Segmentation of the Left Ventricle in Cardiac MRI using a Robust Active Shape Model Approach

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Abstract

The segmentation of the left ventricle in MRI is a required task to evaluate and diagnose cardiac function. The main challenges for the development of an automatic segmentation tool are: i) the presence of misleading anatomical structures, ii) edge fuzziness near the apical and basal slices, and iii) misalignment between consecutive slices. A common approach is to use shape information to guide the segmentation, e.g., using an Active Shape Model (ASM). However, the presence of outliers hampers the accuracy of this approach. This paper proposes an EM framework that takes outliers into account and is able to provide robust segmentation estimates. The proposed method was evaluated on a public dataset with 33 MR sequences and the results show it provides significant improvements over the standard ASM method, and also outperforms another state of the art approach.

1 Introduction

Cardiac MRI is the standard image modality for the assessment and diagnosis of some cardiomyopathies [4]. After acquiring a sequence of MR volumes, covering a entire cardiac cycle, cardiologists have to manually delineate the inner boundary of the left ventricle (LV), called endocardium. Only then are they able to compute specific features of cardiac function, such as ventricle volumes and ejection fraction.

To relieve cardiologists of this morose task, several (semi)automatic segmentation algorithms have been proposed over the years [5]. However, automatically identifying the endocardium is a complex task, due to: 1) wall irregularities, caused by the presence of papillary muscles and trabeculations; 2) edge fuzziness near the apical and basal slices, due to partial volume effects, and 3) misalignment between consecutive volume slices that may appear due to different breath-holding levels during acquisition.

A popular approach is to use shape priors to constrain the final segmentation [3]. Among this type of approaches, one of the most popular is the Active Shape Model (ASM) [2]. This method uses an explicit representation of the contour that is able to deform according to specific modes of variation observed in a training set of annotated data.

Although ASM based methods have achieved state of the art results, their performance is often hampered by the presence of other misguiding boundaries, typically denoted as outliers. This paper proposes a robust ASM that is able to achieve accurate results even in the presence of outliers [6]. The proposed method is based on an Expectation-Maximization (EM) approach that assumes each edge segment detected in the MR volume may either belong to the endocardium or to outliers. Under this assumption, each edge segment is assigned a specific weight during the segmentation process depending on the probability that it belongs to the LV boundary, as will be explained in the following section.

2 Proposed Methodology

2.1 Shape Model

In this work, a 3D shape model is used to define the segmentation of each MR volume. This shape model is learned using the approach described in [7], which provides a framework to overcome the challenge of learning a 3D shape model from annotated volumes with a variable number of slices. Formally, it allows a specific slice model, $\mathbf{x}(s) = [\mathbf{x}^1(s), \dots, \mathbf{x}^N(s)] \in \mathbb{R}^{2N}$, to be obtained from the training set, where $s \in [0,1]$ denotes the

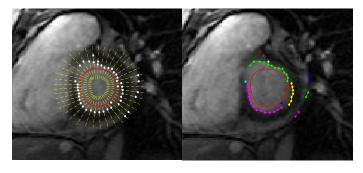


Figure 1: Extraction of candidate edge segments from a volume slice: (left) detection of edge points (white) along lines (yellow) orthogonal to the model (red); (middle) edge segments obtained by linking edge points.

position of that slice in the MR volume, and $x^j(s) \in \mathbb{R}^2$ defines the position of the *j*-th model point within the slice. The position of the model points is defined by the set of parameters, $\boldsymbol{\theta} = \{\boldsymbol{a}, \boldsymbol{t}\}$ and $\boldsymbol{b}(s)$, which correspond to the parameters of the similarity (pose) transformation and the deformation coefficients, respectively, through

$$\boldsymbol{x}(s) = \boldsymbol{T}_{\boldsymbol{\theta}} \left(\overline{\boldsymbol{x}}(s) + \boldsymbol{D}(s) \boldsymbol{b}(s) \right), \tag{1}$$

where $\bar{\boldsymbol{x}}(s) \in \mathbb{R}^{2N}$ is the average model in slice position $s, \boldsymbol{D}(s) \in \mathbb{R}^{2N \times L}$ is the matrix of deformation modes, and $\boldsymbol{T}_{\boldsymbol{\theta}}$ is the linear transformation that defines the pose of the LV.

