Nonrigid Active Shape Model–Based Registration Framework for Motion Correction of Cardiac T1 Mapping

Hossam El-Rewaidy,1 Maryam Nezafat,1,2 Jihye Jang,1,3 Shiro Nakamori,1 Ahmed S. Fahmy,1,4 and Reza Nezafat1*

Purpose: Accurate reconstruction of myocardial T1 maps from a series of T1-weighted images consists of cardiac motions induced from breathing and diaphragmatic drifts. We propose and evaluate a new framework based on active shape models to correct for motion in myocardial T1 maps.

Methods: Multiple appearance models were built at different inversion time intervals to model the blood-myocardium contrast and brightness changes during the longitudinal relaxation. Myocardial inner and outer borders were automatically segmented using the built models, and the extracted contours were used to register the T1-weighted images. Data acquired from 210 patients using a free-breathing acquisition protocol were used to train and evaluate the proposed framework. Two independent readers evaluated the quality of the T1 maps before and after correction using a four-point score. The mean absolute distance and Dice index were used to validate the registration process.

Results: The testing data set from 180 patients at 5 short axial slices showed a significant decrease of mean absolute distance (from 3.3 ± 1.6 to 2.3 ± 0.8 mm, P < 0.001) and increase of Dice (from 0.89 ± 0.08 to 0.94 ± 0.4%, P < 0.001) before and after correction, respectively. The T1 map quality improved in 60 ± 0.3% of the motion-affected maps after correction. Motion-corrupted segments of the myocardium reduced from 21.8 to 8.5% (P < 0.001) after correction.

Conclusion: The proposed method for nonrigid registration of T1-weighted images allows T1 measurements in more myocardial segments by reducing motion-induced T1 estimation errors in myocardial segments. Magn Reson Med 000:000–000, 2018. © 2018 International Society for Magnetic Resonance in Medicine.

Key words: myocardial T1 mapping; motion correction; active shape models; nonrigid registration; MRI

INTRODUCTION

Myocardial interstitial diffuse fibrosis and extra-cellular volume expansion are characteristic of many cardiac diseases (1–4) and alter longitudinal relaxation time (T1) values (4–6). Recent improvements in pulse-sequence development allow reproducible measurement of myocardial T1 values (7–10). In myocardial T1 mapping, a series of T1-weighted (T1-w) images are acquired with different saturation or inversion times (TIs) (11–14) and are used to create T1 maps by voxel-wise fitting through two- or three-parameter fit models (14–16). In the presence of respiratory and cardiac motion, voxels are not aligned in different T1-w images and will cause errors in T1 estimation. Therefore, motion correction is an essential step in myocardial T1 mapping.

To minimize motion artifacts, T1 mapping is often acquired during a breath-hold scan (12,17). Free-breathing T1 mapping sequences have also been developed by using slice tracking or navigator gating (14), but residual motions can still be detected among different T1-w images as a result of respiratory drifting or inability of prospective slice-tracking technique to register the images. To overcome this challenge, postprocessing motion correction is used to align T1-w images (18,19). Xue et al (18) proposed a motion-correction technique that simulates contrast changes of T1-w images by generating free-motion images from an initial T1 estimate. The synthetic images are then matched with the corresponding inversion images to estimate the deformation field and correct the motions, but this framework does not account for T1 variations among different patients at the same TI, where the blood-myocardium contrast can be completely inverted for different cases at the same TI. Roujol et al used a modified optical flow energy function to estimate the elastic deformation field of the myocardium with an additional term to avoid transient structures from through-plane motions (19). However, estimation of the nonrigid parameters was affected by different signal-to-noise and contrast-to-noise ratios of T1-w images. Additionally, these methods were proposed to register T1 mapping images acquired using breath-holding acquisition protocols, in which the respiration-induced cardiac motion is minimized. Furthermore, these intensity-based image-registration techniques require expensive computational power and time, so the need to improve motion correction for T1 mapping is still unmet.

