Boosting and Nonparametric Based Tracking of Tagged MRI Cardiac Boundaries

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Abstract. In this paper we present an accurate cardiac boundary tracking method for 2D tagged MRI time sequences. This method naturally integrates the motion and the static local appearance features and generates accurate boundary criteria via a boosting approach. We extend the conventional Adaboost classifier into a posterior probability form, which can be embedded in a particle filtering-based shape tracking framework. To make the tracking process more robust and faster, we use a PCA subspace shape representation to constrain the shape variation and lower the dimensionality. We also learn two shape-dynamic models for systole and diastole separately, to predict the shape evolution. Our tracking method incorporates the static appearance, the motion appearance, the shape constraints, and the dynamic prediction in a unified way. The proposed method has been implemented on 50 tagged MRI sequences. The experimental results show the accuracy and robustness of our approach.

1 Introduction

Tagged cardiac magnetic resonance imaging(MRI) is a well known technique for non-invasively imaging the detailed myocardial motion and deformation throughout the heart cycle. In the tagged MRI protocol, ECG triggering is used to acquire a time sequence of images at several frames in a heart cycle. Quantitative analysis of the myocardial wall motion requires accurate segmentation of the epicardial and the endocardial boundaries for the whole time sequence. This segmentation problem is difficult due to the presence of tagging lines, the complexities of the cardiac geometry, the fast motion of the myocardium, and the high level of MR image noise. There have been some prior efforts to achieve tagged MRI segmentation. In [1], grayscale morphological operations were used to separate non-tagged blood-filled regions from the tagged myocardium regions. In [2, 3], learning methods including shape, intensity and appearance modeling were proposed.

It has been noted by several researchers that incorporating temporal information would greatly help the segmentation. When a human expert manually delineates the contours, it is common practice to watch the MRI images as a *movie* and use other frames and their motion to segment the current frame. Using this observation, in this paper we propose a dynamic segmentation approach. Several methods in the MRI literature have used temporal information to help segmentation. Sun *et al.* [4] proposed a segmentation and tracking

method for the left ventricle by learning the ventricle dynamics. In [5], tracking of the myocardium is embedded in a nonrigid image registration framework. More myocardial boundary tracking methods can be found in the echocardiography literature. Comaniciu *et al.* [6, 7] proposed a multi-model information fusion framework to achieve robust myocardial boundary tracking. In [8, 9] shape-space based or contour-matching based approaches are proposed.

In this paper, we introduce a new framework for boundary tracking of short axis (SA) tagged MRI sequences, including the boundary contours of the endocardium of the left ventricle (LV), the endocardium of the right ventricle (RV) and the epicardium. In this framework, in order to find strong image features, instead of visually tracking the contour points via profile matching or optical flow related methods, we learn a more complex boundary criterion using AdaBoost. Contour profile consistency between two consecutive frames (the motion feature) is an important feature in tracking, but it has limitations in handling the inherent appearance changes due to tag fading and myocardial deformation, especially the boundary's tangential movement (such as rotation and sliding, see Fig. 2b) and myocardial motion through the imaging plane. Using the boosting algorithm, we demonstrate that for more accurate boundary feature extraction, the local boundary appearances in the current frame (the static feature) are also important. The AdaBoost algorithm gives a natural way to combine both features and generate better boundary criteria. Furthermore, through boosting error analysis, we find the confidence ratings of each criterion and calculate the posterior probability density function of the shape model. In order to lower the dimensionality and constrain the shape variations, we project the shape into a Principal Component Analysis (PCA) subspace [10], and update the PCA parameters instead of the contour points' positions. Since the heart motion has a cyclic contraction and expansion pattern, which exists in both normal and diseased hearts, we treat the systole and diastole separately and find two motion prediction matrices and error covariance matrices via multivariate linear regression. We embed the shape tracking into a nonparametric-based sequential particle filtering framework [11] for its ability of contour tracking through heavy clutter.

Our overall learning and tracking framework is outlined by the flow-chart in Fig. 1. Our experimental results show the accuracy and effectiveness of the proposed algorithm.

