Combining Active Appearance Models and Morphological Operators Using a Pipeline for Automatic Myocardium Extraction

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Abstract. A geometrical model of the human heart is of interest in many fields of biophysics. The myocardium contains the electrical sources responsible for the generation of the body-surface ECG. An accurate geometric knowledge of these sources is crucial when dealing with the electrocardiographic forward and inverse problem. We developed a semi-automatic approach for segmenting the myocardium in order to deal with the electrocardiographic problem. The approach can be divided into two main steps. The first step extracts the atrial and ventricular blood masses by employing Active Appearance Models (AAM). The ventricular blood masses are segmented automatically after providing the positions of the apex cordis and the base of the heart. Due to the complex geometry of the atria the segmentation process of the atrial blood masses requires more information. We divided, therefore, the left and the right atrium into three divisions of appearance: the base of the heart, the lower pulmonary veins from its first up to the last appearance in the image stack, and the upper pulmonary veins. After successful extraction of the blood masses the second step involves morphologically-based operations in order to extract the myocardium either directly by detecting the myocardium in the volume block, or by reconstructing the myocardium using mean model information, in case the algorithm fails to detect the myocardium.

1 Introduction

Atrial and ventricular surface activation time imaging from body-surface ECG mapping data [8, 5, 7] may become a diagnostically powerful clinical tool for assessing cardiac arrhythmias. This cardiac source imaging technique aims to provide information in a noninvasive manner about the spread of electrical excitation in order to assist the cardiologist in developing strategies for the treatment of cardiac arrhythmias. Common cardiac arrhythmias, such as atrioventricular

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reentrant tachycardia, atrioventricular nodal reentrant tachycardia, or atrial fibrillation, can, in many cases, be traced back to accessory pathways, atrial or ventricular foci, e.g., from the pulmonary veins [6, 1], and reentrant circuits [13]. Identifying the site of origin of the ectopic focus or the location of an accessory pathway provides the essential information for treatment strategies, such as catheter ablation [9].

Activation time imaging from three-dimensional anatomical and body-surface ECG mapping data enables noninvasive imaging of the electrical excitation in the heart [12]. The method yields solutions to the electrocardiographic inverse problem and is based on an electrodynamic model of the patient's volume conductor and heart. The volume conductor considers a model of the electrodynamically most relevant compartments including chest, lungs, atrial and ventricular myocardium, and blood masses. A model of the heart comprises separate models for the atria and ventricles since whole heart models still resist a technical implementation with regard to the electrodynamic inverse problem. The crucial point of an atrial and ventricular model is their geometry. Geometric distances between the cardiac sources and the chest strongly influence the electrodynamic-based model and, therefore, the overall model error. The complex geometry of the atria is given by the orifices of the pulmonary veins, orifices of superior and inferior vena cava, tricuspid and mitral annuli, and right and left appendages, and this makes it more difficult, compared to the ventricle, to generate a geometrical model. It is clear that any technique that is capable of generating an atrial model will succeed also for the ventricle. Consequently, we decided to extract the ventricular blood masses using the same technique as used for the atrial blood masses, although especially the myocardium of the left ventricle could be segmented in a direct way. The reason for this decision was to get a consistent way for cardiac modeling and for incorporating the proposed technique into a segmentation pipeline with little user interaction. The main problem of constructing a realistic heart model is that the myocardium can hardly be segmented in volume data (especially the atria are a big challenge) because of the low sensitivity and resolution even for state-of-the-art medical imaging modalities like MRI and CT. We employed AAM for the extraction of blood masses and we use morphological operations to reconstruct the myocardial structure directly, in case the myocardium can be detected in the volume data, or in an indirect way, using a priori knowledge, otherwise.

The paper is organized as follows: Section 2 describes the segmentation approach and the implemented algorithms. Results of geometrical models of the atrial and ventricular myocardium are presented in section 3. The two steps of the approach are discussed in section 4, and finally, we summarize in section 5.

