Myocardium Segmentation Based on Combining Fully Convolutional Network and Graph cut

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Abstract

Myocardium segmentation from cardiac MRI images is an important task in clinical diagnosis of the left ventricle (LV) function. In this paper, we proposed a new approach for myocardium segmentation based on deep neural network and Graph cut approach. The proposed method is a framework including two steps: in the first step, the fully convolutional network (FCN) was performed to obtain coarse segmentation of LV from input cardiac MR images. In the second step, Graph cut method was employed to further optimize the coarse segmentation results in order to get fine segmentation of LV. The proposed model was validated in 45 subjects of Sunnybrook database using the Dice coefficient metric and compared with other state-of-the-art approaches. Experimental results show the robustness and feasibility of the proposed method.

Keywords: Myocardium segmentation, Graph cut, Fully Convolutional network, Deep learning, Cardiac MRI segmentation.

1. Introduction

Cardiac diseases are leading cause of death worldwide [1]. Currently, cardiac magnetic resonance imaging (MRI) is recognized as a valuable tool for cardiac diagnosis, treatment as well as monitoring of cardiac diseases. For quantitative assessment, segmentation of the myocardium from cardiac magnetic resonance imaging is a prerequisite step for cardiac diagnosis [2]. Many clinically diagnosis parameters such as ejection fraction, left ventricular volume, wall thickness, and mass could be derived from the segmentation results of cardiac myocardium [3]. Therefore, accurately exacting the myocardium from cardiac MR images plays an important role in cardiac diagnosis [4]. This task depends on accurate delineation of endocardial and epicardial contours in the left ventricle (LV), which usually is manually performed by specialists. However, manual segmentation is a time-consuming and tedious task. It is also prone to intra- and inter-observer variability [5]. Thus, automatic methods for the left ventricle segmentation are desirable. Nevertheless, automatically segmenting myocardium faces some difficulties presented in cardiac MR images [5] such as the existence of inhomogeneity in intensity due to blood flow. In addition, papillary muscles and trabeculations located inside the LV cavity have the same intensity as the myocardium.

There have been many methods for myocardium segmentation proposed in the literature such as graph cut method [6-8], active contours model [9, 10], and deep learning [11, 12]. Among them, graph cut has the advantage of being fast, achieving globally optimal results. Despite its advantages, graph cuts may not produce an accurate segmentation for objects with weak boundaries. To address this drawback, there have been attempts to add a shape prior to the graph cuts segmentation technique. Freedman and Zhang in [13] presented a method that uses a fixed shape template aligned with the image by the user input. Slabaugh and Unal [14] proposed the usage of an elliptical prior. This method iteratively solves the image segmentation and elliptical fitting problems. Nevertheless, this method cannot give correct results if a bad elliptical prior was provided to the input.

On the other hand, in natural image segmentation, deep learning methods, especially deep convolutional networks, have shown excellent performances [15, 16]. Inspired by the success in natural image segmentation, recently the deep convolutional networks have been applied for myocardium segmentation [11, 12]. In a more detail, there have been some works combining deep learning method and deformable model to segment LV on cardiac MR images [11, 12]. In these works, deep learning methods were employed to produce a rectangle to detect the region of interest of LV, and then other postprocessing methods were used to make

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a final segmentation of LV. However, due to a lack of large training datasets and low signal-to-noise ratio, the myocardium segmentation is limited compared to the natural image segmentation.

Different from these researches, we proposed an automatic method which employed fully convolutional networks and Graph cut for myocardium segmentation. The core idea of the proposed method is to use the dataset consisted of multi cardiac MRI images in different positions in one beat cycle along with the ground truths to train the network. In more detail, the proposed approach including three steps: in the first step, we put the datasets consisted of multi cardiac MRI images in different positions in one beat cycle along with the ground truths as input of a convolutional neural network (CNN). The CNN with multiple layers can extract the feature from the training image and learn from the features. In the second step, the-segmentation results obtained by CNN are used as coarse segmentations. Finally, we performed Graph

cut method on the coarse segmentation results to obtain accurate and robust segmentation.

