Contrast Echography Segmentation and Tracking by Trained Deformable Models

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Abstract

The objective of this work is to segment the human left ventricle myocardium (LVM) in contrast echocardiography imaging and thus track it along a cardiac cycle in order to extract quantitative data about heart function.

Ultrasound images are hard to work with due to their speckle appearance. To overcome this we report the combination of active contour models (ACM) or snakes and active shape models (ASM). The ability of ACM in giving closed and smooth curves in addition to the power of the ASM in producing shapes similar to the ones learned, evoke to a robust algorithm. Meanwhile the snake is attracted towards image main features, ASM acts as a correction factor.

The algorithm was tested independently on 180 frames and satisfying results were obtained: in 95% the maximum difference between automatic and experts segmentation was less than 12 pixels.

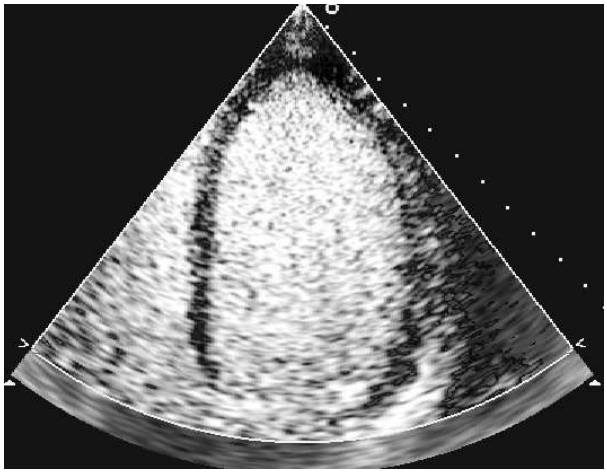

Figure 1. Frame of Contrast Echocardiography. The U-shaped structure is the myocardium to be segmented.

1. Introduction

Heart diseases are one of the most common death causes of the last decades. For this reason, after myocardial infarction, it is important to have tools that allow to evaluate the heart function. Left ventricular wall movement can be used to this end but it is not accurate enough. Additional information about the myocardial perfusion (blood flow) should be obtained in order to determine if we have a reversible or an irreversible heart disfunction.

The most widespread image techniques for myocardial perfusion analysis are SPECT, PET and MR. Although they give high quality information about myocardial perfusion they are not widely available in most hospitals because of their cost. Moreover, the use of ionizing radiation makes them invasive to the patient. The availability, low cost and non-invasiveness of echocardiography, in addition to great progresses in microbubble contrast agents during last decade, have projected the contrast echocardiography [5] as a powerful tool in the myocardial assessment. However, it is difficult to get conclusions directly from images. Quantitative parameters must be extracted to interpret the sequence of perfusion images. This is done by tracking myocardial points along the cardiac cycle meanwhile the process of destroying the microbubbles (using a high energy pulse) and reperfusing again is repeated. Some approaches have been done in the framework of tracking myocardial points but they are reduced to some ROIs which are actualized taking into account the optical flow of the sequence [7],[3]. In [4], it is proposed to segment the ventricle walls by using ACM and ASM. The authors model the shape with the first M coefficients of its discrete cosine transform instead of the raw coordinates. The present work has similarities to them. We segment the full myocardium in order to track the whole contour. To achieve it we also combine ACM and ASM, this allows us to take advantage of the experts knowledge and it is motivated because manual segmentation of the myocardium in the whole cardiac cycle (100 frames approximately) is highly time consuming and suffers from inter- and intra-observer variability.

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2. Background

2.1. Active Contour Models (ACM) or Snakes

A snake [6] can be thought as a set of nodes $S_t = \{(x_{s,t}, y_{s,t})_{s=1}^{M}\}$ which represent an elastic discrete curve. It evolves in time with the objective of minimizing the sum of its internal and external energies:

$$E(u) = E_{int}(S_t) + E_{ext}(S_t)$$

E_{int} imposes the smoothness of the curve and E_{ext} attracts it towards image main features (edges in case of contour segmentation). Given a node in the snake (x_t, y_t) it will evolve according to

$$\begin{cases} x_{t+1} = (A + \gamma Id)^{-1}(\gamma x_t + F_x(x_t, y_t)) \\ y_{t+1} = (A + \gamma Id)^{-1}(\gamma y_t + F_y(x_t, y_t)) \end{cases} \quad (1)$$

