Cardiacnet: Cardiac Arrhythmia Detection and Classification Using Unsupervised Learning Based Optimal Feature Selection with Custom CNN Model

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The irregularity in the heartbeats caused cardiac arrhythmia, which resulted in serious health problems. This cardiac arrhythmia is monitored by electrocardiogram (ECG) signals. As a result, an accurate and timely analysis of ECG data can prevent serious health problems. However, the conventional manual prediction systems and artificial intelligence (AI) methods failed to detect cardiac arrhythmia because they failed to extract the deep salient features from the ECG dataset. So, this research work implements a model named CardiacNet, which is used to identify and classify cardiac arrhythmias from an MIT-BIH-based dataset. Initially, the pre-processing operation is performed to remove the non-linearities from the dataset. Then, unsupervised machine learning algorithm-based principal component analysis (UML-PCA) is used to extract the features of the pre-processed dataset. Further, the optimal feature selection operation is carried out using improved Harris Hawk's optimization (IHHO), which is a naturally inspired model. Moreover, a customized convolutional neural network (CCNN) model performs the classification of various cardiac arrhythmia diseases using IHHO features. The simulation results show that the proposed CardiacNet resulted in an accuracy of 97.57%, sensitivity of 98.29%, specificity of 97.97%, F-measure of 97.40%, precision of 98.66%, Matthew's correlation coefficient (MCC) of 98.17%, dice of 98.96%, and Jaccard of 97.12%. The performance comparisons show that the proposed CardiacNet resulted in improved metrics over all existing methods.

Povzetek: Razvit je sistem CardiacNet za učenje brez nadzora za optimalno izbiro lastnosti s prilagojenim CNN modelom za natančno zaznavanje in klasifikacijo srčnih aritmij iz podatkov EKG.

1 Introduction

Abnormal heart rhythm is known as cardiac arrhythmia. According to the World Health Organization, cardiovascular diseases claim over 17 million lives each year [1]. About 31% of all fatalities may be attributed to this. The American Heart Association reports that heart disease is responsible for one in every three fatalities in the United States. Every year, cardiovascular disease kills more individuals than all forms of cancer and chronic lower respiratory disorders combined [2]. The 2022 research indicated that 2–4% of people in North America and European nations were living with AF. In adults, a heart rate of more than 100 beats per minute is considered tachycardia, whereas a heart rate of fewer than 60 beats per minute is considered bradycardia (less than 60 beats per minute). When the heart begins to contract before it should, this is called a premature contraction. An erratic heartbeat is also known as fluttering or fibrillation. Cardiac arrhythmias are classified not just by the patient's heart rate but also by several other factors. In addition to being utilized as a diagnostic criterion [3], the location of the irregular heart rate may also be used to classify the condition. In most cases, problems with the atrioventricular node are the root cause of arrhythmias in the heart's atrium. The atrioventricular node is situated in the heart, halfway between the two upper chambers (the atria) and the two lower chambers (the ventricles) [4]. During cardiac contraction, blood is pushed from the atria to the ventricles. Some examples of atrial arrhythmias include atrial fibrillation (AF), atrial flutter, atrial tachycardia, premature atrial contractions, and sinus bradycardia. The AF and atrial flutter are types of arrhythmias that, if left untreated, may be life-threatening. AF is a cardiac rhythm disorder characterized by abnormally fast and disorganized atrial contractions and electrical impulses that originate from places other than the sino-atrial node [5].

