MYOCARDIUM SEGMENTATION COMBINING T2 AND DE MRI USING MULTI-COMPONENT BIVARIATE GAUSSIAN MIXTURE MODEL

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ABSTRACT

Accurately delineating the myocardium from cardiac T2 and delayed enhanced (DE) MRI is a prerequisite to identifying and quantifying the edema and infarcts. The automatic delineation is however challenging due to the heterogeneous intensity distribution of the myocardium. In this paper, we propose a fully automatic method, which combines the complementary information from the two sequences using the newly proposed Multi-Component Bivariate Gaussian (MCBG) mixture model. The expectation maximization (EM) framework is adopted to estimate the segmentation and model parameters, where a probabilistic atlas is also used. This method performs the segmentation on the two MRI sequences simultaneously, and hence improves the robustness and accuracy. The results on six clinical cases showed that the proposed method significantly improved the performance compared to the atlas-based methods: myocardium Dice scores 0.643±0.084 versus 0.576±0.103 (P=0.002) on DE MRI, and 0.623±0.129 versus 0.484±0.106 (P=0.002) on T2 MRI.

Index Terms—multi-component bivariate Gaussian mixture model, expectation maximization, probabilistic atlas, myocardial infarction, Magnetic Resonance Imaging

1. INTRODUCTION

Assessing variability of the myocardium is essential in diagnosis and treatment management for patients suffered from myocardial infarction [1-4]. Cardiac MRI sequences are widely used in clinics, in particular the Delayed Enhanced (DE) sequence, which can visualize the infarcts, and the T2-weight MRI, which provides the information of the ischemic regions[1, 2]. To localize and quantify the edema and infarct regions, segmenting the myocardium from the T2 and DE MRI is a prerequisite.

However, the automatic segmentation of the myocardium is challenging due to the intensity heterogeneity, as Fig. 1 illustrates.

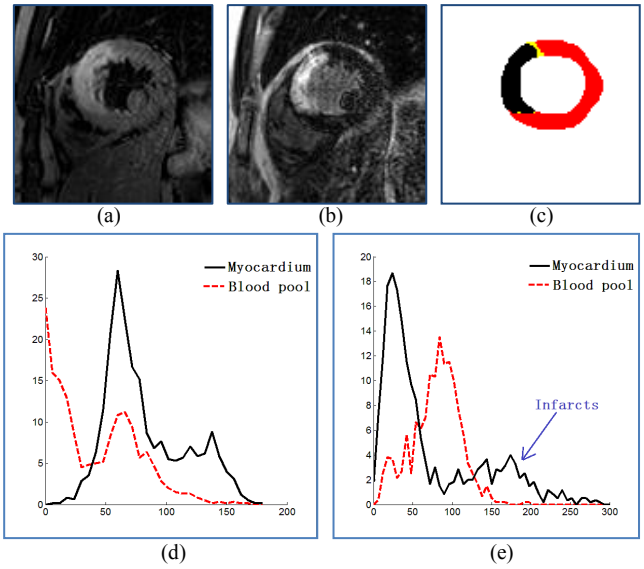

Fig.1. Cardiac MRI images and the intensity distribution: a T2 image (a) and the intensity distributions (d); a DE image (b) and the intensity distribution (e); (c) provides the classification results of the myocardium.

Firstly, the intensity range of the myocardium is overlapped with that of the blood pools, particularly in the DE MRI due to the contrast enhancement to the infarct regions. Hence, the boundary between the infarcts and blood pools is generally indistinct and particularly difficult to delineate.

Secondly, the intensity of the myocardium is not normally distributed in either the T2 or DE sequence. Instead, the intensity distribution is a mixture of at least two components: one for the healthy tissues and the other for the ischemic regions (infarcts in DE MRI, edema in T2 MRI). This challenges the traditional EM-based frameworks [5] and the atlas-based segmentation methods[6], where uniformity of the intensity distribution is commonly assumed.

To deal with the challenges, in this work we propose to combine the complementary information of the two cardiac MRI sequences and perform the segmentation simultaneous-

ly within a unified framework. This is inspired by the previous work [3] that the missing information, such as boundaries, in the DE MRI can be complemented form the T2 MRI, and *vise versa*. In the proposed method, the two MRI sequences are assumed to be pre-registered, and the intensity distribution of the two registered images is then formulated by a Multi-Component Bivariate Gaussian (MCBG) mixture model. The segmentation and model parameters are estimated by using the Expectation Maximization (EM) algorithm. Finally, the segmentation result of the proposed method also has potential to classify the regions of edema and infarcts in the T2 and DE sequences respectively, as the Fig 1 (c) shows.

