Automated Diagnosis of Cardiac Diseases Using Machine Learning and Non-Stationary Heart Sound Signals

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ABSTRACT:
The objective of this research is to employ machine learning techniques for the accurate diagnosis of cardiac diseases by leveraging a combination of diverse features. This study introduces an automated methodology that involves the analysis of non-stationary heart sound signals to effectively identify various heart conditions. In contrast to conventional approaches relying on techniques such as analysis of variance, signal average or standard deviation comparison, the proposed diagnosis is primarily based on diagnostic labels, ensuring a more reliable and robust assessment. The integrated system proposed in this study utilizes the renowned MIT-BIH database to analyze heartbeats and discern different functional states. Training and testing of the data are performed using the K-fold cross-validation procedure, and a novel model is employed to enhance the learning process. Through this innovative diagnostic system, the detection of cardiac abnormalities in electrocardiogram (ECG) signals is achieved with an impressive accuracy ranging from 96% to 99% across a broad spectrum of cases. By harnessing the power of machine learning algorithms and leveraging a comprehensive set of features, this research significantly advances the field of cardiac disease diagnosis. The proposed methodology outperforms traditional approaches by providing a more accurate and efficient means of identifying heart conditions. The utilization of diagnostic labels as the basis for diagnosis ensures enhanced reliability, enabling healthcare professionals to make informed decisions regarding patient care. Ultimately, this research contributes to the ongoing efforts to improve cardiac healthcare, enabling early detection and intervention, and potentially saving numerous lives.

KEYWORDS: Heart Diseases, Machine Learning, Heart Rate Analysis, MIT-BIH Database.

1. INTRODUCTION

Cardiovascular diseases (CVDs) are a significant cause of mortality worldwide, with an estimated 17 million deaths globally due to CVDs according to a 2005 report by the World Health Organization (WHO) [1]. CVDs are also responsible for an estimated 30% of all deaths worldwide [1]. Within this group, approximately 7.2 million deaths are attributed to coronary heart disease (CHD), and 5.7 million deaths are attributed to stroke [1]. By 2030, it is projected that approximately 23.6 million people will die from CVDs [2].

Healthcare professionals typically diagnose heart disease manually by interpreting electrocardiogram (ECG) signals, but recent technological breakthroughs have led to the development of multiple automated diagnostic tools for arrhythmia classification and diagnosis by physicians [3-4]. Some studies in the literature have suggested that heart rate could be a suitable criterion for diagnosis. Khan et al. [5, 6] provided a comprehensive introduction to the research conducted in this field and proposed deep learning (DL)-based methods for classifying three types of arrhythmias. DL has become a practical tool in medical settings, particularly for classifying cardiac arrhythmias, with several studies investigating one-dimensional (1D), two-dimensional (2D), and/or merged 1D/2D deep convolutional neural networks (CNN) [7, 8]. For example, Xiao et al. [7] proposed a novel arrhythmia classification technique that involves pre-processing, a 1D deep CNN using a block-stacked style architecture including clique and transition blocks, and an

attention mechanism and majority voting decision strategy for prediction. However, their experiments did not account for low-frequency noise recorded in arrhythmic beats, and the 2D representation requires additional computations that are not feasible without building and adjusting a large set of hyperparameters. In a similar study, Noman et al. [8] proposed a framework based on a 1D-CNN that directly learns features from raw heart-sound signals and a 2D-CNN that takes inputs of 2D time-frequency feature maps. Despite the numerous advantages of DL, these networks require feeding with an immense volume of input data, and proper decision-making in these networks relies on the adjustment of multiple parameters.

Automated systems for arrhythmia diagnosis have been developed in recent research [9, 10], but these systems are still undergoing strict pre-approval evaluations by healthcare professionals. Other proposed systems suffer from learning challenges and uncertainty [11, 12]. The development of arrhythmia detection systems requires overcoming fundamental issues, such as manual feature selection, feature extraction techniques, and classification algorithms, particularly when using unbalanced data for classification. Extracting features from ECG signals for automatic arrhythmia diagnosis requires an immense volume of data and information. Afkhami et al. [13] proposed a novel method for accurately classifying cardiac arrhythmias, utilizing two inter-beat (RR) interval features as time-domain information exemplars. They also used Gaussian mixture modeling (GMM) with an enhanced expectation maximization (EM) solution to fit the probability density function of heartbeats. In addition, GMM parameters and shape parameters (e.g., skewness, kurtosis, and 5th moment) were included in the feature vector, which was then used to train an ensemble of decision trees. Mathunjwa et al. [9] designed a new DL method for effective arrhythmia classification using 2-second segments of 2D recurrence plot images of ECG signals. Marinho et al. [14] proposed a novel approach to detect cardiac arrhythmias in ECG signals. In [15], an improved CNN called the modified visual geometry group network (mVGGNet) was introduced for automatic heart-abnormality classification using ECG signals. Ref. [16] combined three groups of features for arrhythmia classification, including RR distances, signal morphology, and higher-order statistics (HOS), and validated the proposed method using the MIT-BIH database based on an inter-patient paradigm. The robustness of each group of features against classification faults was also investigated. Despite the promising results of these studies, automated arrhythmia diagnosis systems still need to overcome challenges such as learning difficulties and unbalanced data for classification.

The proposed jitter-based classification system demonstrated a sensitivity of 93.7%, 89.7%, and 87.9% for N, S, and V classes, respectively, according to the experimental results. Kaya et al. [17] used long short-term memory (LSTM) neural networks to classify ECG signals by combining LSTM and angle transform (AT) methods. Rahul et al. [18] proposed an improved RR interval-based cardiac arrhythmia classification approach that utilized the discrete wavelet transform (DWT) and median filters to remove high-frequency noise and baseline wander from the raw ECG. Lee et al. [19] proposed a beat–interval–texture convolutional neural network (BIT-CNN) model for arrhythmia classification by transforming variable-length 1D ECG signals into fixed-size 2D time-morphology representations. They learned comprehensible characteristics of beat shape and inter-beat patterns over time. Zhang et al. [20] proposed a Multi-Lead-Branch Fusion Network (MLBF-Net) architecture for arrhythmia classification by integrating multi-loss optimization to jointly learn the diversity and integrity of multi-lead ECG. The experimental results showed that MLBF-Net achieved the highest arrhythmia classification performance, with an average equation F_1 score of 0.855. Rahul et al. [21] proposed a technique for classifying lethal CVDs, such as atrial fibrillation (Afib), ventricular fibrillation (Vfib), ventricular tachycardia (Vtec), and normal (N) beats.

In this study, an automated method for analyzing non-stationary heart sound signals to identify disease-related classes is proposed. Unlike other methods that do not consider the non-stationarity of the signal, this study uses signal windowing to address this issue. By combining features obtained from analyzing cardiac signals, the diagnosis and classification of cardiac arrhythmias can be improved. The proposed feature extraction structure integrates features from the time and frequency domains based on statistical and fractal indicators, using only two leads. The structure also employs a decision tree for learning. However, the contribution of frequency and time domain features to classification accuracy may differ depending on the feature extraction method. Therefore, an appropriate feature extraction process is crucial for achieving a comprehensive method for combining and classifying features. Additionally, a multi-core overlearning model using group learning methods can address challenges such as overfitting and uncertainty, while also reducing computational complexity. The primary goal of this study is to diagnose heart disease and reduce false and negative faults, thereby improving evaluation criteria.

