

# 4D Cardiac Reconstruction Using High Resolution CT Images

Mingchen Gao<sup>1</sup>, Junzhou Huang<sup>1</sup>, Shaoting Zhang<sup>1</sup>,  
Zhen Qian<sup>2</sup>, Szilard Voros<sup>2</sup>, Dimitris Metaxas<sup>1</sup>, and Leon Axel<sup>3</sup>

<sup>1</sup> CBIM Center, Rutgers University, Piscataway, NJ, 08550, USA

<sup>2</sup> 2 Piedmont Heart Institute, Atlanta, GA, 30309, USA

<sup>3</sup> New York University, 660 First Avenue, New York, NY, 10016, USA

**Abstract.** Recent developments on the 320 multi-detector CT technologies have made the volumetric acquisition of 4D high resolution cardiac images in a single heart beat possible. In this paper, we present a framework that uses these data to reconstruct the 4D motion of the endocardial surface of the left ventricle (LV) for a full cardiac cycle. This reconstruction framework captures the motion of the full 3D surfaces of the complex anatomical features, such as the papillary muscles and the ventricular trabeculae, for the first time, which allows us to quantitatively investigate their possible functional significance in health and disease.

## 1 Introduction

Most countries face high and increasing rates of cardiovascular diseases. Therefore, it is critical to detect and diagnose such diseases in early stages. Computed tomography (CT) and Magnetic resonance imaging (MRI), as non-invasive methods to generate three dimensional images of an organ, have been widely used over the decades. If the detailed cardiac shape features are accurately reconstructed from these images, we can potentially obtain additional clinically valuable information besides the widely used wall thickness and global function features. Many cardiac reconstruction methods have been developed to build 3D models of the heart from cardiac MR images, such as, but not limited to registration-based propagation framework [12] and deformable model [8] [9]. However, due to the sparsity of the data in usual MRI data sets, important anatomic structures, such as the papillary muscles, the ventricular trabeculae and the valves, are often difficult to capture in this modality.

There has also been work on the 3D cardiac reconstruction from CT images [10,7,2]. However, despite the higher level of structural detail potentially available in CT data, most of the prior work has not sought to capture the finer detail structures of the myocardium, such as papillary muscles and trabeculae. The conventional approach to reconstructing cardiac structures from 3D images (e.g., for generating generic or patient-specific models of the heart) is a model-based one that uses a smooth parametric model to guide the segmentation of the cardiac structures from the 3D images. Such parametric models capture the

overall shape of the heart wall, but are too coarse to capture or incorporate many of the finer scale anatomical features. For example, Zheng et al. proposed an automatic method to segment the four-chamber heart [10]. Their method employs Active Shape Model to exploit a large database of annotated CT volumes. It efficiently segments all the four chambers of heart. However, the inner wall of the chambers is simply modeled as a smooth surface.

Recent advances in CT technology have made the acquisition of higher resolution cardiac images possible, which can capture previously unseen cardiac structure details. However, these anatomical details are currently only visualized using methods such as volume rendering, which do not lend themselves to the quantitative analysis of the 3D anatomical structures. Segmentation and reconstruction of the endocardial surface of the ventricles with incorporation of finer details can potentially greatly assist doctors in diagnosis and functional assessment. Chen et al. proposed a hybrid framework for 3D cardiac reconstruction [1]. That method has provided high resolution segmentation results of the complex cardiac structure. Their results captured the papillary muscles and detail structure of the myocardium. However, CT data sets from different time frames were segmented independently. Prior model knowledge from neighboring time frames is not used in their framework. Topological consistency between consecutive time frames is not guaranteed, either.

For the case of 4D cardiac images, two problems have to be considered simultaneously: 1) a heart wall segmentation problem in each image and 2) a tracking problem of the left ventricle motion given the data set. In [3], Mcinerney et al. proposed a method for 4D cardiac reconstruction, in which the output of the previous time frame is used as the initial guess for the current time frame in order to do a sequential segmentation. They used a finite element surface model which may not be able to handle topology changes. Montagnat et al. proposed an extended deformable framework by introducing time-dependent constraints. Thus, in addition to computing an internal force to enforce the regularity of the deformable model, prior motion knowledge is introduced in the deformation process through either temporal smoothing or trajectory constraints [4]. However, these 4D reconstruction methods do not capture detailed features.