This causes an atrial rhythm that is fast and irregular. As a result of the atria's wall fibrillation, the heart is unable to pump blood properly to the ventricles. AF may lead to several potentially deadly consequences, including stroke and heart failure. AF has been connected to a wide variety of medical conditions, including hypertension, an overactive thyroid, coronary heart disease, and rheumatic heart disease. Atrial flutter, like AF [6], may have serious consequences. Atrial flutter is characterized by the fast and regular movement of cardiac electrical impulses throughout the atria, in contrast to the disorganized passage of electrical impulses seen in AF. Premature heartbeats, or ventricular arrhythmias, may originate from an ectopic ventricular focus. Ventricular fibrillation, ventricular tachycardia, and premature ventricular contractions are all examples of ventricular arrhythmias. It's important to note that certain forms of arrhythmia cause no obvious symptoms and don't put the patient's life at risk [7]. However, there are forms of arrhythmia that show no symptoms but may lead to serious complications, including a clot, a stroke, heart failure, or even sudden cardiac death. Arrhythmia is a disorder that may arise when the heart's electrical impulses, which serve to coordinate beats, are not functioning properly [8]. The initial stages in making a diagnosis of this illness are to interpret the ECG and confirm that the ECG shows no symptoms of cardiac arrhythmia [9]. To alter and analyze cardiac arrhythmia ECG data, methods including feature extraction, engineering, pattern analysis, and deep learning are utilized, which increases the diagnostic precision and comprehension of arrhythmia situations. Through a variety of techniques, such as visual inspection, automated pattern recognition, and deep learning, arrhythmia diseases may be identified using amplitude changes in ECG readings, increasing the accuracy and efficiency of identifying cardiac abnormalities. Using ECG data from the MIT-BIH database and another database, several researchers were able to successfully categorize all four types of arrhythmias. The classification of cardiac arrhythmias has received a lot of attention, with ECG data serving as the gold standard [10]. Myocardial infarction is one of the most prevalent and dangerous forms of cardiac arrhythmia documented so far. When the regular beat of the heart is disturbed, a diagnosis of cardiac arrhythmia is made. However, the heart itself is the site of the abnormalities that give rise to this illness. Heart abnormalities lead to abnormal activation, depolarization, and repolarization. The ECG will show a shift in waveform reflective of these alterations. The waveform of an ECG will change depending on the kind of cardiac arrhythmia that is being suspected. So, the conventional AI [11], machine learning [12], and deep learning [13] methods failed to result in better sub-class classification. So, the novel contributions of this work are illustrated as follows:

- Implementation of CardiacNet for classification of Sinus Bradycardia, Right Bundle Branch Block, Old Anterior Myocardial Infarction, Ischemic Changes, Coronary Artery Diseases, and the Normal Heart from the MIT-BIH dataset
- Adoption of both feature extraction and optimal feature selection methods such as UML-PCA and IHHO is necessary for the effective analysis of ECG data.
- The development of a CCNN model for multiple classification classes from IHHO features, which also performs the prediction of disease from test data, Improved Harris Hawk's Optimisation features are used by the CNN model for multiple-class arrhythmia grouping, which calls for the gathering of the data, feature extraction, model design, training, assessment, fine-tuning, installation, and analysis.

The rest of the paper is organized as follows: Section 2 contains the literature survey with existing drawbacks. Section 3 contains a detailed analysis of the proposed method with sub-block explanations. Section 4 contains the detailed simulation analysis. Section 5 contains the conclusion.

2 Literature survey

In [14], the authors implemented the T-wave integral and the total integral from a single cycle of normal and patient ECG data to detect and localize myocardial infarction (MI) in the left ventricle. Through identifying ischemia-related alterations and infarct patterns, the T-wave integral in electrocardiography aids in the assessment of repolarization anomalies in myocardial infarction patients. It aids in diagnosis and prognosis, assisting with therapy selection with objectivity. A whole ECG cycle was used to extract these features. The T-wave integral was used because of the significance of this property to the T-wave in the MI. T-wave integration in machine learning (ML) helps with biometric identity, research and development, ischemia risk assessment, ECG signal quality, therapeutic efficacy, and personalized medicine. The second part of this study considers the integral of a single ECG cycle [15]. This happens because the shape of the ECG signal is altered after an MI alters the total integral. By including additional variables in the classification process, this body of work may increase accuracy. It was shown that MIs may be identified with a high degree of accuracy using a simple technique based on the extraction of just two characteristics from a regular ECG. The diagnostic properties of multiscale wavelet energies and eigenvalues of multiscale covariance matrices were investigated by [16]. Classifiers can take many forms; the K-nearest neighbor technique, and support vector machines (SVM) with linear and RBF kernels [17], to name a few. The diagnostic ECG database provides the data utilized in these tests. There is a wide variety of situations included in the datasets, from healthy controls through anterior, lateral, and septal MI as well as inferior, lateral, and posterior-lateral MI. The findings validated the efficacy of the suggested method in identifying MI disorders.