The remainder of this paper is organized as follows: In Section 2, the proposed approach is described in detail. In Section 3, some experimental results are presented, including a comparison with state-of-the-art methods. Finally, we conclude this work and discuss future applications in Section 4.

2. Method

The pipeline for myocardium segmentation of the proposed approach is presented Fig. 1. First, to get enough training data for deep learning, we employed an appropriate data augmentation method. Second, a deep fully convolutional network (FCN) was applied to obtain the coarse segmentation including endocardium and epicardium masks of all test and validation images. Finally, based on the masks resulted from the FCN, the multi-phase graph cut segmentation-based method is performed to achieve the fine myocardium segmentation results.
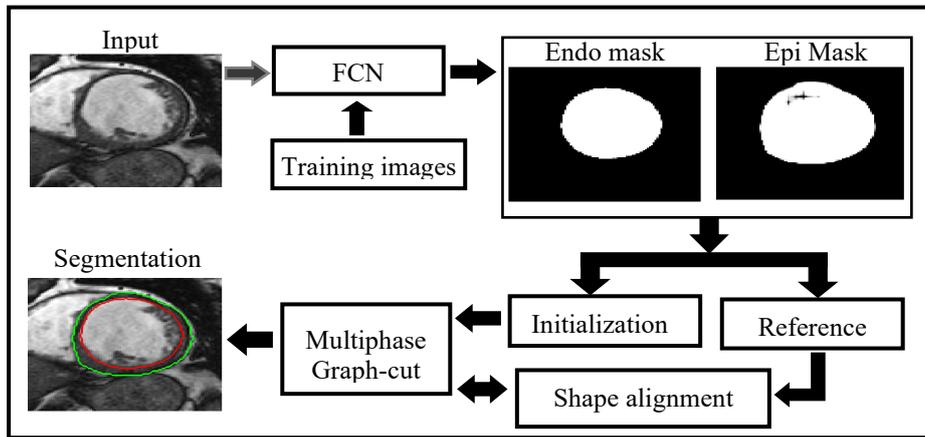
Fig. 1. The overview of the proposed framework
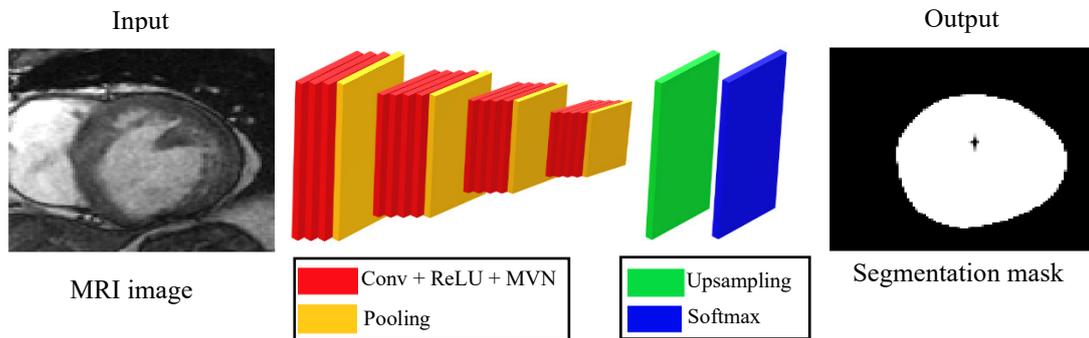
Fig. 2. The basic structure of the FCN- based segmentation for endocardium/epicardium

2.1 FCN Architecture for LV segmentation

The basic structure of the network is presented in Fig. 2. It includes 15 convolution layers (Conv), 3 max pooling layers, upsampling layers and a softmax layer. We can divide the network into two main parts, contracting path and expanding path. The contracting path consists of 3x3 convolution layers with zero padding to preserve the spatial structure of the feature map and 3x3 max pooling layers with stride 2. Each convolution layer is followed by a rectified linear unit (ReLU) and a mean variance normalization.

