Dynamic Heart Modeling Based on a Hybrid 3D Segmentation Approach

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Abstract. A hybrid 3D segmentation approach is proposed in this paper to perform a physical beating heart modeling from dynamic CT images. A Morphological Recursive Erosion operation is firstly employed to reduce the connectivity between the heart and its neighborhood; then an improved Fast Marching method is introduced 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. Every one of 10 heart volumes in a heart beating cycle is segmented individually and finally aligned together to produce a physical beating heart model. This approach is tested on 5 dynamic cardiac groups, totally 50 CT heart images, to demonstrate the robustness of this technique. The algorithm is also validated against expert identified results. These 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.

1   Introduction

Cardiovascular disease becomes one of the leading causes of death for both men and women in the worldwide. However, characterization of myocardial deformation during the systolic contraction is a fundamental step toward understanding the physiology of normal heart and the effects of cardiovascular disease. This effort can lead to more accurate patient diagnosis and potentially reduce the morbidity. An accurate physical beating heart model, which represents all the features of the heart deformation, is considered as a fundamental procedure for cardiac deformation analysis and diagnosis.

   Fast and accurate segmentation of a heart volume is a basic operation to perform a physical dynamic cardiac modeling. 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 and endoscopic or minimal access cardiac surgical simulation.

A new 3D hybrid segmentation algorithm is proposed here to segment and model a complete beating heart 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 2, we present a brief review and improvement of fast marching method and morphological reconstruction techniques, and propose our multistage hybrid segmentation algorithm. We demonstrate this algorithm and present a validation experiment in section 3. The robustness and accuracy of our approach are discussed in section 4.

2   Multistage Hybrid Segmentation Approach

2.1 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:

$$\phi_t + F \mid \nabla \phi \mid = 0 \qquad (1)$$

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:

$$\mid \nabla T \mid F = 1 \qquad (2)$$

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, we employ the fast marching method in our approach to perform the initial propagation of a contour from an user-defined seed to an approximate boundary. However, the traditional fast matching method is hard to control overflow when the front propagates near to the contour boundary in many cases. An improved speed term is introduced into our approach, which is based on a global average image gradient instead of many local

gradients. This global speed term can efficiently stop the entire front when most part of the front tends to stable. We applied it to the front speed function at (2):

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

where $G_\sigma * I$ denotes the convolution of the image with a Gaussian smoothing filter with standard deviation σ. ∇ and N stands for gradient operation and total number of points in the front, respectively. λ is a positive constant.
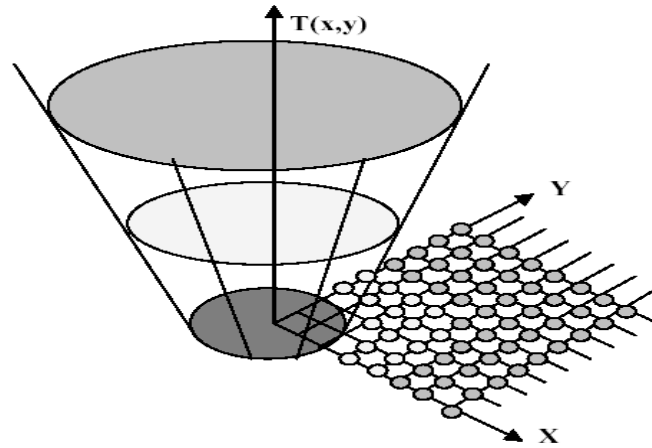
Fig.1 Fast Marching method. T(x,y) demonstrate the time at which the curve crosses the point (x,y).

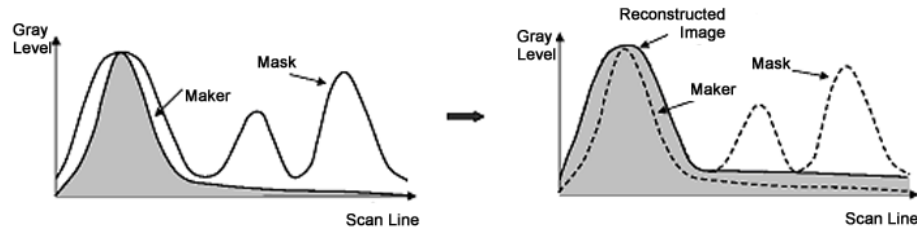## 2.2 Morphological Reconstruction

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

Recursive Dilation:

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

Recursive Erosion: (4)

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

(5)

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

Morphological Reconstruction:

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

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 N.

