A Novel Liver Perfusion Analysis Based on Active Contours and Chamfer Matching

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Abstract. Liver Perfusion gives important information about blood supply of liver. However, in daily clinical diagnosis, radiologists have to manually mark the perfusion position in time-sequence images due to the motion of liver caused by respiration. In this paper, we propose a novel hybrid method using a variation of active contours and modified chamfer matching to automatically detect the liver perfusion position and measure the intensity with a single shape prior. The experiment is taken on abdomen MRI series and the result reveals that after extracting liver's rough boundary by active contours, precise perfusion positions can be detected by the modified chamfer matching algorithm, and finally a refined intensity curve without respiration affection can be achieved.

1 Introduction

Liver perfusion is a quantitative measurement of blood flow of liver, which plays important role in providing information in the assessment and treatment of various liver diseases. For example, it can be used as a noninvasive and repeatable technique in diagnosis of acute rejection in the liver transplant [1]. In clinic, by injecting a contrast agent into the liver while taking abdomen MRI images in a fixed time intervals, the concentration of the contrast agent can be tracked and analyzed. The change of perfusion intensity is tracked in time, resulting in a perfusion curve.

However in the clinical application, the problem is that the liver moves because the patient breathing throughout the series, resulting in the change of perfusion position. Moreover, it is unpractical to keep patients to hold their breaths during the process. So the radiologist has to manually mark the position, which is very tedious and time-consuming.

So far, the automated perfusion measurement process has received a large amount of attentions. In [2], Sebastian modeled the problem using registration method. In his method, Fast Marching Method (FMM) and Level Set Method[3,4,5] were used to segment the liver region, then a distance vector transform was employed to identify the perfusion position along the time sequence images. The result was promising, but the stop criteria of FMM strongly depends on the size of liver region that radiologists may not know exactly. It can lead to over or under segmentation when liver contours are not clear enough. Both of the situations will effect the perfusion localization precision. In [6], a new approach was proposed to get kidney perfusion curves that present the transportation of the contrast agent into the kidney. Then the curves are used in the

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classification of normal and acute rejection in kidney transplants. It used a deformable model with shape prior constrains which is a mean sign distance map of a lot of segmented kidneys. However, it is not suitable to our application. Firstly, it needs a lot of prior shape models, which radiologists can hardly achieve; secondly, liver's shape and size change significantly from different views or different slices, which brings more difficulties to build a mean model.

In our paper, in order to help radiologists automatically tracking the liver's perfusion position with little manual intervention, we employ a hybrid method which contains a variation of active contours [7] segmentation and a modified chamfer matching algorithm[8,9]. Active contour model is used to segment the liver region which has low gradient response on boundary. The segmentation results are distance maps which can be changed to contour lines. Then a modified edge pixel based chamfer matching algorithm is applied to match these contour lines to a single template shape contour whose perfusion position has been marked manually in advance. Finally, we can get all the abdomen MRI slices' relative perfusion position to the template's.

The outline of the paper is as follows: section 2 is a brief review of the active contour model and the chamfer matching algorithm; section 3 illustrates our hybrid method and section 4 presents the experiment results; section 5 is the discussion and conclusion.

2 Active Contours and Chamfer Matching

2.1 Active Contours

Active contours can be used to segment objects automatically, which is based on the evolution of a curve. Its objective is to minimize a metric function defined by the curvature. For example, starting with a curve around the object to be segmented, the curve moves toward its interior normal and stops on the boundary of the object.

Assume Ω be a bounded open subset of R^2, $C=\partial\Omega$ its boundary, and $C(s):[0,1]\rightarrow R^2$ be a parameterized curve, μ_0 is the image. The classical active contour model is defined bellow [7]:

$$J_1(c) = \alpha \int_0^1 |C'(s)|^2 ds + \beta \int_0^1 |C''(s)| ds - \lambda \int_0^1 |\nabla u_0(C(s))|^2 ds \tag{1}$$

Here, α, β, and λ are positive parameters. The first two terms control the smoothness of the evolution which is called the internal energy, and the third term makes the evolutional curve toward the object boundary called the external energy.

Edge-stop criteria is used to stop the evolving curve on the object's boundary. The edge-stop criteria is in the form of an edge stopping function and it depends on the gradient of image μ_0 whose boundary is defined by gradient. A typical edge stopping function [10] is:

$$g(\mu_0) = \frac{1}{1 + |\nabla G_\sigma(x,y) * \mu_0(x,y)|^p}, p \geq 1 \tag{2}$$

Where $G_\sigma(x,y) * \mu_0(x,y)$ is the convolution of μ_0 with the Gaussian:

$$G_\sigma = \sigma^{-1/2} e^{-|x^2+y^2|/4\sigma} \tag{3}$$

It is obvious that the edge stopping function is close to zero in the region where the gradient response is strong and such region always is the boundary of the object.

