Segmentation of the Right Ventricle in Four Chamber Cine Cardiac MR Images using Polar Dynamic Programming

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1. Introduction

Current clinical and research guidelines consider cardiac MR (CMR) a true gold standard for the evaluation of left and right ventricular function ([Karamitsos et al., 2009](#)). The ventricular function is generally calculated by measuring volumetric information from a stack of planes in the short axis (SAX) ([Hundley et al., 2009](#); [Fratz et al., 2013](#); [Tandri et al., 2006](#)). The SAX stack is planed using a single four chamber (4CH) plane because this plane demonstrates ventricular anatomical elements, such as the ventricular apices and the atrioventricular valves (i.e., mitral or tricuspid valve), ensuring that the SAX stacks encompass the entire ventricle.

Volumetric analysis of ventricular size and function relies on manual contouring of the inner wall of the ventricle (i.e., the endocardium), in the end diastolic (ED) and end systolic (ES) frames. Manual contouring is performed using commercial post-processing software such as Syngo.via (Siemens Healthcare, Erlangen, Germany) and CVI42 (Circle Cardiovascular Imaging Inc., Alberta, Canada); these software packages use the 4CH plane to help physicians visualize whether a SAX plane extends outside the RV for a given frame. Despite its utility, the 4CH information is mostly ignored in current CMR segmentation literature given its exclusion from popular CMR segmentation challenges (MICCAI 2009 ([Radau et al., 2009](#)), MICCAI 2012 ([Petitjean et al., 2012](#))). As part of our experiments we identified that RV segmentation in the 4CH plane can be used not only for identifying which SAX planes contain the RV for a given frame but provide a rough estimate of the RV endocardial contour in the SAX

planes; an example is shown in Fig. 1. The 4CH RV segmentation can also be used to calculate fractional area change (FAC), a validated surrogate for RV functional evaluation commonly used in echocardiography ([Lai et al., 2008](#)). Using the FAC as an RV ejection fraction (EF) surrogate can help mitigate the main drawbacks of CMR, which are the length of the scan and requiring patients to perform 8 to 16 breath holds in repeated 5-10 seconds intervals ([Dickstein, 2008](#)).

Fig. 1. Use of the 4CH segmentation for identifying the planes in the SAX stack that contain the RV. Red outline in (a) shows the manually traced RV border including trabeculation in the ED frame. Red outline in (b) shows a rough estimate of the RV endocardial contour in the SAX stack based on the 4CH plane in the ED frame. SAX stacks with no outline are those that do not include the RV. Figure best viewed in color.

Given the diverse disease processes that affect the RV (e.g., pulmonary hypertension, congenital heart disease, valvular disease, coronary arterial disease, heart failure) temporal area/volume information of the RV are critical for non-load dependent measures of ventricular function ([Kuehne et al., 2004](#)).

To provide a reproducible RV segmentation using a single 4CH plane, we present an algorithm utilizing the following steps (shown in): (1) automatic

Fig. 2. 4CH Segmentation Flowchart. Magenta denotes the module that requires user interaction; blue denotes optional modules. Figure best viewed in color.

segmentation of the cardiac region of interest (ROI) (Section 2.2); (2) user identification of the ED and ES frames along with the appropriate landmarks (Section 2.3); (3) automatic propagation of landmarks throughout the cardiac cycle (Section 2.4); (4) automatic identification of the septum (Section 2.5) and (5) final segmentation of the RV (given the septum and the propagated landmarks) (Section 2.6). The segmentation consists of joining three manually selected landmarks. First, the segmentation finds the minimum cost path between the apex and the tricuspid valve (TV) lateral landmarks. This path is known as the free wall (Fig. 3b). Three different techniques are used for finding this free wall: Dijkstra ([Dijkstra 1959](#)), ALCT ([Strandmark et al., 2013](#)) and PDP ([Rosado-Toro et al., 2016](#)). Next, the landmarks between the apex and the TV septal are joined using Dijkstra. Finally, the TV lateral and TV septal landmarks are joined using a straight line. As optional features, (6) the semi-automated RV segmentation masks can be smoothed in the temporal axis to produce a temporally smoothed segmentation mask (Section 2.7) and (7) the proposed technique can exclude the trabeculae if needed, when the user chooses to focus only on the blood pool (BP) part of the RV (Section 2.8). For generating the rough estimates in the SAX stacks (i.e., Fig. 1b) the entire ventricle should be used, but for calculating clinical features such as FAC the BP region should be used instead.

2. Materials and Methods

2.1. Measurements

To evaluate the segmentation performance, we analyzed 175 DICOM images coming from 7 different patients (i.e., 6 healthy and 1 pathological). Each patient has 25 frames. Images were acquired in a Siemens 1.5T Aera scanner, using a cine steady-state free-precession pulse sequence (TR = 2.7-2.8 ms, TE = 1.16 ms, acq. matrix = 168 x 192, FOV = 29.8 x 34 cm; slice thickness = 6 mm) and a phased array flex body coil.