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.

2.3 Segmentation and Modeling Approach

The proposed 3D segmentation and modeling algorithm is a multistage procedure, comprising 5 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 $256 \times 256 \times 100$ 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.

Stage 5. *Model the beating heart*. Finally, a series of dynamic CT volumes involving in a cardiac cycle (totally 10 sets in our experiments) are segmented individually, and the resultant heart volumes are visualized and animated by either surface or volume-rendering methods.

3   Experimental Results

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

The source data employed in our 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 (a).

The proposed segmentation and modeling 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. The results of these experiments are described below.

(a)   (b)
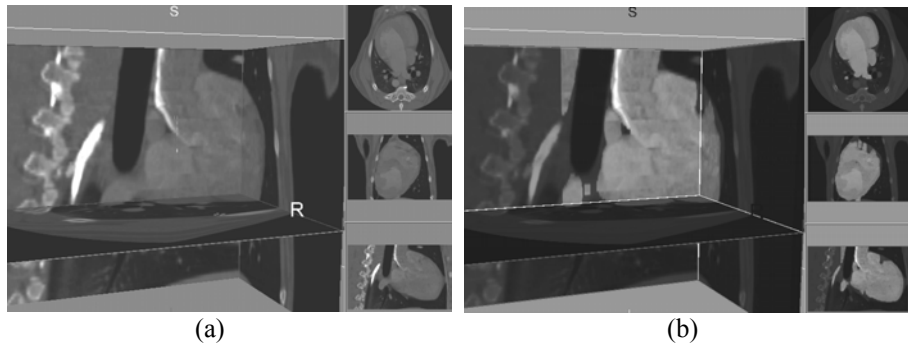
Fig.3 An example of the cardiac images. (a) source data; (b) highlighted segmented heart region. In both (a) and (b), left: ortho-planar view; right top to bottom: axial, sagittal and coronal views.

3.1 Case Study

Five dynamic CT scans of beating hearts, each containing ten individual volumes throughout the cardiac cycle, were employed in this study. Each of the 10 images was segmented individually. An example of the segmented results is shown in Fig.3 (b).

The average segmentation time for one of these volumes is 155 seconds, which is not fast enough 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 and animated to produce a physical cardiac beating model. One set of the heart volumes during a cardiac cycle is shown in Fig.4.
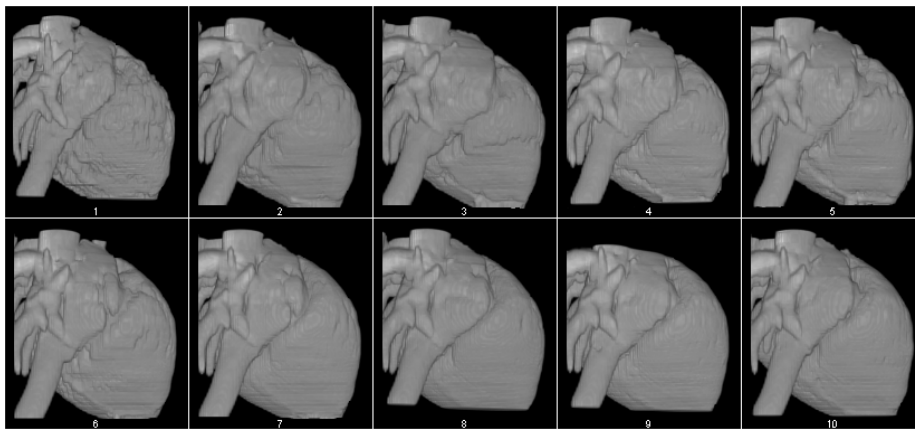

Fig. 4 Segmentation results. 1-10: segmented heart volumes during a cardiac cycle.

3.2 Validation

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

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

4   Discussion

This approach achieves highly accurate segmentation results for the input datasets. Our method identifies and reconstructs the structure of the organ for high quality visualization across a variety of conditions, even in the imperfect world of routine clinical-quality images. Additionally, we 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 a individual heart volume. Compared to existing segmentation algorithms, our new approach represents a significant improvement.

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.

The physical beating heart models were finally produced using the segmented cardiac volumes. The animated beating heart can represent the features of deformation of the heart during a cardiac cycle.

5   Conclusion

A new fully 3D medical image segmentation and modeling approach was described using a 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, we propose to improve the algorithm to make it fully automatic. We are considering the morphological Top-hat transformation [10], 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 we therefore chose not to use it in our current work.

Acknowledgement

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