2.2 Chamfer Matching

Chamfer matching was firstly introduced in [9] by Barrow, which is a method that matches edge points or other low level feature points extracted from a 2D image. There are two binary images involved in the process. The first is a source image in the form of a distance map, and the second is a template image containing object's shape contour. After transforming the template image according to the source image, the shape contour overlaps on the source image's boundary region. An average of the overlapped pixels' value on the source image is the measure of the correspondence between them. A perfect match means that the average is close to zero. Transformations with different parameters are applied and the one with minimum average is selected. Often the root mean square average distance(rms) is used as the measure:

$$rms = ((v_1^2 + v_2^2 + \cdots + v_N^2)/N)^{1/2}/3 \tag{4}$$

Here, v_i is the source image's pixel which overlapped by the shape contour and N is the number of these pixels.

3 Hybrid Perfusion Analysis

In our MRI images, part of the liver boundary is not clear and has no gradient defined, so we employ a modified energy minimization active contour model called active contours without edges proposed in [10]. Our segmentation method is a simplified implementation of [10]. It is based on the following two observations: firstly, the movement of the liver is slight,and the rotation can be ignored. Secondly, as the upper half of the liver has strong gradient response, it always can be segmented well. But the low half nearly has no gradient response defined and its segmentation result is bad.

There are four steps in our hybrid method. Firstly, set a cycle's center point and radius as initial curve for the modified active contours segmentation and all the images can share one center point and radius. In the second step, we apply active contours without edges method to yield contour lines and edge pixels, where the segmentation result is in the form of distance map and the liver shape can be extracted by edge detecting algorithm on that distance map. The third step involves manually selecting an image, refining the contour to make it a nearly complete liver shape as a template contour image for chamfer matching and mark the perfusion position. The forth step is to focus on applying modified chamfer matching to the segmented result, and calculate the quotient of matched edge pixels number and the rms in (4). After matching, all slices are related to the template image, and their perfusion positions can be gotten. Finally, we can measure the perfusion intensity and draw the perfusion curve.

3.1 Set Initial Curve's Center Point and Radius

Because the modified active contours segmentation method is based on curve evolution, we use a circle as the initial curve whose center and radius need to be set carefully. Theoretically, the center point should be at the center of the liver, but as mentioned above, the upper half of the liver has strong gradient response. So it is better to put

the center point near the center of the upper half of the liver. The radius should be big enough to make the initial circle cover most of upper half part of the liver.

Once we have set one image's center point and radius, these parameters could be used in other images, which is based on the observation that the liver's total movement is small respect to patient's breathing.

3.2 Segmentation Using Active Contours Without Edges

In our segmentation stage, we restrict the curve evolving process in a sub-area marked by manual which covers the whole liver shape. Because the movement of the liver is slight, the sub-area's definition is suitable to all of the images. In this way we can reduce the cost of active contour model's calculation.

The original energy function of active contour model introduced by [10] is:

$$\begin{aligned} F(c_1, c_2, C) = \mu \cdot Length(C) + \nu \cdot Area(inside(C)) \\ +\lambda_1 \int_{inside(C)} |\mu_0(x, y) - c_1|^2 dxdy \\ +\lambda_2 \int_{outside(C)} |\mu_0(x, y) - c_2|^2 dxdy \end{aligned} \tag{5}$$

Here, c_1 and c_2 represent the inner and outside curve's average intensity, respectively. In the above, the length of curve C and the area of inside curve C are regularizing term. If we write the third term as $F_1(C)$ and the forth term as $F_2(C)$ while ignoring λ_1 and λ_2, we can see that if the curve C is outside the object, $F_1(C) > 0$, $F_2(C) \approx 0$; if inside the object, $F_1(C) \approx 0$, $F_2(C) > 0$; if partial inside and partial outside the object, then $F_1(C) > 0$ and $F_2(C) > 0$; finally, if the curve C is exactly on the object boundary, then $F_1(C) \approx 0$ and $F_2(C) \approx 0$. Thus the energy function is minimized [10].

