

FAST AND ROBUST LOCALIZATION OF THE HEART IN CARDIAC MRI SERIES

A Cascade of Operations for Automatically Detecting the Heart in Cine MRI Series

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Keywords: Localization of the Heart, Magnetic Resonance Imaging, Cardiac cine MRI.

Abstract: This work presents a robust approach for fast initialization of an Active Appearance Model for subsequent segmentation of cardiac MRI data. The method automatically determines AAM initialization parameters: position, orientation, and scaling of the model. Four steps are carried out: (1) variance images over time are calculated to find a bounding box that roughly defines the heart region; (2) circle Hough-transformation adapted to gray values is performed to detect the left ventricle; (3) thresholding is carried out to determine the orientation of the heart; (4) the optimal initialization is selected using a mean texture model. The method was evaluated on 42 MRI short axis studies coming from two MRI scanners of two different vendors. Automatic initializations are compared to manual ones. It is shown that the proposed automatic method is much faster than and achieves results qualitatively equal to manual initialization.

1 INTRODUCTION

Segmentation of cardiac structures from magnetic resonance (MRI) images has been of great interest in the medical imaging community (Sörgel and Vaerman, 1997; Stegmann and Pedersen, 2005; Lelieveldt et al., 2001; van Assen et al., 2006). The great advantage of model-based segmentation is that it incorporates prior knowledge about the segmented structures.

Active Appearance Models (AAMs) (Cootes et al., 1998) are deformable models which describe possible configurations of shape and gray values by statistical analysis of a training data set. Several authors have proposed the use of AAMs and their numerous extensions to the problem of segmentation of cardiac structures. Methods proposed so far comprise 3D AAMs (Mitchell et al., 2002), temporal AAMs (Lelieveldt et al., 2001), and 3D+time AAMs (Stegmann and Pedersen, 2005).

A concrete instance of an AAM is defined by parameters comprising: position, scaling, orientation, shape and texture parameters. Matching the model to unseen data is equivalent to finding a configuration of parameters that optimally fit the model to the unseen data. The common proceeding is to place

the model onto unknown image data. Then deformations are iteratively applied until a difference measure such as root mean square (RMS) texture difference reaches a minimum. A problem often ignored in literature is robust and fast automatic initialization of the model, i.e. finding reasonable initial position, orientation and scaling. A brute-force method iteratively tries out each and every configuration. However this is very time-consuming since the number of possible initializations is huge. In previous work it has been suggested to perform AAM Search in parallel with multiple different initialization parameters (Stegmann, 2000). However, this approach is quite time consuming, especially when dealing with 3D AAMs. To utilize AAM-based segmentation for cardiac cine MR in daily clinical practice, a more efficient method for initialization is required.

Recently a method based on sparse Markov Random Fields (MRFs) (Donner et al., 2007) has been proposed for fast initialization of model-based segmentation. However this method relies on feature extraction which is not proven to deliver adequate results on cardiac cine MR data. Further more the run times reported for solving the considered MRF are in the order of a few seconds while the method we

present in this paper delivers the result after about one second.

This work presents a method that automatically determines the initial position parameters for an AAM for segmentation of the human heart in MRI short axis data. In earlier work Sörgel and Vaerman (Sörgel and Vaerman, 1997) have introduced a method for automatic heart localization for initialization of active contours. The presented work extends this approach. Instead of initializing active contours the goal of this paper is to initialize an Active Appearance Model. A set of well-established image processing algorithms is used including morphological operators (Soille, 2002) and Hough-transformation for circles (Davies, 1988). In contrast to previous work where Fuzzy Hough-transformation (Philip et al., 1994b) was applied to detect the left ventricle (Philip et al., 1994a) we propose to perform Hough-transformation directly on gray values as will be outlined later in this paper.

This paper is organized as follows: In section 2 an overview of the investigated MRI data is given. The fully automatic method for localization of the heart is described in detail in section 3. Validation and results are presented in section 4 and the paper concludes with section 5.

2 DATA

The 4D data considered in this work consists of cine MRI short axis studies of 42 different patients. The data was captured using two MR scanners from different vendors each one operating at a magnetic field strength of 1.5 Tesla. Each short-axis study consists of 7 to 13 slices with pixel resolutions ranging from 1.17mm to 1.68mm. The spacing between slices ranges from 7.2mm to 12.0mm. Time-resolution lies in the range of 11 to 27 time steps per patient study.