2 Methods

Our goal when developing this segmentation approach was to get a consistent way for cardiac modeling and for incorporating the proposed technique into a segmentation pipeline with little user interaction. We employed AAM for the

extraction of blood masses because this model based technique is able to generate reliable results when segmenting the cardiac blood masses. The use of morphological operations provides a fast method for myocardium reconstruction, in case the myocardium is detectable, or estimation otherwise, and enables an easy implementation in a semiautomatic segmentation pipeline.

2.1 Blood Mass Extraction Using Active Appearance Models

In the year 1991 Craw and Cameron published one of the first appearance modeling approaches [4]. They wrapped faces to a reference shape before doing a Principal Component Analysis (PCA). In 1994 Cootes et al. introduced Statistical Models of shape and texture [2]. In 1998 Active Appearance Models were introduced [3] and since this introduction a lot of enhancements were done. For more information http://www.isbe.man.ac.at/∼bim/ should be picked up.

Objects in images are represented using shapes. A shape can be described by a set of n points. Statistical methods can be applied when using shapes and, therefore, it is possible to analyze the shape differences and shape changes. Shapes can be inserted into an input or training image by searching for corresponding landmarks. Normally a human expert annotates the training sets by hand. Good landmarks are points of high curvature or junctions. Intermediate points can be used to define the boundary more precisely. The vector for representing a shape can formally be defined as

$$x = (x_1, ..., x_n, y_1, ..., y_n)^T. \tag{1}$$

If there are s training examples, then s vectors are generated by the human expert. Before applying statistical analysis on these vectors it has to be guaranteed that all shapes are in the same coordinate-frame. Therefore all shapes are aligned in a way, that the sum of distances of each shape to the mean ($D = \sum |x_i - \overline{x}|^2$)is minimized. An appearance model can represent shape and texture changes learnt in the training sets. The shape of an object is represented as a vector x and the texture as a vector g:

$$x = \overline{x} + Q_s c \tag{2}$$

$$g = \overline{g} + Q_g c \tag{3}$$

where the parameter c controls shape and texture. $\overline{x}$ is the mean shape, $\overline{g}$ is the mean texture and Q_s, Q_g are matrices describing the modes of variation (shape and texture) learnt from the training set. Generally, an AAM seeks to minimize the difference between an unseen image and one created by the appearance model.

For creating the AAM we integrated the AAM-API[1] available at http://www.imm.dtu.dk/∼aam/ into our Medical Segmentation Toolkit (MST) framework. The MST framework is developed using C++ and includes some

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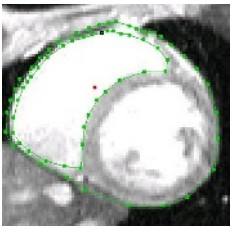

Fig. 1. Training set, annotated using 66 landmark points, of a blood mass from the right ventricle

different standard frameworks like the DCMTK framework for handling medical images (http://dicom.offs.de/dcmtk.php.en), ITK (http://www.itk.org/) for some segmentation methods, and Qt (http://www.trolltech.com/) for creating user interfaces. This toolkit enables to combine different segmentation techniques for each compartment and offers the creation of defined compartment pipelines.

When constructing a realistic cardiac model of a patient the main problem is that the myocardium can only be detected at limited locations in the volume conductor. The only structure which can be seen with sufficient accuracy are the blood masses. But also the blood masses have a big variation in shape and texture. Because of this reason a segmentation approach for this task needs a-priori information for successful and almost error-free extraction of the searched blood masses. Model based approaches like the AAM seem, therefore, to be a good choice for solving this segmentation problem. When trying to segment the atrial and ventricular blood masses from different patients the structures vary in shape and texture. With the help of AAM it is possible to figure out which are plausible variations and which are not. A new data set can, therefore, be segmented by finding the best plausible match between the model and image data.