The authors [18] presented a novel approach to the automated identification and localization of MI using cardiac electrical activity analysis. The 12-lead ECG data from 200 participants is segmented in this research; this contains 125,652 "normal" beats and 485,753 "indicative of myocardial infarction" beats. Initially, a signal was discretely wavelet transformed (DWT) [19] at depths of up to four using data collected from 12 cardiac electrodes. The DWT coefficients are then used to derive a set of twelve nonlinear characteristics. The collected data is then evaluated using a t-score. By using 47 characteristics extracted from lead 11, the suggested technique was able to obtain the greatest average accuracy (91.8%), sensitivity (91.4%), and specificity (91.27%) in identifying normal and MI ECG (two classes). Using an artificial neural network classifier [20], we were able to automatically categorize cardiac arrhythmias into one of five groups. An ANN classifier is trained using the linear and nonlinear parameters retrieved from a heart rate variability (HRV) signal. The suggested method was validated by testing it on the MIT-BIH arrhythmia database, where it achieved a success rate of 92.38 percent.

In [21], the authors proposed an automatic cardiac arrhythmia classification technique using probabilistic neural networks (PNN) trained on multi-channel ECG data. Using the results of this research, we were able to reliably categorize arrhythmias for use in diagnostic decision support systems. In [22], the authors conducted a study on the various approaches for evaluating the HRV signal retrieved from the ECG waveform. After the HRV signals have been described in terms of these characteristics, they are submitted to classifiers, which further classify them (for healthy persons and diseases like heart disease and diabetes) to aid in diagnosis.

To improve the efficiency and accuracy with which AF may be detected in displayed ECG traces, authors investigated and implemented a DL technique, including a recurrent neural network (RNN) and gated recurrent units (GRUs) [23]. This research made use of a public dataset from Physionet at MIT-BIH. As far as we are aware, this is the first time DL has been used to produce a real-time diagnosis of AF. This article presents experimental findings showing that RNN and GRU each attain an accuracy of 0.920 and 0.900, respectively. However, there is a need for further filtering, pre-processing, or de-noising when using this method. Through methods including missing data management, feature selection, and dimension reduction, preprocessing processes normalize dataset dimensions, improving data quality and making it more suitable for statistical analysis and machine learning. Data is normalized to a standard range, resulting in increased algorithm efficiency and assuring consistency and equivalence.

The DL Algorithm used a long short-term memory (LSTM) [24]-RNN to determine the presence and severity of cardiac diseases using ECG data. The model's excellent accuracy was validated using many different cardiac disease datasets. We tested the model on an arrhythmia dataset to see how well it could distinguish between cardiac diseases and arrhythmia (which has a high likelihood of mimicking the associated heart rate variability).

Further, the PhysioBank's [25] goal is to provide researchers with easy access to high-quality digital recordings of physiological signals and accompanying data. So far, it has accumulated databases of multiparameter cardiopulmonary, brain, and other biological signals from both healthy individuals and patients suffering from a broad variety of diseases with serious implications for public health. Some examples of these conditions are life-threatening arrhythmias, congestive heart failure, cardiac diseases, neurological disorders, and old age. The PhysioToolkit is a free and open-source software library for a wide variety of physiological signal processing and analysis tasks, including but not limited to displaying and characterising signals interactively [26]; creating new databases; simulating physiological and other signals; quantitatively comparing analysis methods; and detecting physiologically significant events using both conventional and novel methods based on statistical physics and nonlinear dynamics. PhysioToolkit was developed by the UCSF Physiological Signal Processing and Analysis Group. When it comes to sharing and analyzing recorded biological signals, PhysioNet is the community-driven infrastructure you need. This data bank is available via the World Wide Web. It included functions that encouraged collaborative data analysis and algorithmic improvement by teams.