3 METHOD

Our method takes into account the complete four-dimensional (3D + time) input data and computes the initial parameters for the position of the model: position, orientation and scale-factor. The pipeline is made up of four steps (see figure 1):

- extraction of the region of interest (ROI)
- localization of the LV
- calculation of LV-RV orientation
- model-based candidate selection

In each step elementary digital image processing algorithms are used. This makes the method transparent, comprehensible, and easy to implement. In the following the individual steps of the algorithm are explained in detail.

3.1 Extraction of the Region of Interest

In order to limit more complex calculations to a restricted ROI, the first step is a detection of the image area which contains the heart. Over the period of the cardiac cycle position and size of the heart vary due to contraction of the myocardium. As a result the strongest variations of gray values appear in the region inside the heart. The localization is derived from the variations of gray values over time similarly as proposed by Sörgel and Vaerman (Sörgel and Vaerman, 1997).

For every slice a variance image is calculated. The gray values of a variance image correspond to the variance of the according pixel over the complete cardiac cycle. High gray values indicate strong variance and thus the according pixels belong to the heart region with high probability. Figure 2 shows examples of such variance images for different slices of a single data set.

It has to be considered, especially for MRI data, that high variance of a pixel's gray value might possibly come from noise or imaging artifacts. To reduce the disturbing influence of noise the following image processing steps are carried out for the individual variance images. A threshold is selected such that the according number of pixels above the threshold approximately cover the area of the heart (roughly $10000mm^2$).

To eliminate single pixels and small pixel areas a morphological cleaning is applied to each variance image. The morphological structuring element that is used is a 5×5 mask centered over the considered pixel. If less than 11 pixels in this mask are set the pixel is unset. If more than 15 pixels are set the center pixel is set. Otherwise the old pixel value is kept.

This improves the results significantly but in some cases there still remain misleading pixels set. To increase robustness all masks from all slices are considered jointly. A new mask is generated by summation of the individual variance images. This gives a result as depicted in figure 3(a). Outliers where misleading variances appear in individual slices only are removed with the following operation: All pixels which are set in less than 25% of all slices are deleted. Figure 3(b) shows an example of the outcome of this step. To further reduce artifacts only the largest connected region in the mask is considered (figure 3(c)). A bounding

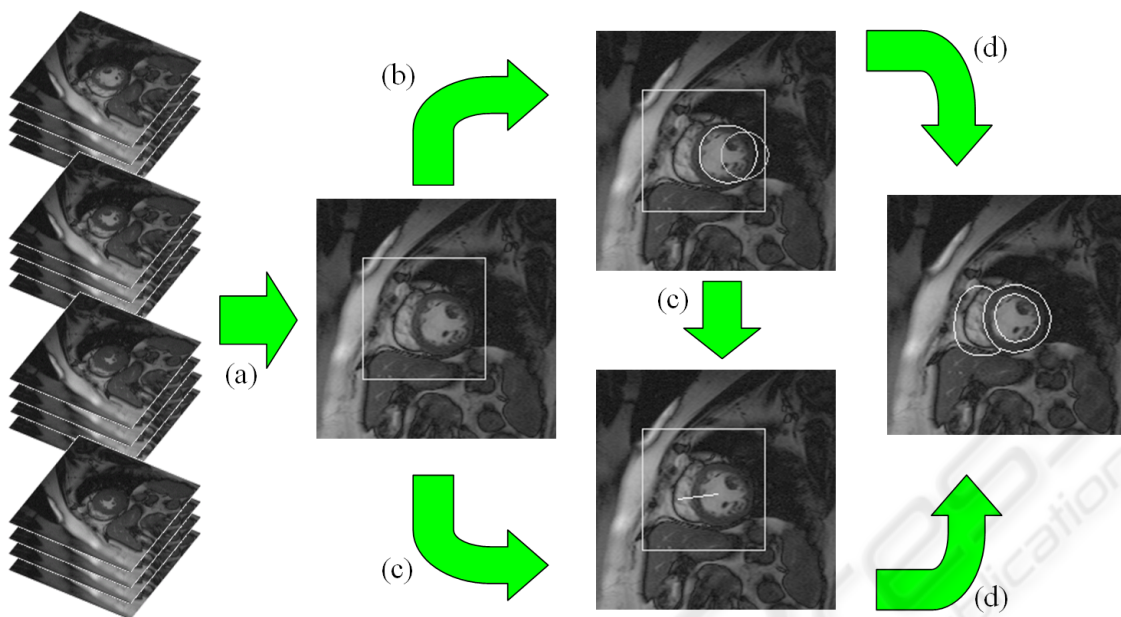


Figure 1: The pipeline: (a) ROI extraction, (b) LV localization, (c) LV-RV orientation, (d) model-based candidate selection.

