

# Fast Template Based Segmentation of Cine Cardiac MR

Guy Shechter<sup>1</sup>, Jérôme Declerck<sup>1</sup>, Cengizhan Öztürk<sup>1</sup>, Elliot R. McVeigh<sup>1,2</sup>

Depts. of Biomedical Engineering<sup>1</sup> and Radiology<sup>2</sup>, Johns Hopkins University, Baltimore, MD

**Introduction:** Existing techniques for assessment of myocardial function from tagged MR images require segmentation of myocardial tags and heart contours. Currently, this is the most time consuming part of the analysis because contours must be explicitly specified for approximately 200 images (10 slices at 20 cine phases). It is hypothesized that using an *a priori* defined 3D template, we can significantly reduce the time needed for segmentation by allowing three dimensional local deformations of the template and interpolation through time.

**Methods:** Polyhedral surface meshes representing the left ventricular epicardial and endocardial surfaces at end-diastole were used as templates. These templates were created by contouring a separate high density data set, fitting a smooth parametric surface to the contours, and finally tessellating the surface.

A template based contouring package was developed to allow interaction with the 3D template for fitting to MR images. This OpenGL software was developed and used on an SGI O2 computer. The program accepts any arbitrary stack of images and can display three orthogonal cross sections. Short axis – long axis pairs can also be handled. Initially, the user can freely translate, rotate, and scale a template for best alignment to the MR images in 3D.

Local refinement of the template is achieved by moving individual mesh points. When adjusting individual mesh points, the inherent smoothness of a surface may be lost. To avoid this problem, the user has the option of deforming a neighborhood of points. A single parameter  $\sigma$ , which can be modified interactively in real time, governs the rate of a spatial gaussian decay, and thus the size of the neighborhood (figure 1). Instead of recontouring each cine phase individually, we take advantage of temporal coherence. Once the mesh has been fit at one cine phase, it can be copied to a later (or earlier) time. The copied mesh can then be locally modified to track deformations evident in the MR images. Linear interpolation of the mesh points provides a good approximation for the contours at intermediate time frames.

To assess the speed enhancements offered by our method, we compared the time required to segment the left ventricle from short axis data using our template based contouring method with two contouring programs currently used in our laboratory : Findtags and gContour. Findtags[1] is a semi-automatic contouring package

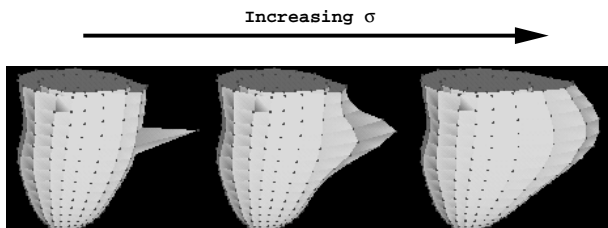


Figure 1: By moving a single point on the mesh, and in real time changing  $\sigma$ , the user can modify a neighborhood of points with a spatial gaussian decay.

for the LV using active contours in 2D polar resampled images. gContour[2] is a manual contouring package that can be used to contour any structure on medical images. The short axis data set contained 10 slices during 27 cine phases.

**Results:** Figure 2 shows an LV mesh after alignment to a short axis data set. Table 1 shows the time required to contour the LV using three different programs. Visual inspection by two independent experts confirms that the quality of contouring is comparable in the three methods.

	Average Time (min)
Findtags	200
gContour	300
Template based contouring	30

Table 1: Summary of the times required to segment the LV using three different contouring programs.

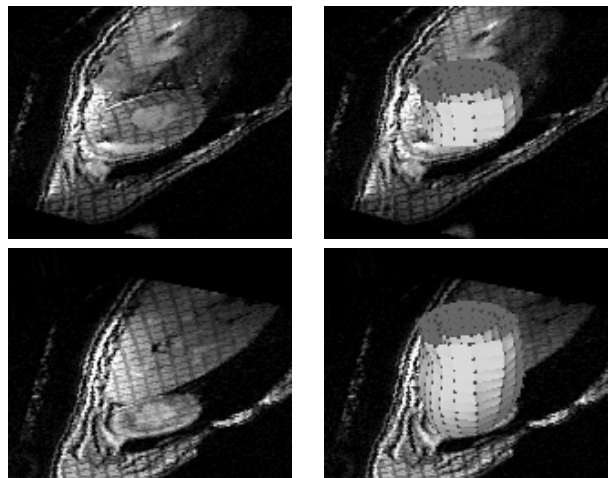


Figure 2: Left : two short axis images at mid (top) and apical (bottom) levels. Right : LV mesh following interactive segmentation overlaid on the corresponding images from the left.

**Discussion:** By interactively contouring in 4D, we have demonstrated a significant reduction in segmentation time for the LV. This will directly reduce the overall time required for completing analysis of myocardial function using MR images. We have the ability to segment any anatomical structure given an initial template.

**Acknowledgements:** This work is supported by a Whitaker Foundation Graduate Fellowship (GS), an INRIA Post-Doctoral Fellowship (JD), a Falk Foundation Post-Doctoral Fellowship (CO), and RO1-HL45683 (ERM,GS).

## REFERENCES:

1. Guttman, MA, Prince, JL, McVeigh, ER, IEEE Tran. Med. Imag., 13:74-88, 1994.
2. Sundaram, TA, *Masters thesis* : “Characterization of Global Heart Properties Using Tagged Cardiac Magnetic Resonance Images”, August 1998.