3D active shape modeling for cardiac MR and CT image segmentation
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'A full heart has room for everything and
an empty heart has room for nothing.'
Antonio Porchia (1885–1968), in Voces

Efficient Reconstruction of LV Endocardial and Epicardial Surfaces Using a 3D Sparse Active Shape Model

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Efficient Reconstruction of Cardiac LV Surfaces Using a 3D Sparse ASM

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Abstract

Among different radiological modalities cardiac magnetic resonance imaging (MRI) has been demonstrated to be the most accurate and reproducible tool for the assessment of human cardiovascular system. However, the traditional quantification methods based on the short- or long-axis slice summation, require acquisition of densely sampled datasets, resulting in increased examination and analysis time. In this study we demonstrate, that comparable quantification accuracy can be achieved with a combination of sparsely sampled data and the use of an Active Shape Model of the cardiac left ventricle.

8.1 Introduction

Cardiac Left Ventricular (LV) function and mass are important prognostic factors in risk assessment and management of heart disease. Among radiological modalities cardiac magnetic resonance imaging (MRI) has been demonstrated to be the most accurate and reproducible tool for these purposes [3]. In clinical routine practice, acquisition of so-called short-axis (SA) slices, covering the whole extent of the heart from the base to the apex in imaging planes perpendicular to the LV axis over multiple cardiac phases, is followed by precise delineation of the myocardial borders. The final volumetric estimate is usually computed as a sum of all short-axis volumetric contributions. The correct identification of the most basal slice may have a tremendous impact on the quantification results and has proven to be the major source of error in the assessment of LV volumes and mass. A recently proposed MRI technique, based on acquisition of the radially (RAD) oriented long-axis (LA) images, provides a clearer depiction of the basal part of the heart and can be alternatively utilized for the quantification of LV volume and mass [4]. The chamber volumes are computed as a sum of the volumes of each individual radial segment spanned between two neighboring slices. However, densely sampled image data (at least 9 slices) are required to achieve clinically acceptable results for the assessment of cardiac function [4].

A new hybrid quantification method, based on feedback-assisted 3D reconstruction of the endocardial and epicardial LV surfaces, was proposed in [101]. User-placed guide points are used to sparsely outline the boundaries of the left ventricle in all available short-axis slices and two longitudinal views and, subsequently, to fit a spline-based surface, representing the LV shape. The volumes, enclosed by the reconstructed endocardial and epicardial surfaces, are utilized for the quantitative assessment of LV dimensions. This approach has proven to be suitable for quick and more accurate analysis of cardiac function due to the better definition of the heart basis. However, it still requires a substantial amount of user interaction and is subject to observer variability.

In this paper a new method for fully automated, rapid, accurate 3D reconstruction of the LV surfaces, based on a special purpose 3D-ASM described in [78], is proposed. Our method is an extension to the classical ASM, introduced by Cootes et al. [19], and because it is able to work with sparsely acquired image slices, it is coined SPASM (SParse data ASM). A 3D statistical shape model of the LV was built using densely sampled data sets [91] and was tuned using a grid-computing approach [78, 90]. However it is applied to reconstruct the shape of the object of interest in a set of sparsely acquired MRI images from a variety of orientations (see Fig. 8.1). In this paper we
turn the focus of our work to assess the minimal number of required slices that allows
the reconstruction of the LV surface with a quality comparable to that of densely sam-
pled data.
To our knowledge, recovery of the shape of increasingly sparsely sampled organs (in
particular the heart) using a statistical shape model based on a dense mesh has not
been reported yet. The same holds for systematic investigation of the influence of data
sparsity on the reconstruction accuracy of organ surfaces.

8.2 Methods

8.2.1 Background
Cootes et al. introduced ASMs [19]. ASMs consist of a statistical shape model, of-
ten referred to as Point Distribution Model (PDM), and a matching algorithm. The
PDM is trained from a population of typical examples of the target shape, and models
shape variability as a linear combination of a mean shape, i.e. a mean set of (pseudo-
landmarks, and a number of eigenshapes. Three dimensional ASMs for cardiac seg-
mentation were described by Van Assen et al. [78] and Kaus et al. [26].

