Active Contours with Automatic Initialization for Myocardial Perfusion Analysis

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ABSTRACT - Quantitative analysis of myocardial perfusion requires detection of myocardial boundaries in many short-axis MR images. Manual tracing of myocardial boundaries is a time-consuming and tedious task, which may limit the clinical use of quantitative analysis. In this paper, we propose an automatic detection algorithm based on active contours. For initialization, starting contours need to be defined. Instead of manually tracing the initial contours, our approach presents an automatic method for finding initial contours of epicardium and endocardium. Once the initial contours are defined, we apply the active contours called stochastic active contour scheme (STACS) for image segmentation.

1. INTRODUCTION

Myocardial perfusion has been used for analyzing coronary artery diseases, such as myocardial ischemia and myocardial infarction. Instead of traditionally measuring myocardial perfusion with single photon emission computed tomography (SPECT) or positron emission tomography (PET) scans, magnetic resonance imaging (MRI) becomes an attractive alternative. Recent development of cardiac MRI provides the possibility to obtain high resolution dynamic images of the heart without radiation effects as in SPECT and PET scans.

Myocardial perfusion with cardiac MR is usually analyzed by comparing rest and stress situations. With these studies, a contrast agent, such as gadolinium-diethylenetri-amine pentaacetic acid (Gd-DTPA), is injected as a bolus into the vein. Under stress situation, adenosine served as pharmacological vasodilation is injected. The performance of the left ventricular myocardium is analyzed through MR sequence images. The myocardium in each image is usually divided into 6 or 8 equiangular segments according to regions of blood from different coronary arteries. Average signal intensity in each segment throughout sequence images provides average signal-time curves, whose upslopes are determined. The ratio of the upslope under stress and the upslope at rest is called perfusion reserve, which is used for quantitative analysis of cardiovascular diseases.

One major problem of myocardial perfusion analysis is tracing myocardial boundaries in all images. A simple way to detect these boundaries is the manual detection by directly drawing the inner and outer contours of the myocardium. However, the manual procedure is very time-consuming and tedious in practice because there are hundreds of MR perfusion images per perfusion study, which may take 3-4 hours to achieve quantitative analysis. This may limit the use of qualitative analysis for clinical routine measurements. Automatic detection of myocardium boundaries would be desirable to facilitate and stimulate more quantitative perfusion analysis in clinical use.

Many existing techniques require some sort of user interaction, such as manually defining a region of interest or manually tracing the first contour as a guidance; therefore, they are not fully automatic. The semiautomated contour detection in a software package called MASS (MR Analytical Software System)[1] has been developed by using the model-based approach and assuming the similarity between the model image and the contour-detected images. Moreover, the model may be needed for every new set of MRI sequences. Spreeuwers and Breeuwer proposed a detection of myocardial boundaries using intensity-time and shape characteristics [2]. However, they indicate that a manual segmentation is required for the image in the first frame for each sequence, so that it can be used as a shape model for the next frame in the segmentation process.

Active contours or snakes are widely used for image segmentation [3, 4]. Recently, they have been introduced to myocardial perfusion for myocardial boundary detection [5]. All of these active contour schemes implicitly assume that the heart is roughly located at the center of the image to be segmented and location of the heart may be cropped out manually. However, the heart in a typical cardiac MR

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image is not usually at the center. Before applying more sophisticated image segmentation schemes, it is important to detect first where the heart is in the image. We do so for two main reasons. First, we want to crop automatically each cardiac MR image in the set to cover only the heart part so that the computational cost is reduced significantly when applying active contours for image segmentation. Second, once the heart region is cropped, we can place automatically the initial contour in the vicinity of the heart for rapid convergence to the final solution using active contours.

In this paper, we propose an automatic method for finding initial contours in myocardial perfusion studies. This approach results in the initialization prior to epi- and endocardial detection with active contours. The initial contours are derived automatically by using all sequence images in one slice. After obtaining the initial contours, we apply the active contours called stochastic active contour scheme (STACS) [6]. STACS is based on the energy minimization approach that combines the characteristic of the curve evolution and the image statistics. It incorporates the prior knowledge of the object's shape, which is an ellipse shape in this problem, onto the properties of the contour; therefore, it can overcome the problem of papillary muscles in the image.