The appearance model represents both the shape and texture variability seen in a training set. The training set consists of labelled images, where key landmark points are marked on each example object. We used 96 different training sets for establishing the right and left ventricular blood mass AAM. Every image set was annotated using 66 annotation points. 33 points were used to describe the left/right ventricular blood mass and 33 points were used to define the pericardium. Figure 1 shows an example of a training set for right ventricular blood mass extraction AAM. The pericardium (whole heart contour) is annotated because this makes it easier to initial locate the desired structure, a manner that was used for each AAM. After the preparation of the ventricular data sets, the training procedure - the processing of the principal component analysis - yielded 55 main components for the right ventricular blood mass and 56 main components for the left ventricular blood mass.

As already mentioned above, the atria show a more complex geometry and, therefore, more information is needed for the segmentation process of the atrial blood masses. In order to simplify the segmentation process we decided to divide the atria into three divisions of appearance: the base of the heart up to the left

upper (LUPV) and the left lower (LLPV) pulmonary vein, the LUPV and the LLPV from its first up to its last appearance in the image stack, and from this position up to the right lower (RLPV) and upper (RUPV) pulmonary vein. We created one training set for each division. All together, we prepared 193 training sets for atrial blood mass extraction and each atrial blood mass was annotated by 66 annotation points. 33 annotation points were used to define the left/right atrial blood mass and the resting 33 annotation points were used to describe the pericardium. The creation of the appearance models yielded 56 main components for the first atrial division, 58 main components for the second division and 51 main components for the third defined atrial division. The main components of our AAMs were defined to include 97% of all shape and texture variations.

Blood Mass Search Procedure. When extracting the ventricular blood masses the user has to provide the position of the apex cordis and the base of the heart in the associated volume block. After this, the AAM approach for the left and the right ventricular blood masses is initialized and then yields the desired segmentation of the ventricular blood masses by applying the fitting procedure until convergence.

The segmentation procedure for the atrial blood masses can be described this way. First initial parameters have to be set: the base of the heart, the end of the first division of appearance and the end of the second division of appearance in the volume block have to be marked. Then the AAM need to be initialized and that means to locate the desired structures in principal. After this process the model fit approach starts and operates until the search process converges.

These steps have to be repeated for each image between the given parameter range in the volume block to extract the ventricular blood masses as well as the atrial blood masses. Because the AAM ranges are defined by the given parameters the associated AAM are used in order to extract the desired structures.

2.2 Myocardium Reconstruction/Estimation Using Morphological Operations

After blood mass extraction using the technique described in section 2.1 the labelset should be smoothed by appropriate tools. Figure 2 shows a triangulation, created by a marching cubes algorithm, of the extracted labelsets of the atrial blood masses. The extracted blood masses are the basic input for the myocardium modeling procedure. The atrial and ventricular myocardium is constructed directly, in case the myocardium can be detected by the algorithm in the volume data, or artificially otherwise by applying appropriate voxel manipulations. The method adds label voxels in the outward normal direction until the user defined wall thickness is reached. Due to given facts in human beings the atrial wall thickness is between 3 to 5mm, the right ventricular myocardium between 6 to 8mm and the left ventricular myocardium between 8 to 12mm. The necessary input parameters for the algorithm are the minimum wall thickness, the mean wall thickness, and the maximum wall thickness. The approach uses operations of mathematical morphology. In principal the dilation operation is used.

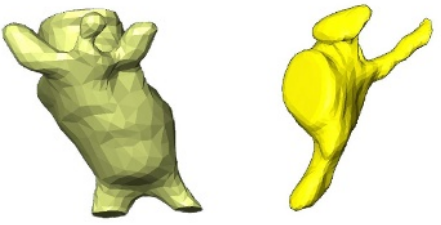

Fig. 2. Left panel shows the triangulated blood masses of the left atrium, and the right panel shows the triangulated blood masses of the right atrium

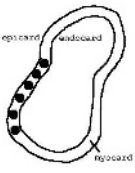

Fig. 3. On each boundary voxel of the endocardium, a virtual circle with a predefined radius rolls around the endocardium in order to reconstruct the atrial myocardium

