Real-Time Myocardial Segmentation in MRI

Q. Duan[1], A. F. Laine[1], and V. M. Pai[2]

[1]Biomedical Engineering, Columbia University, New York, NY, United States, [2]Radiology, SUNY Upstate Medical University, Syracuse, NY, United States

Introduction

Cardiac cine-MRI images are becoming more important in clinical diagnosis and treatment of heart disease. In order to quantitatively evaluate cardiac functional images, segmentation of endocardial and epicardial boundaries of the myocardium is essential. Several automated or semi-automated segmentation algorithm have been developed to minimize human effort involved in this step. Recent advances of high speed imaging, such as Phase Train Imaging (PTI) [1], can provide large image data sets with very high temporal resolution (1.5-3 milliseconds). Such data sets can be very valuable for diagnosing and detecting systolic dyssynchrony, previously limited by temporal resolution. However, the increased data content in high speed imaging necessitates development of highly efficient image processing algorithms in order to minimize processing times. In this context, a fully automated real-time segmentation framework was developed in this paper and illustrated on 414 frames of clinical PTI data.

Method

A novel deformable model framework, Surface Function Actives (SFA), was designed for flexibility and efficiency. As a deformable model parallel to active contour and level sets, the SFA framework was specifically developed [2] for real-time segmentation by approaching a N-D segmentation as an (N-1)-D minimization problem. A previous application [3] on 4D ultrasound segmentation showed that this framework could provide accurate 3D+time endocardial segmentation within 50 milliseconds per 3D volume. In this abstract, we have extended the SFA framework to a multi-phase version by using two coupled active interfaces to *simultaneously* segment endocardial and epicardial surfaces. Unlike other existing methods, the proposed method requires minimal manual involvement, no prior knowledge or training data about the shape or appearance of the heart, no pre-processing such as smoothing, and no additional post processing to prune the segmentation. In addition, papillary muscles are *automatically* excluded by segmentation formulation utilizing a smooth interface representation. The segmentation is automatically driven by the intensity homogeneity measures without computation of image gradients. The proposed algorithm was applied to 414 frames of clinical PTI data with average temporal resolution of 2 milliseconds. Each image frame had a dimension of 160x192 pixels. Manual tracing of the endocardium and epicardium was also performed by an experienced expert serving as a gold standard to evaluate the performance of the proposed multi-phase SFA method. The algorithm was preliminarily implemented in Matlab© (Natick, MA).

Results

Figure 1 shows 10 sample frames of the segmentation results taken from 414 frames at different phases of the cardiac cycle, which are roughly 8 milliseconds or 40 frames apart. Both endocardium and epicardium surfaces were accurately segmented on all frames with papillary muscle nicely excluded. The proposed method took 500 ms to segment all 414 frames. On average, it took SFA 6 iterations to reach a stable endocardial and epicardial segmentation with each iteration using 0.194 microseconds under a Matlab© implementation. All computations were executed on a 2.4GHz 64-bit AMD server, running Red Hat Linux Enterprise AS. Quantitative evaluations were performed both on endocardial and epicardial segmentation volume, in terms of area difference, true positive fraction, and false positive fraction. For endocardial segmentation, the area difference (mean ± standard deviation) was 8.7% ± 5.9%; the true positive fraction was 93.3% ± 7.0%; and the false positive fraction was 7.0% ± 4.6%. For epicardial segmentation, the area difference was 6.8% ± 5.3%; the true positive fraction was 95.5% ± 3.6%; and the false positive fraction was 7.8% ± 5.2%. Average distance between automated segmented surfaces and manually traced surfaces was 3.0 pixels ± 2.4 pixels. Comparison metrics from a recent systematic study on cardiac MRI segmentation [4] were used as a reference, which suggested that our results were comparable to level set based methods as well as inter-observer variance. Note that the PTI images have slightly coarser resolution as well as a slightly blurry appearance than regular cardiac cine MRI due to undersampling in the phase-encoding direction, which may increase the inter-observer variance as presented in [4].