2.2. Identify cardiac region of interest

The first step of our technique is to identify the cardiac ROI. Consider a 4CH image sequence of the cardiac cycle, where we define each pixel as $I(x, y, n)$ where n is the frame number and (x, y) are the coordinates within the given frame. To automatically identify the cardiac ROI, we identify the pixels where there is motion – specifically, we check for a high standard deviation of pixel intensity throughout the cardiac cycle. The *standard deviation image* is defined as

$$\sigma_I(x, y) = \sqrt{\frac{1}{N-1} \sum_{i=1}^N |I(x, y, i) - \mu_I(x, y)|^2}$$

where $\mu_I(x, y)$ is the mean of the image for every (x, y) pair. It is defined as:

$$\mu_I(x, y) = \frac{1}{N} \sum_{i=1}^N I(x, y, i)$$

N is the number of frames in the cardiac cycle; in our experiments $N = 25$. High values of σ_I denote high intensity variability throughout the cardiac cycle, which

we associate with cardiac movement. Therefore, to find the cardiac ROI we threshold σ_I , using k-means++ ([Arthur and Vassilvitskii, 2007](#)); other techniques such as Otsu ([Otsu, 1975](#)) or fuzzy C-means ([Pal and Bezdek, 1995](#)), would also be effective for thresholding. Once we threshold σ_I , we define the cardiac ROI as the bounding box of the largest connected component as illustrated in Figs. 2a-b. For subsequent processing, we only analyze the pixels that reside cardiac ROI.

Fig. 3. 4CH cardiac magnetic resonance image at (a) ED and (b) ES. The zoomed cardiac region of interest at ED and ES is shown in (c) and (d). The RV anatomical landmarks are annotated in (c) and (d). Landmarks that will be selected by users of the technique are shown as circles in (c) and (d). Figure best viewed in color.

2.3. Identify landmarks in ED and ES frames

The second step in our algorithm is the user identification of the ED and ES frames. The ED frame is the frame that qualitatively shows the RV at its largest size. Once selected, the user identifies the four landmarks: the apex, both sides of the TV (i.e. lateral and septal) and the middle of the BP, shown in Fig. 3c. The apex can be found by selecting the region where the free wall and the septum intersect. Standard anatomic landmarks were utilized to identify the TV. The middle of the BP is a point near the center of the RV that has a high intensity (i.e. blood pixel).

The ES frame is the frame that qualitatively shows the RV at its smallest size. There may be multiple frames that qualitatively appear to contain the smallest RV area. In this case, the ES frame is the frame where the midpoint of the TV looks the closest to the apex. Once the ES frame is selected, the user identifies three landmarks: the apex and both sides of the TV (i.e. lateral and septal). Since the TV is closed in the ES frame, the valve is clearly visible in the image and the TV landmarks are selected from the intersection between the TV line with the free wall (TV lateral landmark) and septum (TV septal landmark). The middle of the BP landmark is not selected in the ES frame because the algorithm propagates the landmark automatically from the ED frame, as indicated in section 2.4.

2.4. Propagate landmarks throughout the cardiac cycle

For each of the user-selected landmarks, the technique finds the minimum cost trajectory of the specific landmark throughout the cardiac cycle. Although

there are multiple shortest path algorithms ([Dijkstra, 1959](#); [Strandmark et al., 2013](#)), we use dynamic programming ([Sonka et al., 2015](#)), which we modify so that the path intersects each frame at just a single point.

The cost function (C_f) that is used for the propagating the BP landmarks is the edge strength of $I(x, y, n)$, which is computed with 2-D Gaussian smoothing:

$$G(x, y, n) = \left| \frac{d(G_\sigma(x, y) * I(x, y, n))}{dx} \right|^2 + \left| \frac{d(G_\sigma(x, y) * I(x, y, n))}{dy} \right|^2 \quad (1)$$

Here G_σ is a 2-D Gaussian function with standard deviation σ , and $*$ denotes linear convolution. For the other landmarks, (C_f) is I because the shortest path will follow a low intensity point throughout the cardiac cycle.

To make sure that the technique selects the landmark as part of the path, we add a constant value to C_f , and we set the cost to zero at the user-selected landmark locations. The constant value is the maximum of the number of elements of C_f and the maximum value of the array.

For the path to be smooth, we want the location of the landmark at frame 1 to be adjacent to the location of the landmark at frame N . To add this constraint to the dynamic programming, we extend C_f along the temporal dimension in a periodic fashion from $[1, N]$ to $[-N + 1, 2N]$. This extended version is referred to as C_f^* . Given C_f^* we initialize the cumulative sum used in dynamic programming to be $M_f(x, y, -N + 1) = C_f^*(x, y, -N + 1)$ for each x, y . The other M_f values are recursively computed:

$$M_f(x, y, n) = \left[\min_{\Omega} M_f(x_f, y_f, n - 1) \right] + C_f^*(x, y, n)$$

where Ω is a region of analysis, defined as:

$$\Omega = \{(x_f, y_f): |x_f - x| \leq d_x, |y_f - y| \leq d_y\}$$

for each $n \in [-N + 2, 2N]$ and for each (x, y) , where (d_x, d_y) represent the step size used in the dynamic programming search. For each landmark, the step size (d_x, d_y) is calculated to be the average landmark displacement per frame:

$$d_x = \frac{|x_{ED} - x_{ES}|}{\tau_{ED,ES}}$$

$$d_y = \frac{|y_{ED} - y_{ES}|}{\tau_{ED,ES}}$$

where

$$\tau_{ED,ES} = \min(|ED - ES|, N - |(ED - ES)|)$$

Here (x_{ED}, y_{ED}) and (x_{ES}, y_{ES}) are the landmark's (x, y) coordinates for the ED and ES frame, respectively. For the middle of the BP, we set $d_x = d_y = 1$ to reduce the amount of movement of the landmark throughout the cardiac cycle. Let us denote the path as $P = (p_1, \dots, p_{2N})$, where $p_n = (x_n, y_n)$. Once M_f has been generated, the path is initialized as follows:

$$p_{2N} = \operatorname{argmin}_{x,y} M_f(x, y, 2N)$$

The rest of the path is created as follows:

$$p_n = \operatorname{argmin}_{\Omega^*} M_f(x, y, n)$$

where Ω^* is a region of analysis, defined as:

$$\Omega^* = \{(x, y): |x - x_{n+1}| \leq d_x, |y - y_{n+1}| \leq d_y\}$$

2.5. Identify septum

The septum is a low intensity region within the cardiac ROI that separates the RV from the LV. The free wall is also a low intensity region, so we use the following technique to ensure that the free wall is not accidentally included as part of the septum. On each frame we threshold $I(x, y, n)$ to find the low intensity regions inside the cardiac ROI. Then, we modify those low intensity regions to exclude any pixels that fall outside an ellipse of the form,

$$\frac{(x\cos(\alpha) - y\sin(\alpha) + t_x)^2}{a^2} + \frac{(x\sin(\alpha) + y\cos(\alpha) + t_y)^2}{b^2} = 1$$

where

$$a = \frac{\sqrt{(x_{AP} - x_{TV_s})^2 + (y_{AP} - y_{TV_s})^2}}{2}$$

$$b = \frac{a}{2}$$

$$\alpha = \tan^{-1}\left(\frac{y_{AP} - y_{TV_s}}{x_{AP} - x_{TV_s}}\right)$$

$$t_x = \text{round}\left(\frac{x_{AP} + x_{TV_s}}{2}\right)$$

$$t_y = \text{round}\left(\frac{y_{AP} + y_{TV_s}}{2}\right)$$

Here (x_{AP}, y_{AP}) and (x_{TV_s}, y_{TV_s}) are the (x, y) coordinates for the apex and the septal part of the TV landmarks, respectively. We assume a 2:1 aspect ratio for the ellipsoidal fit of the septum region.

2.6. Segment RV using landmarks

Given the propagated landmarks and the septum at each frame, we proceed to segment the RV throughout the cardiac cycle. The contour that outlines the ventricle is obtained as follows: first the technique constructs an RV ROI; second it outlines the free wall; third it finds the endocardial border; and fourth it joins the septal and lateral sides of the TV, using a straight line, to form the border corresponding to the TV. The endocardial border is the high gradient region that divides the BP from the septum and goes from the apex to the septal part of the TV. A smoothing operation is performed to ensure a smooth RV contour. A morphological filling operation ([Soille, 2004](#)) is carried out to generate a mask from the contour.

2.6.1. *Right ventricular region of interest (RV-ROI)*

The segmentation procedure begins by finding a sub-region within the cardiac ROI that pertains to the RV-ROI. For the ED frame the RV-ROI is the overlap between the cardiac ROI and the rectangle consisting of lines L_1 , L_2 , L_3 and L_4 , shown in Fig. 4. Letting d denote the pixel distance between the lateral and septal sides of the TV, construct L_1 as a line perpendicular to the TV positioned d pixels right lateral from the lateral side of the TV. Construct lines L_2 and L_3 parallel to the TV positioned $d/5$ pixels proximal from the TV and distally from the apex, respectively. Finally, construct L_4 as a line perpendicular to the TV positioned $d/5$ pixels left lateral from the apex. For subsequent frames, the ROI is formed by taking the final, semi-automated RV mask in the ED frame and applying morphological dilation ([Haralick and Shapiro, 1991](#)) using a 3×3

Fig. 4. The RV-ROI is the overlap between the rectangle created by lines L_1 , L_2 , L_3 and L_4 and the cardiac region of interest. Figure best viewed in color.

square operator. The pixel locations that fall outside the ROI but inside the cardiac ROI will be given a fixed cost function value in the subsequent steps of the segmentation procedure.

2.6.2. Outlining the free wall

The contrast between the trabeculae and the BP is greater than the contrast between the trabeculae and the free wall. This is why active contour algorithms that rely on gradient strength to achieve a minimum cost spline ([Bing and Acton, 2007](#); [Bing and Acton, 2008](#); [Mukherjee and Acton, 2015](#); [Li et al., 2010](#)) will latch onto the trabeculae/blood pool boundary rather than the free wall.

Techniques that use the intensity to generate paths or closed contours are also of interest, for example in ([Atehortúa et al., 2016](#)) the technique searches for low intensity paths using a polar representation. Unfortunately, this technique does not include the ability to constrain the paths to pass through certain landmarks. These unconstrained paths may fail to include the propagated landmarks (i.e., the apex), particularly in the ES frames. Since we want a technique that passes through certain landmarks and minimizes a cumulative sum, then minimum shortest path techniques are used.

We compare three different techniques for outlining the free wall: Dijkstra's shortest-path algorithm ([Dijkstra, 1959](#)), Strandmark's ALCT algorithm ([Strandmark et al., 2013](#)) and a modified version of a polar dynamic programming (PDP) algorithm developed by our group ([Rosado-Toro et al., 2016](#)) to find low intensity paths using a polar representation. For ([Dijkstra, 1959](#)) and ([Strandmark et al., 2013](#)) we use $I(x, y, n)$ as the primary component for the cost function. For ([Rosado-Toro et al., 2016](#)) the inputs are the intensity image $I(x, y, n)$ and the gradient strength ($G(x, y, n)$). Instead of using $G(x, y, n)$ as defined by (1) we replace $G(x, y, n)$ with

$$G(x, y, n) = \max_{x, y} I(x, y, n) - I(x, y, n)$$

This change ensures that the free wall does not latch onto the trabeculae/BP boundary. Introducing origins for each frame $(x_0(n), y_0(n))$ allows us to represent $I(x, y, n)$ and $G(x, y, n)$ as $f(\theta, \rho, n)$ and $g(\theta, \rho, n)$ in polar coordinates as follows:

$$\rho(n) = \sqrt{(x - x_o(n))^2 + (y - y_o(n))^2}$$

$$\theta(n) = \tan^{-1} \left(\frac{y - y_o}{x - x_o} \right)$$

$$f(\theta(n), \rho(n), n) = I(x, y, n)$$

$$g(\theta(n), \rho(n), n) = G(x, y, n)$$

Using the polar representation, we define the polar variance image as

$$V(\theta(n), \rho(n), n) = \int_0^{\rho(n)} \int_{\theta(n)-\gamma}^{\theta(n)+\gamma} (f(\phi, r, n) - \bar{f}(\phi, r, n))^2 dr d\phi$$

where

$$\bar{f}(\theta(n), \rho(n), n) = \int_0^{\rho(n)} \int_{\theta(n)-\gamma}^{\theta(n)+\gamma} f(\phi, r) dr d\phi$$

In these equations γ is a smoothing parameter. Given $V(\theta(n), \rho(n), n)$ and $g(\theta(n), \rho(n), n)$ we then define $C(\theta(n), \rho(n), n)$ as:

$$C(\theta(n), \rho(n), n) = \alpha V(\theta(n), \rho(n), n) + \beta \exp(-g(\theta(n), \rho(n), n))$$

where α and β are weighting parameters. To ensure that the path passes over the TV lateral and the RV apex (i.e., delineating the free wall), the algorithm identifies the $(\theta(n), \rho(n))$ pairs associated with the landmarks and sets their cost function value to 0. It then adds a constant value to the other cost function values in each frame (n). The constant value is set to the number of elements in the $C(\theta(n), \rho(n), n)$ array. We resample the cost function into a uniform polar grid with angles from 0° to 360° with an angular sampling interval ($\Delta\theta$) and radii from 0 to the maximum radius in the image with a radial sampling interval of $\Delta\rho$. The next step is to use the image patching algorithm (IPA) dynamic programming

([Sun and Pallotino, 2003](#)) to generate a minimum cost path (i.e., $\rho(\theta(n), n)$ values that minimize the cumulative sum of the cost function). Note that other techniques for finding a minimum cost path can be used, (e.g., [Appleton and Sun, 2003](#), [Qian et al., 2015](#)). Finally, the $\rho(\theta(n), n)$ values and the corresponding angles are converted back to (x, y) coordinates for each n . This generates a closed contour that may include regions that are proximal to the TV or overlap with the septum. Any part of the segmentation mask that is proximal to the TV or in the septum is removed.

To restrain Dijkstra's shortest-path algorithm and Strandmark's ALCT from going into the septum, we set all the pixels in the septum to have the highest value in the cost function for the given frame.

Unlike Dijkstra's algorithm, which uses no parameters, ALCT uses an A* algorithm ([Hart et al., 1968](#)) that incorporates length, curvature and torsion penalties in an active contour model to find the minimum cost path. The method for selecting the parameters for both ALCT and PDP is explained in section 3.4.

2.6.3. Identifying septum-BP border

Given the free wall, the technique proceeds to find the septum-BP border. For each frame we calculate the cost function by first calculating the edge strength

$$G(x, y, n) = \left| \frac{d(I(x, y, n))}{dx} \right|^2 + \left| \frac{d(I(x, y, n))}{dy} \right|^2$$

Next we subtract the edge strength from the maximum edge strength. Given this cost function, the septum-BP border is the minimum cost path from the apex to

the septal portion of the TV. To find the septum-BP border, we use Dijkstra's shortest-path algorithm.

2.7. Incorporate temporal smoothness

Given the semi-automated segmentation of the RV in 4CH cardiac images, we smooth the segmentation by applying a 1D median filter ([Gonzalez and Wood, 2002](#)) in the temporal dimension. For all patients we used a filter size of 5. The median filter in the temporal dimension is implemented as follows: for each (x, y) coordinate, look at its 2 nearby neighbors in the temporal dimension. Apply a median filter to those binary values. We keep the constraint in the previous section that removes every pixel that is proximal to the TV. The temporal smoothness will remove outlying traces at the expense of reducing metrics such as fractional area change.

2.8. Identifying blood pool

As shown in Figs 2c-d, the RV is composed of the trabeculae and the BP. The impact of including the trabeculae in SAX CMR views is assumed to be small in healthy individuals ([Winter et al., 2008](#)); no such analysis has been done for 4CH views. An advantage of the proposed technique is that it can automatically exclude trabeculae from the semi-automated segmentation of the RV if needed. The BP is defined as the largest connected component inside the semi-automated segmentation of the RV that has an intensity value higher than a threshold. To find the threshold, we first calculate the histogram of $I(x, y, n)$ at

the locations of the septum and the RV, respectively and compare the frequency for each intensity bin. The threshold is the highest intensity bin where the frequency of the septum is higher than the frequency of the RV.

3. Results

3.1. Manual tracing protocol

Manual tracing was performed two radiologists and a cardiologist, each with at least 5 years of training and experience in the interpretation of CMR images. To allow for human variability and biases in the manual tracing, each tracer was blinded to the others' work.

3.2. Performance metric

3.2.1. Dice score

The performance metric used for this analysis was the Dice score (DSC). The DSC computes the mutual overlap between the ground truth and a segmented region:

$$\frac{2|X \cap Y|}{|X| + |Y|},$$

where X and Y are binary masks. One of the binary masks is defined as a reference binary mask and the DSC measures how similar the non-reference binary mask is to the reference binary mask. A value of 1 denotes complete mask equality (i.e., $X = Y$), and a value of 0 denotes no overlap (i.e., $X \cap Y = \emptyset$).

