CARDIAC SEGMENTATION IN MR CINE DATA USING INVERSE CONSISTENT DEFORMABLE REGISTRATION

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ABSTRACT
This paper proposes a registration-based segmentation technique to fully automatically segment the left ventricle in cardiac cine magnetic resonance studies. We propose an inverse consistent deformable registration algorithm to recover one set of forward and backward deformation fields that allow us to access the deformation from any frame to any other frame in the cardiac sequence. Cardiac phases are segmented using a shortest path algorithm and time consistency is enforced through the deformation fields. We demonstrate on 52 datasets with expert outlined ground truth that the algorithm produces accurate (1.39 pixels median error, 2.10 pixels RMS error, 0.88 Dice coefficient) and fast (0.3 s/image) results.

Index Terms—Image Segmentation, Image Registration, Cardiovascular System

1. INTRODUCTION
Cardiovascular disease is an important health concern in the western world. Physicians use non invasive technologies such as magnetic resonance imaging (MRI) to observe the left ventricle (LV), which pumps oxygenated blood out to the rest of the body. They are interested in measuring quantities such as the ejection fraction, myocardial mass, blood volume over time, and myocardial thickening that can all be estimated given an outline of the LV myocardium. Manual outlining in all images is very cumbersome, however, and most physicians limit it to the end-diastolic (ED) and end-systolic (ES) phases, which is not enough to estimate most quantities. This paper proposes a technique to automatically segment the LV in all slices and all phases of a cardiac MR cine study.

The main difficulties in segmenting the myocardium are: a) the presence of papillary muscles and trabeculations in the blood pool that contribute to partial voluming between blood and muscle; b) often no clear edge between the myocardium and the liver; c) if there is fat around the heart, the fat/lungs edge is stronger than the fat/myocardium edge; and d) the trabeculations in the right ventricle might also generate partial voluming near the epicardium.

MR cine data consists of 3D+T data and some researchers have attempted 4D segmentation [1]. We believe however that it is very difficult to build a model that is general enough to cover all possible shapes and dynamics of the LV and a model-free approach would not be constrained enough. The opposite approach of segmenting each image individually [2] results in little cohesion between images and unsmooth contours over time. Intermediate approaches consist in segmenting either one phase at a time or one slice at a time. Segmentation of one phase at a time [3] is usually done with a model-based 3D segmentation but faces three main difficulties. First, the model needs to be trained for all possible LV shapes and pathologies and all possible MR acquisition protocols. Second, MR slices are so far apart (8-10 mm) compared to the in-slice resolution (1-2 mm) that the 3D segmentation problem is very anisotropic. Finally, individual slices might have been acquired at different breath hold and be misregistered.

We have chosen instead to segment one slice at a time using deformable registration, taking advantage of the strong temporal correlation between phases, and propagate the segmentation between slices. In the past, Paragios [4] has proposed to incorporate an optical flow based tracked shape as a prior in a level set framework. Sun et al. [5] have learned the dynamics of the LV boundary that they then incorporated in a curve evolution process. The most closely related work is our previous work [6] where we implicitly incorporated deformation fields from a registration algorithm into the energy function of a minimum surface algorithm.

We propose a fully automatic algorithm that combines deformable registration and segmentation. The main idea is to use an inverse consistent deformable registration to register all phases in one slice to the first phase. Then, the segmentation algorithm can be applied to any phase and the contours in the other phases can be recovered through the forward and backward deformation fields. The segmentation that results in the best set of contours is then retained. This can only be done because the deformable registration is inverse consistent and is the main strength of the algorithm. Otherwise, we would have had to recover many deformation fields between all pairs of phases, which would have been completely impractical.

2. LEFT VENTRICLE SEGMENTATION
The detection of the heart and the LV blood pool has already been described in [7]. It uses the first harmonic of the Fourier
transform in each slice to detect the beating heart. Then, blood-like connected components are extracted using Otsu thresholding and characterized by their shape, temporal behavior, position, etc. Finally, isoperimetric clustering is used to group connected components between slices and form the LV blood pool.

