A Spline Model for Sampling of the Right Ventricle Myocardium from Cardiac PET Images

S. Takobana[1,2], A. Adler[2], L. Mielniczuk[1], R. Beanlands[1], R.A. deKemp[1,2], R. Klein[1]
[1]University of Ottawa Heart Institute, Ottawa, Ontario, Canada
[2]Systems and Computer Engineering ,Carleton, Ottawa, Ontario, Canada

UNIVERSITY OF OTTAWA HEART INSTITUTE
INSTITUT DE CARDIOLOGIE DE L'UNIVERSITÉ D'OTTAWA

Carleton UNIVERSITY
Canada's Capital University

Introduction:

Pulmonary hypertension can alter right ventricular (RV) physiology and anatomy, in most cases making it hypertrophic and dysfunctional.[2] RV physiologic and functional function measurement, are desirable for clinical care and research, however segmenting the RV in nuclear images is not currently available in commercial software. We developed a general spline model for segmenting the RV in cardiac PET images of normal and hypertrophic hearts in human and animals. A spline model should minimize the number of control points as well as their degrees of freedom for computational efficiency and usability, yet remain general enough to fit the spectrum of anatomies. The purpose of this study was to evaluate a proposed 12 spline points model with 13 degrees of freedom for sampling the RV in cardiac PET images.

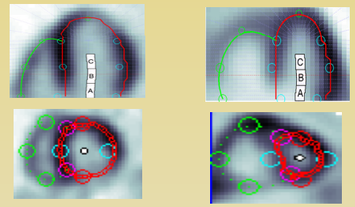


Figure 1. Representative Horizontal Long Axis (top) and short axis (bottom) of a normal (left) and a hypertrophic (right) human heart with super imposed LV (red) and RV (green) contours.

Methods:

A sample set of 5 normal and 5 hypertrophic human, and 5 normal and 5 hypertrophic rat heart FDG PET images was used. Each image was automatically reoriented to a standard left ventricle (LV) short axis (SA) reference frame and LV segmentation was automatically processed. 1 The RV model was manually fit to each image and the quality of fit was evaluated. A pass was granted when the model was judged by the operator to sufficiently trace the RV mid-myocardium and appropriately intersected the LV.

The model consisted of 12 spline points with a total of 13 degrees of freedom as illustrated in figure 2. Each spline point is explained in Table 1 along with an initial placement of the spline points, prior to operator manipulation.

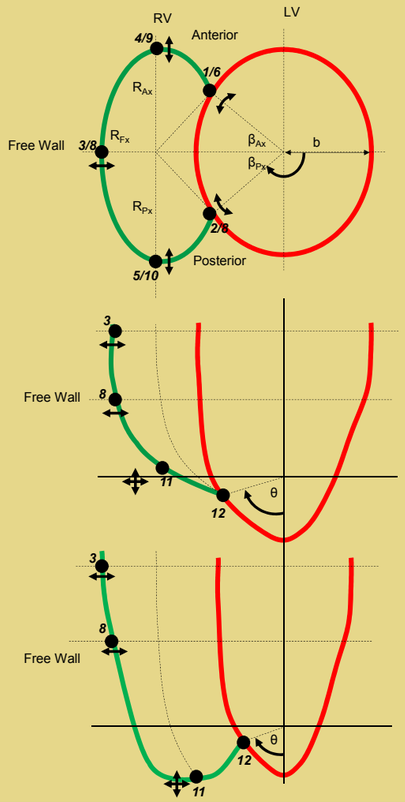


Figure 2. Diagram of the RV spline model (green) relative to the previously described LV spline model[1] (red). Short axis slice (top) and horizontal long axis view of the model in a normal (middle) and hypertrophic (bottom) heart. The control points are shown as black dots and described in Table 1.

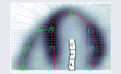
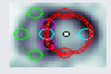
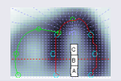
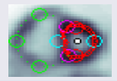
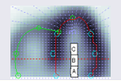
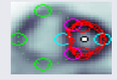
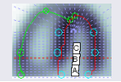
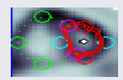
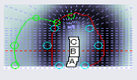
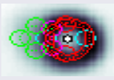
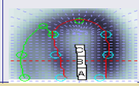
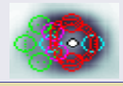
Table 1 Control Points and their degrees of freedom and initial location relative to the LV

Control Point	Degrees of Freedom	Description	Initial Estimate from LV Long axis
1	1	Basal Anterior RV/LV intersect control point	β_{AB} = 120°
2	1	Basal Posterior RV/LV intersect control point	β_{PB}= 240°
3	1	Basal Free wall spline points RV/LV	R_{FB} = 2×*b from LV center*
4	1	Basal Anterior vertical control point	R_{AB} =*b* from RV center
5	1	Basal Posterior vertical control point	R_{PB} = *b* from RV center
6	1	Mid Anterior RV/LV intersect control point	β_{AM} = 120°
7	1	Mid Posterior RV/LV intersect control point	β_{PM}= 240°
8	1	Mid Free wall spline points RV/LV	R_{FM} = 2×*b from LV center*
9	1	Mid Anterior vertical control point	R_{AM} = *b* from RV center
10	1	Mid Posterior vertical control point	R_{PM} = *b* from RV center
11	2	RV Extent spline point –useful particularly in hypertrophic case were the RV shape requires more flexibility to trace out.	Midway between free wall and the RV/LV intersect control point and same vertical with 12
12	1	RV/LV intersect control point	θ=90°

Results:

Table 2 shows sample results of the spline model being, applied including horizontal long axis (HLA) and the short axis (SA) views of the PET images with the LV (red) and RV (green) contours superimposed. The circles designate the spline control points. A PASS indicates model correctly traces out the RV anatomy.
In normal rats, the RV wall was difficult to visualize due to its thinner wall, proximity to the thicker LV, and low image resolution. In all human images and in all hypertrophic rat hearts the model was sufficient for tracing the RV.
The points of intersect of the RV with the LV did not appear to vary between images (β_{AM}=120°±5°, β_{AB}=120°±5°, β_{PM}=240°±5°, and β_{PB}=240°±5°, n=20)

Table 2: Sample Validation of RV Spline Model Quality of Fit

Specimen	View		Result
	HLA	SA	
Human – Normal			PASS
Human – Hypertrophy			PASS
Human – Hypertrophy			PASS
Human – Hypertrophy			PASS
Rat – Normal			FAIL
Rat – Hypertrophy			PASS

Future Work:

Future work will focus on automatic fitting of the spline points so as to reduce operator workload, biases, and errors. The model can than be automatically fit to all phases of the cardiac cycle using ECG gated image sequences, so as to measure ventricle cavity volumes and ejection fractions. Likewise, the model can be used to sample the activity in dynamic image sequences of the tracer redistribution process, so as to quantify molecular function using kinetic models of the tracer.

Conclusions:

The proposed model is sufficiently flexible to describe normal and hypertrophic hearts in human and rat populations. In normal rats, however, image quality may not be sufficient visualize the RV. It is possible that a simpler model, with fewer degrees of freedom may be sufficient, while further reducing the model complexity.

References :

1. Klein, R.; Lortie, M.; Adler, A.; Beanlands, R.S.; deKemp, R.; , "Fully Automated Software for Polar-Map Registration and Sampling from PET Images," *Nuclear Science Symposium Conference Record, 2006.*
2. R. Naeije and S. Huez, "Right ventricular function in pulmonary hypertension: physiological concepts," *European Heart Journal Supplements*, vol. 9, no. suppl H, p. H5, 2007.