where A (the scatter matrix) codifies the smoothness constraints, γ affects to the speed convergence and $F = (F_x, F_y)$ are the external forces that make the nodes move. Depending on the F that we synthesize, snakes behavior will vary. In this text we propose external forces that give a certain coherence between the normal directions of the snake in its nodes and the gradient directions of contours where each node should be attracted. These forces are:

$$F(x, y) = -\langle \overrightarrow{v_c}, \overrightarrow{v_s} \rangle \nabla D(x, y) \quad (2)$$

where D is a distance map, $\overrightarrow{v_c}(x, y)$ is the gradient direction of I in the nearest edge point to (x, y) (in distance D) and $\overrightarrow{v_s}(x, y)$ is the normal vector to the snake, fixed one of the two possible, at the point (x, y). Notice that the same way we previously have created the distance map D, we have to create an angle map D^{Ψ} so that, at each point (x, y) we know the distance to the nearest edge point and the gradient direction of it [8].

Let $\overrightarrow{v_c}$ and $\overrightarrow{v_s}$ be unitary vectors,

$$\underbrace{\langle \overrightarrow{v_c}, \overrightarrow{v_s} \rangle}_{K} = \begin{cases} \text{(0,1]} & \text{if} & \text{angle}(\overrightarrow{v_c},\overrightarrow{v_s}) < \pi/2 \\ 0 & \text{if} & \text{angle}(\overrightarrow{v_c},\overrightarrow{v_s}) = 0 \\ \text{[-1,0)} & \text{if} & \text{angle}(\overrightarrow{v_c},\overrightarrow{v_s}) > \pi/2 \end{cases}$$

The term K makes the snake be attracted by contours that have similar orientation (angle between $\overrightarrow{v_c}$ and $\overrightarrow{v_s} < \pi/2$) and rejects it from contours which have opposite directions (angle $> \pi/2$). In case that $K = 0$, the only forces that act in these points are internal forces.

Using these forces we obtain quite good results but they are not enough to reach our objective. ACM are, in their nature, local methods, the support of a global method is needed.

2.2. Active Shape Models (ASM)

This technique allows us to build compact models of shape by capturing the statistics of sets of labelled points in a set of training images. Once the model is built, only plausible shapes (similar to the ones in the training set) can be obtained [1]. Having N training images, manual segmentation is performed in every image I_j. Let $\widetilde{s_j} = \{(\widetilde{x_i^j}, \widetilde{y_i^j})\}_{i=1}^{M}$ be the ordered set of landmark coordinates. We align $\widetilde{s}_j$ to a reference shape s_0 ($s_0 = \widetilde{s}_1$, for instance) by applying a transformation $s_j = L_{r,\theta,T}(\widetilde{s}_j)$ that scales (r), rotates (θ) and translates $(T = (T_x, T_y))$ $\widetilde{s}_j$. This allow us to capture the intrinsic variation between shapes (avoiding similarities) [2].

Let $\{(x_i^j, y_i^j)\}_{i=1}^{M}$ be the aligned coordinates of the j-th training image $(j = 1, \ldots, N)$. For every j we construct the vector

$$\mathbf{X_j} = (\mathbf{x_1^j}, \mathbf{y_1^j}, \mathbf{x_2^j}, \mathbf{y_2^j}, \ldots, \mathbf{x_M^j}, \mathbf{y_M^j})$$

by concatenating the coordinates of the points so we get N observations in the $\mathbb{R}^{2M}$ space. Applying a PCA to the data, we reduce the dimensionality while maintaining relevant information. Any shape in the training set can now be approximated using the mean shape $\overline{X} = 1/N \sum_{j=1}^{N} \mathbf{X_j}$ and a linear combination of the first $m < M$ modes of variation

$$X = \overline{X} + Pb \quad (3)$$

where $P = (P_1 \quad P_2 \quad \ldots \quad P_m)$ is the matrix of the first m modes with $P^T P = Id$ and $b = (b_1, b_2, \ldots, b_m)$ is the shape parameter.

If we have an aligned shape $\widetilde{X}$ and want to find the most similar plausible shape, we just have to project it into the space to get the parameter b

$$b = P^T(\widetilde{X} - \overline{X}) \quad (4)$$

and ensure that b live into a certain valid m-dimensional hyperbox. Then the plausible shape is exactly are (3).

3. LVM Segmentation

As we told before, our purpose is to segment the LVM (Figure 1) by combining methods exposed in sections 2.1 and 2.3. The procedure is divided in three parts: First of all the model is trained. Then we initialize the snake paying special attention to the case of the first image of the sequence. Finally we explain how the snake evolves.

