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Machine-Learning Algorithms to Automate Morphological and Functional Assessments in 2D Echocardiography

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ABSTRACT

BACKGROUND Machine-learning models may aid cardiac phenotypic recognition by using features of cardiac tissue deformation.

OBJECTIVES This study investigated the diagnostic value of a machine-learning framework that incorporates speckle-tracking echocardiographic data for automated discrimination of hypertrophic cardiomyopathy (HCM) from physiological hypertrophy seen in athletes (ATH).

METHODS Expert-annotated speckle-tracking echocardiographic datasets obtained from 77 ATH and 62 HCM patients were used for developing an automated system. An ensemble machine-learning model with 3 different machine-learning algorithms (support vector machines, random forests, and artificial neural networks) was developed and a majority voting method was used for conclusive predictions with further *K*-fold cross-validation.

RESULTS Feature selection using an information gain (IG) algorithm revealed that volume was the best predictor for differentiating between HCM ands. ATH (IG = 0.24) followed by mid-left ventricular segmental (IG = 0.134) and average longitudinal strain (IG = 0.131). The ensemble machine-learning model showed increased sensitivity and specificity compared with early-to-late diastolic transmitral velocity ratio ($p < 0.01$), average early diastolic tissue velocity (e′) ($p < 0.01$), and strain ($p = 0.04$). Because ATH were younger, adjusted analysis was undertaken in younger HCM patients and compared with ATH with left ventricular wall thickness >13 mm. In this subgroup analysis, the automated model continued to show equal sensitivity, but increased specificity relative to early-to-late diastolic transmitral velocity ratio, e′, and strain.

CONCLUSIONS Our results suggested that machine-learning algorithms can assist in the discrimination of physiological versus pathological patterns of hypertrophic remodeling. This effort represents a step toward the development of a real-time, machine-learning-based system for automated interpretation of echocardiographic images, which may help novice readers with limited experience. (J Am Coll Cardiol 2016;68:2287–95) © 2016 by the American College of Cardiology Foundation.

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ABBREVIATIONS AND ACRONYMS

2D = 2-dimensional

ATH = athletes

E/A = early-to-late diastolic transmitral velocity ratio

HCM = hypertrophic cardiomyopathy

IG = information gain

LS = longitudinal strain

LV = left ventricular

STE = speckle-tracking echocardiography

By 2030, 40.3% of the U.S. population is projected to have some form of cardiovascular disease (1). There is growing interest in precision medicine techniques that can deliver individually adapted medical care by linking genetic pre-disposition, biomarkers, and imaging modalities for refining cardiac risk assessment (2–4). One of the computational approaches that can help to implement precision medicine in cardiology is machine learning: a collection of statistical learning and modeling techniques that can learn from established data and can make predictions on unseen or new data (5). Machine learning has been used for performing complex classification tasks in cardiology, including classification of constrictive pericarditis and restrictive pericarditis (6), classification of arrhythmia (7), quantitative prognosis of mortality in patients with heart failure (8), and for risk stratification in patients undergoing percutaneous coronary intervention (9). Noninvasive imaging is the gatekeeper in the management of cardiovascular diseases, and the use of quantitative imaging data-driven phenotypic differentiation is an active area of investigation with opportunities for developing precision phenotyping models and algorithms (10,11).

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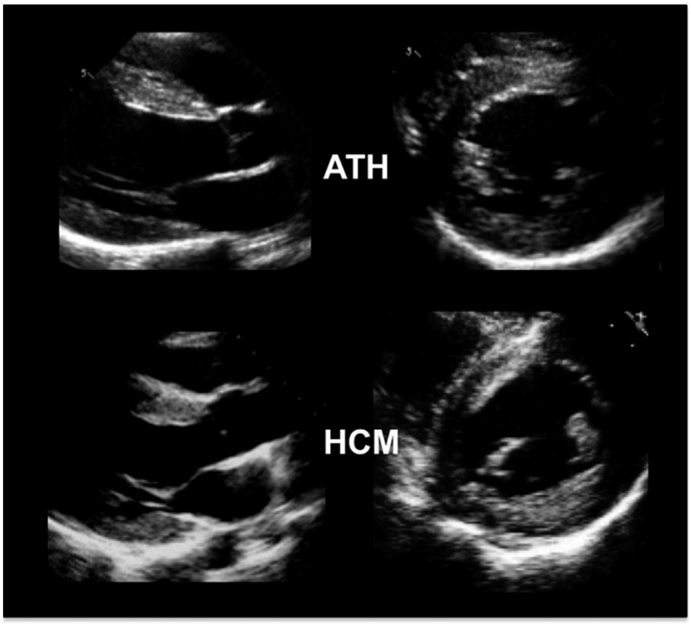
Machine learning offers the potential to improve the accuracy and reliability of echocardiography, which is central to modern diagnosis and management of heart disease (12). Clinical utility depends entirely on the skill of users who are trained in image acquisition, analysis, and interpretation. Automated machine-learning systems may aid in the interpretation of a high volume of cardiac ultrasound images, reduce variability, and improve diagnostic accuracy, particularly for novice users with limited experience (2). This investigation, therefore, explored the development and validation of an ensemble machine-learning framework applied to speckle-tracking echocardiography (STE) data toward the goal of fully automated assessment of left ventricular (LV) morphology and function. Specifically, our machine-learning approach integrated 3 separate approaches into 1 algorithm: support vector machines (13), artificial neural networks (14), and random forests (15). STE by itself uses techniques that provide automated endocardial border detection, to which the current study applied the machine-learning algorithms for clinical decision making in terms of differentiating pathological remodeling, seen in hypertrophic cardiomyopathy (HCM) and physiological hypertrophy in athletes (ATH) as a clinical model to investigate the potential use of machine-learning techniques.

FIGURE 1 Cardiac Imaging



This example shows a morphological resemblance of an athlete's heart with hypertrophic cardiomyopathy (HCM) from the imaging core lab database. ATH = athletes.

METHODS

We identified a convenience cohort of 139 male subjects from the imaging core lab database at our institution (77 verified ATH cases and 62 verified HCM cases) (**Figures 1 and 2**). All subjects were in sinus rhythm. ATH had undergone screening echocardiograms as active, competitive professionals from the United Football League. The clinical diagnosis of HCM was made by the phenotypic presentation of unexplained LV hypertrophy with septal wall thickness >15 mm in the absence of known cardiovascular or systemic disease (16). We also included patients with gray-zone HCM (13 to 15 mm), who were additionally required to have cardiac magnetic resonance imaging demonstrating fibrosis on delayed gadolinium-enhanced images and/or a family history of HCM (17). Thus, echocardiographic diagnosis of HCM was supported by a positive genetic test or family history in 8 cases (13%); phenotypic confirmation was made by cardiac magnetic resonance in 39 cases (63%), of whom 27 (45%) were positive for fibrosis or myocardial enhancement on delayed gadolinium-enhanced cardiac

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