The algorithm uses virtual circles as structuring elements with a radius range from the defined minimum wall thickness up to a maximum wall thickness. These circles roll around the blood mass boundary in order to reconstruct the myocardial structure. If the algorithm is able to determine the myocardium by probing all voxels to be element of a user defined gray value range inside the virtual circles (minimum up to maximum wall thickness) then the myocardial structure can be reconstructed directly. If the myocardial structure can not be detected the mean model information is used to reconstruct the myocardial structure. The mean model is a user defined parameter that describes the myocardium to have a standard wall thickness of 5mm for the left/right atrial myocardium, 7mm for the right ventricular myocardium and 10mm for the left ventricular myocardium, as an example for one possible parameter set.

The situation of estimation occurs predominantly when reconstructing the atrial myocardium because the atrial myocardium is almost always invisible due to its low sensitivity in the image data. This approach processes the volume stack sequentially in z direction without taking adjacent slides into account. For this reason this approach is a 2D version. In spite of the fact that this 2D version of the algorithm yields good results, the marching cubes algorithm can produce holes, especially when the segmentation of the blood masses differs too much between adjacent images or labelsets within the volumestack. Such a variation may occur because of the choosen image modalities (4mm slice thickness) and possible artefacts especially caused by motion. Although a slice thickness of 1mm is possible with new scanners such an image modality setting needs a lot of time that is not available when using the approach in a clinical application nowadays. To overcome this problem, the adjusted variant, the 3D variant, takes one slide

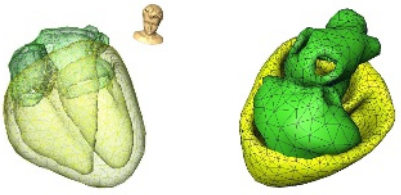

Fig. 4. Segmented ventricles and atria triangulated - for visualization - using a marching cubes algorithm

above and one slide below the initial labelset slide into account. As a main step of the 3D variant the adjacent slides are similarified by the algorithm [10]. To similarify the adjacent sets reduces the likeliness of holes when triangulating the labelset using a standard marching cubes algorithm. Because for the estimation of the electrical spread in the human heart a functional model and not an anatomical one is needed, model variations caused by similarify and smoothing operations influence the inverse solver less than having non existing structures (e.g., holes) in the model caused by above described possible situations.

3 Results

The segmented labelset is triangulated with a standard marching cubes algorithm followed by a remeshing process guaranteeing quality standards (equilaterality of triangles) that qualify for a FEM/BEM formulation used for dealing with the electrocardiographic problem. Our main problem is to get a model of the volumeconductor, on the one hand, in a very fast and efficient way to enable the estimation of the electrical excitation in a clinical application, and, on the other hand, to keep the model error as small as possible to get reliable results when trying to solve the inverse problem - and that means to find the pathological pathway in a non invasively way.

We tested our approach using volume data from eight different patients [12]. The segmentation of the left and the right ventricular blood mass needed $\mu = 148$ seconds. The segmentation of the right and the left atrial blood masses needed $\mu = 167$ seconds. The reconstruction process of the myocardial structure by using the blood masses as the main input source, needs about $\mu = 5$ seconds. For the reconstruction approach we used a *Dual Pentium Xeon* workstation with a clock frequency of 2.8 GHz and 2 GByte main memory (RAM).

Figure 4 shows a triangulated and remeshed ventricular and atrial myocardium model that qualifies for estimating the spread of electrical excitation in the patients volume conductor. Figure 5 shows a ventricular model of a female patient and the atrium with its blood masses.