Active shape models (ASMs) allow robust segmentation of myocardial borders and have been used in left and right ventricular (LV/RV) segmentation from cine MR images (20–22). In ASM, a training data set with pre-delineated contours of the target object (e.g., LV) is used to build shape and appearance models. The shape model is built by estimating the mean shape of the object and

1Department of Medicine (Cardiovascular Division), Beth Israel Deaconess Medical Center and Harvard Medical School, Boston, Massachusetts, USA.
2Division of Imaging Sciences & Biomedical Engineering, King’s College London, London, United Kingdom.
3Department of Computer Science, Technical University of Munich, Munich, Germany.
4Systems and Biomedical Engineering, Cairo University, Giza, Egypt.
*Correspondence to: Reza Nezafat, Ph.D., Department of Medicine (Cardiovascular Division), Beth Israel Deaconess Medical Center, 330 Brookline Avenue, Boston, MA 02215, USA. E-mail: nezafat@bidmc.harvard.edu

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intershape variations among different patients in the training data set, as represented by the covariance matrix (21,23). The appearance model is built to capture intensity variations at the LV myocardial borders (21). A matching algorithm is then used to search for the object’s borders in testing images with the built models.

In this study, we propose a new ASM-based framework for nonrigid registration of T1-w images to reduce motion artifacts in free-breathing cardiac T1 mapping. The epicardial and endocardial boundaries of the LV are modeled and segmented at different values of TI. Contour-based image registration step is then used to estimate rigid and nonrigid parameters from the extracted contours, which are applied to T1-w images to reconstruct motion-corrected myocardial T1 maps. Qualitative and quantitative analyses are performed to evaluate the proposed methods.

METHODS

The proposed motion-correction technique consists of two steps: (i) extraction of the endo- and epicardial contours of all images; and (ii) registration of T1-w images using the extracted contours. The first step is based on the active shape and appearance models (21,23,24). General shape and appearance model training is performed only once (offline) and used to extract the epicardial and endocardial contours of any given T1-w image. In the second step, the given set of T1-w images is registered using both affine and nonrigid transformations, such that the extracted contours of all images are aligned. In the following sections, we describe the steps involved in the proposed motion-correction scheme.

Active Shape Model Construction

A modified formulation of the conventional ASM is used to build a shape model that captures shape variations among the LV boundaries in the given training data set. The LV shape in every image in the training data set is represented by a vector, $\mathbf{x}$, containing the x- and y-coordinates of each point on the endocardial and epicardial contours, as follows:

$$\mathbf{x} = \left[ (x_1, y_2, \ldots, x_{L/2})^{epi}, (x_1, y_2, \ldots, x_{L/2})^{endo}, (y_1, y_2, \ldots, y_{L/2})^{epi}, (y_1, y_2, \ldots, y_{L/2})^{endo} \right]$$  \hspace{1cm} [1]

where $(x)^{epi}$ and $(y)^{epi}$ are the x- and y-coordinates of the epicardial contours, respectively; $(x)^{endo}$ and $(y)^{endo}$ are the x- and y-coordinates of the endocardial contours; and $L$ is the number of landmark points in both epicardial and endocardial contour. To maintain the point correspondences among the training contours, LV contours are aligned by removing rigid transformations (i.e., translation, rotation, and scaling) using Procrustes transformation (23,25). Both epicardial and endocardial contours are aligned simultaneously by applying Procrustes transformation of the $\mathbf{x}$ vectors directly.

Having obtained a shape vector, $\mathbf{x}_n$, for each image in the training data set (with $n = 1, 2, \ldots, N$, where $N$ is the number of images in the training data set), any given LV shape can be represented by a shape vector, $\mathbf{x}$, as follows (23,24):

$$\mathbf{x} = \bar{x} + P\mathbf{b}.$$  \hspace{1cm} [2]

where $\bar{x} = \frac{1}{N} \sum_{n=1}^{N} \mathbf{x}_n$ is the mean shape of the LV contours in the training data set, $\mathbf{b}$ is the model parameters (associated with the given shape, $\mathbf{x}$), and $P$ is a matrix whose columns represent the principal components of the covariance matrix, $C = \frac{1}{N} \sum_{n=1}^{N} (\mathbf{x}_n - \bar{x})(\mathbf{x}_n - \bar{x})^T$. The columns of the matrix $P$ are also referred to as the modes of variations (20,21,23), as they contain the most significant variations that can be linearly added to the mean-shape vector to represent a given LV shape. In this work, only the first 12 eigenvectors of $C$ are used as the principal modes of variations. This number is determined as the smallest number of eigenvectors whose corresponding eigenvalues represent 99% of the total variations (represented by the summation of all eigenvalues) of $C$.

