A New Method to Automatically Identify Left-ventricular Contours from The Gated SPECT Myocardial Perfusion Imaging

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Abstract: Several software packages have been commercially available for the automated quantification of left-ventricular (LV) myocardial viability and mechanical dyssynchrony from the gated SPECT myocardial perfusion imaging (MPI). However, the identification of LV contours is a major issue to influence the reproducibility of the quantification tools. In this paper we present a new method which can automatically identify the LV contours by dynamical programming. The validation with patients suggested that the results of our new method were significantly correlated with those by the technologist.

Keywords: SPECT, Myocardial perfusion imaging, Left ventricle, Dynamic programming

Purpose

Electrocardiography (ECG)-gated single-photon emission computer tomography (SPECT) myocardial perfusion imaging (MPI) is a commonly used method to assess left-ventricular (LV) functions for the diagnosis and prognosis of cardiovascular diseases. We have developed a complete software package to measure LV parameters, such as myocardial viability and mechanical dyssynchrony [1]. However, a few steps in this software require the manual identification of nuclear cardiology technologists, which may influence the reproducibility of the software [3]. The identification of LV myocardial contours, including LV center, radius, apex and base, is a major step requiring the operations of technologists. The purpose of this study was to develop and validate a new method for the automatic identification of LV contours.

Methods

The work is a continuation of another work [1, 2]. The algorithmic steps of the proposed method are summarized as a flow chart in Fig. 1, whose critical steps will be explained below.

A. Dynamic programming to search mid-ventricular contour

In the QGS program [3], the radial count profiles originating from the center of mass (COM) are generated to achieve spherical sampling of the product of the binary mask of the LV myocardium and the short-axis slice. Then, the locus of the profiles' first maxima

This work is supported by the New Star Team of XUPT, by the Key Lab of Contemporary Design and Integrated Manufacturing Technology, Northwestern Polytechnical University, Ministry of Education, China, under Grant KF201401, by the Department of Education Shaanxi Province, China, under Grant 15JK1673, and by Shaanxi Provincial Natural Science Foundation of China, under Grant 2016JM8034.

DOI: 10.12059/Fully3D.2017-11-3202034

represents the maximal count myocardial contour (mid-ventricular). This approach ignored the neighborhood relationship between nearby sampling points on the locus, whereas dynamic programming-based optimization is pretty flexible in emphasizing this neighborhood relationship. Analyzing in details, we may find that a dynamic programming without any constraint on the neighborhood relationship will degrade into the strategy adopted by the general method, while the one with the strongest constraint on the neighborhood relationship will force the maximal count myocardial contour to be a regular circle shape, which is not consistent to the real situations. We believe that both extreme cases are not good to the totally automatic, accurate and stable implementation of a quantification analysis tool. Since the endocardial contour is desired, the maximal count needs to be replaced by the maximal gray level value, and then its maximal differential value along radial orientation is calculated.

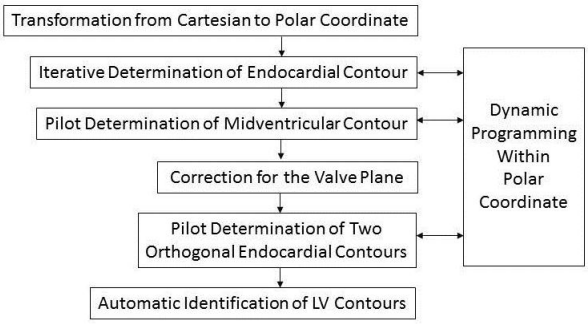


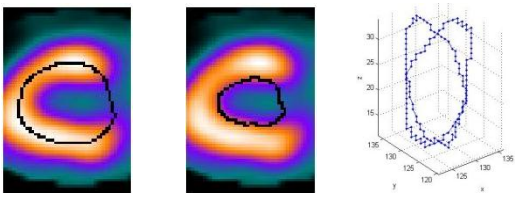
Fig. 1. Flow chart of the algorithmic steps of the proposed method.

B. Pilot determination of endocardial contour

After the mid-ventricular contour is determined, the endocardial contour can be subsequently piloted by the mid-ventricular contour. The piloting is achieved by combining the following constraint with the dynamic programming-based optimization process,

$$\left|c'_{\text{pilot}}(\theta)-c'_{\text{optimized}}(\theta)\right|\le\varepsilon,\theta\in[0°,360°), \qquad (1)$$

where ε is a small boundary, and θ represents the angle variable in the polar coordinate, while c'_{pilot} and $c'_{\text{optimized}}$ are the derivatives of the curves on the pilot contour (Fig. 2a) and the contour being optimized (Fig. 2b), respectively. The same strategy was used to find the epicardial contour. Subsequently, the endocardial, mid-myocardial and epicardial contours in the horizontal and vertical long-axis images were combined to identify the LV contour parameters, including LV center, radius, apex and base.



(a) (b) (c)

Fig. 2. (a) The mid-ventricular contour corrected for the valve plane. (b) The endocardial contour piloted by the mid-ventricular contour in (a). (c) Endocardial contours in the horizontal and vertical long-axis images.

C. Validation with Patient Data

We tested our automatic method with 8 patients from Nanjing Medical University Hospital. A nuclear medicine technologist who was blinded to the results of automatic method conducted a manual study. The correlation between two tests was analyzed by a Pearson statistics.