Unlike typical ASMs, the shape model used in this work includes two additional deformation modes, which grant each slice model the ability to move within the slice plane, thus allowing them to fit misaligned slices.

2.2 EM Framework

The goal of the algorithm is to segment all the slices of a particular MR test volume. Suppose this volume has S slices, and that the position of the m-th slice is given by s_m . In order to fit the shape model to the boundary of the LV in all the slices, the model parameters, $\boldsymbol{\theta} = \{\boldsymbol{a}, \boldsymbol{t}\}$ and $\boldsymbol{b}(s_1), \ldots, \boldsymbol{b}(s_S)$, have to be chosen accordingly. Candidate points are extracted from each slice by searching along lines orthogonal to the model, as depicted in Fig. 1 (left). Then, edge segments are obtained by grouping these candidates, as shown in Fig. 1 (right).

Each of the detected edge segments, denoted by $Y^i(s_m) \in \mathbb{R}^{2M^i}$, may belong to the endocardium or to outliers. Since this information is not known *a priori*, a binary hidden variable, $k^i(s_m)$, is used to allow both possibilities: $k^i(s_m) = 1$ for valid segments and $k^i(s_m) = 0$ for outliers. These two possibilities are assumed to occur with probabilities p_1 and p_0 , and, for each case, a different observation model is used, as follows

$$p\left(\mathbf{Y}^{i}(s_{m})\middle|k^{i}(s_{m})=1,\boldsymbol{\theta}\right)=\prod_{j=1}^{M^{i}}\mathcal{N}\left(\mathbf{y}^{ij}(s_{m});\mathbf{x}^{ij}(s_{m}),\boldsymbol{\Sigma}^{ij}(s_{m})\right),\quad(2)$$

$$p\left(\mathbf{Y}^{i}(s_{m})\middle|k^{i}(s_{m})=0,\boldsymbol{\theta}\right)=\prod_{i=1}^{M^{i}}\mathcal{U}(V_{\mathbf{x}^{ij}(s_{m})}),\tag{3}$$

where $\mathbf{y}^{ij}(s_m) \in \mathbb{R}^2$ is the *j*-th candidate point in $\mathbf{Y}^i(s_m)$ and $\mathbf{x}^{ij}(s_m)$ is the corresponding model point. $\mathcal{N}(\cdot)$ and $\mathcal{U}(\cdot)$ define a Gaussian and a uniform distribution, respectively. $\mathbf{\Sigma}^{ij}(s_m)$ is the variance associated with the corresponding model point, $\mathbf{x}^{ij}(s_m)$, and $V_{\mathbf{x}^{ij}(s_m)}$ defines a validation gate in the vicinity of $\mathbf{x}^{ij}(s_m)$.

Let $\Theta = \{a, t, b(s_1), \dots, b(s_S), p_1, p_0\}$ define the complete set of parameters, and let \mathcal{Y} and \mathcal{K} be the set of all the detected segments in all

the slices and their corresponding labels. The EM framework allows Θ to be iteratively optimized by maximizing the expectation of the complete posterior probability,

$$\widehat{\mathbf{\Theta}}_{(t+1)} = \arg \max_{\mathbf{\Theta}} Q\left(\mathbf{\Theta}; \widehat{\mathbf{\Theta}}_{(t)}\right) = \mathbb{E}_{\mathcal{K}}\left[\mathcal{P}(\mathcal{Y}, \mathcal{K}, \mathbf{\Theta}) \middle| \mathcal{Y}, \widehat{\mathbf{\Theta}}_{(t)}\right], \quad (4)$$

in a two step procedure. In the first step, *E-step*, the probability of each edge segment being valid (or outlier) is updated based on the current model estimate