2. ELECTROCARDIOGRAPHY

Accurate and consistent evaluation of arrhythmias by cardiologists is crucial for effective diagnosis, but it can be challenging and time-consuming. Therefore, automated detection systems are necessary for the accurate identification of cardiovascular diseases. Sophisticated diagnostic systems can assist cardiologists in precise and rapid diagnosis of ECG recordings, reducing the time and cost of clinical interpretation. In recent years, various machine learning-based

models have been proposed for the analysis of cardiac signals to detect different types of arrhythmias. An ECG is a machine that records the heart's electrical activity as a graph, where electrodes are placed at specific spots on the skin to record the electrical impulses generated by the heartbeat. Each recorded ECG graph contains three distinct waves, namely the P wave, the T wave, and the QRS complex. Researchers have used cardiac signals and analyzed various data to propose a range of techniques for identifying heart diseases and classifying the heart's diverse functional states. The developed models are based on feature extraction, feature selection, and classification. Fig. 1 shows segments of a 2s 1D ECG signal for six classes and their corresponding RPs, including data on AF rhythm, normal beats, PAC beats, PVC beats, VF, and noise. As asserted by them, this is the first report of using SCM to extract features with ECG signals.

3. CVDs

According to the World Health Organization (WHO), cardiovascular diseases (CVDs) account for 32% of all global deaths [22]. Congestive heart failure (CHF) is a severe cardiac disorder and a leading cause of mortality worldwide. In CHF, the heart muscle fails to pump enough blood to maintain the bloodstream and meet the needs of body tissues for oxygen and metabolism. Globally, over 26 million adults suffer from CHF, and its prevalence is increasing by 3.6 million annually [23]. However, early diagnosis of CHF can significantly improve treatments and prevent disease progression. Arrhythmias are the next leading heart disorder responsible for several cases of sudden cardiac death (SCD). An arrhythmia refers to an abnormality of the heart's rhythm caused by irregular heartbeats.

Various non-invasive and invasive methods can be used to diagnose CVDs. Invasive methods are available, but they are costly and uncomfortable, particularly in remote areas. In contrast, early diagnosis of CVDs using non-invasive methods is cheap and painless. ECG and phonocardiograph (PCG) signals are among the non-invasive techniques used to diagnose CVDs. However, cardiologists require the necessary equipment and facilities for heart monitoring to perform respective analyses, which are not easily accessible, particularly in remote areas [24].
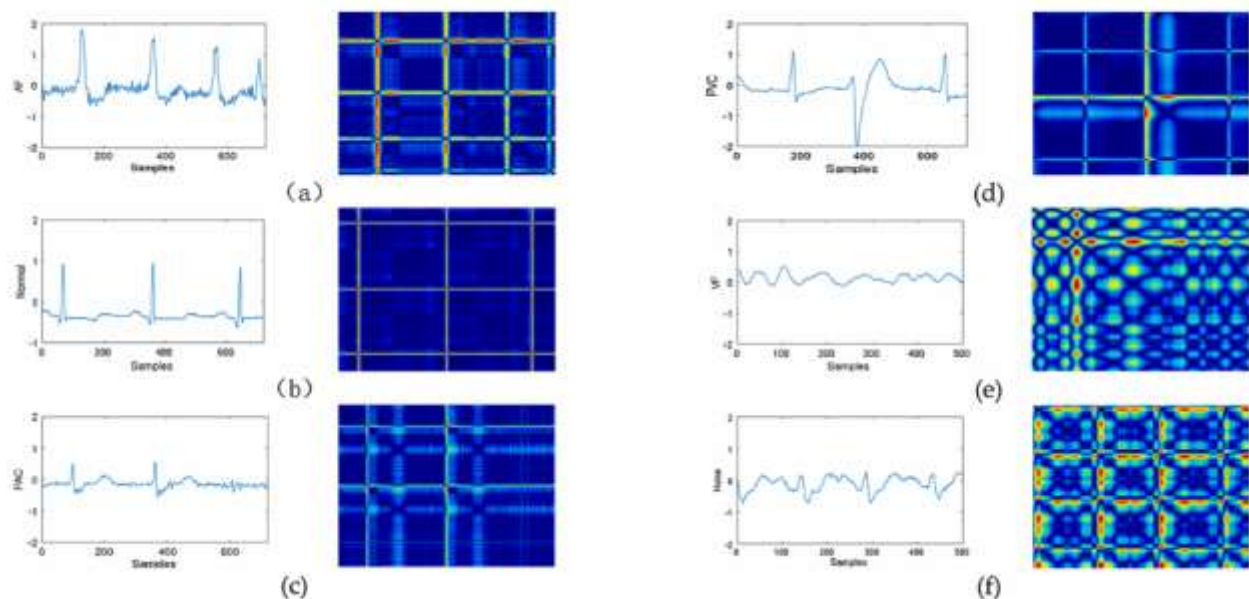

Fig. 1. Segments of the signal for a 2s normal state for six classes and relevant RPs. The 2s segments are shown for AF (a), normal beats (b), PAC beats (c), PVC beats (d), VF (e), and the likely noise (f). The difference in sample size between ECG segments are emanated from various sampling rates for the databases [9].

An ECG is a non-invasive test that monitors and records the heart's function by detecting the electrical activity of the heart muscles. ECGs provide essential data on heart diseases to cardiologists, making them efficient tools for the identification of various CVDs.

4. MIT-BIH DATABASE

This study used data from the MIT-BIH database to conduct experiments. This database includes various common and life-threatening arrhythmias and comprises 48 ambulatory ECG records, each lasting 30 minutes, obtained from 47 patients. Each record consists of two distinct scenarios, where for 45 records, the first lead is the MLII (modified limb

lead), and for the remaining records, the lead is modified V5. The second lead is pericardial, i.e., V1 (for 40 records) and V2, V4, or V5 (for the remaining records). For this study, 23 records were randomly selected from 4000 ambulatory ECG records in the database collected from a diverse population of inpatients. The remaining 25 records were selected from the same collection, featuring less common but clinically significant arrhythmias that are not well-represented in a small random set [14]. Table 1 shows the main labeling of the database, including 16 classes of rhythms.

Table 1. Data from the MIT-BIH arrhythmia database.

No.	Type of heartbeat	Abbreviation	Signal annotation	Total
1	Normal rhythm	NOR	N	74607
2	Left bundle branch block	LBBB	L	8069
3	Right bundle branch block	RBBB	R	7250
4	Atrial premature contractions	APC	A	2514
5	Premature ventricular contraction	PVC	V	7127
6	Heartbeat	PB	/	7020
7	Premature atrial abnormality	AP	a	150
8	Ventricular Fibrillation	VF	!	472
9	Integrated ventricular beat	VFN	F	802
10	Non-conductive P wave	BAP	x	193
11	Nodal escape	NE	X	229
12	Merged fast and normal beat	FPN	J	982
13	Ventricular escape	VE	F	106
14	Nodal escape beat	NP	E	83
15	Atrial escape beat	AE	J	16
16	Unclassified	UN	E	38
Total	-	-	Q	109655

The classes were labeled, and the results of cardiac arrhythmia classification algorithms were represented following the standards set out by the Association for the Advancement of Medical Instrumentation (AAMI). AAMI defines five clinically relevant classes as "N" (sinus node beats), "S" (supraventricular ectopic beat), "V" (ventricular aberrant beats), "F" (fusion beats), and "Q" (unclassified hits). Table 2 maps the classes of the MIT-BIH arrhythmia database to AAMI heart rate classes. Additionally, this table contains plans to train data division and the test set (DS1 and DS2, respectively) [2] for subject-oriented classification. This plan carefully splits the dataset so that the training and test samples are equally distributed among the five mentioned classes, and it also creates false-negative (FN) for four speed records (i.e., 102, 104, 107, and 217) recommended by the AAMI. All 48 records and 16 MIT-BIH annotation classes were used in the class-oriented plan, while the subject-oriented plan employed 44 non-rhythmic records with 5 classes in Table 2 recommended by AAMI.

Table 2. AAMI considering the label of five classes for classification.