3.2.2. Fractional area change

The fractional area change (FAC) is defined as follows:

$$FAC = \frac{a_{RV}(ED) - a_{RV}(ES)}{a_{RV}(ED)}$$

where $a_{RV}(ED)$ and $a_{RV}(ES)$ are the area of the mask in the ED and ES frames, respectively. FAC is commonly used in echocardiography to analyze ventricular function ([Rudski et al., 2010](#)).

3.3. Analysis tools

3.3.1. Correlation coefficient

The correlation coefficient (R) ([Rodgers and Nicewander, 1988](#)) measures the closeness of data points to a regression line of the form $y = mx + b$, and is defined as

$$R = \frac{\sum_{i=1}^P (x_i - \bar{x})(y_i - \bar{y})}{\sqrt{[\sum_{i=1}^P (x_i - \bar{x})^2][\sum_{i=1}^P (y_i - \bar{y})^2]}}$$

where

$$\bar{x} = \frac{1}{P} \sum_{i=1}^P x_i$$

and

$$\bar{y} = \frac{1}{P} \sum_{i=1}^P y_i$$

Here x and y represent two samples. For our experiment, $P = 7$. The sign of R will be the same as the sign of the slope (m) of the regression line. Values of R

close to one indicate a strong positive linear relationship between the variables (x, y) . Values of R close to zero indicate x and y are independent.

3.4. Parameter selection

To achieve best performance the algorithm-specific parameters that yield the highest mean DSC needs to be used. To reduce bias, the traces we used for optimizing the algorithm-specific parameters were not used for the subsequent experiments. The PDP as explained in section 2.6.2 has 5 major parameters $\gamma, \Delta\rho, \Delta\theta, \alpha, \beta$. The values of $\gamma, \Delta\rho$ and β are 5° , 0.5 pixels and $1 - \alpha$ respectively. These values are the same as those selected ([Rosado-Toro et al., 2016](#)) in their original work. The range of α used for optimization was from 0.3 to 0.6 in 0.1 increments. The range of $\Delta\theta$ was from 0.4 to 1.1 in 0.1 increments. We tried all possible combinations of α and $\Delta\theta$ values specified above. The algorithm-specific parameters of $\alpha = 0.6$ and $\Delta\theta = 0.8$ yielded the highest mean DSC.

ALCT identifies 3 major parameters ρ, σ, ν . According to ([Strandmark et al., 2013](#)), a high torsion regularization (ν) forces the curve to stay within a plane; since we are working with 2D images we set $\nu = 0$. For finding the optimum curvature regularization (σ) we set the length regularization to zero ($\rho = 0$), and vary σ from 10^{-4} to 10^4 in $10^{0.1}$ increments. Given the optimum σ , we vary the length regularization from 0 to 1 in 0.025 increments. The algorithm-specific parameters of $\sigma = 10^{2.6}$ and $\rho = 0.35$ yielded the highest mean DSC.

Table 1 Inter-physician manual tracing performance using DSC.

Manual Tracing	Manual Tracing		
	Physician1	Physician2	Physician3
	$\mu^* \pm \sigma^\dagger$	$\mu \pm \sigma$	$\mu \pm \sigma$
Physician1	-	0.8707 ± 0.0561	0.8592 ± 0.0526
Physician2	0.8707 ± 0.0561	-	0.8562 ± 0.0544
Physician3	0.8592 ± 0.0526	0.8562 ± 0.0544	-

Table shows the DSC between the manual traces of different trained physicians. The tracing protocol (described in section 3.1) was used to manually trace the 4CH RV throughout the cardiac cycle.

* Mean of DSC

† Standard deviation of DSC

3.5. Performance analysis

Table 1 shows the results of the DSC analysis (mean and standard deviation based on a total of 175 images) between the physicians. The percent overlap between the traces (which is in the mid to high 80s) reflects the variability between the physicians and serves as reference for evaluating the performance of the semi-automated algorithms.

Table 2 shows the results of the DSC between the semi-automated algorithms and the physicians' manual traces. This metric gives insight as to which free wall outlining algorithm (PDP, ALCT or Dijkstra) provided a better match with the physicians' traces. The first column of Table 2 shows which physician selected the landmarks, each physician selected 7 landmarks per patient and the ED and ES frames. The second column shows whether the mask used to calculate the DSC is the RV (BP + trabeculae) or the BP. The third

Table 2 Comparing physician manual tracing to semi-automated tracing (RV and BP) using DSC.