8.2.2 SPASM model construction
The underlying statistical shape model of the SPASM was constructed using non-rigid
registration [18] of a group of 90 manually labeled cardiac MRI data sets of healthy
and diseased hearts. After automatic landmarking and subsequent Procrustes align-
ment of the landmarked shapes, a mean shape is calculated. A set of eigenshapes is
calculated by application of Principal Component Analysis to the covariance matrix of
the shape samples with respect to the mean shape. For a more elaborate description
of the model training part, we refer to [91].
8.2.3 SPASM matching: edge detection

The second part of the SPASM, the matching algorithm, is based on a Takagi-Sugeno Fuzzy Inference System (FIS) [61] using Fuzzy C-means (FCM) [70] clustering, and propagation of model update information from locations with image information to regions without image information (see Sec. 8.2.4).

In the iterative process of matching the ASM to a (unseen) data set, the model, represented by a 3D mesh, is intersected by the image slices. From the image slices rectangular patches are extracted at the intersections. Thus, a large number of voxels surrounding the model mesh are gathered for classification into three tissue classes (blood, myocardium and air). In the inference part of the FIS, which contains defuzzification of the fuzzy membership degrees, different rules apply to different anatomical locations. Schematically the FIS looks like:

1. **input**
   
   Extract image patches at mesh intersections with images. Pool gray values according to (combinations of) mesh sectors.

2. **fuzzification**
   
   Determine balanced gray value partition using three tissue classes (blood, myocardium, and air) using an FCM clustering operation per gray value pool.

3. **inference of model updates**
   
   Three fuzzy membership degrees (FMDs) per voxel result from fuzzification. Based on the FMDs, infer a mesh update:

   (a) **defuzzification**
   
   for each pixel $T(x, y) = \begin{cases} 
   \text{bloodpool} & \text{if } L(x, y) = \text{bright} \\
   \text{myocardium} & \text{if } L(x, y) = \text{medium bright} \\
   \text{air} & \text{if } L(x, y) = \text{dark}
   \end{cases}$
   
   with tissue label $T$ and gray value $L$, at coordinate $(x, y)$ (see Fig. 8.2).

   (b) **transition inference**

   **endocardial border** from outside to inside take the first transition from myocardium to blood pool

   **epicardial border** from inside to outside take the first transition from myocardium to
   
   - blood pool, at the septum.
   - any other tissue at the lung, anterior and posterior wall,

For a description how a voxel is determined to be bright, medium bright, or dark, we refer to Chapter 5.

8.2.4 SPASM matching: update propagation

In sparsely sampled data sets (see Fig. 8.1), regions exist where the data is undersampled. Therefore, contrary to dense data sets, proper reconstruction of a 3D data volume is impossible. Locally only 2D image information is available, inherently yielding 2D in-plane updates during matching. Consequently, updates from image data cannot be
derived at all landmark locations, as required for ASMs. Ignoring updates at void data regions results in fixating landmarks at the model mean or at the location from the previous iteration, depending on whether updates are calculated with respect to the model mean shape, or incrementally with respect to the model shape from the previous iteration. In any case, ignoring updates prevents proper model deformation.

As a solution, we propose to propagate update vectors calculated at data locations, weighted with a Gaussian kernel (see Fig 8.3(a)) related to the geodesic distance along the model surfaces from update source to void data location

\[
w(\lambda, \omega) = \begin{cases} 
  e^{-\frac{\|\lambda - \omega\|^2}{2\sigma^2}}, & \text{if } \|\lambda - \omega\| \leq \chi \\
  0, & \text{if } \|\lambda - \omega\| > \chi 
\end{cases}
\] (8.1)

where \(w(\lambda, \omega)\) is the weight at the location of the receiving node \(\lambda\), \(\omega\) is the source node, \(\|\lambda - \omega\|\) is the geodesic distance to the origin of the update, \(\sigma\) is the width of the Gaussian kernel, and \(\chi\) is the propagation cut-off distance (\(\chi \equiv 3\sigma\)). Consequently, the weight at the source \((\lambda = \omega)\) is unity. A receiving node accepts propagated updates from any source only once, through the shortest path from source node to receiving node (see Fig. 8.3(b)). Pruning of all node updates is performed after all propagations stopped. A total update per node \(\upsilon\) is computed by summing over all contributions and normalized with the number of weights. The total update to node \(\lambda\) is thus defined as