No.	AAMI class	MIT-BIH class	Total
1	N	NOR, LBBB, RBBB, AE, NE	89665
2	S	APC, AP, BAP, NP	2940
3	V	PVC, VE, VF	7478
4	F	VFN	802
5	Q	FPN, UN	17

5. THE PROPOSED METHOD

Generally, this research is comprised of three fundamental sections: signal windowing, feature extraction, and classification.

a) Signal Windowing: The necessity addressed here is overcoming the non-stationarity of cardiac signals. This issue holds significant importance in improving the accuracy of the examined system. To extract information from the signal, it needs to be divided into short segments in a manner that, according to signal processing sciences, ensures the time required to generate a cardiac complex, which is at least 500 seconds. Essentially, the goal is to apply processing to segments that are sufficiently short, preventing temporal changes in the properties of cardiac signals within them. Considering the overlap between frames, the impact of discontinuities in the signal decreases, and this is a crucial step in improving accuracy, which we have addressed in this research. While some researchers do not use signal windowing and apply feature extraction directly to the entire signal, this approach leads to a reduction in classification accuracy.

b) Feature Extraction: In the feature extraction section, various features are employed to describe the signal, commonly used in vital signals and cardiac signals. The following features are introduced in order, encompassing time and frequency domain features. In (1), the signal integral is represented, where x denotes the input signal and N is the length of the signal.

$$I_{ECG} = \sum_{i=1}^{N} |x_i|$$ (1)

In equations (2) to (5), the absolute mean value of the signal, the absolute value of third-order time moments, the absolute value of fourth-order time moments, and the absolute value of fifth-order time moments are respectively represented.

$$MAV = \frac{1}{N} \sum_{i=1}^{N} |x_i|$$ (2)

$$TM3 = \frac{1}{N} \sum_{i=1}^{N} |x_i^3|$$ (3)

$$TM4 = \frac{1}{N} \sum_{i=1}^{N} |x_i^4|$$ (4)

$$TM5 = \frac{1}{N} \sum_{i=1}^{N} |x_i^5|$$ (5)

In the set of equations (6) to (9), the signal variance, root mean square, waveform length, and zero-crossings are respectively represented.

$$VAR = \frac{1}{N-1} \sum_{i=1}^{N} |x_i|$$ (6)

$$RMS = (\frac{1}{N} \sum_{i=1}^{N} x_i^2)^{0.5}$$ (7)

$$WL = \sum_{i=1}^{N-1} |x_{i+1} - x_i|$$ (8)

$$ZC = \sum_{i=1}^{N-1} [\text{sgn}(x_i \times x_{i+1}) \cap |x_i - x_{i+1}| \geq threshold]$$

$$f(x) = \begin{cases} 1 & if\ x \geq threshold \\ 0 & otherwise \end{cases}$$ (9)

In the set of equations (10) to (13), the mean absolute mean deviation, autoregressive coefficients, V order moments, and separable and simple square integrals are respectively represented.

$$\text{MAVSLP}_k = \text{MAV}_{k+1} - \text{MAV}_k \; ; \; k = 1,2,\ldots k-1 \tag{10}$$

$$\text{x}_i = \sum_{p=1}^{P} a_p \text{x}_{i-p} + \text{w}_i \tag{11}$$

$$\text{x}_i = \left(\gamma m_i^\alpha \right) \text{n}_i$$

$$V = \left(\sum_{i=1}^{N} \text{x}_i^v \right)^{\frac{1}{v}} \tag{12}$$

$$\text{SSI} = \sum_{i=1}^{N} x_i^2 \tag{13}$$

Similarly, in equations (14) to (16), the average range of change, the difference in absolute standard deviation, and finally, the Wilson amplitude range are respectively presented.

$$\text{AAC} = \frac{1}{N} \sum_{i=1}^{N-1} |x_{i+1} - x_i| \tag{14}$$

$$\text{DASDV} = \sqrt{\frac{1}{N} \sum_{i=1}^{N-1} \left(x_{i+1} - x_i \right)^2} \tag{15}$$

$$\text{WAMP} = \sum_{i=1}^{N-1} \left[f(|x_i - x_{i+1}|) \right]$$

$$f(\text{x}) = \begin{cases} 1 & if \ x \geq threshold \\ 0 & otherwise \end{cases} \tag{16}$$

Continuing, frequency domain features are introduced for the analysis of cardiac signals. From (17) to (22), frequency domain features, including mean frequency, median frequency, peak frequency, average power, final power, and frequency ratio, are respectively presented.

$$\text{MNF} = \sum_{i=1}^{N} f_i \ P_i \Big/ \sum_{i=1}^{N} P_i \tag{17}$$

$$\sum_{i=1}^{TTP} P_i = \sum_{i=MDF}^{N} P_i = \sum_{i=1}^{N} P_i \tag{18}$$

$$PKF = \max(p_i) \ . \ i = 1,2,\ldots N \tag{19}$$

$$\text{MNP} = \frac{1}{M} \sum_{i=1}^{N} P_i \tag{20}$$

$$\text{TTP} = \sum_{i=1}^{N} P_i = \text{SMO} \tag{21}$$

$$\text{FR} = \sum_{i=LLC}^{ULC} P_i \Big/ \sum_{i=LHC}^{UHC} P_i \tag{22}$$

In addition to the aforementioned features, we also utilize fractal dimension features. These features are generally considered among the important features that reflect the oscillations and intricacies within the signal, with a high calculation speed. Among these features, known as fractal dimension features, are included Katz dimension, Higuchi dimension, Petrosian dimension, correlation dimension, and other similar measures. Equations (23) and (24) describe the signal's correlation dimension, where we have N points in an M-dimensional space.

$$Z(i) = \left[Z_1(i).Z_2(i).....Z_m(i) \right] \quad i = 1,2,...,N \tag{23}$$

Then, the correlation integral C(ε) is calculated according to equation (24).

$$C(\varepsilon) = \lim g / N^2 (N \to \infty) \tag{24}$$

Where g is the total number of pairs of points with distances less than ε. As the number of points tends to infinity and the distance between them approaches zero, the correlation integral for small values of ε is expressed as in equation (25).

$$C(\varepsilon) \sim (\varepsilon)^\wedge v \tag{25}$$

In the fractal method, the estimation of the fractal dimension is carried out for a new series of input data x according to the equation (26).

$$x = \left\{ x(1), x(2).....x(N) \right\} \tag{26}$$

Where:

$$x_m^k = \left\{ x(m).x(m+k).x(m+2k).....x\left(m + \left[\frac{N-m}{k} \right] k \right) \right\} \tag{27}$$

Where $m = 1, ..., k$ represents the starting point of each series, k is the distance between samples, and $\left[\frac{N-m}{k} \right]$ is the integer part of each number. Therefore, for each m, we have the length L_m(k).

$$L_m(\mathrm{k}) = \frac{\sum \left| x(m+ik) - x(m+(i-1)k) \right| (N-1)}{\left[\frac{N-m}{k} \right] k} \tag{28}$$

In this equation, N represents the number of required samples, and for each value of K, K lengths will be estimated. Then, the average is calculated as the component of the mean length. This process is repeated up to K_{max}, and if L(k) is obtained for the next k^{-1}, Higuchi is then used to form the best approximation line with the least squares error in Log(L(k)) versus Log(k^{-1}).