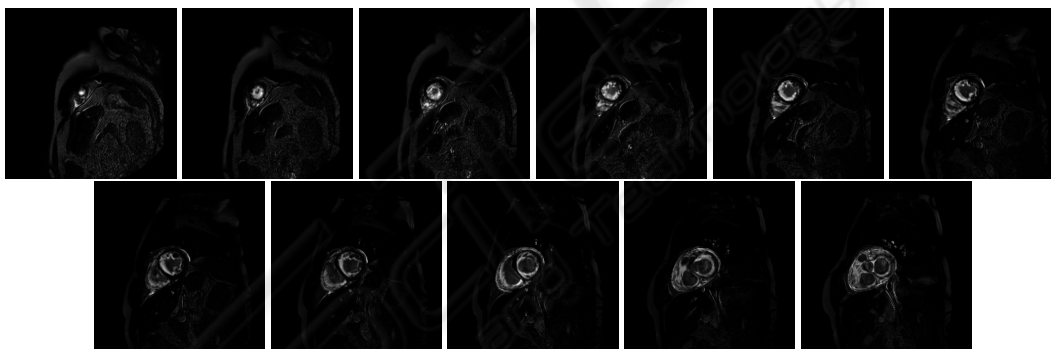


Figure 2: Variance images for individual slices of a single data set.

box around it defines the ROI as shown in figure 3(d). Since information from different time steps and different slices is combined it is argued that the resulting mask robustly identifies the region of the heart.

3.2 Localization of the Left Ventricle

While the first step in the algorithm takes the full 4D data into account the rest of the algorithm is performed on the central slice of end-diastole only. The end-diastole is typically known since the individual time steps are delivered as volumes sorted by time, starting with the end-diastolic volume. Since the captured volume typically covers the left ventricle from apex to base the center slice of a volume is taken for

further refined localization of the heart.

The myocardium of LV has approximately the shape of a circle. This fact motivates the use of a Hough-transformation for circles (Davies, 1988). To reduce the computational burden the Hough-transformation is restricted to the ROI calculated in the previous step.

Typically the first step in Hough-transformation is edge detection. In the experiments carried out on cardiac MRI data it turned out that standard edge detection algorithms like Canny Edge Detection (Canny, 1983) give very poor results for many data sets. On the one hand this is due to properties of MRI data. On the other hand fuzzy anatomical structures such as papillary muscles and trabeculae make it very difficult

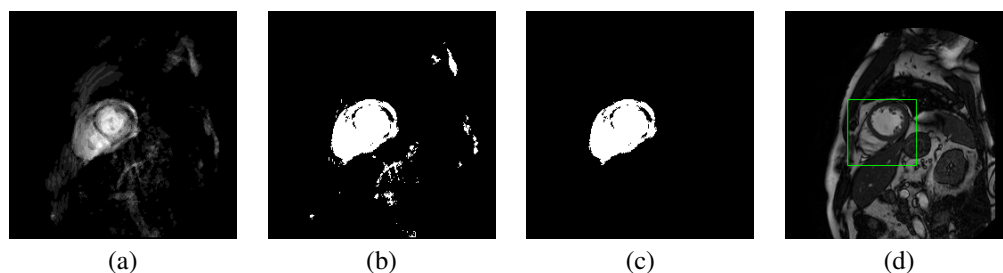


Figure 3: Towards the ROI: (a) Sum of variations, (b) thresholded, (c) largest region extracted, (d) and resulting bounding box.

to calculate meaningful image gradients that clearly represent transitions between objects. Furthermore in experiments it was observed that gray value distributions for MRI images fluctuate significantly inter and even intra patient studies. This makes it very hard to select generic parameters for an elaborate edge detection algorithm.

More elaborate approaches like Fuzzy Hough-transformation (Philip et al., 1994b) try to circumvent the problem of structures deviating from perfect circles. Anyway the problem of strongly misleading edges in the region of papillary muscles remains.

In order to overcome the problems of edge detection, the Hough-transformation is adopted to take original gray-values rather than edge information as input. The assumption is made that gray values of the myocardium are significantly darker than those of the blood inside the ventricles. Thus, for transforming the image into Hough-space low gray values in the image are assumed to belong to the myocardium with high probability. Using this approach the detected circle does not lie on the boundaries of the myocardium but somewhere in between. As a result the circle is detected robustly even if the shape of the left ventricle deviates from the perfect circle. Compared to the Fuzzy Hough-transformation the computational complexity is even reduced (no gradient calculation is required). Note that the even darker gray values in the lung region were excluded since they lie outside the previously calculated ROI.