Landmark Selection	Segmentation	Free Wall	Manual Tracing		
			Physician1	Physician2	Physician3
			$\mu^* \pm \sigma^\dagger$	$\mu \pm \sigma$	$\mu \pm \sigma$
Physician1	RV	PDP	0.8970 $\pm$ 0.0418	0.8639 $\pm$ 0.0723	0.8413 $\pm$ 0.0580
		ALCT	0.8912 $\pm$ 0.0493	0.8691 $\pm$ 0.0667	0.8465 $\pm$ 0.0589
		Dijkstra	0.8879 $\pm$ 0.0392	0.8657 $\pm$ 0.0629	0.8418 $\pm$ 0.0554
	BP	PDP	0.8614 $\pm$ 0.0549	0.8835 $\pm$ 0.0463	0.8690 $\pm$ 0.0477
		ALCT	0.8475 $\pm$ 0.0636	0.8784 $\pm$ 0.0533	0.8616 $\pm$ 0.0596
		Dijkstra	0.8516 $\pm$ 0.0527	0.8790 $\pm$ 0.0442	0.8626 $\pm$ 0.0507
	RV	PDP	0.8953 $\pm$ 0.0434	0.8676 $\pm$ 0.0717	0.8335 $\pm$ 0.0601
		ALCT	0.8884 $\pm$ 0.0539	0.8712 $\pm$ 0.0711	0.8372 $\pm$ 0.0632
		Dijkstra	0.8777 $\pm$ 0.0496	0.8613 $\pm$ 0.0701	0.8254 $\pm$ 0.0615
Physician2	BP	PDP	0.8638 $\pm$ 0.0543	0.8874 $\pm$ 0.0452	0.8623 $\pm$ 0.0469
		ALCT	0.8508 $\pm$ 0.0658	0.8810 $\pm$ 0.0562	0.8554 $\pm$ 0.0592
		Dijkstra	0.8499 $\pm$ 0.0599	0.8778 $\pm$ 0.0523	0.8529 $\pm$ 0.0542
	RV	PDP	0.8969 $\pm$ 0.0410	0.8699 $\pm$ 0.0706	0.8372 $\pm$ 0.0514
		ALCT	0.8860 $\pm$ 0.0577	0.8691 $\pm$ 0.0711	0.8378 $\pm$ 0.0606
		Dijkstra	0.8880 $\pm$ 0.0444	0.8706 $\pm$ 0.0671	0.8363 $\pm$ 0.0542
	BP	PDP	0.8615 $\pm$ 0.0536	0.8872 $\pm$ 0.0452	0.8628 $\pm$ 0.0423
		ALCT	0.8451 $\pm$ 0.0683	0.8772 $\pm$ 0.0584	0.8526 $\pm$ 0.0635
		Dijkstra	0.8559 $\pm$ 0.0547	0.8848 $\pm$ 0.0464	0.8592 $\pm$ 0.0488
Physician3	RV	PDP	0.8953 $\pm$ 0.0434	0.8676 $\pm$ 0.0717	0.8335 $\pm$ 0.0601
		ALCT	0.8884 $\pm$ 0.0539	0.8712 $\pm$ 0.0711	0.8372 $\pm$ 0.0632
		Dijkstra	0.8777 $\pm$ 0.0496	0.8613 $\pm$ 0.0701	0.8254 $\pm$ 0.0615
	BP	PDP	0.8638 $\pm$ 0.0543	0.8874 $\pm$ 0.0452	0.8623 $\pm$ 0.0469
		ALCT	0.8508 $\pm$ 0.0658	0.8810 $\pm$ 0.0562	0.8554 $\pm$ 0.0592
		Dijkstra	0.8499 $\pm$ 0.0599	0.8778 $\pm$ 0.0523	0.8529 $\pm$ 0.0542
	RV	PDP	0.8969 $\pm$ 0.0410	0.8699 $\pm$ 0.0706	0.8372 $\pm$ 0.0514
		ALCT	0.8860 $\pm$ 0.0577	0.8691 $\pm$ 0.0711	0.8378 $\pm$ 0.0606
		Dijkstra	0.8880 $\pm$ 0.0444	0.8706 $\pm$ 0.0671	0.8363 $\pm$ 0.0542
	BP	PDP	0.8615 $\pm$ 0.0536	0.8872 $\pm$ 0.0452	0.8628 $\pm$ 0.0423
		ALCT	0.8451 $\pm$ 0.0683	0.8772 $\pm$ 0.0584	0.8526 $\pm$ 0.0635
		Dijkstra	0.8559 $\pm$ 0.0547	0.8848 $\pm$ 0.0464	0.8592 $\pm$ 0.0488

Table shows the DSC value between the manual traces of the 4CH RV throughout the cardiac cycle and the semi-automated segmentation generated using the physicians' landmarks.

RV, right ventricle; BP, blood pool; PDP, polar dynamic programming; ALCT, A* algorithm using length curvature and torsion.

* Mean of DSC

† Standard deviation of DSC

column of Table 2 denotes the algorithm used for outlining the free wall. Note that although all DSC values are within physician variability, the PDP consistently outperforms the ALCT and Dijkstra algorithms (i.e., has a higher DSC with the

Table 3 Inter-physician performance using semi-automated techniques to do the tracing

a	Landmark Selection	Free Wall	Landmark Selection		
			Physician1	Physician2	Physician3
			$\mu^* \pm \sigma^\dagger$	$\mu \pm \sigma$	$\mu \pm \sigma$
Physician1	PDP		-	0.9629 ± 0.0212	0.9661 ± 0.0218
	ALCT		-	0.9569 ± 0.0396	0.9636 ± 0.0346
	Dijkstra		-	0.9488 ± 0.0315	0.9627 ± 0.0261
Physician2	PDP		0.9629 ± 0.0212	-	0.9670 ± 0.0244
	ALCT		0.9569 ± 0.0396	-	0.9633 ± 0.0355
	Dijkstra		0.9488 ± 0.0315	-	0.9595 ± 0.0303
Physician3	PDP		0.9661 ± 0.0218	0.9670 ± 0.0244	-
	ALCT		0.9636 ± 0.0346	0.9633 ± 0.0355	-
	Dijkstra		0.9627 ± 0.0261	0.9595 ± 0.0330	-
b	Landmark Selection	Free Wall	Landmark Selection		
			Physician1	Physician2	Physician3
			$\mu^* \pm \sigma^\dagger$	$\mu \pm \sigma$	$\mu \pm \sigma$
Physician1	PDP		-	0.9674 ± 0.0190	0.9704 ± 0.0235
	ALCT		-	0.9605 ± 0.0375	0.9653 ± 0.0342
	Dijkstra		-	0.9531 ± 0.0300	0.9624 ± 0.0271
Physician2	PDP		0.9674 ± 0.0190	-	0.9708 ± 0.0261
	ALCT		0.9605 ± 0.0375	-	0.9665 ± 0.0362
	Dijkstra		0.9531 ± 0.0300	-	0.9635 ± 0.0338
Physician3	PDP		0.9704 ± 0.0235	0.9708 ± 0.0261	-
	ALCT		0.9653 ± 0.0342	0.9665 ± 0.0362	-
	Dijkstra		0.9624 ± 0.0271	0.9635 ± 0.0338	-