Appearance Model Construction

Similarly, an appearance model represents the local intensity variations at the LV boundaries are built (21,24). In ASM framework, this is done by modeling the image intensity profile at each landmark point on the given contours. Given the training data set of the images and the corresponding myocardium contours, each landmark point is traced and a line segment perpendicular to the contour is drawn such that it is centered at this point and extends for a distance of $(Z/2)$ pixels on both sides of the point (Fig. 1). The image intensity profile along the line segment is stored as a vector $\mathbf{y}$ of length $(Z + 1)$.

At each landmark point, $l = 1: L$, the mean intensity profile and the covariance matrix are computed as $\mathbf{g}_l = \frac{1}{N} \sum_{n=1}^{N} \mathbf{y}_n$ and $Q_l = \frac{1}{N} \sum_{n=1}^{N} (\mathbf{y}_n - \bar{\mathbf{y}})(\mathbf{y}_n - \bar{\mathbf{y}})^T$, respectively. The appearance model is then given by

$$\mathbf{g}_l = \mathbf{g}_l + S_l \mathbf{h}_l.$$  \hspace{1cm} [3]

where $\mathbf{g}_l$ is the intensity profile captured at the $l$th landmark point; $S_l$ is a matrix containing the first $p_l$ eigenvectors estimated from the covariance matrix $Q_l$; and $\mathbf{h}_l$ denotes the appearance-model controlling parameters. In this work, the number of eigenvectors, $p_l$, is selected so that 99% of the intensity variations at landmark $l$ are included in the model.

Given the highly varying contrast of the training images as a result of different T1-weighting, this model may only be used to represent a specific T1-w image (e.g., a landmark in an image at a specific inversion time). Therefore, different appearance models are needed for the different T1-w images. To achieve this, the range of all expected TIs is divided into a number of intervals, $K$, and a separate appearance model is built to represent the images at each interval (Fig. 1). First, the T1-w images in the training sets are arranged into $K$ groups depending on their TI. Then, an appearance model is built for each landmark point, $l$, and each interval, $i$, using Equation [4], which is similar to Equation [3] but with the subscript, $i$, to indicate that there is a separate model for each inversion time interval.
To account for the large heart motion caused by patient movement or breathing, a multiresolution model is considered in this framework (i.e., coarse-to-fine approach). The finest appearance model (level 1) is built from the original full-resolution T1-w images, whereas the following coarser levels are built from down-sampled versions of the images.

**Left Ventricular Myocardial Segmentation**

Given a set of T1-w images with different inversion times, $I_i(x, y; T_{1i})$, the image with the shortest inversion time (i.e., maximum contrast) is selected as a reference image, $I_{ref}(x, y; T_{1ref})$. The shape model and the appearance model (corresponding to the $T_{1ref}$ interval) of $I_{ref}$ are used to extract the myocardial boundaries in $I_{ref}$. In this step, the initial mean shape of the myocardium is manually deposited on $I_{ref}$ by selecting one point inside the blood pool. The initial contour is then evolved iteratively to delineate the LV myocardium using the standard ASM searching algorithm (21). In each iteration, the matching algorithm uses the appearance models to update the location of the contour points, such that the image-intensity profile at each updated contour point is closest to the appearance model (21). In other words, a displacement vector, $\delta$, is estimated to minimize the following error measure:

$$ e = ||D_{ij}^{1/2} \cdot S_{ij} \cdot (\tilde{g}_{ij}(p_i + \delta) - \tilde{g}_{ij})||, $$

where $D_{ij}$ is a diagonal matrix containing the eigenvalues corresponding to the principal components (or modes of variations) of the matrix $S_{ij}$, as estimated in