In this paper, we present a framework for 4D left ventricle (LV) segmentation with inclusion of small scale anatomical features. Semi-automatic segmentation is used to get the initial segmentation from high resolution CT data for an initial (3D) frame of data. This semi-automatic segmentation is time consuming and tedious, so it is not efficient to use it for segmentation of all the frames. The initial high resolution mesh model is generated as an isosurface of the segmentation. Geometric processing is then applied to the initial model to get a smooth and regular mesh with an appropriate number of vertices. Based on the initial model from one time frame, our method deforms it towards the boundaries on the other frames. During the formation, the topology of the model is kept unchanged. We can also get the one-to-one correspondence between frames, as an additional benefit during the segmentation process. With the one-to-one correspondence, we can easily do interpolation among different time frames to get a

smoother heart cycle animation. We have applied our framework on a whole cardiac cycle. The results have been validated based on the ground truth segmented by multiple clinical experts. These novel and powerful methods can extract the full 3D surfaces of these complex anatomical structures, which allows us for the first time to quantitatively investigate their possible functional significance.

## 2 Methodology

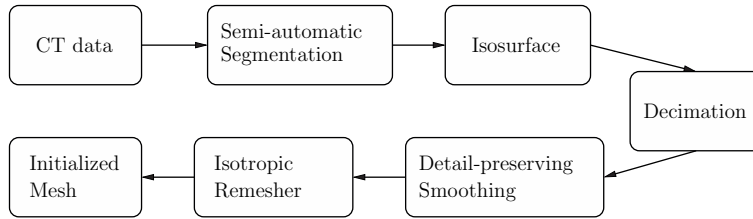
We propose a framework to reconstruct the cardiac model. This framework includes: initial model construction, deformable model based segmentation, and interpolation between time frames. The initial model is generated using 3D snake-based segmentation on one time frame of the CT image. The initial model needs geometry processing, such as decimating, detail-preserving smoothing and isotropic remeshing to get high-quality meshes. Based on the initial model, segmentation of the rest of the CT images is automatically performed using the deformable model. The segmentation of a sequence of CT images is interpolated in time to get a higher effective temporal resolution.

### 2.1 Model Initialization

The model initialization framework is illustrated in Fig. 1.

We use a 3D snake-based semi-automatic segmentation method to get the initial model [11]. This segmentation process is very time consuming and could not be used to segment all frames. Usually it takes several hours to finish a semi-automatic segmentation on one time frame. However, once this model has been generated, it is used to segment the rest of other frames automatically.

Segmentation results are represented as binary images. Isosurface detection is then applied to generate the mesh. However, the resulting mesh is usually bulky, noisy and irregular. To get a better initialization model, some geometric processing should be done on that mesh, such as decimating, detail-preserving smoothing and isotropic remeshing. First, the initial model is too large to readily modify, edge collapses are performed during decimation. After decimation, we get a mesh with much fewer vertices, but that still retains most of the shape details. The meshes have been decimated to about 20,000 vertices. Detail-preserving smoothing is then performed after decimation. The smoothing is restricted to



**Fig. 1.** Initial model construction

the tangential direction. Instead of moving each vertex towards the centroid of its neighbors, which would smooth out the shape details and sharp features, detail-preserving smoothing ensures higher quality meshes without losing details. Isotropic remeshing is important for the mesh quality. In irregular meshes, the vertices with high valences exert strong internal forces to drag other vertices, which can cause unrealistic results in deformable models [6]. An incremental isotropic remeshing technique is used to remesh the given triangular mesh so that all edges have approximately the same target edge length and the triangles are as regular as possible. This process would generally be iterated several times to get the final results.

After all these geometric processing steps, we finally get a high-quality triangular mesh with an appropriate number of vertices. This mesh is used as an initialization for other frames.

## 2.2 Deformable Model Based Segmentation

We want to deform our model normal to the boundaries during tracking. To do so, we define an energy function, including a term, *external energy*, derived from the image so that it is smaller at the boundaries. By minimizing the energy function, it drags the model towards the boundaries. We also want to keep the shape of the model unchanged during deformation. For that, we use another energy term, *model energy*, which reflects the differences between the original model and the deformed model.

Given a gray level image  $I(x, y)$ , viewed as a function of continuous position variables  $(x, y)$ . The model  $M_{t-1}$  derived from the previous frame is used to fit the current frame  $M_t$ . The energy function we want to minimize is defined as follows:

$$E(M_t, I_t, M_{t-1}) = E_{ext}(M_t, I_t) + E_{model}(M_t, M_{t-1}). \quad (1)$$

The external energy  $E_{ext}$  is designed to move the deformable model towards object boundaries.

$$E_{ext}(M_t, I_t) = -|\nabla I|^2, \quad (2)$$

where  $\nabla$  is the gradient operator.