2. METHODS

Our approach to detecting epi- and endocardial boundaries of a heart in myocardial perfusion MR image sequences is based on active contours. However, the algorithm requires a well localization of the initial contours for the active contours to work efficiently and rapidly. Currently, manual tracing of the initial contours is often used. However, we propose in this paper a fully automatic approach for finding the initial contours for active contour based image segmentation.

2.1. Automatic Initial Contours

To develop a fully automatic initialization algorithm, we utilize all images within a slice. Our approach is to first automatically find an image having the most contrast between the myocardium and left ventricle. Using it as a starting point, we determine and place a set of initial contours in the vicinity of the left ventricle. Then a sophisticated image segmentation scheme STACS is applied to accurately trace the epi-and endocardial boundaries of the heart in the image. Finally, the detected final contours for the epi-and endocardial boundaries in the first image are propagated and used as the initial contours in the adjacent images in the sequence. The process is repeated until myocardial boundaries on all images in the sequence of interest are detected. In a case where the boundary between the myocardium and the left ventricular regions in the image is hardly distinguishable by STACS, we use the detected boundaries of the previous image, instead.

The overall process for finding the initial contours in the first image at a slice of interest is shown in Fig. 1. Since the left ventricle becomes brighter when the contrast agent enters the chamber, our idea is to search for the image with the largest contrast variation in the left ventricle region. In the first step, we find the absolute difference image for each adjacent pairs of images in the slice sequence. If there are N images in the sequence, the absolute difference image $D_k(i,j)$ corresponding to the k^{th} pairs of images is defined as

$$D_k(i,j) = |I_k(i,j) \bullet I_{k+1}(i,j)| \quad \text{for } k = 1,2,...,N \bullet 1 \qquad (1)$$

where $I_k(i,j)$ is the k^{th} image in the sequence. Second, each absolute difference image is thresholded to become a binary image. The value of 1 in each "on" pixel, represents the acceptable contrast level in that pixel. Third, we perform morphological closing to merge pixels that are close together, then a median filter is applied to remove the scattering pixels. Finally, the image with the largest "on" area is chosen to be the best contrast variation image among the absolute difference images. We assume that the "on" area in the image belongs to the left ventricle. So we compute the centroid of the "on" area and use it as the center of the initial contours, which are to locate in the vicinity of the left ventricle. Two concentric circles are created as the initial epicardial and endocardial contours.

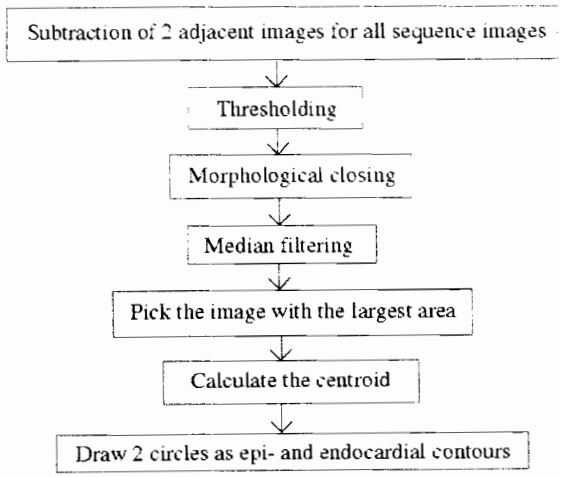

Fig. 1. Diagram of algorithms for initial contours

2.2. Stochastic Active Contour Scheme

After obtaining the initial contours, we apply the active contour called stochastic active contour scheme (STAC) [6] to an MR sequence image to delineate the boundaries of the myocardium. STACS uses an energy minimization approach to segment the heart and its structures. Since an MR image often has low contrast, it is very difficult to segment the myocardium from surrounding tissues, for example, the chest wall. A second major issue arises because the myocardium is essentially the same tissue as