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**FIG. 1. Active shape model training includes building multiple appearance models for the myocardium at different inversion time intervals. The expected range of inversion times is divided into a number of intervals, $i$. An appearance model, $g_i$, is built to represent the intensity variations around the myocardial borders in the T1-weighted (T1-w) images for interval, $i$. To achieve this, intensity profiles along the perpendicular lines at selected landmark points, $L_p$, on the myocardial border are captured. The model is then built by calculating the mean intensity profile and covariance matrix within a data set for each $L_p$. In addition, a shape model is built for the myocardium, where epicardial and endocardial contours from different subjects are aligned and the mean shape and covariance matrix representing the shape variations are calculated.**
Equation [4], and \( p_i \) is the location of the \( i \)th landmark point. The searching algorithm is restricted to window, \( \tilde{g}_{ij} \), of \( \pm 0.8 \) pixels in a direction perpendicular to the contour at the point \( p_i \).

Following the conventional ASM framework, the resulting vector, \( \mathbf{\delta} \), which represents the updated displacement of each contour point, is transformed to the shape model space by removing all rigid parameters following the same alignment procedure as the shape model construction. These updated displacements are projected onto the trained shape model to produce a smooth LV contour (21,23). The previous steps are performed for a fixed number of iterations, and during the search algorithm, the number of modes of variations is exponentially increased so that all of the points within the myocardium region of interest (ROI) and align the set of \( c \) and \( c_{ref} \), using a simple algebraic method (26). The estimated parameters are then used to globally align image \( I_i \) to \( I_{ref} \). Second, a nonlinear image transformation is applied to \( I_i \) such that all of the points within the myocardium are mapped to their counterparts in the reference image. That is, given the displacement vector, \( \mathbf{d} \), that maps contour \( c_i \) to \( c_{ref} \), a displacement field (for the entire image, \( I_i \)) is estimated through a linear interpolation algorithm. For this purpose, a mesh of a large number of concentric contours is generated from the segmented epicardial and endocardial contours in both \( I_i \) and \( I_{ref} \). To generate such mesh, the contours \( c_{ref} \) and \( c_i \) are up-sampled at a high rate. Finally, a number of contours are generated according to the following equation:

\[
v_i(x, y) = w_1c_i^{epi}(x, y) + w_2c_i^{endo}(x, y),
\]

where \( v_i \) is a generated contour on image \( I_i \); \( c_i^{epi} \) and \( c_i^{endo} \) are the epicardial and endocardial contours; and \( w_1 \) and \( w_2 \) are weighting factors. For a contour generated within the myocardium, \( 0 < w_1 < 1 \) and \( w_2 = 1 - w_1 \); for a contour within the blood cavity, \( w_1 = 0 \) and \( 0 < w_2 < 1 \); and for a contour outside the LV, \( w_2 = 0 \) and \( w_1 > 1 \). This results in a mesh of concentric contours (Fig. 3). This meshing operation is done for the image, \( I_i \), and \( I_{ref} \), to obtain two sets of contours (meshes), \( v_i \) and \( v_{ref} \), respectively.

The registration process is accomplished by transforming the given image \( I_i(x, y) \) into \( \tilde{I}_i(x, y) \), and aligning it with the reference image. The transformation is represented by

\[
\tilde{I}_i(x, y) = W(I_i(x, y)),
\]

where \( W \) is a B-spline warping that maps the mesh grid \( v_i(x, y) \) into \( v_{ref}(x, y) \) (27). The previous steps are applied to all images in the T1-w set.

**Algorithm Implementation**

The proposed framework has been executed using parallel central processing unit implementation on MATLAB (version 2014b, The MathWorks Inc, Natick, MA, USA) using a PC with Intel-i7 quad-core processor and 16G RAM. To maintain the smooth intensity profiles in the segmentation step, each T1-w image in the training and testing phases was convoluted with a Gaussian low-pass filter of size \( 5 \times 5 \) pixels and a SD of 2.5. However, after obtaining the myocardial contours, the nonrigid registration step was applied to original T1-w images (i.e., with no smoothing filters applied) to preserve the spatial resolution of the T1 maps. Building the multiresolution appearance model was done through bicubic interpolation of the original image to generate half the original image size in the first level of coarse resolution.