The proposed algorithm is divided into the following steps for the segmentation of each slice: 1) polar space transformation; 2) gray scale analysis; 3) deformable registration; 4) gradient computation; 5) Dijkstra’s shortest path algorithm and; 6) final contour recovery. We will describe each of these steps in more details in the next sections.

The first slice to be segmented is not the first slice in the dataset (the most basal slice) because that one often intersects with the valve plane and is difficult to segment. Instead, we pick a slice that shows as round an approximate blood pool as possible so that there are no interfering papillary muscles.

We have chosen to work in polar space mostly because the segmentation is performed using a shortest path algorithm that is well known to be biased toward small contours in Cartesian space. The center and maximum radius of the polar space are calculated from the blood pool estimates.

2.1. Gray Level Analysis

Because no two MR acquisitions are the same, it is important to determine the gray level properties of the images in the current dataset. In the first step, we use the entire dataset to compute approximate histograms for the blood pool, the myocardium and the whole image using regions that are automatically determined around the approximate blood pool as seen in Figure 1(c). The pixels in the center of the main peaks in those histograms are used to seed a multiseeded fuzzy connectedness (MFC) algorithm, which groups pixels into homogeneous regions. We also define a fourth region for partial voluming seeded with pixels whose gray levels fall between the blood and myocardium peaks.

The MFC algorithm, proposed by Herman and Carvalho [8], consists in building the shortest path from the seeds to all the pixels in the image, with regions competing as the paths are being built. As in [9], we define the cost function as the range of gray level intensities along the path to favor paths that do not vary significantly in gray level and, therefore, stay within one homogeneous region. The final histograms are then computed from the output label image.

The histograms are updated for each slice based on the segmentation that was obtained in the previous slice. New seeds are generated and the MFC algorithm is applied to the current slice to update the histograms and the labels. If during this process, it is observed that the blood class splits into two modes and the highest mode gets close to the myocardium mode, a new class for partial voluming is introduced. On the contrary, if the blood mode moves to the left of the partial voluming mode, then the partial voluming class is eliminated.

Many similarity metrics have been proposed for the registration of medical images and we have found that local cross-correlation (CC) is a robust measure for registering MR cine data. Local CC is defined as:

\[
J_{CC}(f_p, f_q; \Phi_{pq}) = \sum_x \sum_{N} \frac{(f_p(x) - \bar{f}_p)(f_q(\Phi_{pq}(x)) - \bar{f}_q)}{\sqrt{\sum_N (f_p(x) - \bar{f}_p)^2 \sum_N (f_q(\Phi_{pq}(x)) - \bar{f}_q)^2}}
\]

where \(\bar{f}_p\) and \(\bar{f}_q\) are the mean values in the neighborhood around pixel location \(x\) in both images, and \(N\) is the number of elements in that neighborhood. The deformation field \(\Phi_{pq}\) is computed according to [10] using variational calculus and by solving a partial differential equation (descending the gradient of \(J_{CC}\)).

Registration of time series data such as MR cine is usually performed by selecting a keyphase as the reference to which all other phases are registered. This approach is no longer feasible when contours need to be propagated from any arbitrary phase to any other phase. To overcome this issue, we extended the deformable registration algorithm to become inverse consistent.

A deformation field \(\Phi_{pq}\) is inverse consistent if \(\Phi_{pq} \circ \Phi_{pq}^{-1} = \text{id}\) and \(\Phi_{pq}^{-1} = \Phi_{qp}\). \(\Phi_{pq}\) is retrieved by minimizing the inverse consistent similarity metric:

\[
J_{CC}^{ic} = J_{CC}(f_p, f_q; \Phi_{pq}) + J_{CC}(f_q, f_p; \Phi_{qp}).
\]
We have developed an efficient update scheme of the iterative gradient descent, in order to solve Eq. (3) in reasonable time. In essence, each deformation field is alternately updated during descending the gradient of $J_{MC}$ resulting in an accurate computation of the inverse deformation and a quasi-symmetric registration algorithm. The extra computational effort for inverse consistent deformable registration is only about 10%-15% when compared to Hermosillo et al. [10].