2 Shape Modeling and Boosting the Boundary Criteria

2.1 Shape Model

The shape of the mid portion of the heart in SA images is consistent and topologically fixed (one LV and one RV). Therefore it is reasonable to implement a PCA subspace shape model [10] to represent prior shape knowledge and constrain the shape variations during the myocardial wall tracking process. This is particularly desirable in the tagged cardiac MRI case. For many reasons including the noisy nature of tagged MRI and the complex structure of the heart, *accurate* boundary tracking based solely on the MR images is usually not possible. See, for example,

Fig. 1. The flow chart of our proposed framework illustrates the learning and tracking processes. In the manual contour block, the red circles indicate the cusp points between the septum and the RV endocardium. The green circle indicates the location of papillary muscle. In the dynamic block, cooler color turning into warmer color indicates the dynamic model’s evolution during systole.

the manual contour box in Fig. 1, which shows an expert’s manual segmentation results: the two cusp points between the septum and the RV endocardium are always kept, and the papillary muscles in LV and RV are excluded from the endocardium. This cannot be done automatically without strong shape priors.

We use the expert’s manual contours as the PCA input. The manual contours are first centered and transformed to the same scale and orientation. Then they are automatically discretized into 50 ordered landmark points (see the discretization box in Fig. 1) using geometry features such as maximum curvature. Then principal component analysis is applied and the modes of shape variation are found. Any heart shape can be approximately modeled by $X = \bar{X} + Pb$, where $\bar{X}$ is the mean shape vector, P is the matrix of shape modes, and b is the vector of shape parameters weighting the shape variations. The following boundary criterion learning method will be applied on the landmark points individually.

2.2 Learn Boundary Criteria Using Adaboost

Probability Estimation in Adaboost. To reliably and accurately track the myocardial boundary, we try to use all possible image cues, including the static features and the motion features, to make a strong boundary criterion. This cue-integration is performed by Adaboost. Adaboost is a well known classification algorithm [12] that incrementally selects a small number of important features from a huge potential feature set and creates a linear combination of them as an accurate strong classifier. In the learning stage, given training data

$(x_1, y_1) \dots (x_m, y_m)$, where $x_i \in X$, $y_i \in \{0, +1\}$, during the boosting process, each iteration selects one feature, i.e., a weak classifier, h_t from the total potential features pool, and combines it (with an appropriate weight α_t) with the existing classifier that was obtained in the previous iterations.

$$h_t : X \rightarrow \{0, +1\} \quad (1)$$

$$F = \sum_t \alpha_t h_t(x) \quad (2)$$

After t iterations, the linear combination of the selected important features F makes a stronger classifier $H(x)$ with higher accuracy. We denote $\Gamma = \sum_t \alpha_t / 2$ as the threshold value for F . For a new input data x to be classified, if $F > \Gamma$, H classifies x as positive, and vice versa.

$$H(x) = \frac{\text{Sign}(F - \sum_t \alpha_t / 2)}{2} + \frac{1}{2} \quad (3)$$

We perform Adaboost boundary learning at each landmark point on the shape model. Thus the boundary criteria vary according to each model point's location. In order to embed the Adaboost $\{0, 1\}$ classifier into the sampling-based tracking framework, we need to extend it to a probability representation. Influenced by [13], we use a logistic function to estimate the probability of a point x_k , along with its local appearance patch, being on the boundary at the location of landmark point k , with a normalization term Γ_k the same as the threshold value:

$$\text{Pr}(y_k = +1 | x_k) = \frac{e^{F_k(x_k)/\Gamma_k}}{e^{F_k(x_k)/\Gamma_k} + e^{-F_k(x_k)/\Gamma_k}} \quad (4)$$

After the training process, Adaboost provides the error rates e_k on the testing data. We define the confidence rating of the boundary criterion at point k as:

$$c_k = \ln \frac{1}{e_k}; \quad (5)$$

Intuitively, when c_k is big, we trust its probability prediction $\text{Pr}(y_k = +1 | x_k)$ more. We incorporate the confidence rating into the probability $\text{Pr}(y_k = +1 | x_k)$ as a posteriori knowledge. Then the probability density function of the shape model is estimated by:

$$p(Y = +1 | X) \propto \prod_k \frac{e^{F_k(x_k)c_k/\Gamma_k}}{e^{F_k(x_k)c_k/\Gamma_k} + e^{-F_k(x_k)c_k/\Gamma_k}} \quad (6)$$

Boundary Feature Design. The boosting algorithm investigates a large number of weak feature candidates. At each landmark point on the shape contour, the local appearance features are captured by filtering methods in both static and motion cases.