3 Proposed system

Cardiac arrhythmia is the medical term for an irregular heartbeat. Therefore, preventing significant health issues through an accurate and automated examination of ECG data is essential. However, traditional manual prediction systems and conventional AI, ML, and DL approaches were unable to identify cardiac arrhythmias because they were unable to extract characteristics from ECG datasets. By learning hierarchical features from ECG datasets, deep learning algorithms might enhance the identification process while overcoming obstacles such as signal complexity, noise, and model complexity. This can increase the accuracy of recognizing cardiac arrhythmia situations. This is the reason they were unable to detect cardiac arrhythmia. This research aims to apply optimal feature selection, UML, and DL techniques to the problem of identifying heart arrhythmias from raw ECG data. Figure 1 shows the block diagram of the proposed CardiacNet. Here, the MIT-BIH dataset is considered for evaluating the performance of the overall system. Initially, the dataset is split into 80% for training and 20% for testing. Then, the entire operation is going to be performed on both training and testing datasets. To ensure consistent dimensions, maintain data integrity, and facilitate correct analysis, normalization entails activities including preprocessing, managing missing data, encoding, scaling, dimension reduction, feature selection, and outlier treatment. Further, pre-processing operations are carried out to remove the missing symbols and unknown characters, including special characters. To ensure transparency and repeatable findings, text analysis pre-processing comprises managing missing symbols, unknown characters, and special characters using methods including replacement, normalization, regular expressions, spell checking, human inspection, and domain-specific handling. The pre-processing operation also normalizes the number of rows and columns present in the dataset. After that, UML-PCA is applied to the preprocessed dataset to extract its features. By concentrating on critical data patterns, Principal Component Analysis (PCA), a vital data analysis approach, decreases dimensionality, extracts key features, improves model performance, and increases efficiency. In addition, the IHHO model, which is inspired by nature, is used in the process of carrying out the optimum feature selection operation. By imitating the cooperative hunting techniques of Harris's hawks, employing adaptive strategies, reproduction, mutation, and learning to efficiently explore feature space, the Improved Harris Hawk's Optimisation model enhances feature selection. In addition, the CCNN model can categorize the many different cardiac arrhythmia illnesses by using IHHO properties. The Better A more sophisticated version of the Harris Hawk's Optimisation method, the Harris Hawk's Optimisation (IHHO) model was created for the best feature selection in data analysis and machine learning. Iteratively refines feature subsets for better performance, using inspiration from cooperative hawk hunting. Based on ECG signals, CNN models may categorize cardiac arrhythmias, with accuracy varied depending on system design, database effectiveness, and medical knowledge. Finally, CardiacNet classifies sinus bradycardia, right bundle branch block, old anterior myocardial infarction, ischemic changes, coronary artery diseases, and the normal heart. Finally, CardiacNet classifies sinus bradycardia, right bundle branch block, old anterior myocardial infarction, ischemic changes, coronary artery diseases, and the normal heart.

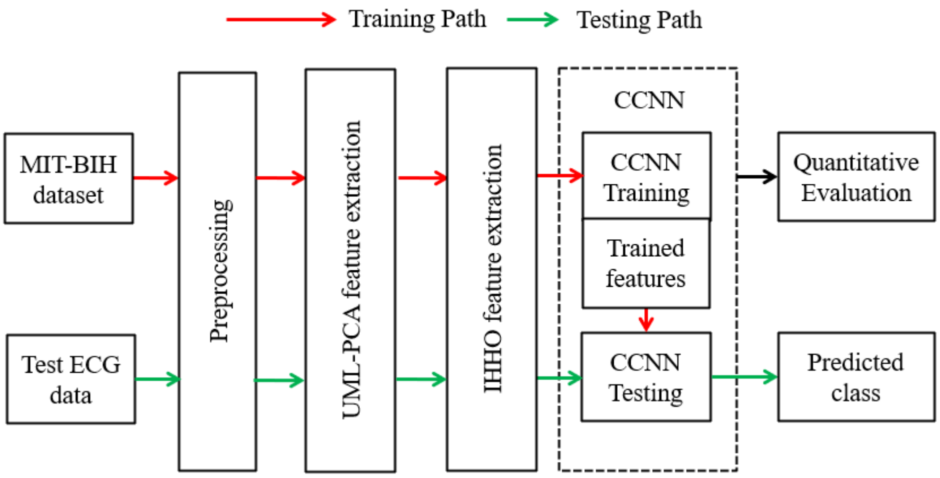
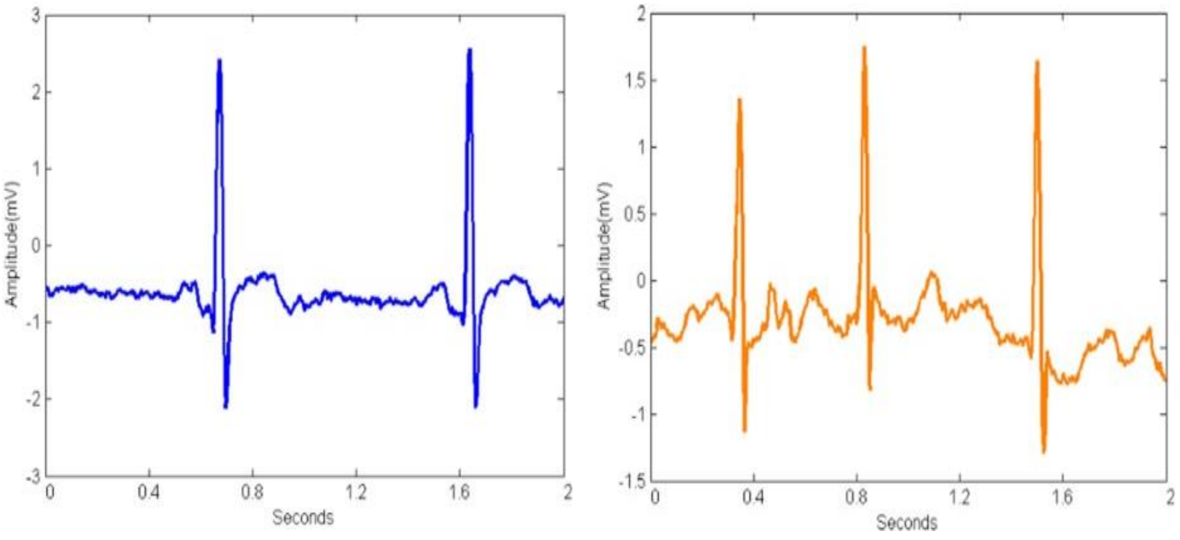