**Data Acquisition and Evaluation**

Informed consent was obtained from each subject, and the imaging protocol was approved by the institutional review board. Imaging was performed using a 1.5T...
Philips Achieva system (Philips Healthcare, Best, Netherlands) with a 32-channel cardiac coil. T1 mapping was performed in 210 consecutive patients (134 males; age 57 ± 14 years) with known or suspected cardiovascular diseases referred for a clinical cardiac MR exam (available online at https://cardiacmr.hms.harvard.edu/downloads-0). The imaging protocol included a free-breathing, respiratory-navigated, slice-interleaved T1 mapping sequence (14) with the following parameters: repetition time/echo time = 2.7/1.37 ms, field of view = 360 × 351 mm², acquisition matrix = 172 × 166, voxel size = 2.1 × 2.1 mm², linear ordering, sensitivity-encoding factor = 1.5, slice thickness = 8 mm, bandwidth = 1845 Hz/pixel, diastolic imaging, and flip angle = 70°.

Each patient data set consisted of five short axial slices covering the LV from base to apex. At each slice location, 11 T1-w images were acquired at different inversion times, T1i, with $i = 1: K$, where $K = 11$, equal to (T1i = ∞, 135, 135 + RR, 135 + 2 RR, ..., 135 + 4 RR, 350, 350 + RR, ..., 350 + 4 RR ms) with 3-s rest periods between the two inversions, and RR as the duration of the cardiac cycle (14).

The epicardial and endocardial boundaries of all images in the database (N=11550 images) were

FIG. 2. Pipeline for myocardial segmentation from T1-w images. Appearance model, $g_{ref}$, for a selected reference image, $I_{ref}$, is combined with the general shape model, built in the training step to segment $I_{ref}$ in the given T1-w images. One point is inserted manually at the middle of the blood pool of $I_{ref}$ to locate the initial left ventricular (LV) shape of the general shape model on $I_{ref}$. The extracted reference contour, $c_{ref}$, is used to generate the number of simulated LV contours. A new slice-specific shape model (SSSM) is built for that set of T1-w images from the simulated contours. Each of the remaining appearance models, $g_i$, built in the training step is combined with the SSSM to segment the corresponding image, $I_i$, and generate new contour, $c_i$. 
manually delineated, with each contour starting from a myocardium point closest to the anterior insertion of the right ventricle into the LV. This unified beginning of each contour allowed inherent alignment of the contours and facilitated the contour handling in the training and testing phases as will be described. Each contour was then resampled to a fixed number of points, $L = 40$, and was subsequently stored for training and testing. For model training purposes, a training data set of 30 patients (approximately 14% of the whole database) was randomly selected and used to train the model, while the remaining 180 patients (testing data set) were used to evaluate the proposed method.

The manually segmented contours of the T1-w images are used as the reference for evaluating the proposed registration framework by applying the estimated image transformation, $W(x, y)$, to the manually segmented contour, $c_i$, and obtaining the registered contour, $\tilde{c}_i$, for comparison to $c_{ref}$. The MAD and Dice similarity index are used as quantitative measures for the accuracy of the registration process (28,29). The MAD is calculated between the registered myocardial contours, $\tilde{c}_i$, and reference contours, $c_{ref}$, as

$$\text{MAD} = \frac{1}{L} \sum_{l=1}^{L} |d(\tilde{p}_l, c_{ref})|, \quad [10]$$

where $d(\tilde{p}_l, c_{ref})$ is the minimum Euclidean distance between the landmark point in $\tilde{c}_i$. The Dice similarity index for LV myocardial area is calculated as

$$\text{Dice} = 2 \frac{\left| H_{after} \cap H_{ref} \right|}{\left| H_{after} \right| + \left| H_{ref} \right|}, \quad [11]$$

where $H_{after}$ and $H_{ref}$ refer to the set of pixels within the myocardial area in the T1-w images after registration and the reference image, respectively.