The rest of this paper is organized as follows: the proposed method is described in Section 2; the experiments and results are presented in Section 3; conclusions and discussions are given in Section 4.

2. METHOD

This work intended to classify image voxels from pre-registered T2 and DE sequences jointly into spatially coherent classes, $\Lambda = \{L_{\text{myo}}, L_{\text{LV}}, L_{\text{RV}}, L_{\text{b}}\}$, namely, myocardium, left ventricle (LV), right ventricle (RV) and background. First, the prior class probabilities for an image voxel were determined by propagating probabilistic atlases constructed from healthy subjects using image registration [5]. Second, image intensity values from both registered images were jointly modeled by a bivariate random vector. Moreover, to account for within class intensity heterogeneities, a multi-component Gaussian mixture (MCGM) model was proposed. The segmentation and model parameters were estimated by maximizing the log-likelihood using the Expectation Maximization (EM) algorithm [7].

2.1. Multi-Component Bivariate Gaussian (MCBG) mixture model

In this study, we assumed, for each class of interest, the joint intensity distribution from T2 and DE sequences followed a multi-component bivariate Gaussian mixture. For observed intensity pair, $\mathbf{y}_i = (y_i^{T2}, y_i^{DE})'$, $i = 1,...,N$, where N is the total number of voxels, the MCBG can be written as,

$$f(\mathbf{y}_i \mid \mathbf{\Phi}) = \sum_{L\in\Lambda}\sum_{j=1}^{n_L} \pi_{iL_j}\phi(\mathbf{y}_i \mid \boldsymbol{\mu}_{L_j}, \boldsymbol{\Sigma}_{L_j}) \tag{1}$$

where n_L is the total number of components for class L. π_{iL_j} is the mixture proportion of the jth component of class L, and $\sum_{L\in\Lambda}\sum_{j=1}^{n_L}\pi_{iL_j} = 1$. $\phi(\mathbf{y}_i \mid \boldsymbol{\mu}_{L_j}, \boldsymbol{\Sigma}_{L_j})$ is a bivariate normal distribution with mean $\boldsymbol{\mu}_{L_j}$ and variance $\boldsymbol{\Sigma}_{L_j}$. All model parameters are denoted collectively by $\mathbf{\Phi}$. Let $\mathbf{z}_i \in \{e_1, e_2, ..., e_k\}$, for $i = 1,...,N$, $k = \sum_{L\in\Lambda} n_L$ be hidden segmentation variables, where e_k is a binary vector with 1 at kth component and 0 elsewhere. $\mathbf{z}_i = e_k$ indicates the ith voxel belongs to the kth component. The hidden data was assumed to follow a Markov Random Field with parameter G[7]:

$$f(z \mid G) = Z(G)^{-1}\exp[-\sum_{i=1}^{N} U_{MRF}(z_i \mid z_{N_i}, G)]$$

where $U_{MRF}\left(\mathbf{z}_i = e_{L_j} \mid z_{N_i}, G\right) = e'_{L_j} G \sum_{k\in N_i} \mathbf{z}_k$ and N_i is the neighborhood of voxel i.

2.2. The maximum likelihood and EM framework

EM algorithm finds the maximum likelihood estimation of MCBG parameters. The segmentation can be found by estimation of the posterior probability of hidden variables $\mathbf{z}_i$, given observed intensity pair $\mathbf{y}_i$, and model parameters for all image voxels.

2.2.1 Initialization

Our EM algorithm was initialized according to the propagated probabilistic atlases $P_L^{Atlas}(i)$. Let ω_{iL} be a function of propagated probabilistic atlas, which assigned a prior probability for ith voxel of class L. Here, we have chosen, $\omega_{iL} \propto (P_L^{Atlas}(i))^w$ subject to the constraint, $\sum_{L\in\Lambda}\omega_{iL} = 1$, where w is a weighting factor determined experimentally.