To decide if the method qualifies, or with other words, if the model represents the for the estimation relevant parameters preferably close, the segmentation result of the blood masses were compared with the blood masses extracted by two

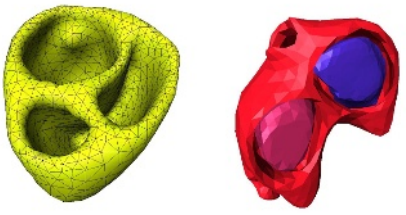

Fig. 5. Left: Reconstructed myocardium of the left and the right ventricle; Right: Atrium with blood masses

different human experts. The correlation coefficient, that was used to measure similarity, resulted in the correlation coefficient range from 0.912 to 0.931. The models of the human experts qualified as well as the automatically extracted models for the estimation of the electrical spread in the human heart.

4 Discussion

We presented a semiautomatic segmentation approach that allows to reconstruct the myocardial structure of the ventricles and the atria even if the myocardium can not be detected in the volume data. The indirect reconstruction/estimation of the myocardial structure enables the creation of a semiautomatic segmentation approach, because the main input for the myocardium extraction, the blood masses, can be seen clearly in the volume data, even if there are artefacts. This fact reduces the necessary user input and the mending process dramatically. Due to the possibility that the myocardium can be reconstructed using the blood masses, or the endocardial structure, the contribution to the model error will be sufficiently small. It is clear that it is important to have only a very small model error when trying to estimate the spread of electrical excitation in the human heart. Note that not only the segmentation task causes a model error. Also the quality of the ECG signal, the positions of the electrodes and other interferences cause an increase of the mean model error. So it is important to hold all these sources of errors down because only if the sum of all errors is low the mean model error has an acceptable value.

It seems to be imperative, when trying to reconstruct the myocardium, to extract the blood masses primary and then to use an indirect technique using the blood masses as a-priori information for the myocardial extraction. The reason for this strategy was that the myocardium can be detected only at limited locations in the medical image data. This myocardium visibility problem occurs because of low image resolutions, artefacts (caused by motion of the patient and/or the heartbeat) and image modality settings. Our cine gated short axis scan image data were acquired using a slice thickness of $4mm$. This slice thickness requires an indirect myocardium extraction approach because the thickness of the atrial myocardium is about $4mm$ and, therefore, it is almost always invisible in the image data. Although it is possible to generate slides with a thickness

of $1mm$ with modern scanners, the acquisition time increases. When using the $4mm$ slice thickness the MRI procedure can be finished in an acceptable time span (about 30 to 45 min). The MRI procedure consists of the preparation of the patient and the acquisition of the axial and the cine-gated short-axis scan. The cardiologist usually starts with the electrophysiology study (EPS) after a two hour intermission. During this break the whole volume conductor model has to be generated in order to enable the non invasive imaging of cardiac electrophysiology (NICE) [11] approach in the catheter laboratory.

5 Summary

The usage of AAM allow the extraction of ventricular and atrial blood masses in a very efficient way, which means that the run time behavior and the quality of the labelsets are in an excellent ratio. Only the annotation or rather the learning procedure of the appearance models need a lot of experience and time. The extraction result of the appearance models, the blood masses of the ventricles and the atria, can be directly used as input by the myocardium extractor. This technique allows to reconstruct the myocardium directly, when the structure can be detected in the volume data, or indirectly by using a-priori information, when the myocardium can not be identified in the volume data. The big advantage of this step is that only a few parameters have to be set and that the algorithm reconstructs the desired structure in a very efficient way.

The approach yields ventricular and atrial models that qualify, according to our experience, for cardiac source imaging. Thanks to the reduction of user interaction, the fast structure detection and the fast reconstruction of the cardiac model, this approach can be used in clinical applications.

The cardiac models were implemented many times in the construction of the patient's volume conductor model needed for solving the electrocardiographic inverse problem. The construction of this volume conductor segmentation pipeline coupled with our inverse solver can provide essential information to the cardiologist, in order to develop treatment strategies like catheter ablation. To get such information in a non invasive manner can help reducing costs, time, and it also reduces the remaining risk for the patient that arises during every invasive treatment.

The combination of AAM and morphological operators allows to create a segmentation pipeline with little user interaction and to reconstruct the desired structure even if not detectable in the volume data.

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