Figure 1: Proposed CardiacNet block diagram.

3.1 MIT-BIH dataset

All the MIT-BIH Arrhythmia Database includes 48 unique 30-minute recordings of two-channel ambulatory ECGs. Between 1975 and 1979, 47 subjects were studied with the use of these recordings by the BIH Arrhythmia Laboratory. Key components such as the dataset, feature extraction, pre-processing, machine learning algorithm, findings, discussion, performance assessment, and conclusion are used to evaluate the efficiency of the MIT-BIH Arrhythmia Database system and make recommendations for further research. Twenty-three recordings were randomly selected from four thousand 24-hour ambulatory ECG recordings taken from inpatients (roughly 60%) and outpatients (roughly 40%) at Boston's Beth Israel Hospital; the remaining 25 recordings were selected from the same set to include less common but clinically significant arrhythmias. Figure 2 shows the sample ECG signals from the MIT-BIG dataset; those are normal ECG signals and cardiac arrhythmia ECG signals. The cardiac arrhythmia ECG signal contains high amplitude fluctuations that can aid in the diagnosis of arrhythmia diseases. High amplitude cardiac arrhythmia fluctuations ECG signals help with illness diagnosis, aberrant rhythm detection, pattern creation, visual identification, clinical decision-support, advancement tracking, and research comprehension.



(a) (b)

Figure 2: Sample signals from MIT-BIH dataset [1]. (a) normal ECG signal, (b) cardiac arrhythmia ECG signal.

3.2 UML-PCA feature extraction

Potential applications of UML-PCA span numerous disciplines, from population genetics to studies of the microbiome to studies of the atmosphere and beyond. A technique called UMAP-PCA reduces dataset dimensions by combining UMAP and PCA, combining global and local structures, and offering a useful lower-dimensional approximation for dealing with complicated high-dimensional data. In a real coordinate system, a collection of points is represented by a list of unit vectors. Each of these scalars represents an orthogonal line segment that best matches the data. For this definition, the best-fitting line is the line with the smallest mean perpendicular distance between the data points and the line. In linear regression, the "best-fitting line" is found by minimizing the sum of squared residuals between the data points and the line, attempting to reduce standard deviation and offer the most accurate approximation. These directions make up an orthonormal basis that ensures the different data dimensions are not linearly connected. UML-PCA is used to execute a change of basis on data by identifying the principal components and then acting on that insight. While using UML-PCA to reduce the number of dimensions might increase efficiency, make interpretation easier, and improve model performance, it also comes with hazards including information loss and incorrect interpretation. Even if it doesn't always happen, UML-PCA usually ignores everything except the most important factors. So, it is often used for assessing massive datasets with several variables or dimensions for each observation. This technology allows for the visualization of data in several dimensions and improves data interpretability without losing any relevant details. To reduce the number of dimensions in a dataset, statisticians might use UML-PCA. Utilizing a transformation matrix, linear transformations change the original coordinate system while preserving data linkages. They are essential in mathematics for data interpretation and analysis and are employed in domains including graphics, image processing, and physics. To achieve this goal, a linear transformation is applied to the data to relocate it to a new coordinate system where the data's variance may be explained using fewer variables. Because of this, we may now further simplify matters. To make it simpler to identify clusters of numbers, many studies simply display the data in two dimensions, depending on the first two primary components. The first two components are critical for doing this and identifying the disease-specific features.