To capture the static local appearance features, we design three different kinds of steerable filters. We use the derivatives of a 2D Gaussian to capture the edges, we use the second order derivatives of a 2D Gaussian to capture the ridges, and we use half-reversed 2D Gabor filters to capture the tagging line breakpoints.

The half-reversed 2D Gabor filters are defined as a 2D sine wave multiplied with the one directional derivative of a 2D Gaussian:

$$F = G'(x, y) \cdot \mathbb{R}\{e^{-j[\phi+2\pi(Ux+Vy)]}\} \quad (7)$$

where G' is the derivative of a 2D Gaussian. U and V are the frequencies of the 2D sine wave, and ϕ is the phase shift.

To capture the motion local appearance features, we measure the intensity consistency between two consecutive frames. In order to avoid the effect of boundary tangential motion, before comparison, a set of Gaussian filters are designed to blur the boundary local patch in a certain orientation and scale (See Fig. 2(b)).

For a 15x15 sized filter patch, by tuning the filters' scale, orientation and frequency, we designed 1840 static filters and 121 motion filters in total. See Figure 2(a) for some sample static filters.

In the manually segmented images, at each landmark point of the contours, a small image patch around it is cut out as a positive appearance training sample for this particular landmark point. Then, along the normal of the contour, on each side of the point, we cut out another two patches as the negative appearance training samples for this particular landmark point. (See boundary appearance box in Fig. 1) For motion features, the consistencies are measured between the current frame sample with the positive sample in the previous frame.

After the training process, the classification error rates on the testing data give the measurement of the boosting performance. After 50 Adaboost iterations, we find that the error rates using both static and motion features are much lower than using either static or motion features alone. See Figure 2(c). This comparison validates our boundary tracking scheme based on both motion and static features.

Fig. 2. (a) shows 3 sample sets of static feature filters, from top to bottom, the derivatives of Gaussian used for edge detection, the second derivatives of Gaussian used for ridge detection, and the half-reversed Gabor filters used for tag line breakpoint detection. (b) illustrates the function of the motion feature filter, which helps remove the tangential motion. (c) shows the testing error rates of the boundary criteria boosting. The red curve which integrates both motion and static features has lower error rates than the other two.

3 Nonparametric Shape Tracking

Sampling-based tracking algorithms have the ability to handle contour tracking problems with non-Gaussian probability density functions (pdfs). Our tracking method is based on a nonparametric particle filtering approach [11], where the pdf is represented by factored sampled particles.

During myocardial wall tracking, we use a state vector s to represent the shape model. $s = [c, \theta, t_x, t_y, b]$, where c is a scaling factor, θ is the orientation angle, (t_x, t_y) is translation, and b is a 12-D variation vector of the PCA shape modes. The myocardial wall tracking algorithm based on particle filtering is as follows:

1. Suppose the total sample number is N , total time frame number is T . At $time = 1$, $s_1^{(n)}$ is initialized as the manual contour shape at the first frame. Weights $\pi_i^{(n)} = \frac{1}{N}$.
2. For $time = 2 : T$,
 - Factored draw samples $s_t'^{(n)}$ from s_{t-1} based on the weights $\pi_{t-1}^{(n)}$.
 - Predict new $s_t^{(n)}$ by sampling from a dynamic model $p(x_t|x_{t-1}) = s_t'^{(n)}$.
 - Measure and weight the new shape in term of the measurement y_t by Eq. 6. $\pi_t^{(n)} \propto p(Y_t|X_t = s_t^{(n)})$, and $\sum_n \pi_t^{(n)} = 1$
 - Estimate the solution via the strongest local mode.
 - End for

There are two main difficulties in implementing the algorithm. The first one is how to find a proper dynamic model. The second is how to decide the sampling size N .