The achieved inverse consistency not only allows for propagating contours between any two phases, but also for more accurate quasi-symmetric image registration.

2.3. Gradient Computation and Minimum Cost Path

The gradients are computed for every image as follows. First, probability images $P_M$ and $P_B$ are computed as responses from the myocardium and blood histograms. The gradient magnitude and direction, of these probability images as well as of the original image $f$, are computed using the Deriche filter. In addition, the label image $C$ is examined for the upwards transitions from myocardium label to non-myocardium label. These transitions are then smoothed to produce a pseudo-gradient image $\nabla L$. Finally, the following gradient formulations for the endocardium and epicardium were found to highlight the important features in the images:

$$G_{\text{endo}}^p(x) = \begin{cases} 0, & \text{if } \frac{\nabla L}{\nabla P_M} < 2\pi \text{ or } \nabla P_B < \pi \frac{\nabla L}{2\pi} \text{, otherwise} \\ 0, & \text{if } 0 < \frac{\nabla P_B}{\nabla P_M} < \pi \frac{\nabla L}{2\pi} + 0.5\nabla f(x) + \nabla L(x), \text{ otherwise}. \end{cases}$$

$$G_{\text{epi}}^p(x) = \begin{cases} 0, & \text{if } 0 < \frac{\nabla P_B}{\nabla P_M} < \pi \frac{\nabla L}{2\pi} + 0.5\nabla P_M(x) + \nabla f(x), \text{ otherwise}. \end{cases}$$

We use Dijkstra’s algorithm to compute the minimum path in the polar image. All the pixels in the leftmost (resp. rightmost) column in the image are initialized as starting (resp. ending) points on the path. To guarantee that the path is closed, we use the branch and bound algorithm proposed by Appleton and Sun [11]. The energy function for a contour $C$ is defined as $E(C) = \sum_{x \in C} \frac{1}{\epsilon + D(x)}$.

2.4. Contour Recovery in One Slice

The contours for all the phases in one slice are recovered as follows. First, the deformation fields $\Phi^1_p$ and $\Phi^1_p = \Phi^1_p 1$ are recovered by registering all phases $p$ to the keyphase 1. For a given phase $p$, Dijkstra’s algorithm is applied to recover the best contour $C_p$ for that phase. The contours $C_q$ on the other phases $q$ are generated using the deformation fields (that have been converted to polar space) by $C_q(C_p) = \Phi^1_q \Phi^1_p^{-1}(C_p)$. This can only be done because the deformable registration is inverse consistent. Then, the energy of this series of contours is given by $K(p) = \sum_q E(C_q(C_p))$. This same process is applied to all phases $p = 1, ..., P$ and the final segmentation in polar space is the one whose energy is lowest: $K = \min_p K(p)$.

Once the best sequence has been recovered, the best polar contour in the best phase is converted to Cartesian space and propagated to the other phases using the forward and backward deformation fields in Cartesian space. In addition, the convex hull of the endocardium is generated to further enforce that it goes behind the papillary muscles.

