SHAPE MODELING OF THE MULTIOBJECT ORGAN HEART

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Abstract

Heart diseases result in or from morphologic variations; therefore analysis of shape variability is important for diagnostic classification and understanding of biological processes. In a pilot study we analyzed 16 individual human hearts, the common shape of the main chambers and of the combined structure including their interindividual variations for a fixed time phase. The electrocardiogram triggered MRI scans were segmented semi-automatically to derive an object ensemble containing the left and right ventricle, the left and right atria, and the pericardium for each individual heart. These objects were modeled using a medial based representation method providing interindividual shape correspondence due to object intrinsic coordinate system. Based on this concept of correspondence a common shape model was generated both for the single object and for the object ensemble. The interindividual variations were analyzed using an extended PCA method showing that almost 80% of variations are lying within the first 5 modes for both, the single and the combined structures. These so far results promise the method to be a big value in quantifying interindividual shape changes of clinical relevant populations and may serve as a potential tool for segmentation, classification, and diagnosis.

Key Words
Cardiac Modeling, Cardiac Image Analysis, Statistical Shape Analysis, Medial Representation, Multi Objects

1. Introduction

Analysis of shape has begun to emerge as a useful area of medical image computing because it has the potential to improve the accuracy of medical diagnosis, the correctness of image segmentation, and the understanding of processes behind growth and disease. Therefore over the last years a number of different techniques have been developed to generate and apply shape models. In the field of modeling and analyzing the complex shape of the human heart, different surface and volume based methods were applied as well as approaches based on finite element methods (FEMs) [1], active shape models (ASM) [2], harmonic maps [3, 4], or statistical shape models [5-8]. A global survey of recent proposals of cardiac shape modeling is given in literature [9]. All proposed methods have in common the challenge of establishing geometric correspondence between the individuals of a population. Frequently, landmark based registration and deformation is applied and therefore the correlation itself may change the shape under study. In a more recent paper from Frangi et al. volumetric B-spline deformation is proposed for automatic landmark generation [6]. Moreover, focusing the complex anatomy of the heart most of these approaches will have major problems in allowing a representation and analysis of the whole organ as well as of its constituents at different scale levels.

Therefore we used a medial based approach (m-reps) proposed by Pizer et al. [7, 10] that promises both, a straightforward method to establish correspondence without altering the individual shape on one hand and a hierarchical and multiscale representation scheme on the other hand. Up to now several single objects have already been successfully modeled and analyzed with this method [11-13], but a mechanical interacting and complex object ensemble, like the heart, has not been modeled yet. We divided the task of modeling a population of human hearts into two steps: First, the shape of the major objects i.e. left and right ventricle, left and right atrium, and the pericardium are represented via single m-rep models. Secondly we demonstrate the statistical shape impact on each object and the whole object ensemble on the population of 16 hearts.

2. Methods

• Data Sets and Pre-processing

For the pilot study we used MRI scans of 16 subjects, two healthy volunteers and 14 arrhythmia patients, which are accounted to be morphologically healthy. Atrial and ventricular geometry was acquired in CINE mode during breath-hold (expiration) using short-axis scans with 4 mm slice thickness for the atria and 6 to 8 mm thickness for the ventricle. In a first step we generated isotropic data sets to guarantee anatomically correct dimensions. Controlled semi-automated segmentation provided labeled data sets for each subject. In the segmentation of the left ventricle, the
papillary muscles are considered part of the blood pool, as is usual in functional cardiac analysis.

- **M-Rep Modeling**

The concept and application of m-reps already have been described in detail [7, 10]. The key idea of establishing geometric correspondence for a population of subjects with shape variations is the use of a discrete n x m grid of atoms forming a medial sheet which is representing the interior morphology of the object and is implying the outer boundary (Figure 1). This basic grid then can be matched to each subject in an iterative optimization process. For the matching two criterions are used: the image match based on a gradient descent method and a geometry weight, which preserves the given geometry of the atom grid. The whole optimization process consists of the following steps:

1. **Figural stage:** A global positioning (rotation, translation, magnification) of the whole atom grid is performed to achieve maximum object similarity.
2. **Atom stage:** The atoms are moved within a certain range to achieve an optimal image match while keeping the given geometry of the grid weighted by the geometry weight.
3. **Boundary stage:** This stage refines the yet rough boundary by keeping the geometry of the grid to an optimal image match (up to 100%).

As an example the resulting lattices of medial atoms consisting of 20 atoms (4x5) for the right ventricles of two different subjects are shown in Figure 1. The same atom grid describes two individual right ventricles with corresponding atoms. In this way we constructed the m-rep models for the whole population and all the major objects, which enables the generation of a common shape model and the analysis of shape variations by comparing individuals atom by atom.

The resulting m-rep models for each subject are representing the individual shape on one hand and provide an object intrinsic coordinate system on the other hand, in which each coordinate is corresponding to the identical coordinates of all other objects within the topological invariant population.