the papillary muscles but they are not to be included in the segmented left ventricle. To successfully overcome these problems, STACS defines an energy functional that has four terms

$$J(\mathbf{C}) = \lambda_1 J_1(\mathbf{C}) + \lambda_2 J_2(\mathbf{C}) + \lambda_3 J_3(\mathbf{C}) + \lambda_4 J_4(\mathbf{C}) \quad (2)$$

where $\mathbf{C}$ is the contour that delineates the boundary of the desired heart structures, and λ_1, λ_2, λ_3, λ_4 are the relative weights of the four terms J_1, J_2, J_3, J_4, respectively. In the first term $J_1(\mathbf{C})$, we assume two different stochastic texture models: M_1 for the object, residing within the contour, and M_2 for the background, residing outside the contour. This term is called the region-based term because it utilizes the regional statistics within the image to help evolving the contour $\mathbf{C}$ during the segmentation process. The second term $J_2(\mathbf{C})$is the edge-based term. Its purpose is to attract the contour $\mathbf{C}$ to clues given by prominent edges within the edge map, derived from the image. The third term $J_3(\mathbf{C})$ regulates the global properties of the contour to resemble the prior knowledge about the heart shape $\mathbf{C}_H(\theta)$. Assuming an ellipse shape for the heart contour, we have

$$\mathbf{C}_H(\theta) = \{ (x, y): \theta^T \mathbf{v} = 0; 4ac \bullet b^2 > 0 \} \quad (3)$$

where the parameter vector $\theta = [a\ b\ c\ d\ e\ f]^T$ and $\mathbf{v} = [x^2\ xy\ y^2\ x\ y\ 1]^T$. The last term $J_4(\mathbf{C})$ enforces the smoothness (the local properties) of the contour.

When actually minimizing the energy functional (2), STACS adopts a level set approach [7] where the contour $\mathbf{C}$ is embedded as the zero level set of a function $\phi(x, y)$, i.e.,

$$\mathbf{C} = \{ (x, y) \in \Omega : \phi(x, y) = 0 \} \quad (4)$$

where Ω is the image domain. Hence, $J(\mathbf{C})$ becomes $J(\phi)$

$$\begin{aligned} & J(\phi) \\ & = \lambda_1 J_1(\phi) + \lambda_2 J_2(\phi) + \lambda_3 J_3(\phi) + \lambda_4 J_4(\phi) \\ & = \int_\Omega \left[\lambda_1 M_1(x, y) H_\epsilon(\phi) + \lambda_1 M_2(x, y)\left[1 - H_\epsilon(\phi)\right] + P(x, y)\delta_\epsilon(\phi)\|\nabla\phi\| \right] dxdy \end{aligned} \quad (5)$$

where

$$M_k = \frac{1}{2}\ln(2\pi\sigma_k^2) + \frac{(u(x, y) - m_k)^2}{2\sigma_k^2} \quad \text{for} \quad k = 1, 2 \quad (6)$$

are the negative log of the probability density functions of the object and the background models, respectively; H_ϵ and δ_ϵ are the regularized Heaviside and delta functions used to mask the pixels inside and on the contour $\mathbf{C}$, respectively; and the potential function

$$P(x, y) = \lambda_2 \Upsilon(x, y) + \lambda_3 D^2(x, y) + \lambda_4 \quad (7)$$

where Υ is the edge map [4] derived from the image, and $D = \theta^T \mathbf{v}$ represents the signed distance to the ellipse contour of the heart.