2.5. Propagation to Other Slices and Prior Information

To propagate to the other slices, we apply the deformable registration up toward the base and down toward the apex one slice at a time. The deformed contours from the previous slice are then used as priors. The gradient-based energy function is combined with the distance function $D(x)$ from the prior contours:

$$E'(x) = \min \{E(x) + D^2(x), \frac{1}{\epsilon} \}.$$  (6)

For the first slice to be segmented, the priors come from the approximate segmentation after LV blood pool detection. However, since these contours are very imprecise, the influence of the distance in the energy function is weakened:

$$E'(x) = \min \{E(x) + \frac{D(x)}{\epsilon \pi \max D(x)}, \frac{1}{\epsilon} \}.$$  (7)

For the epicardium in the first slice, we have designed a 2-step process. First, a rough estimate of the thickness of the myocardium is determined by finding the shortest path in every phase and averaging the distance between the epicardium and the endocardium. Then the distance map to the expected thickness is combined with the gradient-based energy function as in Eq.(6). All the steps in this section are applied to each slice, one slice at a time using the energy function in Eq.(6) or Eq.(7).

3. EXPERIMENTAL RESULTS

We have tested our algorithm on 52 datasets with expert outlined ground truth. The first 22 datasets were acquired on
Table 1. RMS distance (smaller is better) and Dice coefficient (larger is better) between ground truth and segmented contours.

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<th>RMS</th>
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<td></td>
<td>(pixels)</td>
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<tr>
<td>overall</td>
<td>avg  2.10</td>
<td>min  0.94</td>
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<tr>
<td>endocardium</td>
<td>2.00</td>
<td>0.87</td>
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<tr>
<td>epicardium</td>
<td>2.12</td>
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Siemens scanners from 4 different clinical sites. The other 30 datasets were acquired on GE scanners as part of the MICCAI 2009 Workshop on 3D Segmentation in the Clinic: A Grand Challenge. We ran our fully automatic algorithm and generated the segmentation contours. The algorithm is fast, it takes 1 minute to segment an average dataset with 200 images (approximately 256×256) on a dual core laptop (2.93GHz and 4GB RAM), 0.3 s per image.

Distances between ground truth and segmented contours were computed by first subsampling the contours so that their vertices are one pixel apart. Then, for each vertex on each contour, the distance to the closest point (not necessarily a vertex) on the other contour was estimated. These distances can then be histogrammed for all contours, all images, and all datasets. Figure 2 shows the cumulative histograms where a point (x, y) on the curve indicates that x% of all distances are below y pixels. The median distance is then 1.39 pixels. Table 1 shows the average, minimum, and maximum for the RMS distance and Dice coefficient for all datasets. Pixel sizes for the 22 Siemens datasets vary between 1.32 and 2.47 mm and are 1.25 mm for the GE datasets. It can be seen from both Figure 2 and Table 1 that the results for endocardium and epicardium are very similar.

The shortcoming in our previous method [9] is that the deformation fields were only implicitly integrated into the energy function of the minimum surface algorithm. As a result, the epicardium contour was not always tracked correctly and the contour could start at the myocardium/fat boundary at ED and slowly move to the fat/fat boundary by ES, as can be seen from Figure 3(a). Since this mostly happened when the two boundaries were very close to each other, the distance between ground truth and segmented contours was still small. However, the contoured heart appeared to beat abnormally, which might be confusing to the physician. Instead the proposed method uses the deformation fields explicitly and the epicardium contour is tracked much better as can be seen from Figure 3(b). We have had very positive feedback from our clinical experts after visual assessment of the results.

Another way to look at the consistency of the segmentation is to compute the LV mass, which is expected to be constant over time. We computed the standard deviation of the mass over time and averaged over the 52 datasets. It was very small (4.75 g) compared to the average mass of the 52 test left ventricles (166.5 g).

4. CONCLUSIONS

We have proposed an algorithm to segment the left ventricle myocardium in cine MR studies. It is based on an inverse consistent deformable registration that generates a single set of forward and backward deformation fields to align any pair of phases in a time series without the need to reapply the registration algorithm to all pairs of phases. Different segmentation contours are generated on each phase, propagated to the other phases and the best combination of contour series is retained. This makes the algorithm fast and efficient. We demonstrated that the segmentation is accurate and very consistent in time on a large number of clinical datasets.

5. REFERENCES