Hybrid 3D Heart Segmentation from Dynamic CT Images

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Abstract—**In this paper, a fast hybrid 3D segmentation approach is proposed to identify entire heart region from dynamic CT images. Firstly, a Morphological Recursive Erosion operation is introduced to reduce the connectivity between the heart and its neighborhood; then an improved Fast Marching method is employed to greatly accelerate the initial propagation of a surface front from the user defined seed structure to a surface close to the desired heart boundary; a Morphological Reconstruction method then operates on this surface to achieve an initial segmentation result; and finally Morphological Recursive Dilation is employed to recover any structure lost in the first stage of the algorithm. The approach is tested on 5 dynamic cardiac datasets, totally 50 CT heart images, to demonstrate its robustness. The measurements revealed that the algorithm achieved a mean similarity index of 0.956. The execution time for this algorithm extracting the cardiac surface from a dynamic CT image, when run on a 2.0 GHz P4 based PC running Windows XP, was 36 seconds.**

Keywords—**Hybrid Segmentation, Dynamic CT, Fast Marching, Similarity Index**

I. INTRODUCTION

Identification of the anatomic region of interest (ROI) is a fundamental requirement of quantitative analysis of medical images in many clinic applications. The ROI identification has traditionally been done by an interactive user tracing operation, which is tedious, time-consuming, and none reliably reproducible. Although many new and sophisticated imaging techniques have been developed to circumvent these problems, the development of fast, accurate and fully 3D segmentation technique for cardiac diagnosis and surgical simulation is still relatively primitive.

There are several segmentation algorithms described in the literature to facilitate cardiac image visualization and manipulation [1-5]. Most of the researchers paid their attentions to the left and/or right Ventricles from cardiac MRI images [2-5]. Some of them performed in 2D manner and the computing time were rarely mentioned. However, the deformation inspection of the whole heart volume including myocardium is also very important for cardiovascular disease study as well as endoscopic or minimal access cardiac surgical simulation.

A new 3D hybrid segmentation algorithm is proposed here to segment complete heart region from dynamic cardiac CT images, which operates in a multistage manner to perform segmentation rapidly and precisely. Both the computing time and accuracy of the proposed approach are measured here. This study is improved from our previous researches [6],[7].

The rest of the paper is organized as follows: in section II, After a brief review of fast marching method and morphological reconstruction techniques are presented, the multistage hybrid segmentation algorithm is proposed based on their improvement. Demonstration of this algorithm and presentation of an experimental validation are described in section III. The robustness and accuracy of the proposed approach are discussed in section IV.

II. METHODOLOGY

A. Level Set and Fast Marching

The level set method [8] is an interface propagation algorithm. Instead of tracing the interface itself, the level set method builds the original curves (so-called front) into a level set surface ϕ (a hyper surface), where the front propagates with a speed F in its normal direction. To avoid complex contours, the current front $\phi(x,y,t=i)$ is always set at zero height $\phi=0$. Hence, the level set evolution equation for the moving hyper surface can be presented as a Hamilton-Jacobi equation:

$$\phi_t + F \mid \nabla \phi \mid = 0 \tag{1}$$

The fast marching method [8] is a special case of the Level Set approach. Suppose we now restrict ourselves to the particular case of a front propagating with a speed F, which is either always positive or always negative. This restriction allows us to simplify the level set formulation. If we assume T(x,y) be the time at which the curve crosses the point (x,y), as shown in Fig.1, the surface T(x,y) satisfies an Eikonal equation where the gradient of surface ∇T is inversely proportional to the speed of the front F:

$$\mid \nabla T \mid F = 1 \tag{2}$$

The fast marching method is designed for problems in which the speed function never changes sign, so that the front is always moving forward or backward and the front crosses each pixel point only once. This restriction makes the fast marching approach much more rapid than the more general level set method.