c) **Classification**: Classification in the network is performed by considering a suitable classifier, initial training of the network, and finally testing it for the detection of cardiac arrhythmias. The classification utilizes an ensemble method based on a decision tree. There are various ways to combine predictions of a group, or bagging, but the most common method used in the research is majority voting. The main causes of error in learning stem from noise, bias, and variance. This ensemble approach helps minimize these factors. The combination of multiple classifiers reduces variance. To use bagging and boosting, we choose a base learner algorithm. For instance, if we select a classification algorithm, bagging and boosting would involve an ensemble of trees as large as desired. Bagging and boosting methods create N learning patterns by generating additional data during the training phase. New training datasets are produced by random sampling with replacement from the original dataset. With sampling and replacement, some observations in each new training dataset may be repeated. In the case of bagging, each element has an equal probability of being present in the new datasets. To enhance the method, observations are assigned weights, so some of them participate more in the new datasets. In bagging, for training data with size D and dimension n, the model creates a new training sample set Di with size n' by sampling from D uniformly and with replacement. These types of samples are essentially bootstrap samples. Next, m models are created using m bootstrapped samples, and their outputs are combined by averaging in regression or majority voting in classification. This method can be a combination of numerous classifiers, each utilized in the bagging process. However, decision tree-based learning methods are efficient and can be beneficial in ensemble methods like bagging, even in semi-supervised settings. Bootstrap aggregation, also known as bagging, leverages the aggregation

of inputs in a way that an algorithm is used to create stability and improve accuracy, typically applicable in statistical classification and regression processes. This approach not only improves accuracy but also reduces variance and dispersion, aiding in preventing overfitting. While decision tree-based methods are commonly used in bagging, this technique is applicable with various methods. In the stages of bootstrap aggregation in bagging, with sampling and replacement, some observations may be repeated in each *Di*. In a scenario where it can be assumed that a set of observations is independently and equally distributed from an accessible population, bootstrap can be implemented by creating multiple subsamples, where each of these subsamples consists of randomly selected observations with replacement from the original dataset. The use of the bootstrap method in bagging can significantly contribute to improving accuracy and other factors such as variance and dispersion. However, in decision tree-based learning, it essentially involves modeling using one of the prediction model methods that utilize a decision tree (as a predictive model) to draw conclusions about the target value of a case (as presented in the leaves) from observations related to that case (discussed in the subsections). This model, where the target variable can have a set of discrete values, is referred to as decision trees in classification. In these tree structures, the leaves represent class labels, and branches represent combinations of features that lead to the assignment of class labels. Decision trees in which the target variable can have continuous values, typically real numbers, are called regression trees. The predictions of decision tree models are aggregated to create a final combined prediction. This aggregation can be based on the predictions made by individual bootstrapped models or the probability of the predictions made by the individual models. The main drawback of the bagging method is that it does not allow for fine-tuning the aggregation of learner models. If not modeled properly, it may lead to overfitting and become a challenging decision-making problem. Another weakness is that while bagging provides higher accuracy, it can be computationally time-consuming and resource-intensive, making it less desirable for large datasets depending on the use case. The main advantage of the bagging or bootstrap aggregation method used in this study has been its ability to improve the accuracy of a model without risking an increase in its variance. This makes it a suitable choice for situations where we want to reduce the variance of predictions without sacrificing a significant amount of accuracy. The precise and automated identification of the presence or absence of a disease based on cardiac signal analysis in the algorithm set forth in this study can contribute to establishing an effective connection between individuals and healthcare professionals. It can also help prevent a reduction in the error rate in the design of assistive systems and assess changes in error rates. Through proper differentiation of binary or multi-class states, the system could estimate the severity of the disease based on cardiac signals among samples or individuals, fostering more accurate diagnoses.

Overall, for cardiac signals, the accuracy of the proposed method is more than 98% using 30 segment division and 40% overlap. Also, the overlapping situations less than 20% and more than 30% are well analyzed.

In other studies, the issue of uncertainty has not been addressed, but in this study, by plotting the ROC curve, it is possible to make a statement about this issue to a large extent. Therefore, in other experiments, the criterion of the area under the curve was calculated and estimated, which was done for the experimental data and also for the credit data, respectively.

Previous research did not address the non-stationary nature of the ECG signal, but we have addressed it in this research, and to overcome this problem, we have used windowing, which is very effective in improving accuracy. Also, by considering the overlap between frames, the effect of discontinuous points on the signal is reduced, which is an important step in improving accuracy.

In previous studies, techniques such as variance analysis, mean comparison, or standard deviation were used to diagnose the disease, but this study is based on diagnostic labels.

Furthermore, in other studies, the issue of uncertainty has not been addressed. However, in this research, we have addressed this matter by utilizing ROC curves and calculating the area under the curve to overcome uncertainty.

In general, the use of signal windowing involves creating input structures from signals, reducing the length of windowed signals, diminishing the dimensions of extracted features, improving processing time, and enhancing accuracy. This is considered an innovative aspect of the research.

The proposed method in this study consists of three main parts, as illustrated in Fig. 2: 1) windowing of various types of cardiac signals, including different cardiac arrhythmias, 2) feature extraction, and 3) final classification. The algorithm used in this study was simulated in MATLAB (version 2022) on a computer with a Windows 10 operating system for both the learning section and the splitting of the signal into equal frames. The hardware used was conFig.d with an Intel® Core™ i7-7500U Processor (Processor Base Frequency 2.70 GHz; 4GB RAM). All processes were performed offline. The data were split into several stages, where the first stage involved dividing the data into 80% (operational) and 20% (unseen) data groups.
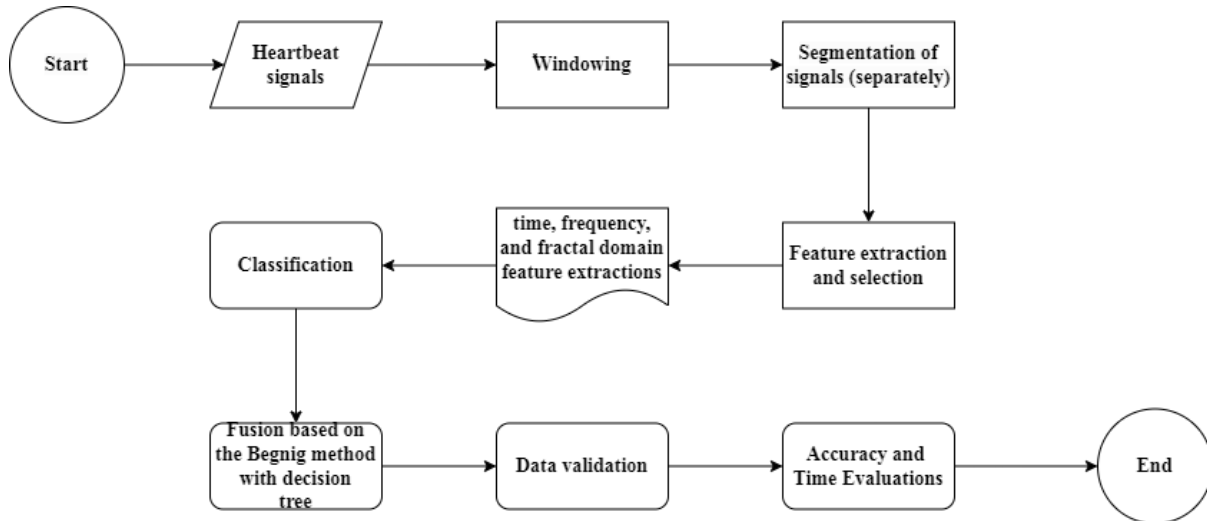
Fig. 2. Schematic representation of the proposed method in recognizing cardiac arrhythmias from the ECG signals.

The 20% of data mentioned in the final stage was used to estimate the performance of the final model obtained. The data were split using the K-fold validation method with K=5, where two groups of data (training and testing) were used for the evaluation process. The training data were included in the model, and then re-split into new training data and validation data using the K-fold method to adjust the fusion classification appropriately. The classification errors were estimated based on the obtained features and the application of validation data. Fault calculation was also performed based on the validation data. After that, the parameters were transferred to the model and evaluated based on the testing data 2. The built model and the unseen data were eventually applied to the model. To determine the best window length, the length of the windows was varied from 800 ms to 2500 ms, considering the properties of the cardiac signal to cover at least one cardiac cycle. The rate of overlap between two consecutive frames was measured by balancing accuracy and time.