The Hough-space considered is a three-dimensional space of parameters. Its axes are x , y (position of the circle's center) and r (radius of the circle). x and y are constrained by the bounding box defining the ROI. r is restricted to an interval of 25mm to 40mm – a typical range of radii for LVs.

Although Hough-transformation as we have described it works quite robustly there is still a small chance that the highest evidence for a circle is not correctly describing the LV. Our experiments showed that the correct contour of the LV always corresponds

to one of the first two largest peaks in Hough-space. Thus the first two most prominent candidates for position and scaling of the LV are considered at the last stage of the algorithm.

3.3 Heart Orientation

From previous steps two possible candidates for the left ventricle are extracted. Each of these candidates described by position and size of the two Hough circles. What remains is to determine the *orientation* of the heart, i.e. where the right ventricle is located relative to the left ventricle.

The ROI computed in section 3.1 is thresholded such that the 20% brightest pixels remain. As experiments showed, the two largest connected regions robustly correspond to the blood inside LV and RV. The centroids of these regions already indicate the spatial relation between the ventricles. It is however not known which region corresponds to the left ventricle and which to the right one. To resolve this ambiguity the region with its centroid closer to the center of a Hough candidate is identified as the left ventricle.

This way a unique orientation is assigned to both Hough-candidates.

3.4 Model-based Candidate Selection

The preceding steps reduced the initialization search space from millions (possibly every pixel with multiple different orientations) to two candidates: two Hough circles for the myocardium of the LV together with estimates of LV-RV orientation. Each of the two candidates defines position, scaling, and orientation for a possible initialization of the model.

To select the optimal candidate the root mean squared (RMS) texture errors between model and both initialization candidates are calculated. The candidate which produces the smaller error is identified as the final result.

4 VALIDATION AND RESULTS

The method has been evaluated for a total of 42 MRI studies. Automatic initializations have been compared to manual ones: five users interactively initialized the model. To assess the quality of the automatic method three figures of merit have been evaluated: average point-to-surface distance, texture error, and time performance.

The average point-to-surface (PTS) distance is calculated for the manually and automatically placed mean model shape relative to the accurately done manual ground truth segmentation. This was only possible for a subset of 31 data sets where ground truth segmentation was available. Figure 4 (top) summarizes PTS measures achieved by users and the automatic method. It is observed that automatic initializations come close to the manual ones. Please note that the average discrepancy of 6mm only refers to rigid initialization of the mean model. In this work only initialization is investigated – no subsequent deformations of the model are applied in attempt to achieve final segmentations.

In order to evaluate initializations for which no ground truth was given, the texture difference between mean model and image data was determined. Figure 4 (middle) shows the quality of matches for all (unsegmented) 42 data sets after manual/automatic initializations with respect to texture difference. It is again concluded that the automatic method generates initializations qualitatively comparable to those of the users. The final results – the initializations – for all validation data sets are visualized in figure 5 for the central slices of end-diastole.

While similar in quality figure 4 (bottom) proves another advantage of the automatization over user interaction – the speed-up. The average initialization of 1 second has been achieved by a Java implementation.

5 CONCLUSIONS

This work has introduced an automatic and robust method for localization of LV and RV in 4D cardiac MRI data. The method has been designed with help of few elementary image processing operators. The Hough-transformation for circles was adapted to operate on original image gray values instead of gradient magnitudes which makes the detection of the LV highly robust. The overall quality of initialization has been assessed by a user study. Time performance of the method indicates a high potential for daily clinical use.

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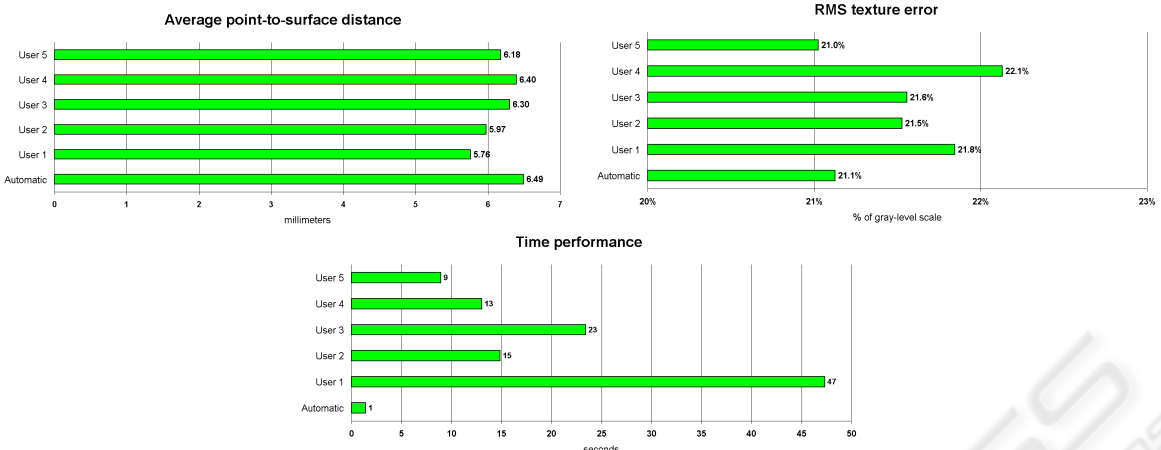