\[
\upsilon(\lambda) = \sum_{m=0}^{M-1} \frac{\upsilon_{\omega m} \cdot w(\lambda, \omega_m)}{K_\lambda}
\] (8.2)

with the total number of contributions from source nodes to \(\lambda\)

\[
K_\lambda = \sum_{m=0}^{M-1} k_m, \text{ where } k_m = \begin{cases} 
  1, & \text{if } \|\lambda - m\| \leq \chi \\
  0, & \text{if } \|\lambda - m\| > \chi 
\end{cases}
\] (8.3)

and with \(M\) the total number of update sources in the mesh.

Thus, a Gaussian smoothing of the model deformation is applied between calculation of the single model updates and application of model shape constraints with respect to the shape training set. Gaussian smoothing of a mesh surface was previously applied by Paulsen et al. [102] in combination with a Markov Random Field for restoration of point correspondences in an ASM of an ear canal.

### 8.2.5 Experiments

The method described in this paper was used to automatically determine LV borders in MRI data sets with different image slice orientations and varying number of image slices present. Image data was acquired from a group of healthy volunteers with a 1.5T Gyrosan NT5 (Philips Medical Systems, Best, The Netherlands) MR scanner using the QBody coil, during breath hold in end expiration. With the Balanced Fast Field Echo (BFFE) protocol, a scout view and 2- and 4-chamber views were acquired, followed by SA views (typically 10-12 image slices). Every image slice was acquired in a separate breath hold. With the Turbo Field Echo (TFE) protocol, a radial scan was performed comprising four LA image slices in a single breath hold in end expiration, with inter-slice angle of 45° (see Fig. 8.1(b)). This protocol was applied to 15 subjects. For five more subjects data was acquired for additional multi-view (MV) data sets (see
Figure 8.2: (a) Classified set of image patches from a radial image. (b) Classified set of image patches from a short-axis image. (A=LV blood pool, B=RV blood pool, C=myocardium, D=air, E=outside image patches)

below). Image slices had a $256^2$ matrix and covered a field-of-view of 300-400 mm. Slice thickness and slice gap for the SA acquisitions were 8 mm and 2 mm respectively; for the RAD TFE acquisitions, the slice thickness was 8 mm. Due to the acquisition of multiple slices in a single breath hold with the TFE protocol, no breathing induced slice shifts occurred. For the method used to correct breathing induced shifts in the data acquired with the BFFE protocol, we refer to [77]. Different slice combinations were created and used for evaluation:

**RAD-4** Full data set of four images acquired in a radial orientation with the TFE protocol and inter-slice angle of 45°.

**RAD-2a** Sub-set of slices 1 and 3 from RAD-4, with inter-slice angle of 90°.

**RAD-2b** Sub-set of slices 2 and 4 from RAD-4, with inter-slice angle of 90°.

**MV-4** Multi-view combination of an apical and a mid-ventricular SA slice, and a 2-chamber- and a 4-chamber view.

**SA-full** Full short-axis stack (11 slices)

**SA-4, SA-5, SA-6, SA-7, SA-8, SA-9, SA-10** Short-axis stack sub sets of 4, 5, 6, 7, 8, 9, and 10 SA slices. All possible combinations of 4, 5, 6, 7, 8, 9, and 10 SA slices were tested.

For quantitative evaluation of segmentation performance of SPASM, in all data sets endocardial and epicardial contours were manually drawn. 3D chamber's surfaces were reconstructed by equiangular resampling of the manual contours and connecting the sample points from neighboring slices to form triangulated surfaces. These surfaces served as gold standard. Point-to-surface (P2S) distances were measured from node locations (points) on the segmentation results of SPASM to the surface of the manual segmentation. With the P2S distances (see Fig. 8.4(a)) as performance
8.3 Results

The best segmentation results, optimal values for $\sigma$, and the best slice combinations per data set are shown in Table 8.1. Based on the results of the P2S distance mea-

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Figure 8.3: (a) Gaussian propagation of single model updates projected on the mesh. Top left, no propagation, this shows the three update vectors from the first level triangle update. Corresponding nodes are surrounded with open squares in (b). Top right, propagation kernel $\sigma=4$ mm, and at the bottom, $\sigma=8$ mm. (b) Propagation of single model updates. Update sources are indicated as large dots. Propagation is shown for the update sources surrounded with a circle. From each source, an update vector originates. Updates are transferred (longer solid arrows) to the nearest nodes in the mesh (open squares). Updates are propagated to adjacent nodes weighted with a Gaussian kernel. Secondary updates are indicated in dotted lines, tertiary updates in dashed lines.