By formulating the energy function using level set, the evolving curve C can be represented by the zero level set of signed distance function ϕ. After simplifying the energy function and adding the curve term, the liver can be segmented by solving the Euler-Lagrange partial differential equation:

$$\frac{\partial \phi}{\partial t} = \delta(\phi)[\mu \cdot div(\frac{\nabla \phi}{|\nabla \phi|}) - \nu - \lambda_1(u_0 - c_1)^2 + \lambda_2(u_0 - c_2)^2] = 0 \tag{6}$$

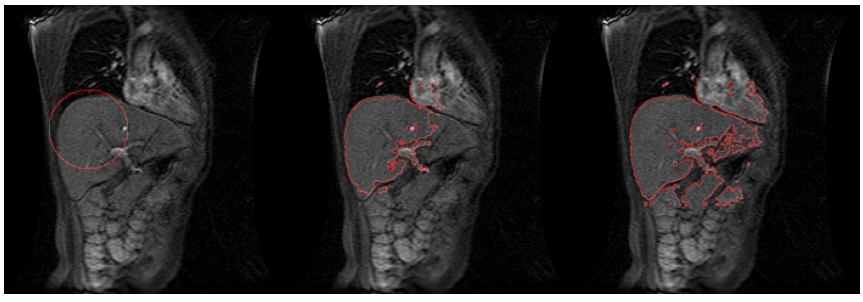

Fig. 1. Active contours procedure. (left) The initial stage. (middle) The middle stage. (right) The final stage.

The time complex is: $O(n^2)$. After nearly 1500 iterations a roughly liver contour 's distance map can be gotten. The modified active contours segmentation method works well but not fast enough to be a real-time application. Also it needs a lot of parameters tweaking, and still very application specific. For example it can not segment images which are very dark. Fig. 1 shows the evolving curve's initial, middle, and final stages.

3.3 Select and Refine Template Image

After segmentation, we get the distance map of liver's shape. We use an approximation method to extract the zero level set which is the boundary of the liver. If a pixel $\Phi(i, j)$ on the zero level set, the sign of 4 neighbourhood pixels' sign can't be the same, in mathematics:

$$\begin{aligned} max(\phi_{i,j}, \phi_{i+1,j}, \phi_{i,j+1}, \phi_{i+1,j+1}) > 0 \\ min(\phi_{i,j}, \phi_{i+1,j}, \phi_{i,j+1}, \phi_{i+1,j+1}) < 0 \end{aligned} \tag{7}$$

Once getting the shape contour, we need to manually select an image, refine the contour to make it to a nearly complete liver shape which is used as a template contour image for the modified chamfer matching. Also need to mark the perfusion position in the selected image. Then the modified chamfer matching algorithm can get other slices' perfusion position relate to the template image. Fig. 2 shows the selected shape before and after the refinement.

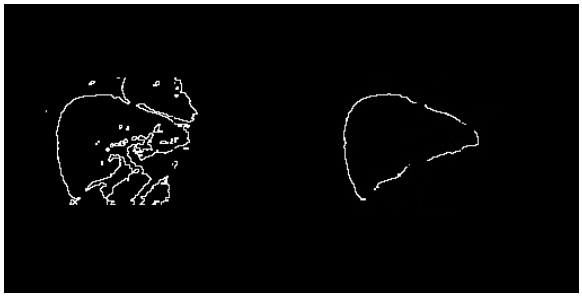

Fig. 2. Selection of the template image. (left) shape before refinement. (right) shape after refinement.

3.4 Modified Chamfer Matching

In chamfer matching, the two input images are not symmetrical. The source image is a distance map which is formed by assigning each pixel a value to the nearest edge pixel. The template image is a binary image containing the shape want to match. In our application, the active contour model's evolving result is naturally a distance map and the template image is selected and refined in step 3, where the two images are from different slices. Because of the low quality of our MRI image series, it is always a challenge to distinguish liver's boundary region with others, which results in a very noisy distance map.

To solve this problem, we propose two methods. Firstly, the noise part of the distance map is ignored, which can be realized by deleting the corresponding noisy pixels in the template image. So these noise regions will not influence the root mean square average. Secondly, the hit edge pixels' number is introduced. After transformation, the template image is aligned to the source image. The corresponding pixel in source image near zero means it is on the boundary of liver shape. These pixels are called hit edge pixels and the more the hit edge pixels, the better they are matched. So, let v_i be the hit edge pixel and N be the number of them, we want to get the maximum of following formula under different transformations:

$$F(N, v_i) = \frac{N}{((v_1^2 + v_2^2 + \cdots + v_N^2)/N)^{1/2}/3} \tag{8}$$

Then we can get the X and Y axis's relative transformation dx_i and dy_i of the *ith* image to the template image's perfusion position. Assume x_0 and y_0 are the template image's perfusion position, and x_i, y_i are the *ith* image's, we have:

$$\begin{aligned} x_i &= x_0 + dx_i \\ y_i &= y_0 + dy_i \end{aligned} \tag{9}$$

4 Experiments

We implement the active contour model using Level Set to solve the partial difference equation and modified chamfer matching in C program language. To evaluate our implementation of the proposed hybrid liver perfusion analysis method, we use a series of two-dimensional 256×256 abdomen MRI images. They are taken with a GE Medical Systems Genesis Signa HiSpeed CT/i system at the Shanghai First People Hospital, and the parameters are: slice thickness 15.0, repetition time 4.7, echo time 1.2, magnetic field strength 15000, flip angle 60 degrees.

