Myocardial Infarction Segmentation by GMM Clustering Method with Free-breathing 3D Navigator-Gated DE-MRI

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Introduction

Computer segmentation may provide faster and more accurate measurements of the extent of myocardial infarction than manual tracing for delayed enhancement MRI (DE-MRI). A number of algorithms have been proposed recently [1] including thresholding, full width at half maximum (FWHM), region growing, and level set algorithms. However, the effectiveness of these advanced methods in the presence of noise and low infarct contrast is problematic. GMM (Gaussian Mixture Model) clustering method has been successfully applied in image segmentation for color texture [2] and brain tissues [3]. In this study, we employed this method for myocardial infarction segmentation of free-breathing 3D DE-MRI images.

Methods

Imaging: Six patients with history of myocardial infarction were imaged at 1.5T using a free-breathing navigator-gated 3D DE-MRI sequence [4]. An eight-channel cardiac phased array was used for signal reception and vector electrocardiographic (ECG) gating was used for cardiac synchronization. DE-MRI was initiated approximately 10 minutes after the contrast administration (Gd-DTPA, 0.2 mmol/kg). The typical imaging parameters were: TR = 4.8 ms, TE = 1.5 ms, flip angle = 20º, readout bandwidth = ±62.5 kHz, FOV = 36 cm, matrix size = 256x256, voxel size = $1.5x1.5x5$ mm^3, 24 short-axis slices.

Image analysis: A GMM clustering method was adopted in this study. In GMM, each cluster is represented by a Gaussian distribution and the entire data can be modeled by a mixture of Gaussian distributions. The parameters of each distribution are resolved by EM (Expectation-Maximum) algorithm [5]. Since myocardial infarction appears as hyperenhancement in DE-MRI, there are distinct clusters inside the epicardial border which could be healthy myocardium, infarction or blood. Myocardial infarction is assumed to be the cluster with the highest mean intensity. Given the manually traced epicardial and endocardial borders, the voxels within these boundaries were processed by the proposed method. In this study two GMM methods were used: 1) three cluster GMM with both epicardial and endocardial contours (GMM3); and 2) two cluster GMM with only epicardial contour (GMM2). The volume of segmented infarction was then calculated. The thresholding and FWHM methods [1] were also implemented and compared with manual tracing by a clinical expert as a standard reference. For the thresholding method, a remote normal myocardial region was chosen (shown as a small blue region in Fig.1e) and the mean + 5 standard deviation (SD) of this region was regarded as the threshold. For the FWHM method, a seed point was selected at the position of potential infarction area. All algorithms were implemented in Matlab.

Results

(a) Original image (b) Manual tracing (c) GMM2 (d) GMM3 (e) Thresholding (f) FWHM
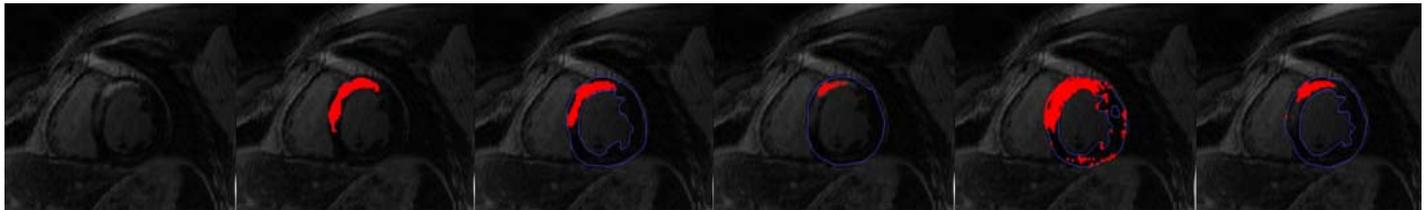
Fig.1. Comparison of myocardial infarction segmentation by different methods for one short-axis image slice. The epicardial and endocardial contours are shown in blue, while the infarction areas are depicted as red pixels.

Figure 1 shows the representative results obtained with the manual, GMM2, GMM3, thresholding and FWHM methods. It is clear in this example that GMM2 provided the most accurate segmentation. Figure 2 shows the correlation between each implemented algorithm and the manual method. Six images (one image per case) were used in the regression and cross correlation analysis. GMM2 provided the largest linear correlation coefficient (R = 0.98), followed by thresholding (0.90), FWHM (0.81), and GMM3 (-0.18), indicating GMM2 was the most accurate.

Discussion and conclusion

This preliminary study in a small subset of patients suggested that the GMM clustering approach is an effective method for semi-automated myocardinal infarction segmentation. Further improvements of this method may include automatic contouring of epicardium and endocardium for more complete automation and Osirix implementation [6] as a plug-in to provide a user-friendly interface.

References

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[5] Theodoridis S et al. Pattern Recognition, China Machine Press, 2006.
[6] Rosset A et al. JDI 2004;17: 205-216.

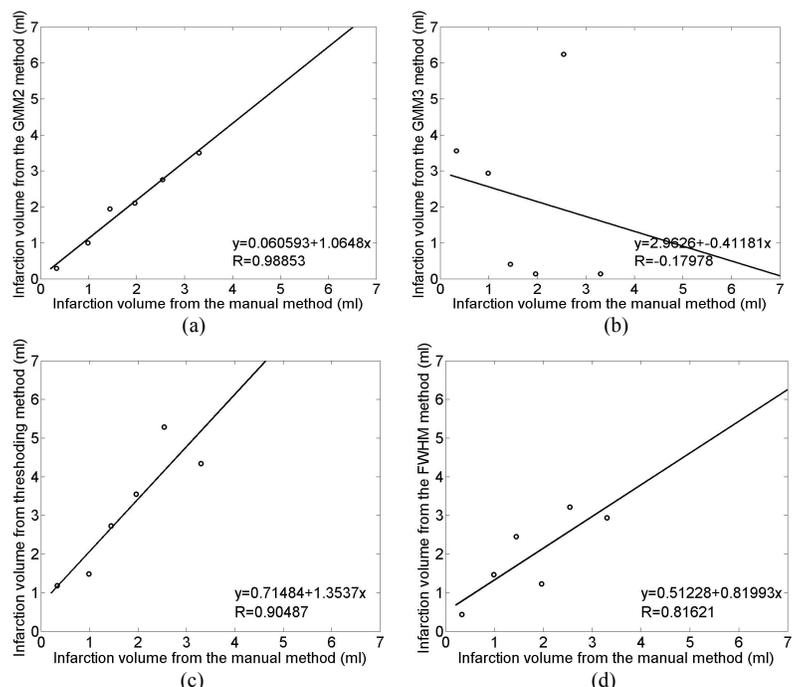**Fig.2**. Correlation between the computer methods and manual tracing: (a) GMM2. (b) GMM3. (c) Thresholding. (d) FWHM.