

Fast and Automated Creation of Patient-Specific 3D Heart Models from Tagged MRI

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Abstract— Tagged MRI provides a useful way to assess regional cardiac mechanical function. However, it only provides 2D data, and does not provide direct access to functional parameters, nor does it allow easy comparisons between patients. Our approach to this problem is to create a patient-specific 3D model from a generic heart shape model and segmented image data. Results show that the model fits the data quite well, even when only sparse data is available. This approach is promising for both individual patient analysis and creation of statistically based analysis of regional cardiac function.

B. Previous work

Some previous approaches modeled the heart as a volumetric finite element mesh, and tried to fit all the heart structures at the same time [1], [2]. However, the relative position of the ventricles and the wall thickness tend to vary a lot from patient to patient. Large deformations are thus required, and can result in a degenerated mesh, which is a problem for finite element based methods like the ones cited previously.

Other approaches rely on a simplified shape model [3]. However, the simplified model does not give a realistic anatomy. We believe a model based on real data should be able to fit the data more closely, especially when the data is sparse.

Another option is to use a statistical model of the heart, such as in [4], [5]. In this paper, we use such a model for segmentation, but our main focus is to use the segmented data to fit a geometrical model, rather than designing a model specifically for segmentation.

The approach we pursue in this paper is to use a generic model of the anatomy of specific cardiac structures extracted from patient data. Then, using deformable model theory, we adapt individually each of these structures, e.g. the left ventricle, to the anatomy of a particular patient.

In order to achieve this goal, we employ automated contour segmentation methods and we present a novel method to assign correspondences between the segmented data and the points on a deformable model.

II. METHOD

This section details the method we used to create a patient-specific model of the heart from tagged images. The method consists of three steps: construction of a generic shape model, segmentation and labeling of MR images, and registration of the generic model with the segmented data.

A. Initial Model Creation

In order to create the original model, cine MR images were acquired of a healthy volunteer. Manual segmentation with validation by an expert was then performed to extract three cardiac structures: the left and right ventricular cavities and the epicardium. The meshing algorithm described in [6] was then used to create surface meshes from the extracted contours. The whole process is illustrated in figure 1.

I. INTRODUCTION

A. Motivations

Some cardiac disorders have direct consequences on the mechanical efficiency of the heart pump. However the cardiac contraction is complex, and can vary greatly between patients. Current medical imaging techniques such as magnetic resonance imaging (MRI) or computed tomography (CT) allow non-invasive evaluation of cardiac function. In particular, tagged MRI is a technique that allows the detailed visualization of myocardial motion and deformation throughout the cardiac cycle. However, these imaging techniques do not directly allow estimation of clinically relevant parameters, such as volume variations, or local velocities and stress in the myocardium. Study of these functional parameters can be very useful for both research and clinical applications.

Detailed analysis of cardiac function should also allow comparisons to be made between patients. Statistical analysis of this data could lead to a better understanding of different pathologies. However, due to anatomical variability between patients and differences in the conditions of image acquisition, it is generally not possible to directly compare image datasets.

A potential solution to both problems could be the use of a generic geometrical heart model, that can be adapted to fit the specific patient data. A good model adaptation scheme should be able to fit the patient data as closely as possible in order to extract detailed functional parameters, while remaining generic enough to allow easy comparisons between patients. Applying such a method to a number of different subjects would provide data that can be used for statistical analysis of regional shape and function variations.

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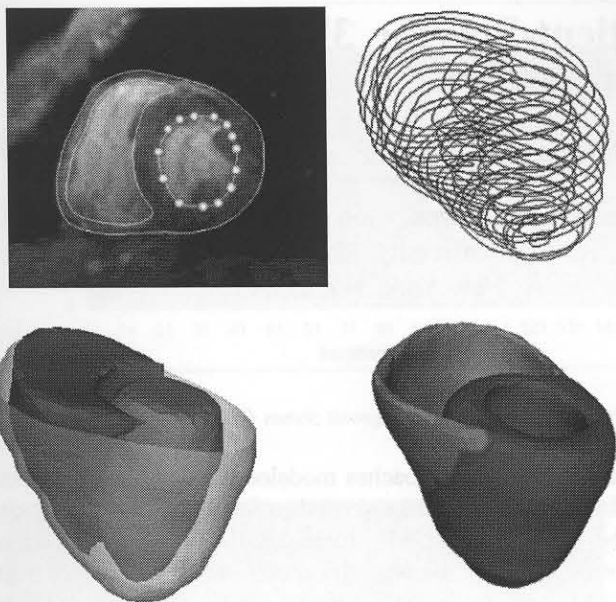


Fig. 1. Initial model construction: manual segmentation, 2D contours, surface meshing, and final result.