The parameters were initialized as follows: for the jth component of class L,

$$p_{iL_j}{}^{(t)} = \frac{\pi_{L_j}{}^{(t)}\phi(\mathbf{y}_i \mid \boldsymbol{\mu}_{iL_j}{}^{(t)}, \boldsymbol{\Sigma}_{L_j}{}^{(t)})}{\sum_{L\in\Lambda}\sum_{j=1}^{n_L}\pi_{L_j}{}^{(t)}\phi(\mathbf{y}_i \mid \boldsymbol{\mu}_{iL_j}{}^{(t)}, \boldsymbol{\Sigma}_{L_j}{}^{(t)})} \tag{2}$$

$$\pi_{iL_j}{}^{(t+1)} \sqcup f(\mathbf{z}_i = e_{L_j} \mid p_{N_i}{}^{(t)}, G^{(t)}) = \frac{\exp\left[-U_{MRF}\left(e_{L_j} \mid p_{N_i}{}^{(t)}, G^{(t)}\right)\right]}{\sum_{L\in\Lambda}\sum_{j=1}^{n_L}\exp\left[-U_{MRF}\left(e_{L_j} \mid p_{N_i}{}^{(t)}, G^{(t)}\right)\right]} \tag{3}$$

(1) mean parameter,

$$\boldsymbol{\mu}_{L_j}{}^{(0)} = \left(\mu_{L_{jT2}}^{T2}, \mu_{L_{jDE}}^{DE}\right)'$$

for $j_{T2} = 1,...,n_L^{T2}$ and $j_{DE} = 1,...,n_L^{DE}$, where n_L^{T2} and n_L^{DE} are the total number of components for class L on T2 and DE sequences respectively. And,

$$\mu_{L_{j_s}}^{s} = \mu_L^s - \sigma_L^s + \frac{2(j_s - 1)\sigma_L^s}{n_L^s - 1}$$

for $s \in \{T2, DE\}$.

$$\mu_L^s = \frac{\sum_{i=1}^{N} \omega_{iL} y_i^s}{\sum_{i=1}^{N} \omega_{iL}},\ \sigma_L^s = \frac{\sum_{i=1}^{N} \omega_{iL}\left(y_i^s - \mu_L^s\right)^2}{\sum_{i=1}^{N} \omega_{iL}}$$

(2) covariance parameter,

$$\boldsymbol{\Sigma}_{L_j}{}^{(0)} = \begin{pmatrix} (\sigma_L^{T2})^2 n_L^{-1} & 0 \\ 0 & (\sigma_L^{DE})^2 n_L^{-1} \end{pmatrix}$$

(3) the mixture proportion,

$$\pi_{iL_j}{}^{(0)} = \frac{\omega_{iL}}{n_L}$$

2.2.2 Update equation

Starting from a proper initial parameter values, EM interleaves two steps. E-step finds the conditional expectation of log likelihood of complete data, given the observed intensity and current estimates of parameters. During E-step, posterior probability p_i is calculated. In M-step, $\boldsymbol{\mu}_{L_j}$ and $\boldsymbol{\Sigma}_{L_j}$ are updated by maximizing the conditional expectation.

E-step:

$p_{iL_j}{}^{(t)}$ is updated as given in (2)

M-step:

$$\boldsymbol{\mu}_{L_j}{}^{(t+1)} = \frac{\sum_{i=1}^{N} p_{iL_j}{}^{(t)} \mathbf{y}_i}{\sum_{i=1}^{N} p_{iL_j}{}^{(t)}}$$

$$\boldsymbol{\Sigma}_{L_j}{}^{(t+1)} = \frac{\sum_{i=1}^{N} p_{iL_j}{}^{(t)} \left(\mathbf{y}_i - \boldsymbol{\mu}_{L_j}{}^{(t)}\right)\left(\mathbf{y}_i - \boldsymbol{\mu}_{L_j}{}^{(t)}\right)^T}{\sum_{i=1}^{N} p_{iL_j}{}^{(t)}}$$

Due to the interaction effects between voxels in the MRF, approximate techniques were used in calculating π_{iL_j} [7], as given in (3). We added ω_{iL} as a constraint here and the formula used to update π_{iL_j} is:

$$\pi_{iL_j}{}^{(t+1)} \propto \frac{f(\mathbf{z}_i = e_{L_j} \mid p_{N_i}{}^{(t)}, G^{(t)}) \omega_{iL} n_L^{-1}}{\sum_{L \in \Lambda} \sum_{j=1}^{n_L} f(\mathbf{z}_i = e_{L_j} \mid p_{N_i}{}^{(t)}, G^{(t)}) \omega_{iL} n_L^{-1}}$$

The update of G is not trivial and we refer the interested reader to [7] for detail.

Upon convergence, the posterior probability for ith voxel of class L is finally given by,

$$p_{iL} = \sum_{j=1}^{n_L} p_{iL_j}$$

Results from the EM algorithm were generally not smooth and the myocardium segmentation could contain parts of the papillary muscle. We therefore computed the convex hull of the blood pool in each slice to cover the papillary muscle and removed higher harmonic phases of the epicardial contour to generate the final smooth segmentation [8].