Figure 4: User study at a glance: Averaged point-to-surface distances for 41 data sets (top left), RMS texture errors for all validation data sets (top right), and time performance for all validation data sets (bottom).

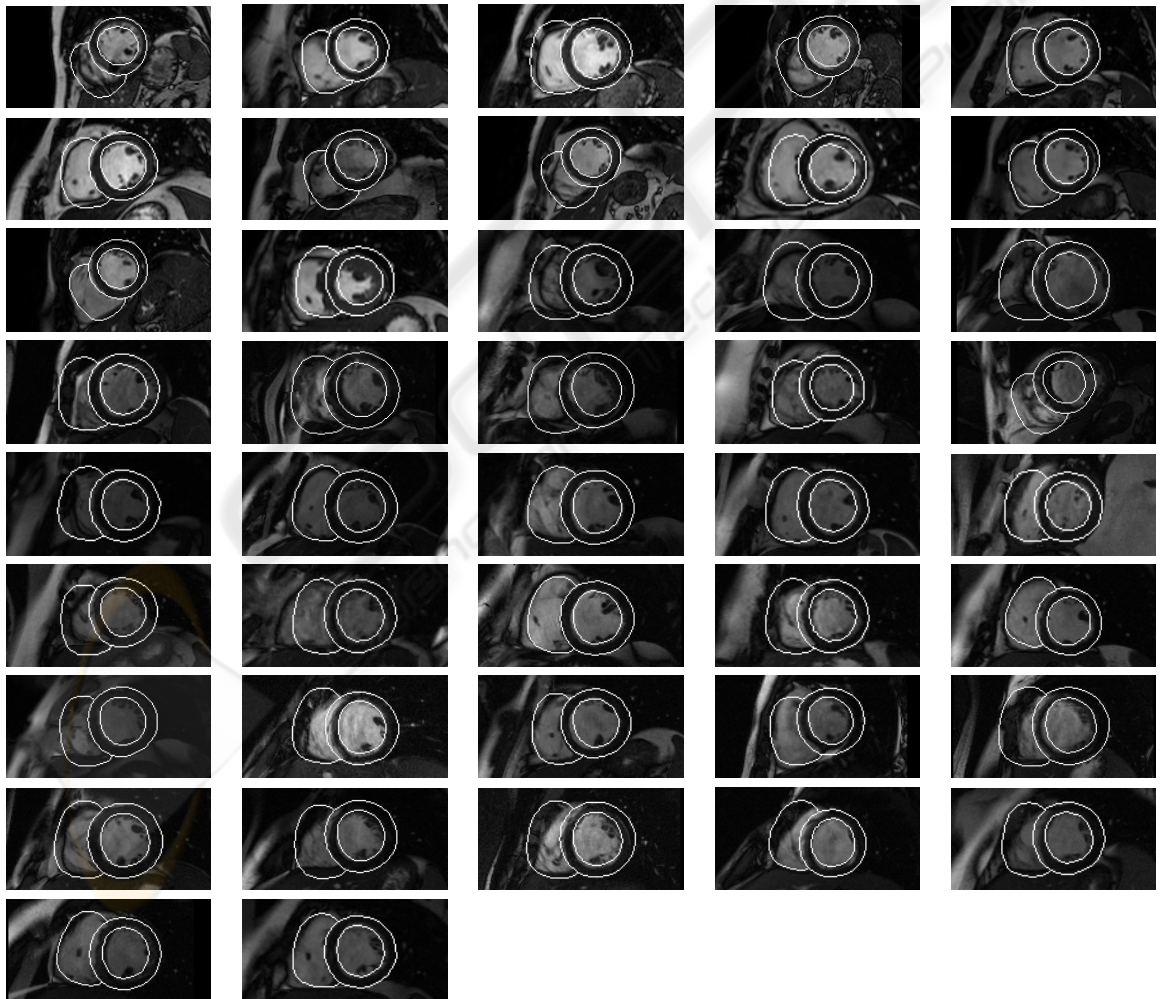


Figure 5: The result: Initialization of the AAM's mean at the central slices.