B. Automated Contour Segmentation method

Following is a short description of the segmentation method we used to process the tagged MR images. A more complete description can be found in [7].

Segmentation of tagged MR Images is difficult for several reasons: boundaries are often blurred and corrupted by nearby tagging lines; moreover, tagged images have lower signal-to-noise ratio and contrast than regular MR images. Because of these difficulties, strong priors for both shape and appearance are needed. Our method uses an active shape model as a shape prior, and a boundary appearance learning technique based on the Adaboost algorithm [8].

1) *Active shape model*: Active shape models [9] are a well known method for learning shape variability. Shapes are represented as a collection of landmarks. Principal Component Analysis is performed over a training set, giving the modes of principal shape variability. The resulting model can be used as a strong prior for segmentation.

In order to train the active shape model (ASM), 220 datasets were manually segmented. The resulting contours were labeled using the method described in [7], providing landmarks for the ASM training. The method is based on localizing high curvature points in the contours, and linearly interpolating between them. The result is a set of 50 landmarks or semi-landmarks. An illustration of the results can be seen in figure 2.

2) *Local boundary appearance modeling*: Because of the complicated boundary and region appearance in tagged MRI, we need to use all available information to form a complex rule. At different locations on the boundary, the rules and our confidence in the rules must be different. However, it is difficult to manually designate the rules and their confidence ratings. Our method uses the Adaboost learning approach to generate the local boundary criteria and their confidence

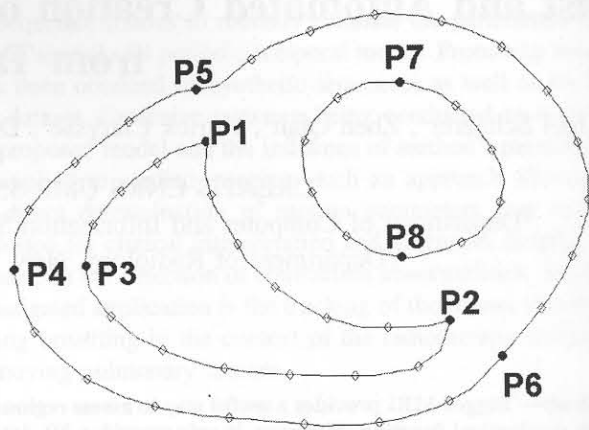


Fig. 2. Result of the automatic method used to place the landmark points. Black points are key points which are automatically found based on curvature and location. A fixed number of other points (represented with diamonds) is equally placed in between.

ratings. Adaboost selects a small number of important features from a huge potential feature set (i.e., weak classifiers) and creates a weighted combination of them to use as an accurate strong classifier.

Three kinds of steerable filters are used as the weak classifiers, for a total of 1840 filters.

3) *Segmentation*: In order to perform segmentation using the shape and appearance models, the heart is first detected using an Adaboost detection method, which is described in [7]. The detection is used to choose an initial position for the ASM. For each model landmark, several possible landmark locations are then searched along the model normal, and their likelihood of being on the heart boundary is estimated using the appearance model. The location with the highest likelihood is selected, and the following force is applied to the model at the location of the landmark:

$$\mathbf{F} = \mu \frac{(\mathbf{x}(j) - \mathbf{x}(i))c(i)}{\|\mathbf{x}(j) - \mathbf{x}(i)\|} \quad (1)$$

where $\mathbf{x}(i)$ is the current location of the landmark, $\mathbf{x}(j)$ is the candidate location of the landmark, and $c(i)$ is the confidence of the detection, given by the Adaboost classifier. This operation is then repeated several times to ensure convergence.

C. Correspondence between the heart model and segmented contours

In order to register the generic heart model to the extracted contours, some kind of correspondence must be found between the model and the contours. Such a correspondence can be found automatically, as with the Iterative Closest Point algorithm [10], for example.