6. RESULTS

To evaluate the effectiveness and success of the proposed model, the confusion matrix and the ROC curve (receiver operating characteristic curve) were used. The confusion matrix was used to analyze the classification and identification of the target class and other classes, and it was estimated by examining various states when diagnosing the disease or an abnormal heart condition in the cardiac signal. The confusion matrix consists of four moods, including true positive (TP), true negative (TN), false positive (FP), and false negative (FN), each having a specific meaning. TP is the number of signals or segments of the signals that indicate the presence of a cardiac abnormality, while TN is the number of signals or segments of the signals that do not indicate the presence of a cardiac abnormality. FP refers to the number of signals or segments of the signals that indicate the presence of a cardiac abnormality, but the simulation software has wrongly determined the presence of that class of cardiac abnormality. FN refers to the number of signals or segments of the signals that indicate the presence of a cardiac abnormality, but the simulation software has wrongly determined the absence of that class of cardiac abnormality. Based on these definitions, the accuracy, sensitivity, and specificity values were estimated using equations (29) to (31).

$$Accuracy: \left(N_{TP} + N_{TN} \right) / \left(N_{TP} + N_{TN} + N_{FP} + N_{FN} \right) \tag{29}$$

$$Sensitivity: \left(N_{TP} \right) / \left(N_{TP} + N_{FN} \right) \tag{30}$$

$$Specificity: \left(N_{TP} \right) / \left(N_{TP} + N_{FN} \right) \tag{31}$$

NTP represents the number of true positives, NTN represents the number of true negatives, NFP represents the number of false positives, and NFN represents the number of false negatives in the diagnosis of a specific class of cardiac abnormality. In the first step, it is necessary to evaluate the performance of the heart recognition model for signals selected from the database. The average recognition accuracy should be acceptable, and the average false rate should be less than 5% (with a small number of features). These values are ideal when the model is applied to the database.

Table 3. An estimation of criteria such as accuracy by estimating the maximum (Max), minimum (Min), and average (Ave) values using the proposed method and considering the change in frame length.

Results of test folds while altering the frame length		A model without feature fusion and classification fusion	A model with feature fusion and classification fusion
K-fold 1	Long frame length	0.89 ± (0.07)	0.95 ± (0.03)
	Average frame length	0.88 ± (0.07)	0.97 ± (0.03)
	Short frame length	0.89 ± (0.07)	0.95 ± (0.04)
K-fold 2	Long frame length	0.90 ± (0.07)	0.95 ± (0.03)
	Average frame length	0.91 ± (0.05)	0.97 ± (0.03)
	Short frame length	0.90 ± (0.07)	0.95 ± (0.04)
K-fold 3	Long frame length	0.90 ± (0.06)	0.95 ± (0.03)
	Average frame length	0.89 ± (0.07)	0.98 ± (0.04)
	Short frame length	0.90 ± (0.07)	0.95 ± (0.03)
K-fold 4	Long frame length	0.89 ± (0.07)	0.95 ± (0.03)
	Average frame length	0.89 ± (0.06)	0.96 ± (0.03)
	Short frame length	0.89 ± (0.07)	0.95 ± (0.04)
K-fold 5	Long frame length	0.89 ± (0.07)	0.95 ± (0.03)
	Average frame length	0.89 ± (0.06)	0.98 ± (0.03)
	Short frame length	0.89 ± (0.07)	0.96 ± (0.04)

The irregular heart signals were analyzed separately to compare cardiac functioning. Table 3 presents the differences in the results obtained from the proposed techniques. The cardiac dataset was analyzed independently using the proposed algorithm with the K-fold method, where K is 5. The short frame length varied from 800 ms to 1300 ms, the average frame length ranged from 1300 ms to 1800 ms, and the long frame length varied from 1800 ms to 2300 ms.

The representation of the confusion matrix can significantly contribute to the algorithm analysis process in terms of classification results. Thus, Fig. 3 illustrates the confusion matrix for 5 folds of a single run of the algorithm for classification in the set. The estimation is performed separately for each of the five classes, and investigating the dispersion among the algorithm outputs contributes to the estimation and investigation of challenges like repeatability and uncertainty. The final accuracies were estimated to investigate the dispersion among the responses in the next experiment, as shown in Fig. 4. Nearly 80% of the features could result in an acceptable accuracy when included in the classification process, indicating that the steadiness in selecting the number of features largely depends on the initial volume of the features. In other words, an efficient feature-selection strategy will select fewer features, and the selected features will function appropriately.
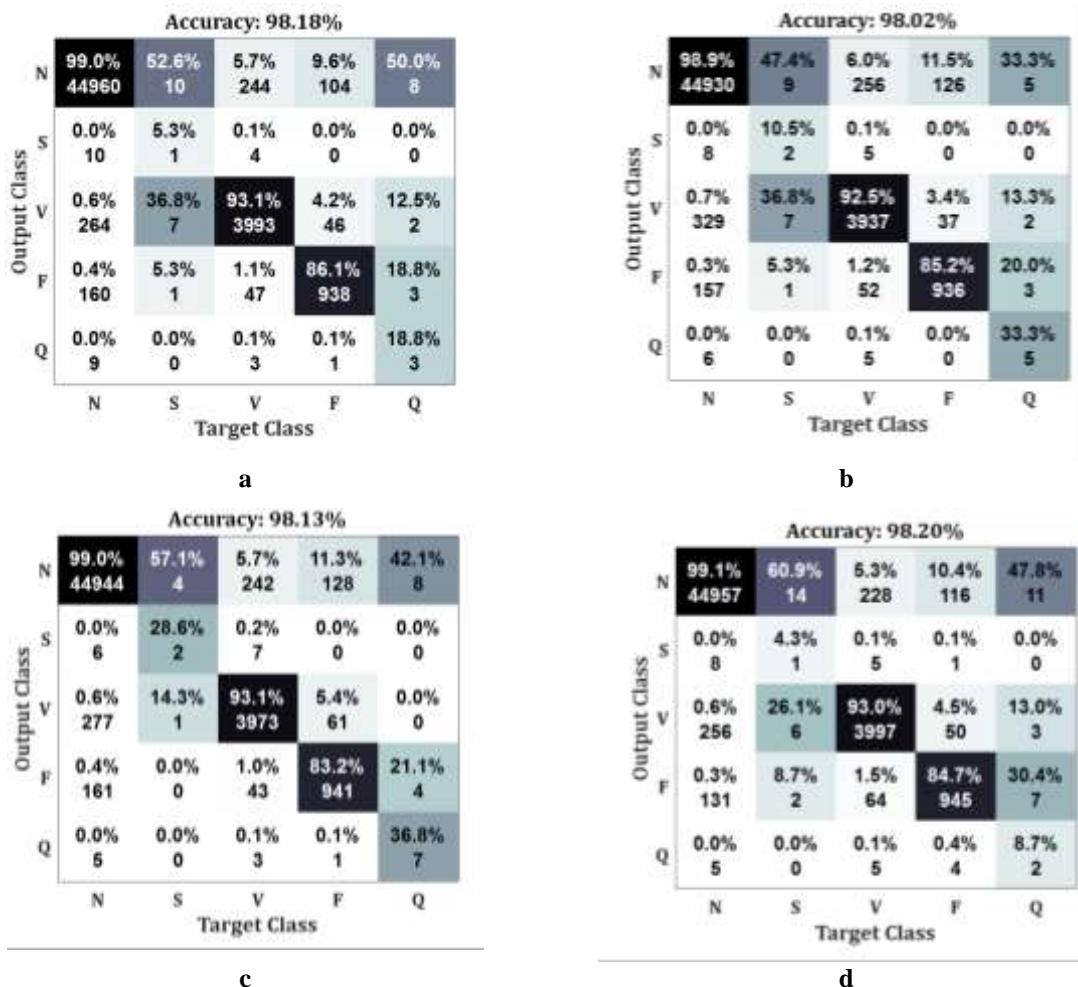
a

b

c

d

Fig. 3. The representation of multiple folds of a single running of the algorithm: a) accuracy98/18%, b) accuracy98/02%,c) accuracy 98/13%,d) accuracy98/20%. the average accuracy is estimated at 98.2%. The purpose of displaying multiple folds of a single running of the algorithm is to indicate the quantitative dispersion of the proposed algorithm.