Model energy is defined as the differences of attribute vectors. An attribute vector is attached to each vertex of the model [5], which reflects the geometric structure of the model from a local to global level. In 3D, for a particular vertex  $V_i$ , each attribute is defined as the volume of a tetrahedron on that vertex. The other three vertices form the tetrahedron are randomly chosen from the  $l$ th level neighborhood of  $V_i$ . Smaller tetrahedrons reflect the local structure near a vertex while larger tetrahedrons reflect a more global information around a vertex. The attribute vector, if sufficient enough, uniquely characterizes different parts of a surface of a boundary. The normalized attribute vectors are affine-invariant [5].

The volume of a tetrahedron is defined as  $f_l(V_i)$ . The attribute vector on a vertex is defined as:

$$F(V_i) = [f_1(V_i), f_2(V_i), \dots, f_{R(V_i)}(V_i)], \quad (3)$$

where  $R(V_i)$  is the neighborhood layers we want to use around  $V_i$ .

As we elaborated earlier in this section, the model energy term reflects the differences of attribute vectors between the original model and the deformed model.

$$E_{model}(M_t, M_{t-1}) = \sum_{i=1}^N \sum_{l=1}^{R(V_i)} \delta_l (f_{t,l}(V_i) - f_{t-1,l}(V_i))^2, \quad (4)$$

where  $f_{t,l}(V_i)$  and  $f_{t-1,l}(V_i)$  are components of attribute vectors of the model and deformed model at vertex  $V_i$ , respectively.  $\delta_l$  here denotes the importance of the  $l$ th neighborhood layers.  $R(V_i)$  is the number of neighborhood layers around vertex  $V_i$ .

A greedy algorithm is used here to minimize the energy function. The proposed algorithm is iterative. During each iteration, the first step is to minimize the external energy, moving vertices towards the minimum gradient of a image; the second step is to minimize the model energy; a neighborhood of a vertex has been examined and the point in the neighborhood with the minimum model energy would be chosen as the new location of the vertex. The iterations continue until the energy converges. While this greedy algorithm might fall into a local minimum, the experiments show satisfactory results.

During the deformation, we suggest moving a surface segment as a whole, rather than a single vertex. This would avoid this risk of getting trapped in a local minimum, and also speed up the convergence. Let  $V_i$  be the vertex to be deformed during a particular iteration. The first to  $R(V_i)$ th neighborhood layers are about to move together as a surface segment. Suppose  $V_i$  is to move to  $V_i + \Delta$  as a tentative position. Then the new position of each vertex  $nbr_{l,m}(V_i)$ , the  $m$ th vertex on  $l$ th neighborhood layer, is set to move to

$$nbr_{l,m}(V_i) + \Delta \cdot \exp\left(-\frac{l^2}{2\delta^2}\right), \quad (5)$$

where  $\delta$  is a parameter determining the locality of the transformation. We make the deformation unchanged on the boundary of the surface segment, such that the continuity has been maintained.

The parameter  $R(V_i)$  that determines the locality if the deformation is chosen to be large in the initial iteration, and is then gradually reduced to 1. Therefore, initially there are more vertices involved in the deformation. More global features are used in deformation. In later states, more local deformations are performed.

### 2.3 Interpolation

Segmentation for all frames are deformed from one single model, such that not only the topology is consistent, but also we have one-to-one correspondence of different time frames. All the meshes are interpolated in time to get a smooth animation of the cardiac cycle. We use periodic cubic spline interpolation. The last frame is set as the previous frame of the first frame in the interpolation process to get a circular animation of the heart cycle. Periodic cubic spline

interpolation makes heart meshes continuous on the second derivatives. The interpolation results are used in simulation of blood flow in the left ventricles.

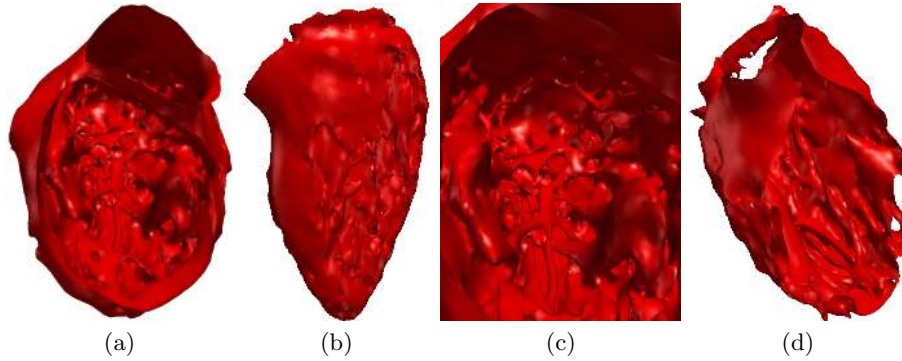
### 3 Results and Validation

We applied our reconstruction framework to 10 cardiac CT volumes, which captures a whole cycle of cardiac contraction. The CT data were acquired on a 320-MDCT scanner using a conventional ECG-gated contrast-enhanced CT angiography protocol. The imaging protocol parameters include: prospectively triggered, single-beat, volumetric acquisition; detector width 0.5 mm, voltage 120 KV, current 200 – 550 mA. Reconstructions were done at 10 equally distributed time frames in a cardiac cycle. The resolution of each time frame is 512 by 512 by 320.