In our case, however, the segmentation method directly provides a number of semi-landmarks, which can also be identified on the model. The knowledge of such a point-to-point correspondence simplifies the problem and allows for more efficient (direct) implementations of the registration methods.

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To find the landmarks on the model, we must first identify the planes that correspond to the image slices. Since the process is conducted at end-diastole, we know that the top and bottom slices correspond to the base and the apex of the heart, respectively. From this knowledge, we can deduce the relative positions of the image slices on the model, and extract the model contours by cutting it along planes corresponding to the image slices. The resulting contours are labeled using the same method that is used to train the ASM.

We now have a set of points extracted from the images and corresponding to the anatomy of the patient, and the location of the corresponding points on the generic model. The next step is to use this knowledge to compute a global non-rigid registration for each heart structure and apply it to the model.

D. Registration

The ASM segmentation provides the location of 50 landmarks per image slice, which we are also able to find on the generic heart model. In order to fit the model to the patient, we need to compute a dense transformation from this information.

A good transformation should fulfill two competing requirements: it should fit the image data as closely as possible, while preserving an anatomically plausible shape for the model. We have explored a hybrid approach [11], using a similarity transform to first roughly find the location and scale the model, and a smoothing thin-plate deformation to fit it locally while preserving its smoothness.

It is generally observed that the configuration of the different heart structures can vary significantly from patient to patient. Therefore, instead of fitting all structures at the same time, we propose to fit them independently, using an independently computed hybrid transformation for each of them. The structures can later be put back together in a single volumetric mesh, for example. In order to do that, landmarks are separated in groups corresponding to the heart structure they belong to: left ventricle, right ventricle and epicardium. The registration methods described in the next sections are applied to each set of landmarks individually.

1) *Affine registration:* To roughly place and scale the model, a 7 parameter similarity transform is used, including: translation, rotation and isotropic scaling. This transform is preferred to a full affine one because anisotropic scaling and shearing can lead to anatomically impossible shapes. Since this transformation is linear, the best fit can be computed using linear least squares. This only requires the solving of a linear system and is very efficient.

2) *Non rigid thin-plate spline registration:* Once the model is located correctly, a local non-rigid transform can be used to fit it more closely with the data. The method presented in [12] provides a reasonable solution, based on smoothing thin-plate splines. The resulting transforms are a linear combination of basis functions whose coefficients can be computed as the solution of a linear system. This is also very computationally efficient.

III. RESULTS

The method was applied to several datasets, and in this paper we present two datasets with different parameters. The

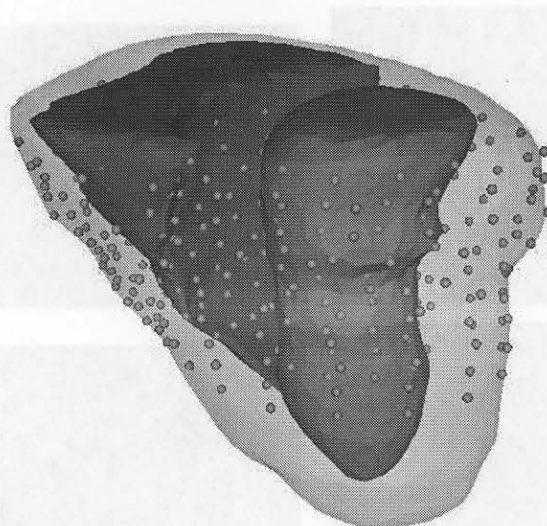


Fig. 3. Left and right ventricular cavities and epicardium of the constructed model for a sample image set. The yellow dots are the landmarks extracted by the ASM.

first dataset was acquired with 192x192 pixels, an in-plane resolution of 1.3mm, a slice thickness of 0.5cm, and 18 slices spaced by 4.8mm. The second dataset was acquired with 132x192 pixels, an in-plane resolution of 1.7mm, and 7 slices separated by 12.5mm. Both datasets were acquired on a 1.5T Siemens Sonata MR Scanner. We show reconstruction of the whole ventricles, even though segmented data was sparse and didn't include the apical portion of the heart.

The method was implemented in Python using the Open Source VTK library. The registration process took less than 10 seconds on 2.4GHz Pentium M computer with 1GB of RAM. The reconstructed model corresponding to the first dataset can be seen on figure 3.