Mean-variance normalization (MVN) is a technique that normalizes the pixel intensity distribution of the feature map after the ReLU. After MVN procedure, the pixel values of the feature map have zero mean and unit variance. The expanding path consists of 3x3 convolution-transpose layers with stride 2, which are used to reconstruct the spatial structure of image. After each convolution-transpose layer, the feature map in this path is combined with the corresponding feature map in the contracting path. Finally, the 'softmax' layer will produce class probabilities for each pixel of the image. The network has roughly 11 million parameters to be learned. Training a deep model like that with a small dataset might lead to overfitting, so we used some well-known techniques to prevent overfitting like data augmentation, dropout and regularization during training.

2.2 Preprocessing and data augmentation

The MRI dataset have huge differences in the pixel intensity distribution between images due to different machines. This might affect the accuracy of networks. This problem is solved by using MVN operation as described in the previous section. The pixel values of the input image then have zero mean and unit variance. We augment the data for training process by performing some affine transformations techniques like rotation (90, 180 and 270˚), vertical and horizontal flipping.

We also use 'transfer learning' for FCN model to reduce training time and increase predictive accuracy. First, the model will initialize the weight values according to the 'Xavier initialization' and train on the LVSC data set. The weight of the convolution layer with the 'Up-sampling' layer after training with the LVSC dataset will be used as initial value when training with Sunnybrook data. The weights of the remaining layers will be randomly generated.

2.3 Myocardium segmentation by multiphase Graph cut framework

In this study, to simultaneously segment endocardiumand epicardium of the left ventricle, we employ the multiphase graph cut framework [17] to achieve fine segmentation results. In image segmentation by graph cut approach, segmentation task can be regarded as pixel labeling problems.

Let $L = \{l_1, l_2, \cdots, l_m\}$ be discrete label sets. In the current work, we consider a special label set, which contains only two labels: 0 and 1 ($L = \{0, 1\}$). Here 0 represents background pixel, while 1 represents object pixel. The energy functional, $E(f)$, in graph cut framework is defined as

$$E(f) = \sum_{p \in P} V_p(f_p) + \sum_{p \in P, q \in N} V_{pq}(f_p, f_q) \qquad (1)$$

where f_p denotes label of pixel $p \in P$, N is set of pixels in the neighborhood of pixel p. The energy function E is composed of two terms. The first term V_p is the data term, which represents the penalties of assigning label $f_p \in L$ to pixel p. The second term V_{pq} is an interactive term, which penalizes the label disparities between neighboring pixels. We can optimize this energy by graph cut method when V_{pq} is a submodule function [18]. Note that, in this paper, we focus on object/background segmentation with only two labels. The energy functional $E(f)$ is maximized by graph minimum cut, hence, the problem is reduced to finding max-flow/min-cut.

This framework is extended to multiphase graph cuts in order to segment multi objects [17]. The energy functional in the case of multiphase graph cuts is defined as:

$$E(\mathbf{f}) = E_D(\mathbf{f}) + \sum_{j=1}^{M} \left(E_{pq}\left(f_p^j, f_q^j\right) + \lambda_S E_S\left(f_p^j, f_q^j, \psi^0\right) \right)$$

$$(2)$$

where $\mathbf{f} = \{f_1, f_2, \cdots, f_M\}$ is set of M object labelings, E_D is sum of data penalties of all labelings, which is defined based on the image intensity, E_S is shape prior energy, and ψ^0 is shape prior of the segmented objects. ψ^0 is reconstructed from the training data [10]. E_{pq} is an interactive term, which is defined as

$$E_{pq}(f_p, f_q) = \exp\left(-\frac{\left(I_p - I_q\right)^2}{2\sigma^2}\right) \frac{1}{\text{dist}(p,q)}\left|f_p - f_q\right|$$