The experiments are performed on a PC with Pentium-M 1600Mhz, 512Mb RAM. Most part of liver's contour can be extracted from the segmentation result by finding the hit edge pixels after the modified chamfer matching. In order to compare the

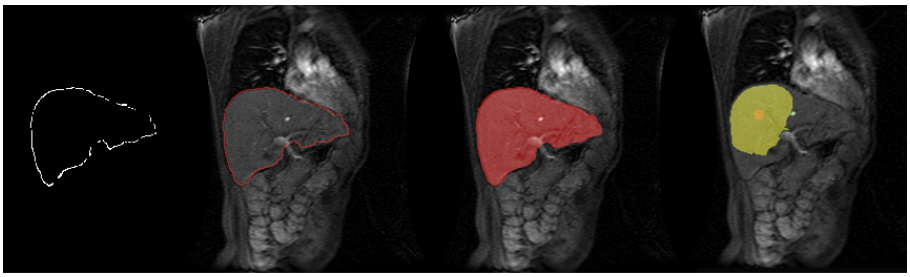

Fig. 3. Comparison between our segmentation and FMM+Level Set Method. From left to right are: hit edge pixels; complete liver shape by connecting hit edge pixels; segmented liver by our method using level set method to smooth; segmented liver by FMM+Levle Set Method.

segmentation quantity to FMM + Level Set Method, we connect the contour and make it complete. By taking it as an initial zero level set for level set method, we can get smooth segmented liver shape after 20 iterations. It is compared to the segmentation result which only use FMM + Level Set Method. Fig. 3 shows the comparison between our model to FMM + Level Set Method. It shows that FMM(2500 iterations) + Level Set Method(200 iterations) only can segment the upper part of the liver, while more iterations will result in over-segmentation. Our method has the potential to segment the whole liver more precisely.

The perfusion curve is confirmed by radiologists from the Shanghai First People's Hospital. Our hybrid method can effectively compensate the liver's movement. Fig. 4 shows the perfusion intensity curve, comparing to the perfusion curve ignoring liver's movement by using a fixed position across the whole series.

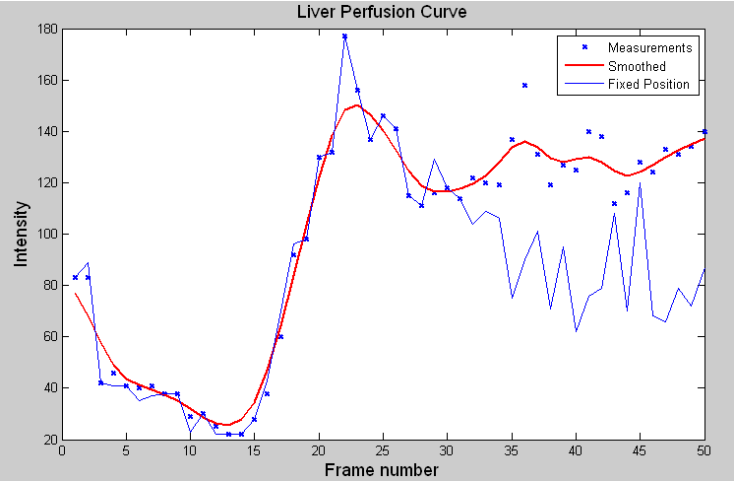

Fig. 4. Liver perfusion intensity Curve. Points labeled 'x' are obtained by our hybrid method and they are smoothed by Gaussian filter. It is compared to the result of the original method using a fixed position across the whole series.

5 Conclusions

This paper introduce a hybrid method which contains active contour model and chamfer matching algorithm to automatically detect the liver perfusion position and measure the intensity. The experiment reveals that the hybrid method can segment most part of the liver and the modified chamfer matching algorithm can get other slices' relative perfusion position to the selected template slice. The modified chamfer matching algorithm is efficient because it not only calculates the rms(4), but also takes the number of matched edge pixels into consideration. We also compare our segmentation result to FMM+Levle Set Method which reveals that our hybrid method with level set smoothing has the potential to segment the liver region correctly even there has lower gradient.

The future work is to extend the approach to automatically locate perfusion area in 3D volume data, in order to meet the challenge of more complex movement of the liver.

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