Figure 8.4: (a) Point-to-surface distances are measured from points on the model to the closest points on the manual surface. (b) Closed model (c) Closed manual shape.

criterion, the optimal propagation kernel width $\sigma$ (mm) was achieved for every slice combination separately using the same grid-computing approach as described in [78]. Tuning was done on the same data set used for evaluation. SPASM was initialized manually in the respective data sets.

8.3 Results

The best segmentation results, optimal values for $\sigma$, and the best slice combinations per data set are shown in Table 8.1. Based on the results of the P2S distance mea-
Table 8.1: Point-to-surface distances from points on the automatically segmented surfaces to the manually segmented surfaces, measured per subject between manual and automatic surfaces, averaged over the total population (15 subjects for RAD and SA, 19 subjects for MV), and volumes averaged over the populations. All values are $\mu \pm \sigma$.

<table>
<thead>
<tr>
<th></th>
<th>Average P2S errors (mm)</th>
<th>Average volumes (ml)</th>
<th>$\sigma$</th>
<th>planes</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>endocardium epicardium</td>
<td>endocardium epicardium</td>
<td></td>
<td></td>
</tr>
<tr>
<td>SA-full Manual</td>
<td>1.27 ± 0.30</td>
<td>1.14 ± 0.29</td>
<td>112.2 ± 26.1</td>
<td>188.6 ± 35.7</td>
</tr>
<tr>
<td>RAD-4</td>
<td>2.24 ± 0.54</td>
<td>2.83 ± 0.78</td>
<td>132.5 ± 18.5</td>
<td>243.0 ± 35.0</td>
</tr>
<tr>
<td>RAD-2a</td>
<td>2.41 ± 0.53</td>
<td>3.15 ± 0.80</td>
<td>132.9 ± 27.4</td>
<td>249.9 ± 50.2</td>
</tr>
<tr>
<td>RAD-2b</td>
<td>2.62 ± 0.76</td>
<td>3.29 ± 0.97</td>
<td>126.8 ± 24.9</td>
<td>240.6 ± 46.6</td>
</tr>
<tr>
<td>SA-full</td>
<td>1.97 ± 0.54</td>
<td>2.23 ± 0.46</td>
<td>122.0 ± 27.3</td>
<td>219.3 ± 41.3</td>
</tr>
<tr>
<td>SA-4</td>
<td>2.14 ± 0.58</td>
<td>2.46 ± 0.50</td>
<td>125.2 ± 26.3</td>
<td>223.0 ± 40.6</td>
</tr>
<tr>
<td>SA-5</td>
<td>2.08 ± 0.54</td>
<td>2.39 ± 0.44</td>
<td>124.7 ± 25.9</td>
<td>222.0 ± 39.4</td>
</tr>
<tr>
<td>SA-6</td>
<td>1.97 ± 0.52</td>
<td>2.30 ± 0.50</td>
<td>123.4 ± 25.2</td>
<td>220.3 ± 39.0</td>
</tr>
<tr>
<td>SA-7</td>
<td>1.99 ± 0.47</td>
<td>2.25 ± 0.40</td>
<td>122.0 ± 26.7</td>
<td>218.8 ± 40.3</td>
</tr>
<tr>
<td>SA-8</td>
<td>1.99 ± 0.47</td>
<td>2.25 ± 0.40</td>
<td>122.0 ± 26.7</td>
<td>218.8 ± 40.3</td>
</tr>
<tr>
<td>SA-9</td>
<td>1.95 ± 0.50</td>
<td>2.25 ± 0.44</td>
<td>122.1 ± 26.9</td>
<td>219.6 ± 39.5</td>
</tr>
<tr>
<td>SA-10</td>
<td>1.97 ± 0.54</td>
<td>2.23 ± 0.46</td>
<td>122.0 ± 27.3</td>
<td>219.3 ± 41.3</td>
</tr>
<tr>
<td>MV-4 Manual</td>
<td></td>
<td></td>
<td>131.9 ± 31.5</td>
<td>227.1 ± 52.1</td>
</tr>
<tr>
<td>MV-4</td>
<td>2.02 ± 0.93</td>
<td>2.29 ± 0.53</td>
<td>127.5 ± 28.1</td>
<td>229.1 ± 41.6</td>
</tr>
</tbody>
</table>