The following experiment examined the changes in results when the performance of the proposed method was evaluated without reflecting the effect of the "fusion step of feature selection." It was observed that the feature selection step improves the response by up to about 2%. This observation is also reflected in the confusion matrix, where four out of five folds are displayed without the feature selection conditions. The dispersion among the responses is significant, and on average, a 1.5 to 2% reduction in accuracy occurs. This classification is illustrated in Fig. 4.
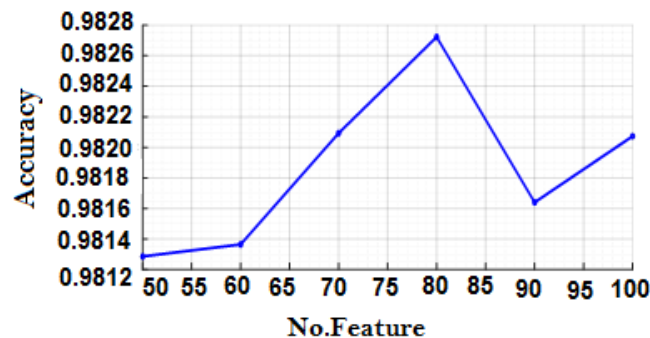

Fig. 4. A representation of the classification accuracy versus the number of features, indicating the maximum accuracy that is obtained when selecting 80% of the features.
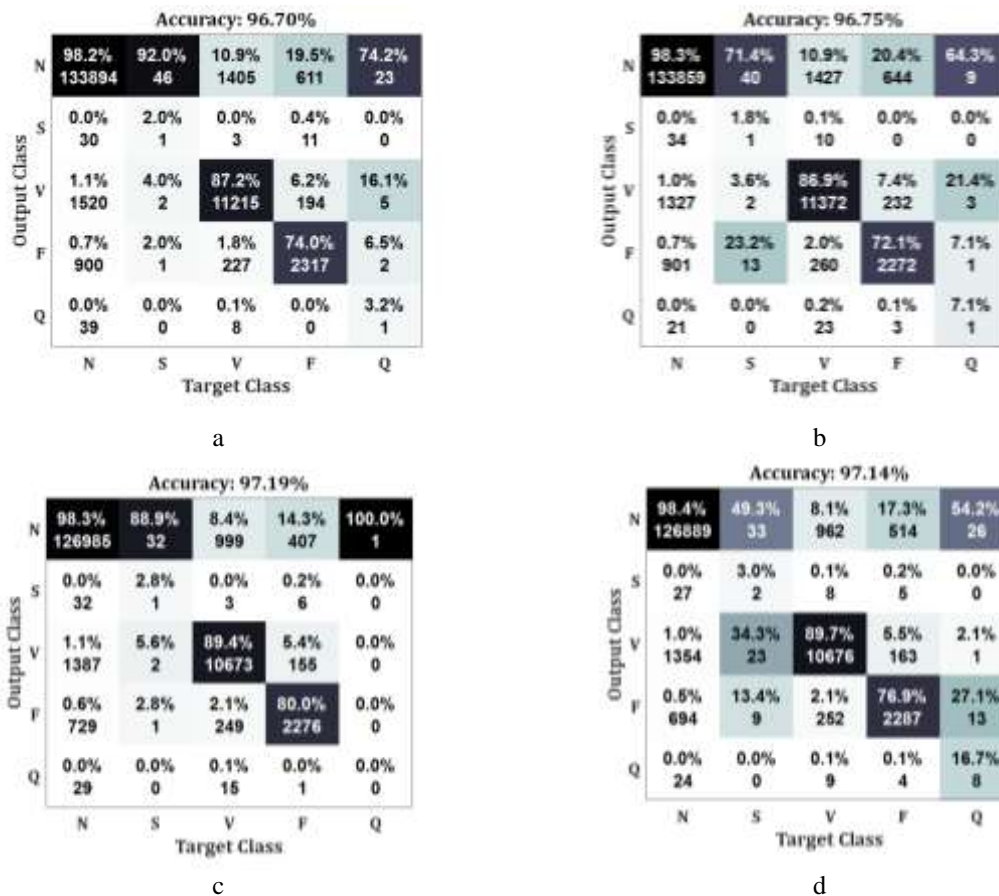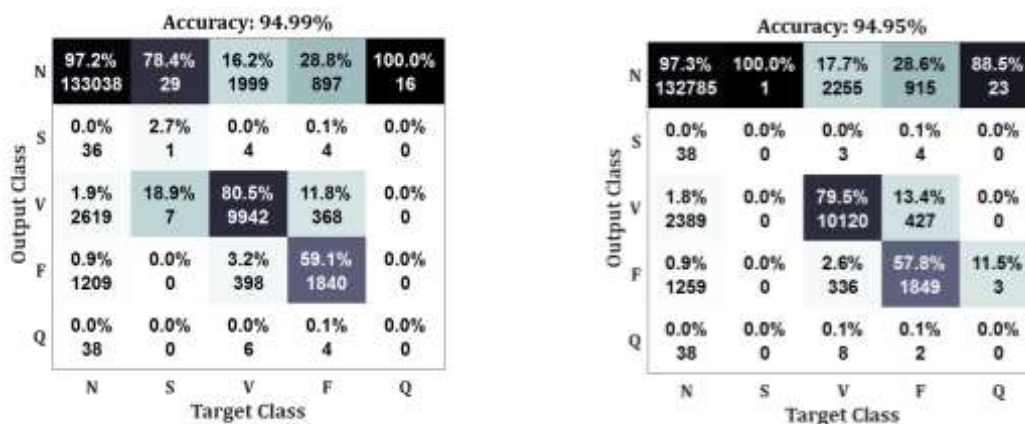
Accuracy: 96.70% (a)

Output Class	N	S	V	F	Q
N	98.2% 133894	92.0% 46	10.9% 1405	19.5% 611	74.2% 23
S	0.0% 30	2.0% 1	0.0% 3	0.4% 11	0.0% 0
V	1.1% 1520	4.0% 2	87.2% 11215	6.2% 194	16.1% 5
F	0.7% 900	2.0% 1	1.8% 227	74.0% 2317	6.5% 2
Q	0.0% 39	0.0% 0	0.1% 8	0.0% 0	3.2% 1

Target Class: N S V F Q

Accuracy: 96.75% (b)

Output Class	N	S	V	F	Q
N	98.3% 133859	71.4% 40	10.9% 1427	20.4% 644	64.3% 9
S	0.0% 34	1.8% 1	0.1% 10	0.0% 0	0.0% 0
V	1.0% 1327	3.6% 2	86.9% 11372	7.4% 232	21.4% 3
F	0.7% 901	23.2% 13	2.0% 260	72.1% 2272	7.1% 1
Q	0.0% 21	0.0% 0	0.2% 23	0.1% 3	7.1% 1

Target Class: N S V F Q

Accuracy: 97.19% (c)