$$w_1^i(s_m) = p\left(k^i(s_m) = 1 \middle| \mathbf{Y}^i(s_m), \widehat{\mathbf{\Theta}}_{(t)}\right)$$
 (5)

$$w_0^i(s_m) = p\left(k^i(s_m) = 0 \middle| \mathbf{y}^{ij}(s_m), \widehat{\mathbf{\Theta}}_{(t)}\right), \tag{6}$$

such that $w_1^i(s_m) + w_0^i(s_m) = 1$. In the second step, *M-step*, the model parameters are updated by maximizing (4). This leads to a weighted least squares regression that minimizes the distance between the model points and the corresponding edge segments, where each segment is weighted by (5).

Since outliers typically receive lower weights, their influence in the estimation of the model parameters is reduced, leading to more robust results. The algorithm iterates between the two steps until the parameters converge.

3 Results

The proposed algorithm was evaluated on a public dataset [1], which contains 33 MR sequences, each with 20 volumes. The results were obtained using a leave-one-sequence-out scheme: for each test sequence, the shape model was learned using the remaining 32 sequences.

The segmentations were evaluated by comparison with the ground-truth using two metrics: 1) the Dice coefficient, which measures the agreement between two segmented regions, and 2) the average distance (AV) between the model points and the ground-truth. Statistical results for another state of the art approach [6] are also provided for comparison.

Fig. 2 shows some examples of the segmentations obtained using the proposed method. It is possible to see that the proposed segmentation is similar to the ground-truth in most cases. Fig. 3 shows other examples with a color-coded evaluation of each slice segmentation. Two conclusions can be drawn. First, volumes in the end-dyastolic frame are easier to segment, which is expected since the LV is dilated and its borders are more noticeable. Second, the segmentation of the apical slice is typically poorer than the remaining slices, due to the partial volume effect mentioned in Section 1.

Table 1 summarizes the statistical results obtained using the proposed approach and using the RANSAC algorithm proposed in [6]. The results show that the proposed method outperforms the RANSAC approach, even though the latter also brings significant improvements over the standard ASM proposed in [2].

Table 1: Statistical performance of the proposed algorithm (mean and standard deviation) and comparison with other approaches.

	Dice (%)	AV (mm)
ASM [2]	73.1 (13.1)	4.7 (3.0)
RANSAC [6]	83.0 (7.5)	2.7 (1.0)
Proposed	85.8 (6.7)	2.2 (0.6)

4 Conclusion

This paper proposes a robust Active Shape Model approach that is able to deal with the difficulties associated with cardiac MRI analysis: the presence of other anatomical structures that misguide the model (outliers) and the existence of misaligned slices. The proposed approach is based on an EM framework that takes into account the presence of outliers. By assigning weights to candidate edge segments extracted from the image, the algorithm is able to reduce the influence of outliers in the estimation of the model parameters, thus leading to robust segmentations. Significant improvements over the standard ASM and another state of the art approach are achieved and show that the proposed method is able to provide good LV segmentations.

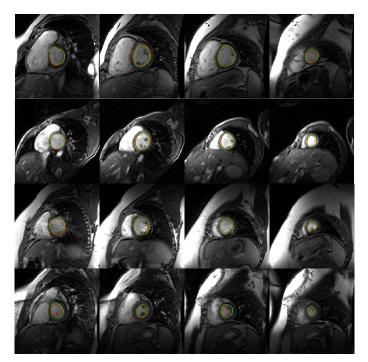


Figure 2: LV segmentation. Each row shows four slices of a different volume depicting: the segmentation obtained using the proposed method (red), and the ground truth (green).

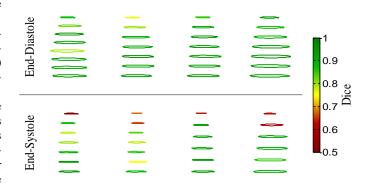


Figure 3: Examples of the estimated 3D segmentation and corresponding evaluation.

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