Subjective T1 map quality was assessed to evaluate the performance of registration. T1 maps were reconstructed before and after motion correction using two-parameter curve fitting of the T1-w images (19). Two experienced readers independently assessed the image quality using a 1-4 score for each segment (19): Score 1 = nondiagnostic/severe motion artifacts (the T1 map at the myocardium should be completely distorted and T1 cannot be measured at any of its segments); Score 2 = fair/large motion artifacts (the myocardial T1 map could be partially distorted or disappeared, but can still be used for diagnosis in some segments); Score 3 = good/small motion artifacts (the myocardial T1 map could be partially distorted or disappeared, but can still be used for diagnosis in some segments); Score 4 = excellent/no motion artifacts (the myocardial T1 map should be clear with sharp edges). Figure 4 shows an example of images scored by readers. In this evaluation, all T1 maps have been anonymized and each reader has evaluated the performance of the registration process.
separately been asked to give a score to each map and determine the corrupted segments in each map, based on the 16-segment model.

Accuracy and precision of T1 mapping within each segment are assessed before and after motion correction, and with respect to T1 values, were measured using the ROI. To calculate the ROI-based T1 values, the manually segmented LV contours are used to automatically select the ROI from each myocardial segment in T1-w images. The ROI-based T1 values are estimated by fitting the ROI pixels within each segment across different T1-w images. Similarly, ROIs are selected from T1 maps before and after correction at each segment, to be compared with the ROI-based T1 values. Accuracy and precision of T1 values are calculated as the mean and SD of Diff(T1), respectively, where Diff(T1) is the difference between T1 values in the ROI-based T1 and corrected (or uncorrected) maps. Only T1 values within the range of the myocardial relaxation time (i.e., 900 < T1 < 1400 ms) are included in this analysis (14).

Statistical Analysis

The average number of T1 maps in each quality score from both readers before and after motion correction, in addition to the mean SD, was statistically compared using a paired student’s t-test. Interreader variability of T1 maps scores before and after motion correction was tested using intraclass correlation coefficients. Statistical significance was defined at P < 0.05. The average of MAD and Dice index measures before and after motion correction were also compared using a paired student’s t-test.

RESULTS

Figure 5 shows an example of T1 maps at five short axial slices before and after motion correction. The corrupted segments of myocardial T1 maps were restored after applying motion correction despite the vague myocardial borders and large motion at apical slice, as indicated by the corrupted T1 map before correction. Registration of 11 T1-w images of the heart at basal slice is illustrated in Figure 6 (and Supporting Fig. S1). Inner and outer myocardial contours of the reference image are copied to all other T1-w images in both uncorrected and corrected sets. Improved correspondence of myocardial pixels of all T1-w images showed improved registration, and the proposed framework also showed a consistent performance at images of low myocardial contrast, where displacement and orientation of the myocardium was preserved as indicated in the third and fourth images in Figure 6.
Figure 7 illustrates the qualitative assessment of 900 myocardial $T_1$ maps (Supporting Fig. S2). Before motion correction, 68 ± 0.2% of the $T_1$ maps were considered motion-affected maps (i.e., scores of 1, 2, and 3), with 7.5 ± 3.5% of the maps with severe motions artifacts, 17 ± 0.0% with large motions, and 43.1 ± 17% with small motions. After motion correction, 37% ($P < 0.001$) of $T_1$ maps were considered motion-affected maps with only 2.6 ± 1.4% ($P < 0.001$) with severe motions, 5.5 ± 0.2% ($P < 0.001$) with large motions, and 29 ± 8.5% ($P < 0.001$) with small motions. Motion-corrected $T_1$ maps showed improvement in 70 ± 0.2% of the motion-affected maps than before motion correction, whereas no change occurred in 27 ± 0.3% of the $T_1$ maps before and after correction, and $T_1$ map quality was also degraded for 3.2 ± 0.2% of the maps after correction. $T_1$ map quality at apical slices contributed to 59 ± 10.7% of the non-diagnostic score after motion correction, primarily because of large motions and increased partial-volume artifacts at LV apex. Intraclass correlation coefficients between both readers of $T_1$ maps scores were 0.86 and 0.82 before and after motion correction, respectively.

Figure 8 demonstrates the regional analysis of $T_1$ maps before and after motion correction. The bullseye depiction of myocardial segments for five short axial slices indicates a higher number of motion-corrupted myocardial segments before correction (i.e., 21.8 ± 10.4% of total segments versus 8.5 ± 4.6% ($P < 0.001$) after correction). An increased number of corrupted segments are observed at apical slices versus basal or midcavity slices before and after correction. The number of corrupted $T_1$ segments at apical slice was significantly decreased after motion correction to 15.6 ± 7% from 30 ± 8.6% ($P < 0.001$). In addition, the number of corrupted segments in basal and midcavity slices significantly decreased to 6.7 ± 4.2% from 19.7 ± 10.8% ($P < 0.001$) after correction.

