

29 AUG 2017 **Research article HEALTH TECHNOLOGY** 

# Automating Cardiac Disease Detection



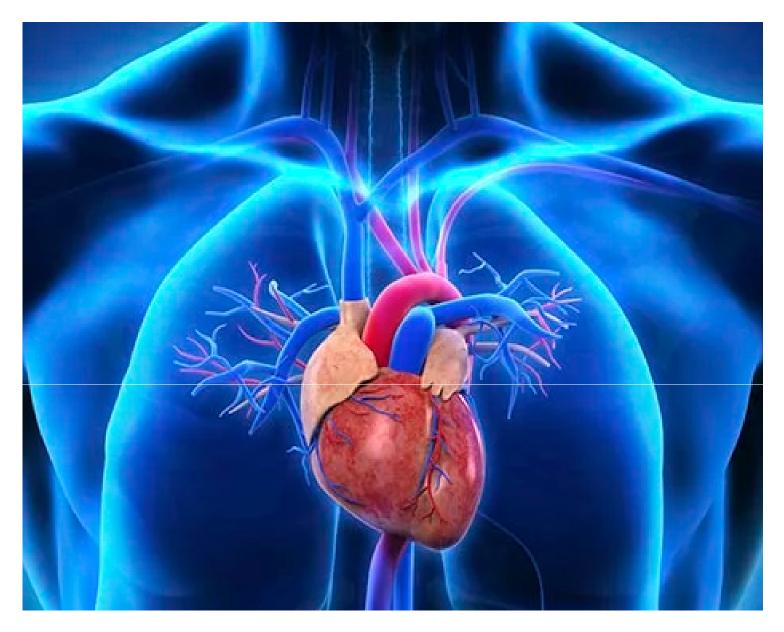




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Automating the detection and localization of segmental (regional) left ventricle (LV) abnormalities in magnetic resonance imaging (MRI) is challenging, with much room for improvements in regard to accuracy. The purpose of the study is to investigate a real-time machine-learning approach which uses some image features that can be easily computed, but that correlate well with the segmental cardiac function. Starting from a minimum user input in only one frame in a subject dataset, we build for all the regional segments and all subsequent frames a set of statistical MRI features based on a measure of similarity between distributions. We demonstrate that, over a cardiac cycle, the statistical features are related to the proportion of blood within each segment. Therefore, they can characterize segmental contraction without the need for delineating the LV boundaries in all the frames. Compared against ground-truth evaluations by experienced radiologists, the proposed algorithm performed competitively, with an overall classification accuracy of 86.09% and a kappa measure of 0.73. Key words: image statistics, linear support vector machine, LSVM, magnetic resonance imaging, MRI

#### Introduction

Early and accurate detection of segmental (regional) left ventricle (LV) abnormalities in magnetic resonance imaging (MRI) is widely accepted as a predictor of cardiac diseases, the leading cause of death worldwide [1]. In routine clinical procedures, segmental cardiac function is considered an essential diagnosis and follow-up component [2]. It is often assessed visually following the American Heart Association (AHA) [3] standard, which prescribes selecting representative 2-D cardiac slices so as to generate 17 standardized LV segments. Based mainly on visual assessments, current radiologic practices are subject to high inter-observer variability [4], [5], and are subjective and nonreproducible.

Alternatively, automating the detection and localization of regional abnormalities has recently sparked an impressive research effort [6]–[11], with promising performances and a breadth of techniques. However, despite such efforts, the problem is still acknowledged challenging, with the need for significant improvements in accuracy.

#### **Problem Statement**

Most of the existing methods require delineations of the endo- and/or epi-cardial boundaries in all frames of a cardiac sequence, using either a manual time-consuming process [6]–[9] or an automatic/semi-automatic segmentation (delineation) algorithm [13], which is itself a challenging and computationally expensive task that may result in high estimation errors [13]. In general, segmentation algorithms require either careful user interventions and/or intensive manual training, along with a heavy computational load. Furthermore, the ensuing segmentation results often hinge on the choice of a large set of ad hoc parameters and training data, which may yield high errors. These difficulties inherent to segmentation algorithms might impede significantly segmental motion abnormality detection. Moreover, some of the existing algorithms, e.g., those based on shape analysis techniques [8], require such delineations in the training phase, which increases significantly the amount of manual inputs and training complexity.

While existing techniques are labor intensive, we believe that there are other characteristics of the images that can be computed with less effort, but that nevertheless correlate with the segmental cardiac function. One such technique that we describe below is based on image features and machine learning.