Table shows the DSC value between the semi-automated segmentation generated using different two sets of landmarks. Comparison is done comparing semi-automated (a) RV and (b) BP masks. PDP, polar dynamic programming; ALCT, A* algorithm using length curvature and torsion.

* Mean of DSC

† Standard deviation of DSC

manual traces). When comparing the DSC between the physicians' manual traces and the RV or BP semi-automated masks, we can see that physician 1 has a better overlap with the RV; meanwhile for physicians' 2 and 3 have a higher DSC with the BP. This means that the traces from physician 1 included more trabeculae, while physicians 2 and 3 tended to exclude more trabeculae.

Table 3 measures the difference between the semi-automated segmentation when physicians use different landmarks. We had the physicians independently identify the 7 landmarks as well as the ED and ES frames. Once the RV segmentation was generated, the DSC values were calculated. The first column in Table 3 denotes which physician selected the first set of landmarks. The second column in Table 3 denotes the algorithm used for outlining the free wall. Columns 3-5 denote which physician selected the second set of landmarks. Table 3a focuses on RV portion of the masks; Table 3b focuses on BP portion of the masks. The landmarks selected by Physician 3 generated results that were like the other physicians. Although the DSC values are in the mid to high 90s, the PDP consistently outperforms the ALCT and Dijkstra algorithms. Table 3 shows that the proposed technique is robust to inter-physician landmark selection variability.

In Table 2, we showed that the semi-automatic techniques generated DSC values that were within human variability. Therefore, we wanted to see if this translates to similar FAC values. The FAC analysis for Tables 4 and 5 was done using the semi-automated segmentation masks generated by the PDP free wall technique.

Table 4 Comparison of FAC derived from three different measurements; manual traces, RV and BP.

Segmentation	Free Wall	Patient						
		1	2	3	4	5	6	7
		$\mu^* \pm \sigma^\dagger$	$\mu \pm \sigma$	$\mu \pm \sigma$	$\mu \pm \sigma$	$\mu \pm \sigma$	$\mu \pm \sigma$	$\mu \pm \sigma$
Manual Trace	-	0.4977 $\pm$ 0.0474	0.4823 $\pm$ 0.0459	0.5105 $\pm$ 0.0520	0.2655 $\pm$ 0.0143	0.5435 $\pm$ 0.0192	0.4365 $\pm$ 0.0574	0.5269 $\pm$ 0.0848
RV	PDP	0.4143 $\pm$ 0.0134	0.3622 $\pm$ 0.0251	0.3706 $\pm$ 0.0268	0.2152 $\pm$ 0.0103	0.4485 $\pm$ 0.0100	0.2470 $\pm$ 0.0445	0.3303 $\pm$ 0.0277
BP	PDP	0.4943 $\pm$ 0.0079	0.4424 $\pm$ 0.0150	0.5207 $\pm$ 0.0221	0.2394 $\pm$ 0.0133	0.5195 $\pm$ 0.0083	0.3107 $\pm$ 0.0324	0.5355 $\pm$ 0.0251

Table shows the variance of the FAC using physicians' manual traces (row 1) semi-automated segmentation of the RV (row 2) or semi-automated segmentation of the BP (row 3). RV, right ventricle; BP, blood pool; PDP, polar dynamic programming.

* Mean of FAC

† Standard deviation of FAC

Table 4 shows the mean FAC and standard deviation derived from the manual traces, the RV and the BP values. The results show that the FAC derived from the RV and BP has lower standard deviation than the FAC derived from the manual tracers. In general, the FAC derived from the BP is similar to the FAC derived from the manual tracers; this is expected since 2 out of the 3 tracers excluded the trabeculae region as part of the RV. The FAC derived from the BP is generally higher than the one derived from the RV. This is because in the ES frame a larger percent of the RV is trabeculae and when excluded, the area in the ES frame is lower, resulting in a higher FAC.

Table 5 R score and P value using FAC.

a	Manual Outlining		
	Physician1	Physician2	Physician3
	R	R	R
Manual Outlining			
Physician1	-	0.7364 [†]	0.9377 [*]
Physician2	0.7364 [†]	-	0.7809 [‡]
Physician3	0.9377 [*]	0.7809 [‡]	-
b	Manual Outlining		
	Physician1	Physician2	Physician3
	R	R	R
Landmark Selection			
Physician1	0.8382 [‡]	0.8321 [†]	0.8143 [‡]
Physician2	0.9238 [*]	0.8225 [‡]	0.9114 [*]
Physician3	0.8692 [‡]	0.7886 [‡]	0.8680 [‡]
c	Landmark Selection		
	Physician1	Physician2	Physician3
	R	R	R
Landmark Selection			
Physician1	-	0.9745 ^Δ	0.9740 ^Δ
Physician2	0.9745 ^Δ	-	0.9843 ^Δ
Physician3	0.9740 ^Δ	0.9843 ^Δ	-

Table shows the correlation coefficients between the different methods for generating FAC measurements. Either (a) comparing FAC derived from physicians' manual traces only (i.e., Table 1); (b) comparing FAC derived from physicians' manual tracings and semi-automated segmentations of the BP using physicians' landmarks (i.e., Table 2), or (c) comparing FAC derived from semi-automated segmentations generated of the BP using physicians' landmarks (i.e., Table 3b).