Figure 9 shows the accuracy and precision of the estimated $T_1$ values before and after motion correction with respect to ROI-based $T_1$ values within each segment. Motion-corrected $T_1$ maps showed significant increased $T_1$ accuracy and precision compared with uncorrected maps (−8.2 ± 33.9 and −36.8 ± 62 ms, respectively; $P < 0.001$). The MAD distance between extracted and reference myocardial contours significantly decreased from 3.3 ± 1.6 mm to 2.3 ± 0.8 mm ($P < 0.001$) after motion correction. In addition, the Dice similarity index significantly increased from 0.89 ± 0.08 before correction to 0.94 ± 0.4 ($P < 0.001$) after the correction. The computation time of the proposed method to register the $T_1$-w set of 11 images was approximately 5 s.
DISCUSSION

In this work, we introduced an ASM-based framework for motion correction of myocardial T1 mapping. The proposed framework uses a two-step algorithm: segmentation of the myocardial boundaries followed by a contour-based registration of the acquired set of T1-w images. Myocardial segmentation is automatically achieved by applying ASM, which incorporates prior knowledge from trained shape and appearance models. In ASM, the appearance model guides an iterative search process for the myocardium borders in the T1-w images. In each iteration, myocardial contours are estimated and then smoothed through projection on the trained shape model. The computation time of this registration process is 5 s per 11 T1-w images, which is less than that of current conventional intensity-based registration methods (110 or 10 s per 9 or 8 T1-w images as reported in (19) and (18), respectively).

The high blood-myocardium contrast and brightness variations at different TIs and among different patients make the registration process of T1-w images challenging. In intensity-based methods, a matching algorithm is applied to look for similar intensity patterns across the T1-w images; however, contrast/brightness variations among T1-w images hinder its performance. The variations in brightness at different TIs have been previously addressed by applying variable-brightness tracking of feature points on the myocardium (19); nevertheless, the contrast/brightness also varies for different patients at the same TI. In the proposed framework, both types of contrast/brightness variations are handled through two steps: (i) building multiple appearance models at different TIs to take into account the variations among different T1-w images, and (ii) building each appearance

FIG. 7. Graphical illustration of T1 map quality distribution (total of 900 T1 maps) based on a four-point scoring system for quality evaluation averaged from two independent readers. Scores 1, 2, 3, and 4 indicate nondiagnostic, fair, good, and excellent T1 map quality, respectively. The number of T1 maps at each score is displayed in purple and cyan for before and after motion correction, respectively. The status of T1 maps before and after correction is represented by arrows of varying thickness, according to the number of T1 maps moving in a given direction. The enhanced T1 maps are represented by green arrows (i.e., T1 maps moved from a lower score to a higher score). The T1 maps that moved from a higher score to a lower score are represented by red arrows, and T1 maps whose scores did not change are represented by blue arrows.

FIG. 8. Bullseye representation of the number of corrupted segments of five short axial slices before and after motion correction. The myocardium at basal and midcavity slices is divided into six standard segments, whereas the apical slice is divided into four segments. We see a significant decrease in the number of corrupted T1 myocardial segments (represented by dark color) after motion correction than before motion correction (represented by bright color).
model from actual patient data to capture the intrapatient T1 variations.

Different patterns of blood-myocardium contrast can still be noticed at the same TI interval (i.e., intervals near zero-crossing of MR recovery, such as at $i = 3$ or $4$) in different patients: brighter blood than myocardium, fainter blood than myocardium, or blood and myocardium with equal brightness. Modeling such contrast patterns using one appearance model is challenging. However, ASM is able to represent them in different modes-of-variation vectors in the training phase. Additionally, the search algorithm, which depends on projecting the intensity profiles of testing images onto the appearance model, successfully recognizes these different patterns during segmentation. These projection-based matching criteria show better performance than correlation and other edge detection methods in previous studies (21,23).