- **Principal Geodesic Analysis**

Principal component analysis (PCA) has proven to be useful for understanding geometric variability in populations of parameterized objects. The statistical framework is well understood when the parameters of objects are elements of a Euclidean vector space. However shapes which are represented by m-reps are operating in a figural space and naturally are not elements of Euclidean space. Therefore the PCA was extended by Fletcher et al. [11, 14] to principal geodesic analysis (PGA) which is also valid in figural space.

- **Application to Data**

The different tasks to generate m-rep models for a given grid are implemented in the Pablo framework, developed from the MIDAG group. The image match fitting criteria were more than 80% in the atom stage and more than 90% in the boundary stage.

Figure 1: Right ventricles from two different subjects (left, right) with the same atom grid of 4x5. The upper part shows the solid shaped model, the lower part shows the interior atom grid representing the medial sheet. The arrow indicates corresponding atoms.

Figure 2 gives an 2D impression of an original MRI image (left) and a m-rep model for the right ventricle showing the image match for the boundary stage (right). PGA analysis was applied to the resulting m-reps, in a first step to each single object and in a second step to the whole object ensemble.

Figure 2: Original MRI image (left) and the results of m-rep generation of the right ventricle for the boundary stage (right).
3. Results

- **Single Object Modeling**

The numbers of atoms satisfying the required match criteria for the five objects are within a range from 12 to 20 atoms. In detail the left ventricle is described with 15 atoms (3x5), the right ventricle with 20 (5x4), the left atrium with 16 (4x4), the right atrium with 12 (3x4) and the pericardium with 16 (4x4). The two main component distribution of the four chambers are given in Figure 3. Two subjects are marked with a filled circle – statistically indicated as diametrically opposed shapes. They are indeed different in size and elongation, especially for the atria.

![Figure 3](image)

- **Multi Object Modeling**

The distribution of the complete object ensemble over the population for the two main components is given in Figure 4, left hand side.

![Figure 4](image)

On the right hand side the percentage weight of the eigenvalues, describing the shape space is shown. The first 5 main components cover a shape space of almost 80% of shape variations within this population (Figure 4, right hand side). The derived mean m-rep model of the heart is shown in Figure 5.

![Figure 5](image)

4. Discussion

This paper presents the application of the m-rep method including shape statistics to the organ heart. It is shown, that this method is able to describe the shape of such complex organs as the heart, consisting of the major objects: left and right ventricle; left and right atrium; and the pericardium. The m-rep method, already successfully applied to some non structured anatomical objects [13] works for the more complicated major heart components as well. The high image match, more than 80 % for each object in the atom stage and the grid correspondence allows the comparison of single objects and furthermore the whole ensemble between the different subjects. This allows global and local analysis as well as common and individual analysis, not provided by any other method yet. Moreover this method requires neither landmark setting nor deformation, as used e.g. by Frangi et al. [6].

All the subjects lie inside a normal statistical Gaussian distribution, both for the statistic of the single objects as for the object ensemble, as is demanded for a uniform population. Two subjects (4,15) are pointed out, to confirm empirically the correctness of establishing spatial correspondence based on atom-wise correlation of the medial sheets. These both are indicated to be opposed in the distribution, more for the atria and the object ensemble, than for the ventricles. Looking at the subject attributes, these are both anatomically quite different structures of this population consisting of 13 male and 3 female subjects (mean age: 37 years, mean weight 85 kg). Subject 4 was the oldest man (57 years, weight: 85kg), whereas subject 15 was a young female (25 years, the lightest with: 45 kg).

Based on this result and on the correspondence concept, a first characterization of the major shape variations is
enabled. This allows either a single mode interpretation, or the interpretation of potential combined modes. The 1st main component especially describes the size differences of the hearts among the subjects. This may be seen in the statistical distributions concerning the two marked subjects (see Figure 3 and Figure 4). The 2nd mode describes a shortening and vice versa an elongation in the horizontal plane. This could either be a morphologic difference (the heart of subject 4 is more shortened, and that one from subject 15 is elongated), or probably a volume shift between the atria and the ventricle (due to a possible different filling state for the same time), or a combination of both of them. However, a detailed interpretation of the first two and the following modes which are including variations like twisting, elongation, stretching, dilation, rotation or others may be postponed due to the small number of subjects. For the current population almost 80% of the shape space will be covered with the first 5 modes (see Figure 4, right hand side). Since the model currently is based on 16 subjects, it is not valid in a statistical sense, however it turns out, that m-reps are a powerful method to model the complex shape of the human heart, which leads to a promising valuable tool for clinical applications.

5. Conclusion

To summarize, the method works for complicated interacting organs, and provides statistically rather promising results. Our next step will be to try this technique for a larger defined population and include motion to allow biological interpretations, which may be helpful especially in diagnostics, therapy, and image analysis.

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References