3.1. Training the model

To train the model, we took a training set of 50 images extracted from 4 different cardiac cycles which covered

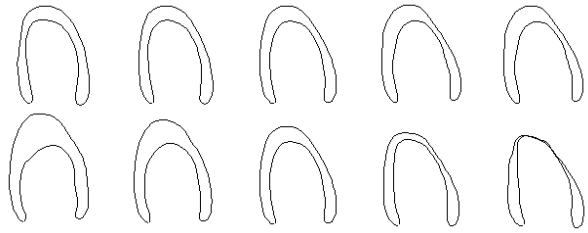

Figure 2. 2^{nd} and 3^{rd} modes of variation of the shape model.

a wide range of shape variation and asked an expert to segment them. 100 landmarks were marked at every image and, after having applied the PCA on the aligned data, we got a shape model (3) with 9 principal variation modes that explained the 98% of the shape variation. Figure 2 shows the effects of varying second and third modes. Notice, for instance, how the second and third modes model the thickness of the myocardium in different locations. ASM also controls that never downside contour surpass the upside one.

3.2. Initialization of the snake

In order to get good results, a first step of preprocessing must be done to smooth the speckle appearance (typical in ultrasound images) but preserving as much as possible the image contours. For this reason we used an anisotropic diffusion filter [9]. An example is shown in Figure 3.(a)

To avoid the snake falling into a local minimum, the initial one must be placed next to the desired result. As initial snake S_0 we take the mean shape $\overline{X}$ of the model in which we have marked 4 special landmarks (Figure 3.(b)). Then we warp $\overline{X} \longmapsto S_0$ so that these points can fit 4 key points found in the target image $I(x, y)$. Basically these are the two corners (C_L and C_R) and the top (internal T_I and external T_E) of the myocardium as shown in Figure 3.(c). To find the corners we use the Harris Corner Detector. Once found, we look for the most significant gradient of $I(x, y)$ along the line defined by points $C = (C_L + C_R)/2$ and T, where T is the top point of the sectorial ROI that contains the echocardiogram, this gives us T_I. As we could observe in most of the frames, the point T_E remains almost fixed, so we consider it fix. Now that we have placed S_0 (Figure 3.(d)), it is ready to evolve according to equation (1). Notice that when instead of working with a single frame we are performing LVM tracking, this can be used to segment the first frame I_0 and, for the other frames I_{n+1} we use $S_0^{n+1} = S_k^n$ as initial snake (where S_k^n is the result of the previous frame).

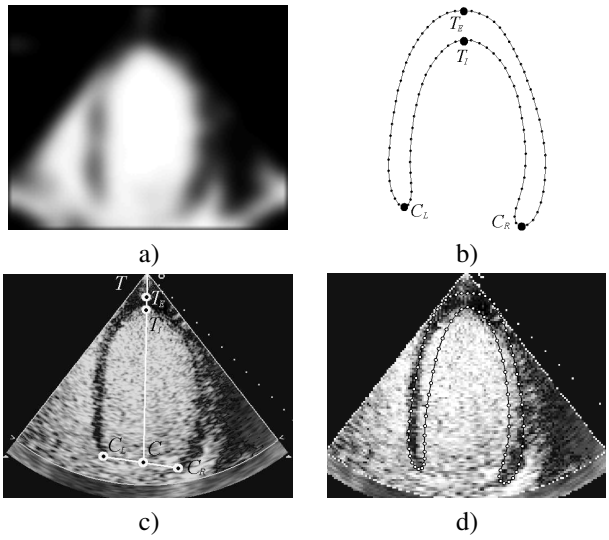

Figure 3. Filtered image a). Mean shape $\overline{X}$ b). Key points found in the target frame c). Initial Snake: mean shape warped to fit the key points d).

3.3. Controlled evolution of the snake

Given the snake at time t, $S_t = \{(x_{s,t}, y_{s,t})_{s=1}^{M}\}$ we predict the new position of the snake nodes $\widetilde{S}_{t+1}$ by applying eq. (1). We correct $\widetilde{S}_{t+1}$ looking for the most similar valid image given by our shape model. First of all, we have to align $\widetilde{S}_{t+1}$ and then project it into the shape space to get the parameters b as in (4). Then we get the plausible shape by (3) and finally, to get the next snake S_{t+1}, we dis-align X. This can be condensed by the following equations:

$$\begin{cases} \widetilde{S}_{t+1} = (A + \gamma Id)^{-1}(\gamma S_t + F) \\ S_{t+1} = L_{r,\theta,T}^{-1}[\overline{X} + PP^T(L_{r,\theta,T}(\widetilde{S}_{t+1}) - \overline{X})] \end{cases} \quad (5)$$

If we iterate the process, once evolving followed by correcting, we realize that the shape constraints given by the shape model are too strong and hardly lets the snake search for new positions. To solve this we apply the corrections every P steps. In our case we used $P = 2$, but this depends on each application.