With respect to rapidly computing a segmentation result, the fast marching method is employ in the approach to perform the initial propagation of a contour from an user-defined seed to an approximate boundary. However, the traditional fast matching method unable to prevent overflow when the front propagates near to the contour boundary in many medical study cases. An improved speed term is introduced into this hybrid approach, which is based on a global average image gradient, instead of traditional local gradients. This global speed term can efficiently halt the entire front when most part of the front tends to stable. It is applied to the front speed function at (2) and described as:

$$F(x,y,z,t) = F(x,y,z).e^{-\lambda\frac{1}{N}\sum_{(x,y,z)\in I}|\nabla G_\sigma * I(x,y,z)|}, \lambda > 0 \quad (3)$$

Where, $G_\sigma * I$ denotes the convolution of the image with a Gaussian smoothing filter with standard deviation σ. ∇ and N stand for gradient operation and total number of points in the front, respectively. λ is a positive constant.

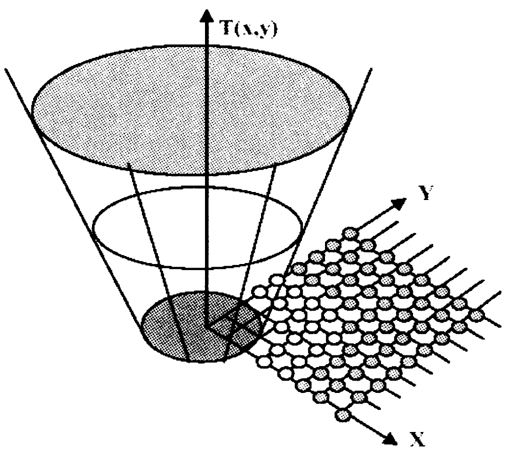

Fig.1 Fast Marching method. T(x,y) demonstrates the time at which the curve crosses the point (x,y).

B. Morphological Reconstruction

Mathematical morphology is a powerful methodology for the quantitative analysis of geometrical structures. The recursive erosion, dilation and morphological grayscale reconstruction techniques are employ in this research. They are defined below:

Recursive Dilation:

$$F\overset{i}{\oplus}K = \begin{cases} F & if\ i=0 \\ (F\overset{i-1}{\oplus}K)\oplus K & if\ i\geq 1 \end{cases} \quad (4)$$

Recursive Erosion:

$$F\overset{i}{\ominus}K = \begin{cases} F & if\ i=0 \\ (F\overset{i-1}{\ominus}K)\ominus K & if\ i\geq 1 \end{cases} \quad (5)$$

Morphological Reconstruction:

$$B_i = (B_{i-1} \oplus_g k) \cap |f|_G \quad (B_i \in R^3, i=1,2,...) \quad (6)$$

In the above, i is a scale factor and K is the basic structuring element (e.g. 1 pixel radius disk). $\oplus_{gray}$ denotes a dilation operation in grayscale, and $|f|_G$, represents the mask of the operation, achieved via a threshold operation using a gray level G. The iteration in (6) is repeated until there is no further change between B_{i-1} and B_i.

Recursive Erosion is employed here to reduce connectivity of objects from neighboring tissues while Recursive Dilation recovers the region lost during the reduction after the objects have been totally segmented. Each step employs the same number of iterations i.

Morphological Reconstruction is a very accurate and efficient tool for recovering the object on a pixel-by-pixel basis. The seed, which results from the output of the fast marching algorithm, is recursively grown under the supervision of the mask until it converges to a stable shape. Morphological reconstruction operations on a grayscale image are depicted in Fig.2.

C. Segmentation and Modeling Approach

The proposed 3D segmentation algorithm is a multistage procedure, comprising 4 major stages:

Stage 1. *Reduce the connectivity between the object region and the neighboring tissues*. Recursively erode the input 3D image using a structuring element base (e.g. a sphere with 1 pixel radius) until the desired object region is completely separated from the neighboring tissues. Record the iteration number i for later use in stage 3. This stage is designed to prevent overflow during the propagation in stages 2 and 3.