3. RESULTS

We acquired the T2 and DE sequences from six patients after myocardial infarction. The voxel sizes of the T2 and DE sequences were respectively $1.3672 \times 1.3672 \times 14$ mm and $0.7617 \times 0.7617 \times 5$ mm. The DE images were registered and resampled, with the same resolution, to the corresponding T2 images. Each slice was manually segmented by a clinician using the ITK-SNAP [9].

For comparisons, the two MRI sequences were first segmented using the traditional atlas and registration-based segmentation method, where an atlas constructed from the mean of a set of cardiac MRI was used[6]. This method also combined the information of the two sequences for the registration in the atlas propagation procedure[3]. Also, to evaluate the efficiency of the proposed MCBG mixture model in combining information of two sequences, the T2 and DE sequences were segmented separately using the traditional EM segmentation framework, where the multi-component univariate Gaussian model was used[8].

Table 1 provides the segmentation performance of the three methods: the Dice metric was used as the error measure: Dice=$(2|S_a \cap S_b|)/(|S_a| + |S_b|)$, where S_a and S_b are the manual and automatic segmentation results respectively.

Fig. 2 provides a typical example of the segmentation results by the three compared methods. Neither of the atlas based segmentation method or the traditional univariate EM segmentation algorithm performed well on the infarct regions in the DE MRI image. By contrast, the proposed method combined the information from the T2 image and more accurately delineated the myocardium in both the two MRI sequences.

4. DISCUSSION AND CONCLUSION

In this paper, we have presented an automatic method for the segmentation of myocardium from MRI data of myocardial infarction patients. We proposed a novel MCBG mixture model to combine the complementary information from the two sequences. The EM framework was adopted to

Table 1. The Dice score of the myocardium segmentation with respect to manual segmentation.

Methods	T2	DE
Atlas-based [1]	0.484±0.106	0.576±0.103
Separate MC	0.624±0.146	0.601±0.105
Proposed MCBG	0.623±0.129	0.643±0.084

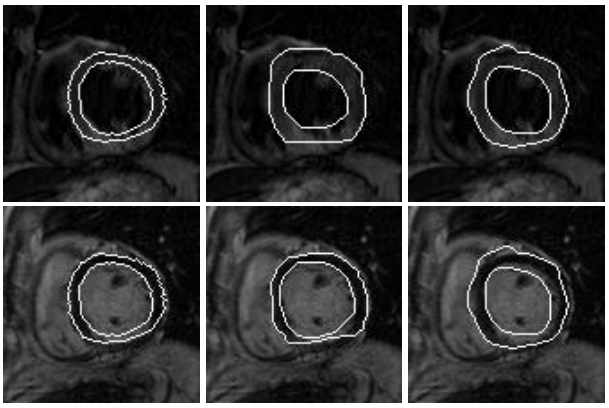

Fig.2. Segmentation results and dice score of one data set. Left column: atlas-based; Middle column: Separate MC; Right column: Proposed MCBG. Top row: T2 sequences; Bottom row: DE sequences.

estimate the segmentation and model parameters, where a probabilistic atlas was also used.

The proposed method has been tested on six datasets. The results showed that the performance of the proposed method achieved Dice score 0.623±0.129 for T2 MRI and 0.643±0.084 for DE sequences. This was significantly better than the result of the atlas-based method, which achieved Dice score 0.484±0.106 and 0.576±0.103 for T2 and DE images respectively. This is because the EM algorithm can iteratively calculate the parameters of MCBG mixture model to fit the intensity of the images and thus improves the voxel-based classification on the base of probabilistic atlas. Also the results of the proposed MCBG were improved compared to multi-component segmentation solely from the DE sequences (Dice score 0.601±0.105), though no improvement was observed on the T2 segmentation (Dice score 0.624±0.146). This is attributed to the fact that the DE sequence has much worse contrast for myocardium compared to T2, especially the infarcted area which can be easily misclassified as the blood pool. And the effect of the complementary information in DE MRI is covered up in the Dice score of T2 segmentation. Therefore, we conclude that the MCBG mixture model has the potential to classify the infarcts from the DE MRI and identify the edema from the T2 sequence, by combining the complementary information of the two MRI sequences.

The MCBG provides a generic framework to model multivariate and complex intensity distributions, for low contrast and heterogeneous regions. In the future, besides classifying the ischemic regions, extending the model for image pairs with different resolutions and marginal misalignment will be considered, to improve the applicability of the algorithm.

5. ACKNOWLEDGMENT

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