Output Class	N	S	V	F	Q
N	98.3% 126985	88.9% 32	8.4% 999	14.3% 407	100.0% 1
S	0.0% 32	2.8% 1	0.0% 3	0.2% 6	0.0% 0
V	1.1% 1387	5.6% 2	89.4% 10673	5.4% 155	0.0% 0
F	0.6% 729	2.8% 1	2.1% 249	80.0% 2276	0.0% 0
Q	0.0% 29	0.0% 0	0.1% 15	0.0% 1	0.0% 0

Target Class: N S V F Q

Accuracy: 97.14% (d)

Output Class	N	S	V	F	Q
N	98.4% 126889	49.3% 33	8.1% 962	17.3% 514	54.2% 26
S	0.0% 27	3.0% 2	0.1% 8	0.2% 5	0.0% 0
V	1.0% 1354	34.3% 23	89.7% 10676	5.5% 163	2.1% 1
F	0.5% 694	13.4% 9	2.1% 252	76.9% 2287	27.1% 13
Q	0.0% 24	0.0% 0	0.1% 9	0.1% 4	16.7% 8

Target Class: N S V F Q

Fig. 5. The representation of four folds of a single running of the algorithm: a) accuracy96/70%, b) accuracy96/75%,c) accuracy 97/19%,d) accuracy97/14%. the effect of "the fusion step of feature selection" has been ignored. Under this condition, the classification accuracy will be reduced by 1.5 to 2% and the dispersity among the responses will be significant.

The impact of fusion in classification was examined in the subsequent experiment, and the results are presented through the confusion matrix. This state takes into account the feature selection step, but the classification is based on decision-making using the decision-making tree. The accuracy drop is more significant in this state, where the results are 2 to 3% less than the ideal state. Fig. 6 illustrates four random folds of a single run of the algorithm. Under some conditions similar to classification (such as classification while excluding the effect of fusion in feature selection and/or excluding the effect of fusion in classification), the diagnostic accuracy of some classes is notably low. However, when using the proposed method, the reduction in accuracy (even with fewer samples) is much lower than in similar states.
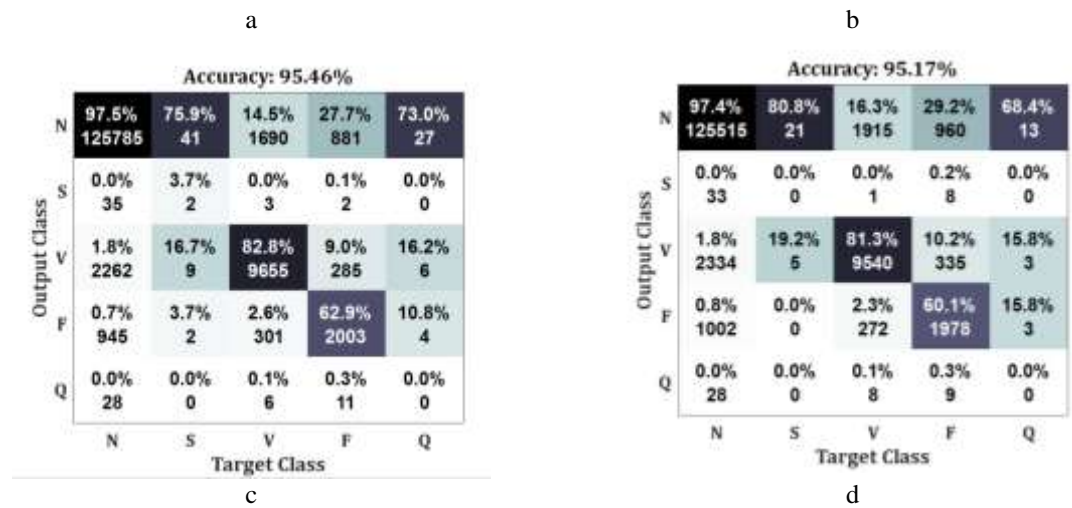
Accuracy: 94.99%

Output Class	N	S	V	F	Q
N	97.2% 133038	78.4% 29	16.2% 1999	28.8% 897	100.0% 16
S	0.0% 36	2.7% 1	0.0% 4	0.1% 4	0.0% 0
V	1.9% 2619	18.9% 7	80.5% 9942	11.8% 368	0.0% 0
F	0.9% 1209	0.0% 0	3.2% 398	59.1% 1840	0.0% 0
Q	0.0% 38	0.0% 0	0.0% 6	0.1% 4	0.0% 0

Target Class: N S V F Q

Accuracy: 94.95%

Output Class	N	S	V	F	Q
N	97.3% 132785	100.0% 1	17.7% 2255	28.6% 915	88.5% 23
S	0.0% 38	0.0% 0	0.0% 3	0.1% 4	0.0% 0
V	1.8% 2389	0.0% 0	79.5% 10120	13.4% 427	0.0% 0
F	0.9% 1259	0.0% 0	2.6% 336	57.8% 1849	11.5% 3
Q	0.0% 38	0.0% 0	0.1% 8	0.1% 2	0.0% 0

Target Class: N S V F Q

a   b

c   d

Fig. 6. The representation of several folds of a single running of the algorithm: a) accuracy94/99%, b) accuracy94/95%,c) accuracy 95/46% ,d) accuracy95/17%. the effect of "the fusion step of feature selection" has been ignored. Under this condition, the classification accuracy will drop by 2 to 3% and the dispersity among the responses will be significant.

Some other conditions can be considered to demonstrate the capability of the proposed algorithm. For instance, fusion has improved classification in both the feature selection step and the classification step compared to the typical state (i.e., feature selection and classification using a simple strategy), where the average accuracy reaches 95%. However, other factors, such as the type of features, the length of the selected frames, the number of selected features, and the initial parameters of the adjustment process, contribute to classification. When evaluating the algorithm's ability to process both testing and validation data, the issue of uncertainty needs to be addressed. Plotting the ROC can help assess this problem to a great extent. Therefore, in the other experiments, the area under the ROC was investigated, and estimations were made for both testing and validation data (Fig. 6).

Fig. 7 displays the ROC, which shows the area under the curve for both testing and validation data. Fig. 8 examines sensitivity and specificity, where the estimation of these factors indicates the performance of the proposed method in terms of unseen cardiac signals. In this experiment, these factors were estimated separately for each class of the two sets of unseen cardiac signals.

The proposed method has shown greater efficiency in detecting N, V, and F states in classifying various cardiac disorders in the ECG signal. However, it has been more prone to errors in detecting S and Q states. The main reason for this issue is the lack of data on S and Q states, which has resulted in insufficient training of the algorithm. If more data on S and Q classes were available, the learning model would be more effective in distinguishing the various classes optimally.
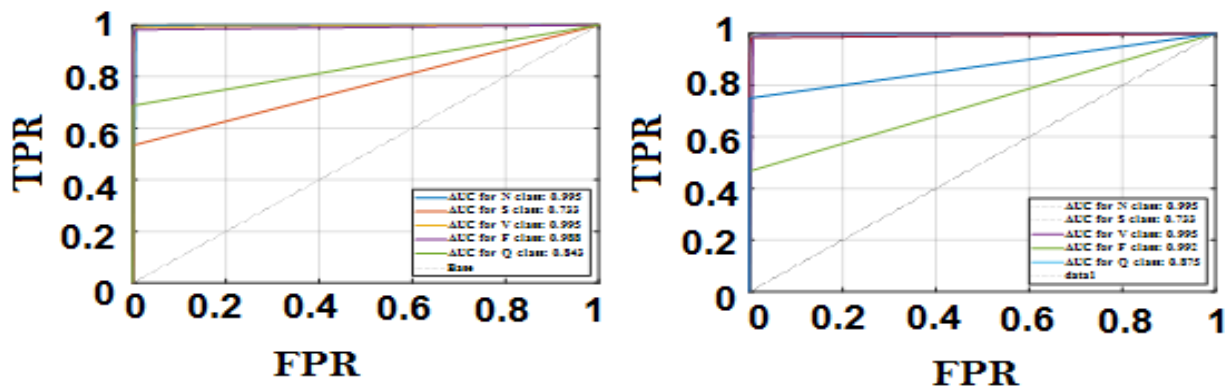