Discussions

Under a non-optimized Matlab© implementation, the proposed method still achieved a computational cost of 1.2 ms per frame, which is already less than the temporal resolution of the data. If implemented under C/C++, more than a 3-fold reduction in computation time can be expected. With this extraordinary efficiency, the proposed method can not only be used for offline analysis, but also enable online *real-time segmentation*, which can also use applied to other applications requiring real-time feedback, such as an interventional procedure or calibrating cardiac synchrony.

Conclusions

An automated real-time segmentation based on multi-phase SFA was developed. The proposed method was tested on 414 frames of PTI data with 2ms temporal resolution. The performance of endocardial and epicardial segmentation was visually and quantitatively validated. Implemented in Matlab©, current method took less than 1.2 ms per cardiac phase. The computation time can be easily reduced by at least 3-fold by using C/C++, allowing realization of true real-time online segmentation.

References

[1] V. Pai, L. Axel, and P. Kellman, J Cardiovasc Magn Reson, vol. 7, pp. 98-99, 2005. [2] Q. Duan, et al, JVCIR, submitted, 2007. [3] Q. Duan, G. Shechter, et al, SPIE Medical Imaging, vol. 6509, pp. 65090V1-11, 2007. [4] Q. Duan, D. Moses, et al, ISMRM 14th Scientific Meeting & Exhibition, pp.1014, 2006.

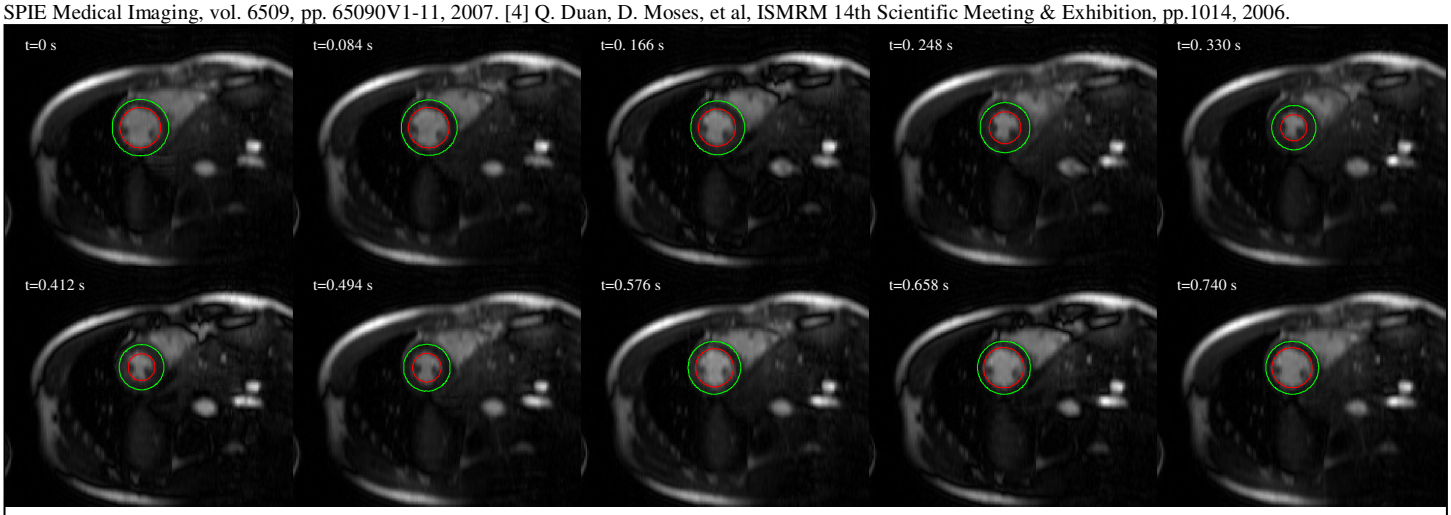

Figure 1: Illustration of segmentation of endocardium and epicardium on 10 frames out of 414 frames. The red curves indicate the automated endocardium segmentation; the green ones are automated epicardium segmentation.