Results

The preliminary new method failed in only one patient (the results cannot be accepted by the nuclear cardiology technologist). The result of this patient was excluded in our statistics.

A. Statistical analysis

Statistical results of automatic and manual methods are listed in Table 1. Values of left-ventricular functional parameters are presented as mean±std. r, correlation coefficient by Pearson; p, significance level. $p<0.05$, statistically significant.

Table 1. Statistical results of automatic and manual methods. Values of left-ventricular functional parameters are presented as mean±std. r, correlation coefficient by Pearson; p, significance level. $p<0.05$, statistically significant.

	Automatic	Manual	r	p
Scar	7.65±4.88	8.42±4.70	0.94	<0.01
PSD	12.48±4.40	11.45±3.89	0.85	0.02
PBW	37.25±13.42	38.71±12.63	0.92	<0.01

B. Patient examples

Fig 3 shows a patient example to automatically identify the LV contour parameters. Fig 4 shows the measured LV myocardial viability and mechanical dyssynchrony using these parameters [2].

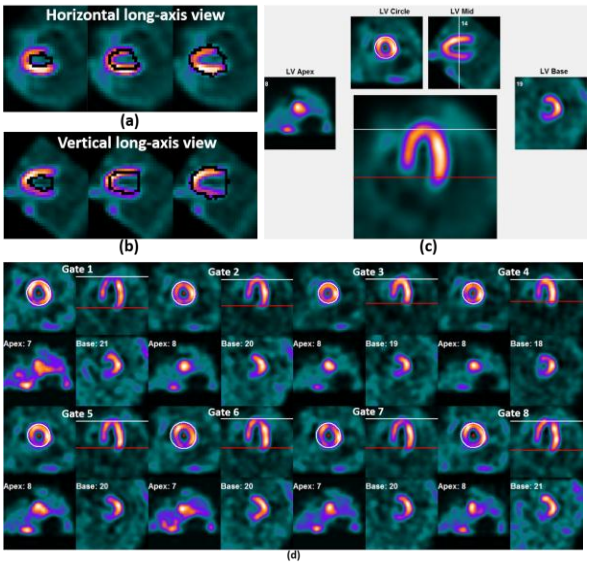


Fig. 3. Patient example to automatically identify left-ventricular (LV) contour parameters, including LV center, radius, apex, and base. (a) Endocardial contour (left), mid-myocardial contour (maximum count contour, middle), and epicardial contour (right) on horizontal long-axis images of left ventricle, automatically detected by a dynamical programming method. (b) Endocardial contour (left), mid-myocardial contour (maximum count contour, middle), and epicardial contour (right) on vertical long-axis images of left ventricle, automatically detected by a dynamical programming method. (c) LV parameters on ungated SPECT MPI images. (d) LV parameters on ECG-gated SPECT MPI images. Red star, LV center; white circle, LV circle; white line, LV apex; red line, LV base.

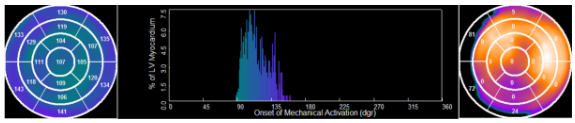


Fig. 4. Measured left-ventricular myocardial viability, mechanical dyssynchrony of the patient example in Figure 1. (a) Polar map of myocardial viability. Bright color, viable myocardium. Numbers, the percentage of scar in this region. (b) Polar map of mechanical dyssynchrony. Bright color, late onset of myocardial contraction. (c) Histogram of mechanical contraction onset.

Fig 5 shows the patient in which our method failed. The cause of the failure was the abnormal uptake of bowel or liver, as illustrated in the vertical long-axis view.

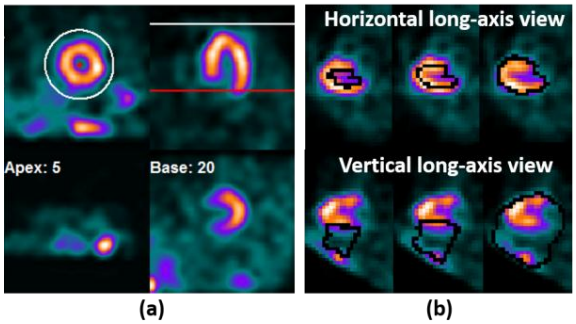


Fig. 5. A patient case in which the automatic method failed to find left-ventricular (LV) contours. (a) LV contour parameters identified by the automatic method. (b) Endocardial, mid-myocardial, and epicardial LV contours on MPI horizontal and vertical long-axis images.

New work

This work presents our continuous effort to build a clinically applicable software system for the automated quantification of LV functions from gated SPECT MPI [2,4]. The presented automatic method is a major improvement for the reproducibility of our software package. Noteworthy, only uptake counts of the SPECT tracer was used in this method, which can be further improved when combined with LV

anatomy to remove the artifacts caused by patient motion or abnormal tracer update.

Conclusions

A new method to automatically identify LV contours from gated SPECT MPI has been developed. The validation with patients suggested that the preliminary results of our method were significantly correlated with those by the technologist of nuclear cardiology. Nevertheless, abnormal tracer update of bowel and liver influences the accuracy of our results in a small portion of patients.

Acknowledgement

We acknowledge Jianyou Shi in the Department of Cardiology at the First Affiliated Hospital of Nanjing Medical University, Nanjing for data collection and related work.

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