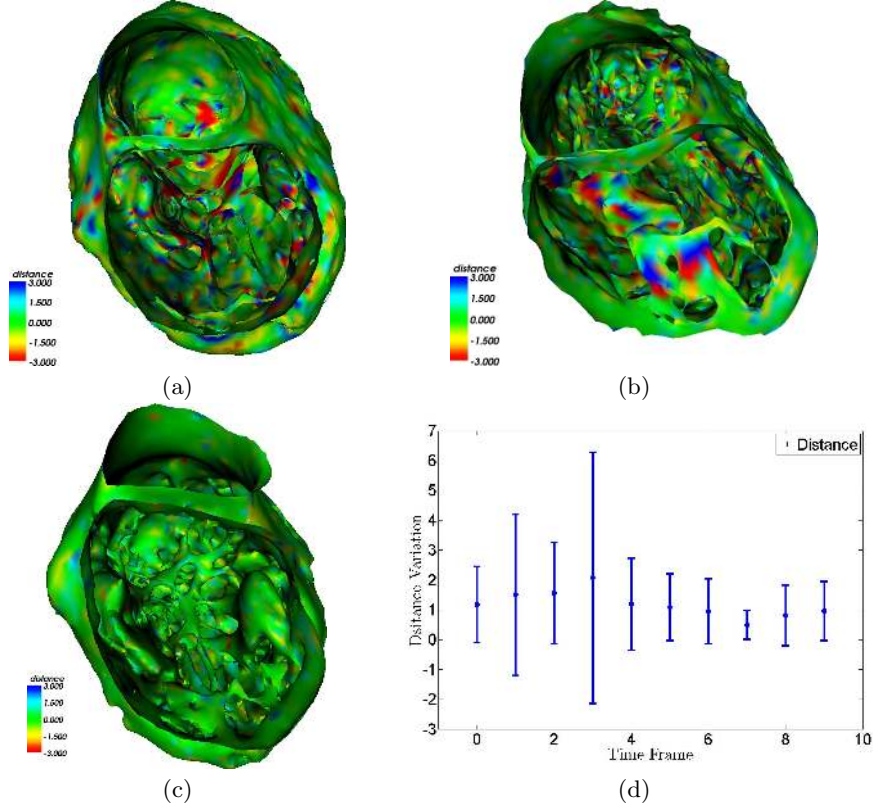
Our reconstruction method successfully captured the papillary muscles and the trabeculae of the left ventricle. Figure 2 illustrates the anatomic structure of the papillary muscles and the trabeculae of the left ventricle. The three-dimensional structures, their relationship and their movement during the cardiac cycle are much more readily appreciated from the model than from the original volumetric image data.

We compare our results to the ground truth from the annotations of clinical experts. Figure 3 shows the differences of the results from the manual segmentations. The color indicates the distance from each vertex of our results to the manual segmentation.

Figure 3(d) shows the quantitative evaluation of the results. The mean distance from every vertex to the semi-automatic segmentation is about one voxel. During the diastolic frames, which are frames 4 to frame 9, there are smaller



**Fig. 2.** Reconstruction results of left ventricle at one time frame. Papillary muscles and the trabeculae are clearly captured. (a) shows a view of the left ventricle from the top, through valves (b) shows a view of the trabeculae of left ventricle from the front (c) shows a zoom-in view of the papillary muscles and the trabeculae. (d) shows that papillary muscles and trabeculae being clipped by a user-defined plane.



**Fig. 3.** Differences of the left ventricle to the ground truth. Green colors mean that the distances are within one voxel. Red colors mean under-segmentation while blue colors mean over-segmentation. (a)(b)(c) Different frames of the differences of the left ventricle to the ground truth. (d) Distances distribution of every frame.

distances and less distance variations. On the other hand, during cardiac systole, because of large deformations between neighboring frames, the results have larger errors.

The interpolation results have made possible a smooth animation of the full cardiac movement cycle.

## 4 Conclusion

In this paper, we have presented a framework using high resolution CT data to reconstruct 4D motion of the left ventricle for a full cardiac cycle. The framework has been applied to a sequence of cardiac CT volumes. High resolution details, such as papillary muscles and ventricular trabeculae, were successfully captured

in this framework. In the future, we plan to use this framework to capture more fine structures of the heart, e.g., the valves and wall surfaces of all the four chambers.

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