In our study, we chose a training data set of 30 patients (1650 T1 images). The optimal size of a training data set for ASM is not fixed and depends on the complexity and interpatient variations of the LV. In a pilot study, we investigated the effect of choosing different sizes of training data sets on registration performance. The proposed models were constructed with a data set representing 10 to 60 patients, and evaluated the performance of the registration using MAD and the Dice index. The resulting indices show that the performance reaches a plateau with 30 patients and there is no significance improvement in performance (Supporting Fig. S3). Further studies are warranted to investigate the optimal size of the training data sets.

The contour-based image registration allows efficient use of both rigid and nonrigid transformations estimated from the extracted contours. However, it is crucial to preserve the point correspondence among all extracted myocardial contours of T1-w images. The ASM maintains a consistent arrangement of landmark points, similar to that used in training (21,23). Because all of the manually delineated contours extracted in training have the same

FIG. 9. Accuracy and precision of the estimated T1 values, with respect to region of interest (ROI) based T1 values, for each myocardial segment at five slices before and after motion correction. Accuracy and precision of T1 mapping is calculated as the mean and standard deviation of T1 differences between corrected/uncorrected maps and region of interest–based T1 at each segment, respectively. Both accuracy and precision are reported for each segment.
contour point arrangement, the resulting contours in the testing step have the same arrangement. In this work, we used the lower insertion point of LV and RV as a starting point in the manual delineation, because of its fixed anatomical characteristics, and a fixed number of landmark points selected with equidistant steps from each contour. The qualitative assessment showed motion artifacts in 66% of the T1 maps in our data set before correction. After applying the proposed methods, the number of motion-affected maps significantly decreased. T1 maps with severe and large motions showed a significant decrease after motion correction, which indicates the ability of the proposed method to capture large motions of the myocardium. Additionally, 63 ± 0.3% of the small-motion-scored maps completely recovered and were assigned the no-motion score after correction, indicating the ability of the proposed methods to correct for fine myocardial deformation caused by cardiac motion in the through-plan direction. However, small motion artifacts were noticed after correction in 10.6 ± 4.3% of the uncorrected motion-free maps (representing approximately 28 T1 maps) as a result of inaccurate segmentation of the LV myocardium. Qualitative analysis of myocardial segments also showed a significant decrease in the number of motion-corrupted segments down to 8.5% of all segments, with approximately 38.4 ± 5.3% of the corrupted segments at the apical slice. The increased number of motion-corrupted segments at apical slices is primarily caused by the increased myocardial motions at the LV apex and degraded myocardial contrast caused by partial-volume artifacts. We also noticed an increased average number of motion-corrupted segments for both corrected and uncorrected maps at LV inferior wall in all slices—basal, midcavity, and apical—as previously reported (10).

The high variability of myocardial morphology caused by different diseases (e.g., hypertrophic and dilated cardiomyopathies) poses a challenge in building the shape model. To circumvent this problem, patients with different cardiac diseases should be sufficiently represented in the training data set. In the proposed registration approach, the contours for epicardium and endocardium borders are extended and aligned instead of pixel-by-pixel alignment. One potential disadvantage of this approach, compared with intensity-based image registration, is that only contour information is used in registration. The registration of contours does not automatically guarantee alignment of myocardial pixels and may cause registration error within the myocardium. In addition, in the proposed model-based framework, new training of shape and appearance models is needed for images acquired with different orientations (e.g., long axis view) or different ranges of T1 (e.g., postcontrast T1 mapping). Although the multiresolution implementation of the proposed framework alleviates large motions of the myocardium, there are still trade-offs in the model flexibility for capturing the fine variations of the myocardium and capturing the large motions. The parallel implementation of this framework is found to be effective, because every T1-w image within a given case (except for the reference image) can be processed independently from others. Thus, all T1-w images are segmented and registered simultaneously on multiple processing cores, leading to a shorter processing time by a factor of the number of central processing unit cores (i.e., one-fourth in our experiments) to the regular implementation time.

CONCLUSIONS

The proposed method for nonrigid registration of T1-w images allows T1 measurements in more myocardial segments by eliminating motion-induced T1 estimation errors in the myocardium segments.

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