$$(3)$$

where I_p and I_q denote the intensities of pixel p, q, respectively, $\text{dist}(p,q)$ is Euclidean distance between pixel p and q, σ is a positive value that can be considered as an estimate of "camera noise".
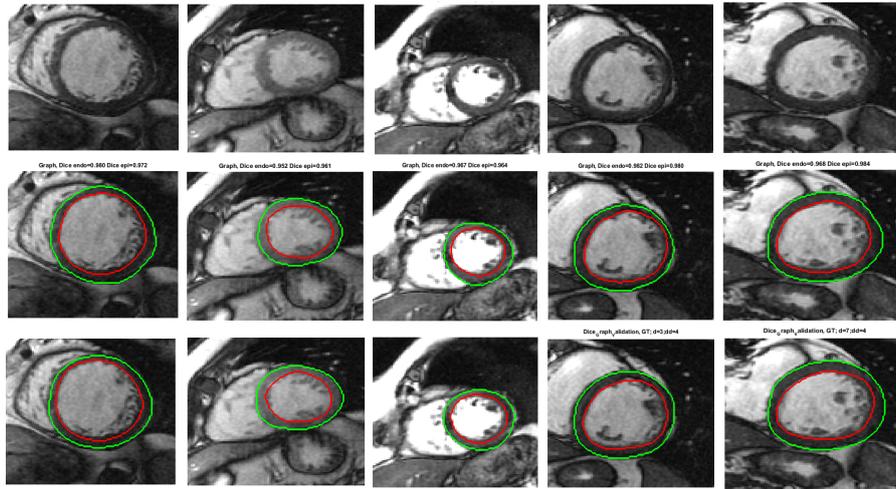
Fig. 3. Representative segmentation by the proposed approach. First row: Input images; Second row: results; Last row: Ground truth endocardium/epicardium mask

3. Evaluation and Results

3.1. Dataset

Images from the Sunnybrook [19] public dataset were used to train and validate the proposed methodology. This dataset consists of DICOM anonymized cardiac magnetic resonance images, with 256 ×256 pixels. The dataset contains several cardiac planes from 45 patients, acquired from healthy and diseased subjects. For each patient, an image sequence includes from 6 to 12 slices. The Sunnybrook data includes three parts, each part contains 15 subjects: Training data includes 135 images; Validation data includes 138 images; and Testing data includes 147 images. The augmentation data process is applied for the training data during training process, with the number of augmented images are about four times larger than the original training images. The reported evaluation results are the average score for validation and Test data.

In all slices, endocardial and epicardial contours were drawn at end diastole and end systole phases, manually segmented by experienced cardiologists and are considered as ground truths.

3.2. Evaluation

To evaluate the quantitative accuracy of segmentation results, we used the Dice similarity coefficient (DSC). The Dice coefficient measures the similarity between automatic and manual segmentations and is calculated as follows

$$DSC = \frac{2\mathbf{S_{am}}}{\mathbf{S_a} + \mathbf{S_m}} \tag{4}$$

where $\mathbf{S_a}$, $\mathbf{S_m}$, and $\mathbf{S_{am}}$ are, respectively, the automatically delineated region, the manually segmented region, and the intersection between two regions.

3.3. Results

We applied the proposed model to segment all images from the Sunnybrook Data [19]. Some representative samples of the results for such data set are given in Fig. 3. The ground truth by human expert are also given in the last row. From this figure, we can see, there is a good agreement between the results by our approach and the ground truths.