4. Results

Our images were acquired with an Agilent Sonos 5500 (Andover, MASS) scanner and the contrast used was Sonovue®. Visualization was performed by the Power-Angio technique.

To test our algorithm, we took 180 images of dimension (480 x 385), from 4 cardiac cycles, different from the 50 used to create the training set and applied (5) to each of

them independently. When we compared the results to the experts segmentations we found that in 95% of the cases the maximum difference reached was less than 12 pixels and the mean difference less than 4 pixels (Figure 4). Errors in segmentation are caused basically by a wrong initialization of the snake. In some frames, myocardium corners are not well defined (because of the image noise) and Harris corner detector can not deal with this. Another reason could be that the shape we are trying to segment do not belong to the learned shapes. In Figure 5 we show the evolution of the initial Snake under the correction effects of the ASM.

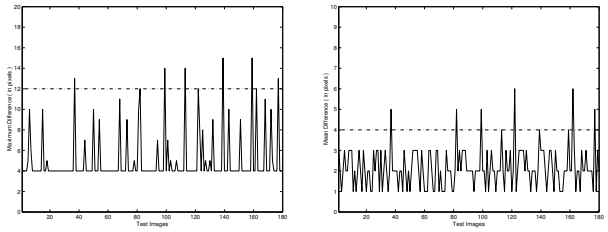

Figure 4. Maximum difference a) and mean difference b).

5. Conclusions

Finding a concrete shape in an image when all information is not available or the present is corrupted can be extremely difficult for a snake. This is precisely our case and is due to the fact that it is a local method of segmentation. Each node evolves according to an external force and some smoothness constraints in its neighborhood, but it does not take into account information about distant nodes. Despite the external forces we have introduced can guide each node more coherently, some global information must be used. This is the contribution of the ASM. They take into account information about all nodes to act over them. So we conclude by pointing that meanwhile snakes predict the position of the nodes, ASM is able to rearrange them so that only plausible shapes can be retrieved and thus the target structure is recovered.

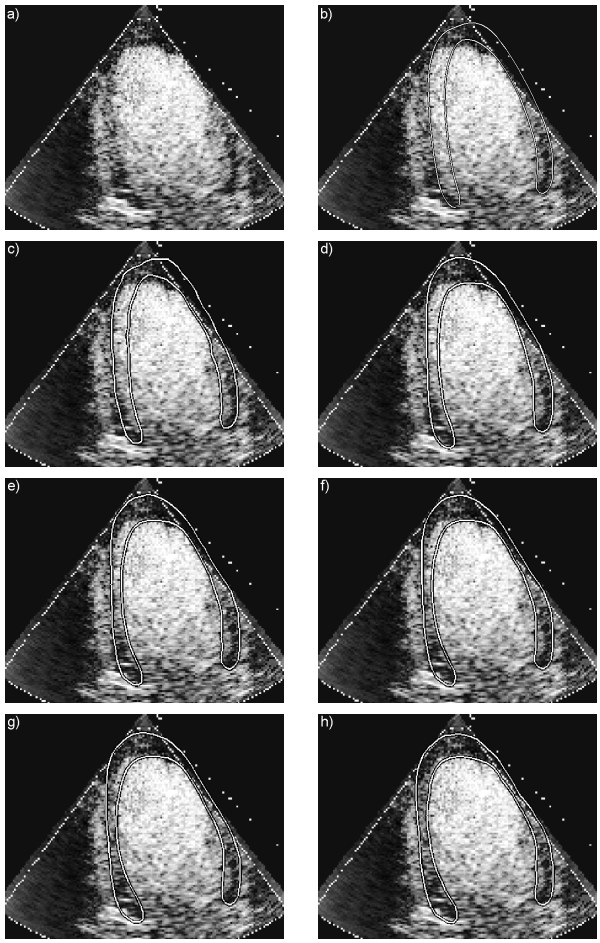

Figure 5. Segmentation process: Target frame a). Initial Snake b). Snake at time steps $t = 1, 2, 5, 7, 10$. Convergence at $t = 17$.

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