Stage 2. *Perform initial evolution of the front*. The improved fast marching method is employed here to initially propagate the user-defined seed to a position close to the boundary without overflow. It performs rapidly, typically less than 10 seconds for a $256\times256\times100$ volume, running on a 2.0 GHz P4 based PC.

Stage 3. *Refine the contours created in stage 2*. Since the speed function in the fast matching method falls to zero sharply, the front could stop a few voxels away from the real boundary. Here, a gray scale morphological reconstruction algorithm is employed to refine the front as a "final check". The output from stage 2 is employed as a *marker,* while the original image is used for the *mask*.

Stage 4. *Recover the lost data elements from stage 1*. During the recursive erosion in stage 1, part of the object (usually around the edges) is also often eliminated. To recover these lost components, the recursive dilation method is employed. The reconstructed object surface is dilated recursively using the same number of iterations i as recorded in stage 1, which results in the recovery of the object surface to the "original" position, ensuring a highly accurate result.

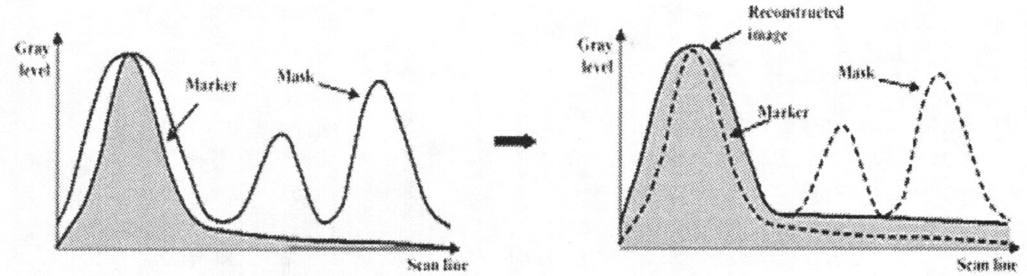

Fig.2 Morphological Reconstruction in grayscale where regions in marker image are used to select regions of the mask image to be reconstructed.

III. Experimental Results

A segmentation environment, "TkSegment", is developed based on the Visualization Toolkit (VTK) and the Python language, into which the multistage hybrid segmentation algorithm was integrated.

The source data employed in the experiments include 50 CT datasets from heart studies. Five groups of canine CT datasets were employed for the cardiac modeling study. Each was a dynamic volume, acquired with a gated acquisition technique on an 8-slice GE helical CT scanner, consisting of 86 slices at each of 10 equally spaced snapshots during the cardiac cycle. The images were each 512×512 pixels (0.35mm×0.35mm), with an axial spacing of 1.25 mm. One example of them is shown in Fig.3.

The proposed segmentation algorithm was applied to these 50 volume datasets. A 2.0 GHz P4 based PC running MS-windows XP was employed to run the segmentation.

A. *Case Study*

Five dynamic CT scans of beating hearts, each containing 10 individual volumes throughout the cardiac cycle, were employed in this study. Each of the 10 images was segmented individually.

The average segmentation time for one of these volumes is 155 seconds, which is not as fast as expected due to the additional time required to segment the blood vessels. However, if the blood vessels are removed early in pre-processing, computational time reduces dramatically to 36 seconds.

The segmented heart volumes were visualized using a Ray Cast volume rendering method. Two segmented example heart volumes of diastolic phase and systolic phase indicated along with their ECG are shown in Fig.4.

B. *Validation*

The segmentation results on the 5 experimental datasets were examined by eye, and deemed to be sufficiently accurate.