# **Proposed algorithm**

The main contribution of this work is in building statistical image features that do not require segmentations and can be easily computed, but that can characterize well segmental cardiac function. The new features remove the need for delineating the endoand epi-cardial boundaries in all the images of a cardiac sequence. Starting from a minimum user input in a single frame of subject data, we build for all the regional segments and all subsequent frames a set of statistical MRI features based on a measure of similarity between distributions. We demonstrate that, over a cardiac cycle, the statistical features are related to the proportion of blood within each segment. These features can therefore characterize segmental contraction without the need for delineating the LV boundaries in all the frames. We first seek the optimal direction along which the proposed image features are most descriptive via a LDA. Then, using these results as inputs to a linear support vector machine (LSVM) classifier, we obtain an abnormality assessment of each of the standard cardiac segments in real-time.

#### **Comparison with Other Methods**

Table 1 compares the proposed method with several other recent methods with respect to the user-input/segmentation requirements, accuracy, processing time, size of the used data sets, and types of the processed slices. In the second column, the description "manual-first" means that the corresponding method requires a manual segmentation of the first frame, while "manual-all" means that manual segmentations are required for all frames. "Reg" means that the corresponding method requires an inter-frame registration process so as to find the LV boundaries in all the frames of a sequence. In the last column, A, B, and M denote apical, basal, and mid-cavity, respectively. All the methods in Table 1 analyze apical, basal and midcavity slices except the method proposed by Lu et al. [7] which shows preliminary results for basal slices only.

Method	User-input/Reg	Accuracy	Time	Dataset	slice
Proposed method	mnl-first	0.86	0.15 sec	58 subj cine MRI	A,B,M
Punithakumar et al. [10], [35]	mnl-first + Reg	0.87	62 sec	58 subj cine MRI	A,B,M
Suinesiaputra et al. [15]	mnl-first + Reg	0.78	N/A	53 subj CE MRI	A,B,M
Garcia-Barnes et al. [36]	mnl-first+Reg	0.85	N/A	28 subj Tagged MR	A,B,M
Suinesiaputra et al. [8]	mnl-all	0.77	N/A	89 subj cine MRI	A,B,M
Lu et al. [7]	mnl-all	0.86	N/A	17 subj cine MRI	В
Qian et al. [6]	mnl-all	0.87	N/A	22 subj Tagged MR	A,B,M

## Conclusion

We proposed a real-time machine-learning and image statistic based approach to automating the detection and localization of segmental (regional) myocardial abnormalities in MRI. Unlike the existing techniques, the proposed method did not require delineations of the endo- and/or epi-cardial boundaries in all the frames of a cardiac sequence. Starting from a minimum user input in only one frame in a subject data set, we built a set of statistical MRI features, based on the Bhattacharyya measure of similarity between distributions, for all the regional segments and all subsequent frames. We demonstrated via synthetic and real examples that, over a cardiac cycle, such statistical features are related to the proportion of blood within each segment, and can therefore characterize segmental contraction at a much lower cost in terms of both computation and user effort. We sought the optimal direction along which the proposed image features are most descriptive via an LDA. Then, using these results as inputs to a LSVM classifier, we obtained an abnormality assessment of each of the standard cardiac segments in real-time.

We reported a comprehensive experimental evaluation of the proposed algorithm over 928 cardiac segments obtained from 58 subjects. Compared to ground-truth evaluations by experienced radiologists, the proposed algorithm yielded an overall classification accuracy of 86.09% and a kappa measure of 0.73. We further reported meta-analysis comparisons with several recent methods, which showed that the proposed method can yield a competitive performance, while significantly reducing the computational load and user effort. It is worth noting that the proposed method assumes the global/local motion between two frames is not substantial. Such an assumption may not be valid for abnormal hearts, which undergo twisting motion and/or large shifts in short- or long-axis direction. In such cases, the proposed features may not fully characterize regional motion abnormality. A possible extension would be to investigate the use of motion features. Another possible extension of the proposed algorithm would be to apply a segmentation algorithm [13] to the first frame so as to fully automate the process.

## Additional information

For more information on this subject, we invite you to read the following article: Afshin, Mariam; Ben Ayed, Ismail; Punithakumar, Kumaradevan; Law, Max; Islam, Ali; Goela, Aashish; Peters, Terry; Li, Shuo. 2014. <u>Regional Assessment of Cardiac Left Ventricular</u> <u>Myocardial Function via MRI Statistical Features</u>. *IEEE Transactions on Medical Imaging*. Vol. 33. No 2 p. 481-494.



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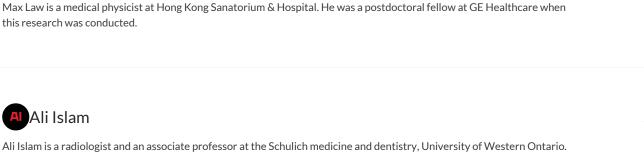
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#### Field(s) of expertise : Computer Assisted Diagnosis Medical Image Analysis & Processing

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#### Images references

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