The motion pattern differs greatly among human hearts, especially between the normal and the diseased. Our strategy is to find a common dynamic model whose constraint is loose but can help in decreasing the sampling range. Since the tagged MRI sequences are acquired with an ECG trigger, the end systolic (ES) frame is easy to locate. We train the dynamic model based on systole and diastole separately. For a given state vector $s^{(t)} = [s_1^{(t)}, s_2^{(t)}, \dots, s_n^{(t)}]'$ at time t , we make an assumption that it can be approximated by a linear transform of $s^{(t-1)}$.

$$s_i^{(t)} = a_0 + a_1 s_1^{(t-1)} + a_2 s_2^{(t-1)} + \dots + a_n s_n^{(t-1)} + N(0, r_i^2) \quad (8)$$

This is a multivariate linear regression problem. We solve it to get $A_i = [a_0, a_1, \dots, a_n]$ as the prediction vector of s_i and r_i^2 as the error variance. Then the conditional probability of the prediction dynamic model is:

$$p(s_i^{(t)}|s^{(t-1)}) = \frac{1}{\sqrt{2\pi r_i}} \exp\{-(s_i^{(t)} - A_i \cdot s^{(t-1)})^2 / 2r_i^2\} \quad (9)$$

The sampling size N is experimentally set. For 12 sequences of the testing data, we find the tracking typically stops improving after $N \geq 1000$. Thus we set $N = 1000$.

4 Experimental Settings and Results

We acquired 50 time sequences of short-axis tagged MR images from 5 normal subjects and 3 patients. Each sequence contains 12 to 18 frames (images). In total, we collected 776 images. The spatial positions of these SA images vary from near the ventricle apex to near the ventricle base, but their topologies, only one LV and one RV, are consistent. The tagging line orientations are either 0° , 90° or $\pm 45^\circ$. An expert was asked to segment the epicardium, the LV endocardium and the RV endocardium from the images. The manual segmentations were used as the training data, as well as the ground truth in validation based on a leave-6-out scheme, in which each time 44 sequences were grouped as the training data while the other 6 were used for testing. If two sequences were taken from the same subject and at the same spatial position, but with different tag orientations, we grouped them in the same training or testing set. In this way, we strictly separated the training and testing data.

Each training image is rotated and scaled to contain a 80×80 -pixel image of the heart with the interior chest wall on top. The size of the boundary appearance patches is set to 15×15 pixels. In the tracking process, the initial contour is set semi-automatically [3] allowing manual correction. Our algorithm implementation is coded in Matlab 6.5 and runs on a 3GHz PC workstation. For a tracker with a sampling size of 1000, it takes 60 seconds to track a frame on average.

See Fig. 3 for some representative tracking results. Since the resulting contours are represented by 50 landmark points, we measure the tracking error by calculating the distances from the landmark points s_i to the expert's manual

Fig. 3. Snapshots from three example sequences of our experimental results. The solid contours are from our tracking method, while the dashed are from manual segmentations. The first 2 rows are data from 2 normal subjects. The last row is from a patient with heart failure. Note that our tracking method can exclude the papillary muscle from the ventricle endocardium, and always keep the cusp points at the RV-LV junctions.

contour C : $error(s_i, C) = \min_{c_i \in C} \|s_i - c_i\|$. Fig. 4(a) shows the mean error in pixels for each time sequence; the mean error for the LV, RV and epicardium are also drawn. In Fig. 4(b) some error analysis are performed in millimeters.

Conclusion/Discussion. In this paper, we have proposed a tracking framework for tagged MRI. Our method integrates the boundary appearance (both static and motion), the shape constraints and the dynamic model naturally in a boosting and nonparametric tracking framework. We strictly test the algorithm on data that are excluded in the training set. The experimental results show the accuracy. With the error analysis shown in Fig. 4(b), we find that in general we have achieved sub-millimeter accuracy while MRI accuracy is approximately $1mm$. Our method works slightly better on the mid-ventricle slices and on normal hearts. In the future we will train more shape and motion models for different slice positions and extend up to the valve region, where the RV separates into distinct inflow and outflow regions. We will also extend the method by training on different diseases, where the shape and motion of the patient data can be very different from the normal (see the last row of Fig. 3, which is from a patient with heart failure).

	$error (mm) \quad \sigma (mm)$	
LV	1.24	0.66
RV	0.79	0.81
Epi	0.67	0.91
Near Base	0.77	0.89
Mid	0.71	0.81
Near Apex	0.87	0.99
Normal	0.76	0.86
Patient	0.89	1.03

Fig. 4. (a) The mean error for each time sequence measured in pixel. The red solid curve represents the overall error. The blue dashed, black dash-dot and green dotted curves represent the mean error distances in the LV, RV endocardium and epicardium respectively. (b) Error analysis in millimeters.

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