estimate motion parameters. To avoid redundant over-sampling, Brown and Kuperman [14] introduced a motion correction method during MR scanning through the automatic rescanning of severely motioned subjects. Ahmed et al. [28] suggested a new k-space acquisition process with 50% overlapping for motion correction. On the whole, these algorithms require a longer acquisition time because of the extra data acquisition process. Welch and Felmlee [15] introduced a motion correction algorithm using the k-space phase difference of orthogonal acquisitions, which is only applicable to the standard 2-D Fourier transformation imaging.

The other post-processing category is motion correction algorithms on the image space without extra acquisitions [1,16,17]. Moore's algorithm [16] is related to the high resolution algorithm for cardiac MR image. It uses registration/averaging of the image to improve the signal-to-noise ratio (SNR). The method by Rohlfing et al. [1] uses inverse interpolation by estimating the pass-to-pass motion. In fact, most of the EPI sequences are acquired by interleaved data sets. Interleaved MRI acquires all the data points required to make up the image in several free-induction decays (FIDs). The main idea of Moore's and Rohlfing's methods is based on the assumption that the movements occur during the FIDs. It involves a registration process among passes and interpolation for the missing data. The slice-to-volume registration technique was introduced for motion estimation of fMRI [17]. All slices of fMRI are registered to an

anatomical high-resolution volume for the rigid motion estimation. Anatomical volume is used for the reference data and the same algorithm is used for motion estimation for the fMRI time series correction [20]. Similarly, Rousseau et al. [18] also used a slice-to-volume registration for motion estimation in the fetal MR brain. More recently, Gedamu et al. [19] introduced a motion correction algorithm using iterative pass-to-volume registration process to minimize the motion artifact. They used a Kaiser-Bessel function for interpolating missing data during the reconstruction process. Dowling et al. [2] suggested the non-rigid correction of interleaving artifacts in pelvic MRI. Most of these methods have a similar algorithmic framework; in that they use registration for motion estimation. After computing the motion parameters, missing data are interpolated.

In this study, we develop a new motion correction algorithm for the interleaved-MR acquisition. The general framework of the proposed method is similar to that of Rohlfing [1] but we introduce the following fundamental modification: in order to reconstruct volume images from a data acquired on an irregular grid (e.g., 3-D co-registered data), the proposed algorithm uses a data-adapted moving least squares (MLS) method to better match the local structures [21]. The interleaved image acquisition is used in MRI to minimize crosstalk between neighboring slices. TR is chosen so as not to be too short to allow data from all slices to be collected in a single pass. After acquiring two interleaved volumes, they are combined to form a high-resolution 3-D image volume. Fig. 1 illustrates the flowchart of the proposed algorithm. The whole 3-D image volume is separated into two sub-volumes: even and odd volumes. The discontinuity index (defined in the Eq. (5)) is computed on each sub-volume to determine whether one of the sub-volumes is corrupted. The proposed motion correction algorithm is applied to the case that both sub-volumes are not corrupted. In this study, rigid image co-registration is performed between two sub-volumes. As a result, a set of scattered data is generated in 3-D, which is used to build up a whole 3-D volume on uniform grid. On the other hand, if one of the sub-volumes is uncorrupted, a simple interpolation method can be applied to form a high-resolution volume [7,21].

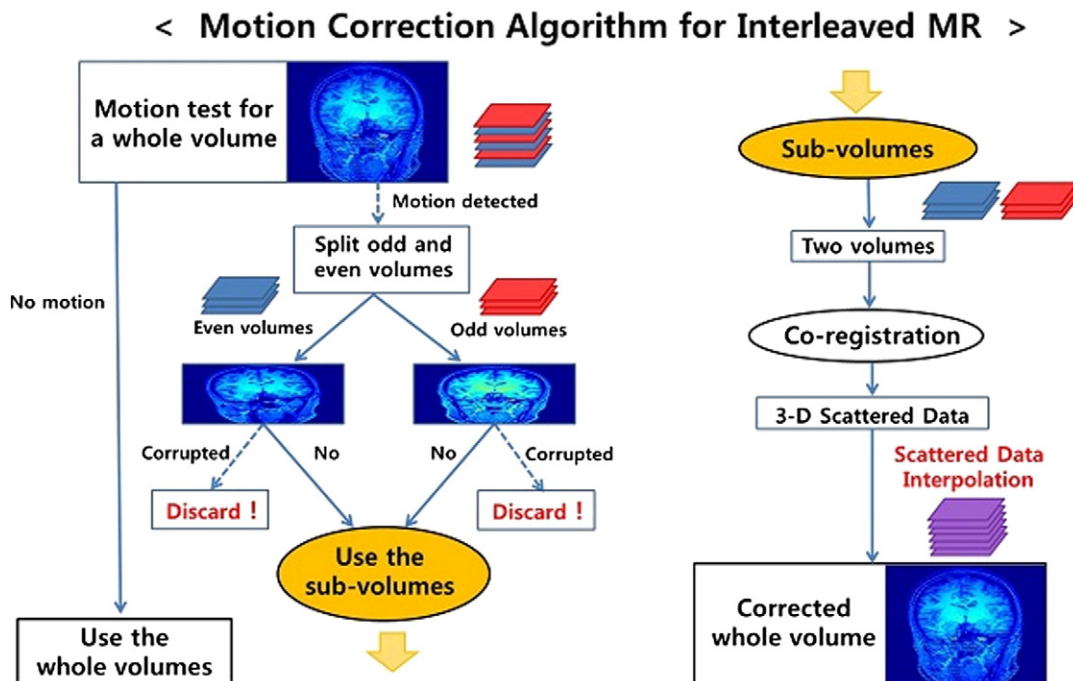


Fig. 1. Flowchart of the proposed algorithm.

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