[†]p value < 0.1

[‡]p value < 0.05

^{*}p value < 0.01

^Δp value < 0.001

In Table 5 we use R and confidence intervals from FAC measurements to measure the linear relationship and determine whether the relationship is

statistically significant. The statistical analysis was performed comparing the inter-physicians' FAC values (Table 5a), FAC derived from the semi-automated segmentation of the BP with the physicians' FAC based on their manual tracing (Table 5b), and FAC derived from the semi-automated segmentation of the BP (Table 5c). Table 5a shows that the correlation coefficients range from 0.9377 to 0.7364 and only the FAC between physicians 1 and 2 turns out to have a p value > 0.05 . Table 5b shows that the correlation coefficients range from 0.7886 to 0.9238 with p values < 0.05 . Finally, Table 5c shows the overlap between the semi-automated technique using different physicians' landmarks. Note that all the R values are higher than 0.95 and their respective p values < 0.01 .

4. Discussion

Understanding the functional properties of the cardiac chambers is important for diagnosing both LV and RV related cardiovascular disorders. However, over the years most of the attention has been on the LV, in part due to the lack of optimal imaging tools for looking at the RV ([Sanz et al., 2012](#)). With the advent of CMR, it is now possible to quantify the function of the LV and the RV providing new capabilities related to the latter. Most of the analysis tools available in the clinic are still focused on the LV. The algorithm presented above was developed to provide an easy-to-use tool for the functional analysis of the RV. The algorithm was designed to segment the RV in 4CH including or

excluding the trabeculae (i.e., the BP segmentation) to accommodate for different trends in RV segmentation ([Driessen et al., 2014](#)).

The results described previously show that the proposed technique yields results that are within human variability (Table 2), while also being robust to physicians' landmarks (Table 3). Using as measurement DSC, PDP outperformed Dijkstra and ALCT in the delineation of the free wall. When the analysis turned to a more clinical measure, finding the FAC derived from the BP yielded results similar to the physicians' traces (Table 4, Table 5b) because two out of the three tracers excluded the trabeculae. We also showed that the FACs values obtained from the semi-automatic segmentations are robust to the physicians' landmarks (Table 5c).

One of the main reasons for the variability among the manual outlines is the trabeculae. For instance, if the DSC between tracers is calculated based on the ED frame, where the amount of visible trabeculae is minimal, the values are in the low 90s. If the DSC is calculated based on both the ED and ES frames (as done in Table 1), the values are in the mid to high 80s; thus the increase in variability stems from trabeculae found in the ES frame. The question whether the trabeculae should or should not be included as part of the physicians' trace is still up for debate ([Driessen et al., 2014](#)). An example of the outline variation can be seen in Fig. 5. One of the physicians included almost no trabeculae while another physician included most of the trabeculae. These discrepancies lead to the high variability seen throughout the study (i.e., Table 1, Table 4 and Table 5a).

Fig. 5. ES physicians' trace. Trace from physician 1 (in red) includes most of the trabeculations, while the other trace (orange) excludes most of the trabeculations. Figure best viewed in color.

Looking at Table 4 we can see that the mean FAC derived from the semi-automated segmentation of the BP is outside a standard deviation of the FAC using the manual tracers in patients 2 and 6. The main problem with patient 2 was the selection of the ES frame. When performing the manual traces, the physicians consistently found that the RV in the 13th frame had the smallest area (i.e., identified the 13th frame as the ES frame). Consequently, when the physicians had to identify the ES frame for the semi-automated segmentation (section 2.3), the physicians consistently identified the ES frame in the 9th or 10th frame. When the error between the selected ES frame and the real ES frame is more than 2 frames, the performance, as measured by the FAC will suffer. Patient 6 shows the importance of selecting the correct landmark locations. The difference in FAC for this patient can be attributed to the landmark selection, in

this case, the location of the septal portion of the TV, shown in Fig. 6. An incorrect landmark selection may affect the area of the ventricle in the ED or ES frame and consequently affect the final FAC value.

An important aspect of the proposed technique is the time advantage in time reduction in the analysis of the RV offer by the semi-automatic segmentation. The proposed method using PDP for outlining the free wall, took on average 2 minutes per patient, while manual tracing took the physicians approximately 15 minutes per patient.

Fig. 6. BP FAC for different user-selected landmarks in the (a) ED and (b) ES frame. The outline in green yielded the highest BP FAC, while the outline in cyan yielded the lowest BP FAC. Figure best viewed in color.

5. Conclusion and Future Work

We developed an algorithm based on landmark selection and polar dynamic programming for the semi-automatic segmentation of the RV in 4CH cine CMR images. The results show that the proposed technique matches the physicians' manual traces and reduces variability among tracers. The results

indicated that the algorithm can optimize the workflow associated with the analysis of the RV by reducing the time required for the RV segmentation. Future work will include using the 4CH RV segmentation to generate volumetric SAX RV segmentation.

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