Measurements, for the MV test, one subject was excluded due to a mismatch of the model. For the SA and RAD tests, for all 15 subjects usable results were obtained. The optimal data configuration for SA-6 is shown in Fig. 8.1(c). T-tests were performed on the point-to-surface errors comparing all data combinations to results achieved with SA-full. Volumes were calculated by closing the model at the base (see Fig. 8.4(b)) and the manual shapes at both the apex and the base (see Fig. 8.4(c)). Endo- and epicardium volumes were calculated and compared for all combinations to those achieved with SA-full. For the comparison of MV-4 to SA-full independent samples t-tests were used. For all other comparisons paired t-tests were used. The results can be found in Table 8.2.

### 8.4 Discussion and Conclusions

Point-to-surface results from all SA and MV data combinations were better than or comparable to results obtained by Lötjönen et al. [32], and better than Mitchell et al. [31] and Kaus et al. [26]. Results from the RAD-4 data set were comparable to [26, 31], while [32] perform slightly better. SPASM however uses considerably less image slices in the sparser data combinations, whereas others used 8-12 slices. Apparent advantage of SPASM is that the method can be applied to arbitrarily oriented image slice combinations.

From the t-tests (see Tab. 8.2), it appears that the accuracy with respect to surface localization achieved on the SA-6 data configuration (6 planes) does not differ sig-
Table 8.2: Significance of point-to-surface errors from all data sets compared to the interobserver variability and to SA-full. Volumes compared to SA-full. Numbers are \( p \)-values. Asterisks mark statistical significance at the 0.05 confidence level. A \( p \)-value cannot be calculated for SA-10 due to equal results to SA-full (see Table 8.1). We also left SA-10 out of other comparisons, because of this.

<table>
<thead>
<tr>
<th></th>
<th>RAD</th>
<th>MV</th>
<th>SA</th>
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<tbody>
<tr>
<td></td>
<td>4</td>
<td>2a</td>
<td>2b</td>
</tr>
<tr>
<td><strong>point-to-surface errors compared to interobserver variability</strong></td>
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<tr>
<td>endocardium</td>
<td>.000*</td>
<td>.000*</td>
<td>.000*</td>
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<tr>
<td>epicardium</td>
<td>.000*</td>
<td>.000*</td>
<td>.000*</td>
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<tr>
<td><strong>point-to-surface errors compared to SA-full</strong></td>
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<td></td>
</tr>
<tr>
<td>endocardium</td>
<td>.078</td>
<td>.049*</td>
<td>.001*</td>
</tr>
<tr>
<td>epicardium</td>
<td>.027*</td>
<td>.003*</td>
<td>.002*</td>
</tr>
<tr>
<td><strong>volumes compared to SA-full</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>endocardium</td>
<td>.065</td>
<td>.002*</td>
<td>.135</td>
</tr>
<tr>
<td>epicardium</td>
<td>.000*</td>
<td>.000*</td>
<td>.001*</td>
</tr>
</tbody>
</table>

Significantly from that achieved when SPASM was applied to SA-full (11 planes). The same was already observed in Chapter 7 for the MV-4 data configuration (4 planes). Volumes could not be compared to manual volumes directly, because the model includes the apex, which the manual shapes did not. This leads to systematic volume differences. From the volumetric t-tests (see Tab. 8.2), volumes were not significantly different to SA-full from 6 SA slices and more and from MV-4 (as seen in Chapter 7). Thus, a limited set of differently oriented images in combination with the model-based approach provides an accurate and efficient way of reconstructing the endocardial and epicardial LV surfaces and yields accurate quantification of LV volumes.