Superposition of the reconstructed model with the original images can be seen on figure 4. The results show that the model fits the original data quite well even in the areas where no data was available to guide it (in our case, near the apex), showing the usefulness of such a model.

In order to quantitatively assess the accuracy of the proposed method, the reconstructed meshes were compared to the original data points. First, the reconstructed meshes were cut along the original image planes. Then, connected contours were created from the segmentation data points. In order to increase their resolution, the contours were linearly interpolated. Finally, the original and reconstructed contours were compared using the method described in [13]. The average distance between reconstructed and data contours on the two datasets was of 0.42mm for the left ventricle and the epicardium, and 0.59mm for the right ventricle. Further analysis shows that this difference is mainly due to the low resolution of the data contours, and could be improved by using more data points. The reconstruction error is small compared to the error induced by typical segmentation methods, which is at least 2mm in state-of-the-art methods (see [5] and [4]).

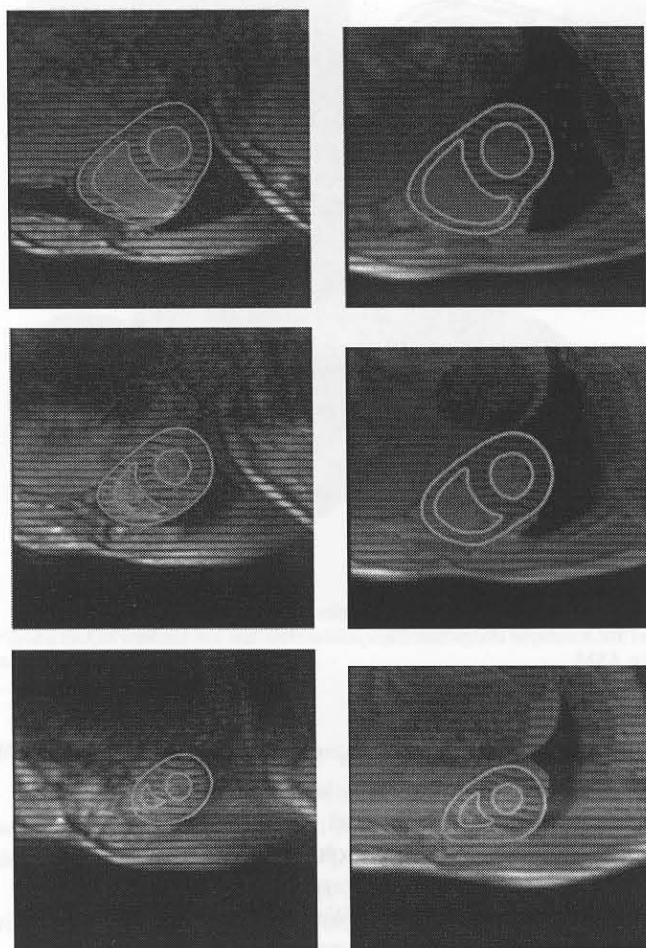


Fig. 4. Contours of the reconstructed model, superimposed on corresponding images from the two datasets. Left column is dataset #1, right is #2. Top is a slice near the base, the middle images represent a slice near the mid-portion of the ventricles, and the bottom images are near the apex. Note that no segmented data was available for the lower portion of the heart.

IV. DISCUSSION AND PERSPECTIVES

The method presented in this paper is a first step towards a detailed automated functional analysis of the cardiac function from tagged MR images. It allows creation of a patient-specific model from a generic geometrical model and arbitrarily located segmented landmarks.

In this paper the method was applied only to the case of cardiac imaging, however, it is obviously more generally applicable. It could be applied to any case where a generic geometrical model can be designed, and a correspondence can be found between the segmented data and the model.

Results could be further improved in a few ways. In figure 3, the effects of inter-slice misregistration can clearly be seen. This effect is due to the fact that different slices are acquired during different patient breatholds, which may be inconsistent with each other. This problem can be partly solved using automated motion compensation algorithms, such as the one presented in [4].

Most functional parameters need the complete geometry of the ventricles, in order to be accurately estimated. The current model does not include the basal part of the heart. Further

work will include extending the segmentation algorithm to long axis images, which are the only way to accurately acquire the heart geometry near the base. The method presented in this paper should be easily extensible to different orientations of data.

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