To validate the performance of the proposed model, we compared obtained results with manual segmentation by the expert (ground truth) that were provided along with the dataset. The agreement between the endocardium and epicardium areas by the proposed model and those by manual segmentation are depicted in Bland-Altman [20] and linear regression plots shown in Fig. 4. It can be seen from the plots in Fig. 4, the areas obtained by the proposed model are in good agreement with those from the expert with high correlation coefficients, above 98% for both endocardium and epicardium. We can observe from the Bland-Altman plots, the data obtained by the proposed model are close to those by manual segmentation, which illustrates the small differences between them. This is because the proposed approach takes advantages of both Fully convolutional network and Graph cut methods into account. In addition, by using multiphase graph cut, approach, the endocardium and epicardium are segmented simultaneously and the correlations between geometric properties of the two regions are can be used, thus improving segmentation results.
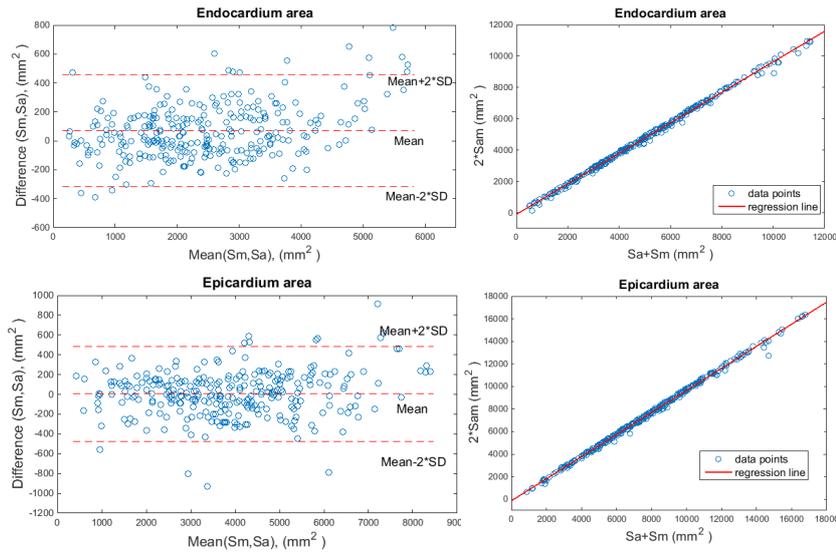
Fig. 4 plots Bland–Altman (left) and Linear regression plots (right) of the automatic segmentation versus the ground truth for the endocardium (a) and epicardium (b) of all datasets

Table 1. The mean and standard deviation of obtained DSC between other state-of the-art and the proposed models on the Sunnybrook Dataset.

Method	Dice Coefficient	
	Endocardium	Epicardium
Ngo and Carneiro method [12]	0.90 ± 0.03	--
Avendi et al. method [11]	0.94± 0.02	--
Hu et al. method [22]	0.89± 0.03	0.94± 0.02
Queirós et al. method [23]	0.90± 0.05	0.94± 0.02
Phi Vu Tran method [21]	0.92± 0.03	0.95± 0.02
Our approach	0.94± 0.03	0.95± 0.02

3.4 Compared to other works:

We now evaluate the performances of the proposed model with other models when applying models on the Sunnybrook Dataset. In particular, we compare the proposed model with the model of Phi Vu Tran [21] and then evaluate the results with those by the radiologist. Along with showing representative segmentation results, we also provide the Dice similarity coefficient, with other state-of the art in Table 1. As can be seen from Table 1, for epicardium segmentation, the proposed approach and method by Phi Vu Tran [21] obtained the same Dice coefficient results, and both methods achieve better results than other comparative methods. However, for endocardium segmentation, the proposed method obtained the highest Dice coefficient value that shown

the advantages of the proposed approach. It is also noted that, the proposed model uses end to end training process without using pre-trained data as in the method by Phi Vu Tran [21].

4. Conclusion

This paper demonstrated the advantages of combining the FCN architecture for segmentation problem in cardiac magnetic resonance imaging and graph cut method. Experiments showed that this model achieves high accuracy on the benchmark of popular MRI datasets. Moreover, the model is fast, and can be applied to other larger scale databases for cardiac myocardium segmentation as well as right ventricle segmentation.

Acknowledgments

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