Fig. 7. The representation of the ROC matrix for validation data (left inset) and testing data (right inset).
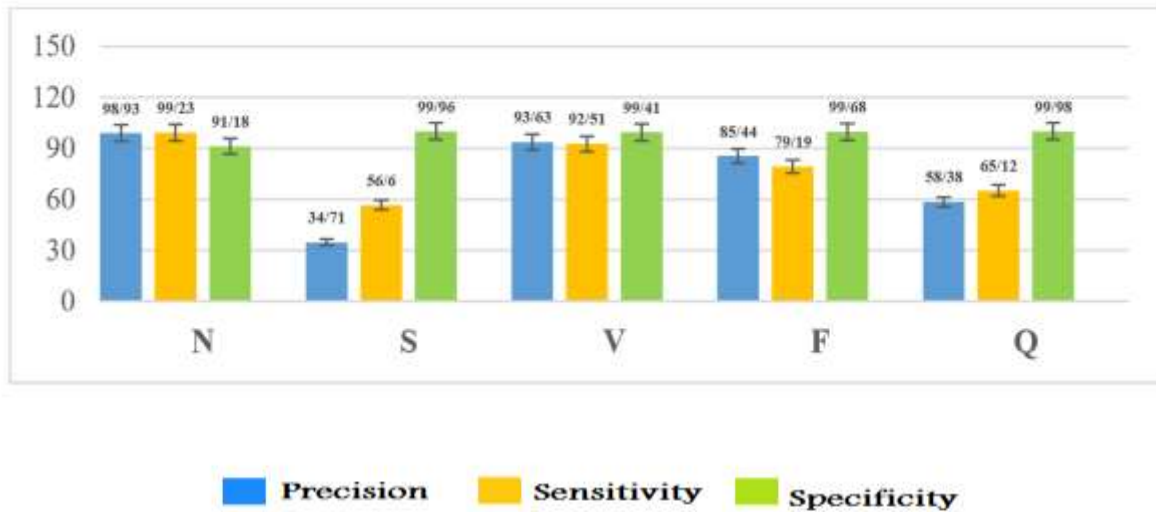
Fig. 8. An estimation of the sensitivity, accuracy, and specificity for cardiac unseen signals.

Overall, the performance of the proposed method is satisfactory. Although it has created some errors in relation to two classes, previous algorithms have either ignored these classes or considered the estimation criteria for all the concerned classes. The proposed model can respond to various sets of cardiac signals. In previous methods, the classification error has been even higher than that in the method proposed in this study. For instance, in previous studies such as Llamedo et al. [25], Ye et al. [26], De Chazal et al. [27], Afkhami et al. [13], both the number of classes and samples are lower than those in this study. Furthermore, these studies offer moderate accuracy, and when considering the excluded classes and samples, the accuracy of their proposed methods will significantly decrease. Some methods have high computational complexity, while others suffer from prolonged response times in both training and testing steps. Table 5 compares the proposed method with methods proposed in other studies.

7. CONCLUSION

The proposed integrated system in this study is a procedure that identifies various states of cardiac functioning by analyzing heartbeats through exploring the MIT-BIH database. Unlike other methods proposed thus far, which simply use techniques such as ANOVA, comparison of the mean or SD of signals, and/or estimation of the accuracy in diagnosing cardiac diseases, the method proposed in this study diagnoses CVDs based on diagnosis labels.

Table 5. The drawbacks and advantages of the proposed method compared to the methods proposed in recent years in relation to the diagnosis of various cardiac functioning states based on heartbeats.

Ref.	Features	Classifier	Classification Accuracy (%)	Advantages	Drawbacks
Afkhami et al. (2016) [13]	Modeling of statistical features and RR intervals	GMM	96.15	Creating low-level, appropriate features; the possibility of decision-making for 4 classes	Excluding some classes and samples; sensitivity to the number of samples; the possibility of overfitting
Ye et al. (2012) [26]	Wavelet; analysis of independent components; RR pick	Support vector machine (SVM)	99.71	Proper accuracy in the two-class state; utilizing low-level features; satisfactory outcomes	Investigation of only two classes; high volume of features; sensitivity to noise

Rodriguez et al. (2005) [27]	Waveform and signal morphology	Classification based on the "strict voting method"	96.13	Proper accuracy in the two-class state; instant classification	Investigation of only two classes; high volume of features; sensitivity to noise
de Oliveira et al. (2011) [28]	Waveform and signal morphology; RR features	Dynamic Bayesian Network (DBN)	98	High number of classes for analyzing heartbeat in the signal	Sensitivity to noise in the input signal; high computational complexity
Zubair et al. (2016) [29]	Deep CNN	Softmax function	97	Creating high-level features; the capability of decision-making for four classes	The need for a high volume of data; high dimension of the extracted features; high computational complexity
Chandra et al. (2018)	A 8-layer CNN and learning	Softmax function	92.7	Creating high-level features; the capability of decision-making for five classes	The need for a high volume of data; high dimension of the extracted features; relatively high computational complexity
Acharya et al. (2017) [31]	A 11-layer CNN and auto-learning	Softmax function	94.9	Creating high-level features; the capability of decision-making for five classes	No interpretability of features; dependence on the length of the window in the signal
Chu et al. [32]	A 12-layer CNN with the LSTM structure; SVM; particle swarm optimization (PSO) algorithm	Optimized SVM	97.8	Creating high-level features; the capability of decision-making for five classes	No interpretability of features; dependence on the length of the window in the non-stationary signal
Avanzato et al. (2020) [33]	CNN with the normalizing step	LSTM and Softmax function	98.3	Creating high-level features; the capability of decision-making for three classes	No interpretability of features; dependence on the length of the window in the non-stationary signal
Zhang et al. (2023) [34]	Deep CNN; features of the time and frequency domain	Softmax function	99.1	Creating high-level and low-level features; the capability of decision-making for eight classes	The need for a high volume of data; high dimension of the extracted features; relatively high computational complexity; dependence on the length of the window in the non-stationary signal
The proposed method	Feature extraction using the	Feature selection using the	98.28	Investigation of five classes; investigation of non-stationary signals and the problem of	Inappropriate output in cases where the signal is affected

features of the time, frequency, and fractal domains	fusion method; classification based on the fusion among the decision-making trees		uncertainty; acceptable accuracy of classification; low sensitivity to noise	with too noises and/or when there are artifacts in the recorder. There is no functional mechanism for when the signal and classification are lost.

This is achieved by training and testing data through the data splitting procedure, the K-fold validation method, and using a classic and efficient model in the learning process. The classification accuracy in this study was 98.28%. The diagnosis system in this study is inspired by soft computing algorithms and serves as a tool to identify the presence of abnormalities in ECG signals and heartbeat signals in the dataset of samples.

The proposed method uses manual feature extraction and appropriate model adjustment, which presents some challenges. Using other feature extraction methods, such as nonlinear features based on efficient descriptors of the ECG signal, and combining manual and automated features will likely enhance the diagnosis accuracy. Therefore, it is recommended to extract features based on various methods to obtain more optimal features. The integration of features increases the likelihood of choosing the best feature and enhances the rate of diagnosing abnormalities through analyzing ECG signals.

In this study, the classes were classified using a classic learning algorithm. However, it is suggested to enhance the function of the classifier. There are various classifiers used to distinguish output labels, but clustering would be more efficient if it can produce low errors and classify new data based on the correct separation. Furthermore, deep learning methods could be useful in these settings.

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