STACS minimizes the functional (5) by iterating between three tasks. In the first and second tasks, it fixes the contour $\mathbf{C}$, and then estimates the parameters m_k and σ_k^2 for $k = 1, 2$ of both models in $J_1(\phi)$ and the parameters θ of the ellipse contour in $J_3(\phi)$. In the third task, it fixes all these parameters, and then evolves the contour $\mathbf{C}$, or equivalently the level set function ϕ, according to the contour evolution equation

$$\frac{\partial\phi}{\partial t} = \delta_\epsilon(\phi)\lambda_1(M_1 - M_2) - \nabla P \cdot \frac{\nabla\phi}{\|\nabla\phi\|} - P_k \delta_\epsilon(\phi) \quad (8)$$

where $\cdot$ is the vector dot product; ∇ is the gradient operator;

$$K = div\left(\frac{\nabla\phi}{\|\nabla\phi\|}\right) \quad (9)$$

represents the curvature along the contour $\mathbf{C}$; and the potential force field

$$\nabla P = \lambda_2 \nabla\Upsilon + 2\lambda_3 D \nabla D \quad (10)$$

Details on the energy functional (5), the derivation of the partial differential equation for the contour evolution (8), and the estimation of all parameters are in [6].

3. RESULTS

Short-axis views of a heart are acquired on a Philips 1.5-T MR system with an image size of 256x256, a pixel size of 1.6mm, a slice thickness of 8mm, and 70 sequence images per slice. Figure 2 shows the results of the proposed automatic initialization algorithm described in Section 2.1. The gray scale images in the top row are the absolute difference images D_k (i, j) calculated by eq.(1). Here we present only three adjacent absolute difference images for comparison. The binary images in the bottom row are the results after applying the thresholding, morphological closing and median filtering algorithms to the corresponding images above. Due to its largest "on" region, the image in the middle column is choosen to be the best contrast variation image among the absolute difference images.

Figure 3 shows two concentric circles placed as initial contours at the vicinity of the left ventricle in the best contrast image. The inner and outer initial contours are used for detecting the epi-and endocardial boundaries, respectively. The radius of the initial contours is roughly estimated from the physical measurement of the endocardium and epicardium. We can see that the center of

the initial contours is not exactly at the center of the endocardium because the papillary muscles lie inside the left ventricle causing the centroid shifted to the left.

Figure 4 shows an example of the detected boundary of endocardium using STACS. In this figure, the papillary muscles are not detected as parts of myocardium. To obtain the boundary of the epicardium, another STACS contour will be applied using the initialized epicardium contour in Fig. 3 separately.

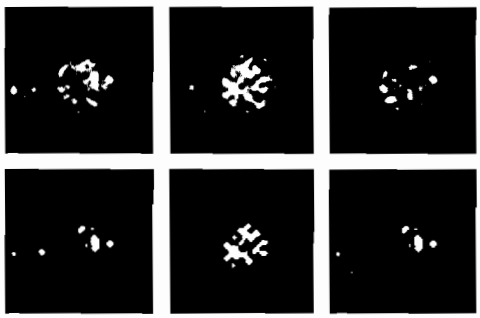

Fig. 2. Images in the first row are the absolute difference images. The binary images in the second row are the results after thresholding, morphological closing and median filtering. The image in the middle column is chosen to be the best contrast variation image among the absolute difference images due to its largest "on" area.

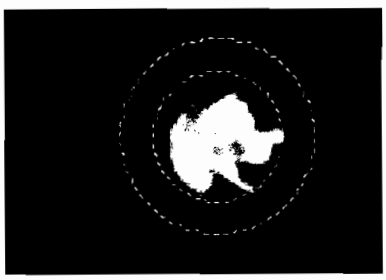

Fig. 3. Initial contours of epicardium and endocardium

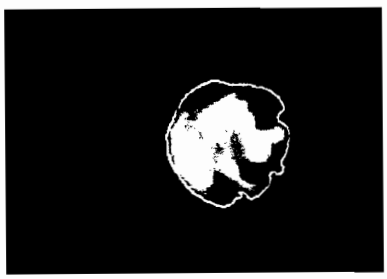

Fig. 4. Detected contour of endocardium using STACS

4. CONCLUSION

An automatic technique for finding the initial contours of epicardial and endocardial boundaries is presented. This technique does not require user interaction and the initial contours are derived using the whole set of sequence images in a slice. With the computed initialization, the stochastic active contours, STACS, can converge to the decent boundary of myocardium. For future work, more data sets need to be evaluated for verification.

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