Automated Myocardial Segmentation for Quantitative Analysis of First-Pass Cardiac Perfusion MRI

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Introduction

Myocardial segmentation is essential for quantitative evaluation of first-pass cardiac perfusion images. In this work, we propose a vector-based multi-phase Active Geometric Functions method to realize automated segmentation of endocardial and epicardial contours for cardiac perfusion data. Active Geometric Functions (AGF) [1], (also referred as Surface Function Actives (SFA) [2]), is a novel deformable model framework parallel to Active Contour and Level Set, aiming for real-time segmentation. In our previous work [2], AGF framework was extended to multi-phase version for simultaneous multi-object segmentation, and applied to myocardial segmentation for cardiac cine data. In this abstract, we further extended the method to work with temporal series like perfusion images, where signal intensity is changing over time.

Method

General Active Geometric Framework

In all deformable segmentation models, interface representation is fundamental. Mathematically, there are two possible descriptions for the interface: 1) Explicit representation: Representing the surface by explicitly listing the coordinates of the boundary points (i.e. a parametric representation) like Active Contour; 2) Implicit representation: Representing the surface by embedding the boundary as the iso-value curves of some function *f* called the representation function like level set. Level set functions add one extra dimension beyond the dimensionality of the image data to allow topological changes in the segmentation. By looking the *opposite* way of level set frameworks, dimensionality reduction in surface representation can be used to reduce the computational complexity, i.e. using a representation function which has fewer dimensions than the image data, i.e. using a 2D function to represent a 3D surface in space. We call such function a geometric function. Mathematically, in *N* dimensional space, we can define a geometric function $g:\mathrm{R}^{N-1}\to\mathrm{R}$ as a special set of functions representing one of the coordinates constrained by the others. Without losing generality, we can assume that this special coordinate is x_0 and the other coordinates are x_1 to x_{N-1}. That is $x_0 = g(x_1,\ldots x_{N-1})$.

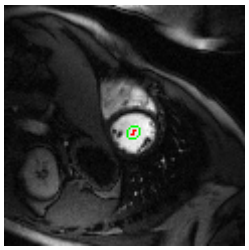

Fig. 1: Segmentation initialization

Multi-phase Vector AGF

In order to segment myocardium from cardiac perfusion time series, we extended AGF in to vector space by treating the time course of each pixel as a vector. Since endocardium and epicardium are target boundaries, a multi-phase extension of AGF as in [2] was used to realize simultaneous segmentation of two boundaries. A variational framework was adopted for its convenience of combining different components of segmentation energy. The final segmentation energy functional was a combination of similarity measurements within each phase of segmentation, smoothness constraints on each curve, and a membership penalty function to keep two curves from collapsing. Mathematically, the functional is:

$$E(C_1,C_2)=\lambda_{11}\int_{\substack{inside C_1\\inside C_2}}\left\|\vec{u}-\overrightarrow{c_{11}}\right\|_2+\lambda_{10}\int_{\substack{inside C_1\\outside C_2}}\left\|\vec{u}-\overrightarrow{c_{10}}\right\|_2+\lambda_{01}\int_{\substack{outside C_1\\inside C_2}}\left\|\vec{u}-\overrightarrow{c_{01}}\right\|_2+\lambda_{00}\int_{\substack{outside C_1\\outside C_2}}\left\|\vec{u}-\overrightarrow{c_{00}}\right\|_2+\gamma_1\oint_{C_1}ds+\gamma_2\oint_{C_2}ds+\upsilon\oint\left|d(g_2-g_1)\right|^2$$

with C_1, C_2 as endocardial and epicardial segmentations, $g_1$and g_2 as corresponding geometric functions, $\vec{u}$ as the temporal vector at each pixel, $\overrightarrow{c_{ij}}, i=0,1; j=0,1$ as the mean vector within each segmentation phase, $\|\bullet\|_2$ as the l_2-norm, $d(\bullet)$ as a soft-thresholding-like membership function, $\lambda_{ij}, i=0,1; j=0,1$ as the parameters balancing the homogeneity measures, γ_1,γ_2 as the weighting for the smoothness constraint for each AGF model, and υ as the parameter controlling the weighting for membership penalty.

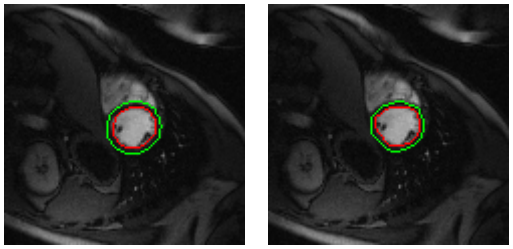

Fig. 2: Segmentation comparison: AGF (left) and manual segmentation (right).

MR Imaging

A TurboFLASH pulse sequence was employed on a whole-body 3T scanner (Siemens; TIM Trio) equipped with a 12-element coil array. The relevant imaging parameters include: FOV = 320 x 320 mm, image matrix = 128 x 128, slice thickness = 8 mm, flip angle = 10°, TE/TR = 1.3/2.5 ms, BW = 1000 Hz/pixel, saturation recovery time delay (TD) = 10 ms, repetitions = 40. The AGF model was initialized as two tiny circles inside LV of the frame at peak blood enhancement as shown in Fig.1. 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 vector AGF method. The algorithm was implemented in Matlab© (Natick, MA). The resulting contours were propagated forward and backward for the remaining repetitions.

Results

Fig. 2 shows segmentation comparison from AGF (left) and manual tracing (right). It took AGF 16 iterations to reach a stable endocardial and epicardial segmentation under a Matlab© implementation. Total processing time was 31ms. All computations were executed on a 2.3GHz Intel Xeon workstation, running Windows XP. 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 was 6.8%; the true positive fraction was 91.4%; and the false positive fraction was 1.9%. For epicardial segmentation, the area difference was 1.5%; the true positive fraction was 97.8%; and the false positive fraction was 3.7%. These results are comparable to a recent systematic study on cardiac MRI segmentation [3]. Signal-time curves in LV blood and myocardium derived from AGF and manual tracing are shown in Fig. 3. Average errors in SI curves (mean ± stdev) are 1.8%±0.7% for LV and 2.8%±0.7% in myocardium.

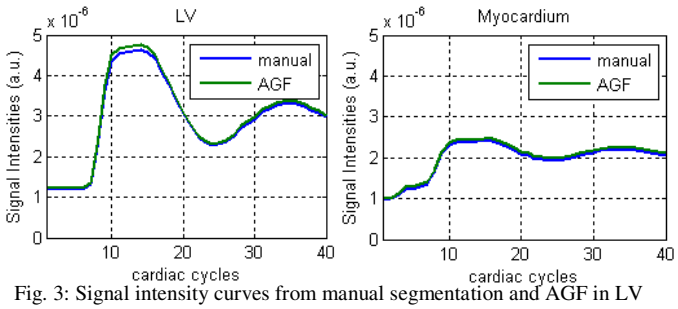

Fig. 3: Signal intensity curves from manual segmentation and AGF in LV (left) and myocardium (right).

Conclusions

An automated segmentation based on multi-phase vector AGF was developed. The performance of endocardial and epicardial segmentation was visually and quantitatively evaluated with good agreement with manual segmentation. The proposed method only takes 31ms to segment the myocardium from the multi-phase data set. Besides offline data analysis, the proposed method could be applied to other cardiac applications where real-time feedback is preferred, e.g. MR guided intervention, or online processing while image acquisition and reconstruction.

References

[1] Duan et al ISBI 2008, 233-6. [2] Duan et al ISMRM 2007, 3172. [3] Duan et al, ISMRM 2006, 1014.