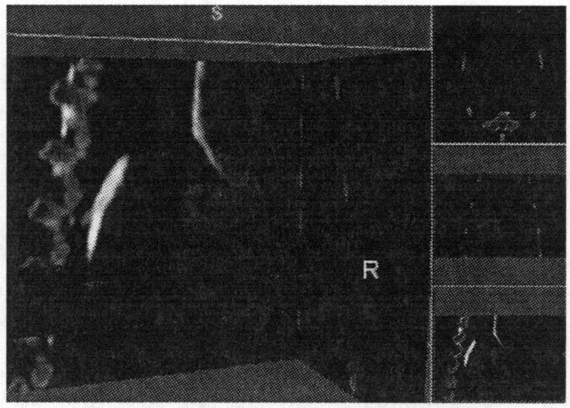

Fig.3 An example source data of the cardiac images. Left: ortho-planar view; right top to bottom: axial, sagittal and coronal views.

To quantify the segmented results, The *similarity index* definition introduced by Zijdenbos[9] is used, where manually traced contours were employed as the gold standard. An average *similarity index* of 0.956 was finally obtained from these heart segmentation studies.

IV. Discussion

The proposed approach achieves highly accurate segmentation results for the input datasets. The method identifies and reconstructs the structure of the heart for high quality visualization across a variety of conditions, even in the imperfect world of routine clinical-quality images. Additionally, I believe that it represents the first near real time, full 3D segmentation approach.

Robustness of the multistage hybrid segmentation approach was tested by 5 cardiac datasets in dynamic CT modality. No failed segmentations were reported even in low quality clinical images. Based on our test using VTK build-in algorithms and running in the same computing environment, morphological operations alone require 9 minutes to segment an individual heart volume. Compared to existing segmentation algorithms, the new approach represents a significant improvement.

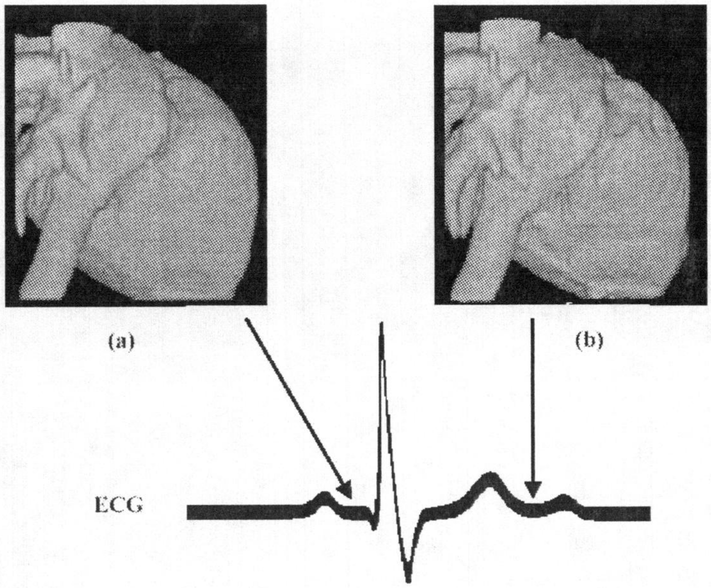

Fig. 4 Examples of 2 of the 10 segmented heart volumes in a cardiac cycle. (a) Diastolic phase; (b) Systolic phase.

The hybrid approach has been optimized for 3D volume segmentation. It combines the speed advantage of model-based methods with the high accuracy of region-based methods, resulting in an algorithm that is both fast and accurate. Over all our experiments, segmentations achieve a mean similarity index of 0.956.

V. Conclusion

A new fully 3D medical image segmentation approach was described using a improved fast multistage hybrid algorithm. The algorithm takes advantage of the speed and accuracy of both model-based and region-based segmentation methods. It was tested on 5 dynamic cardiac CT datasets, demonstrating excellent segmentation results. Quantitative validation demonstrated an average similarity index of 0.956.

While the procedure currently requires a minimal user-interaction to place seeds, I propose to improve the algorithm to make it fully automatic. The morphological Top-hat transformation [10] is considered as one solution, which can extract regions of high intensity of similar size to the objects to be segmented. The detected regions can then be employed as initial seeds. However, this step is still quite computationally expensive, and I therefore chose not to use it in the current work.

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