3.3 IHHO algorithm

In recent years, there has been a surge in interest and understanding of how to implement evolutionary algorithms and swarm intelligence algorithms effectively, cheaply, and efficiently. The No Free Lunch (NFL) theorem states that no algorithm is a universally optimal optimizer for any issue. According to the NFL theorem, no one optimization method can be the best in all application domains. To overcome these constraints, new optimizers that employ population-based strategies, hybrid methods, adaptive techniques, parallel computing, and transfer learning are being developed. The NFL theorem has led to new optimizers with specific local and global searching strategies. Strategies for local and global searches are essential for fine-tuning a new optimizer and boosting productivity and effectiveness. Efficiency is improved by combining both approaches in a new optimizer, encouraging speedier convergence and robust exploring. Figure 3 shows the flowchart of the IHHO algorithm for optimal feature selection. The unique nature-inspired optimization approach was inspired by Harris' Hawks, one of the world's most intelligent birds. Because of their outstanding team-chasing skills, flexibility, energy efficiency, and social cohesiveness, Harris's hawks excel at cooperative hunting. Their communal feeding and specialized tasks increase their success on the hunt. Unlike other raptors, the Harris's hawk forages cooperatively with other members of its stable group, whereas other raptors are more likely to attack and take prey alone. Due to its highly evolved inventive team-chasing abilities, this desert predator can hunt down potential prey, encircle them, flush them out, and then attack them. Predators in the desert use complex team-chasing tactics to identify and catch prey. These tactics include coordinated attempts, disorientation, stress, herding behavior, strategic placement, and group learning. The following steps show the optimal feature selection process.

Step 1: Set T, and N as the HHO parameters, which hold the properties of IHHO.

Step 2: Initialize the location of the population of Harris Hawks X of N random particles with n, t dimensions.

Step 3: The objective function for each element of X is evaluated. The average location of hawks

$$X_m(t) = \frac{1}{N}\sum_{i=1}^{N} X_i(t) \tag{1}$$

where $X_i(t)$ signifies each hawk position in iteration t, where N is the total number of hawks in the iteration.

Step 4: Set the location of the rabbit (best location) as Xrabbit.

Step 5: For each hawk Xi calculate E. The prey's energy is represented as:

$$E = 2E_0\left(1 - \frac{t}{T}\right) \tag{2}$$

Here T signifies the maximum number of repeats and E_0 is energy at its starting point.

Step 6: Depending on the energy value of his prey update the location of Harris Hawks X.

$$X(t+1) = \begin{cases} X_{rand}(t) - r_1|X_{rand}(t) - 2r_2X(t)| & q \geq 0.5 \\ (X_{rabbit}(t) - X_m(t)) - r_3(LB + r_4(UB - LB)) & q < 0.5 \end{cases} \tag{3}$$

Here, $X(t + 1)$ denotes the position vector of hawks in the next iteration, $X_{rabbit}(t)$ denotes the rabbit position, $X(t)$ denotes the hawks' current position vector, $X_{rabbit}(t)$ denotes random numbers between (0,1) that update in each iteration, and the number of iterations is R. The variables' upper and lower limits are represented by the letters LB and UB, $X_{rand}(t)$ represents any randomly picked hawk in the current members population, and X_m represents the current population hawks' average location.

Step 7: The t index is increased in 1, if the stop criteria (t ≥ T) are not satisfied jump to step 5. Finally, the optimal features are selected from the available data.

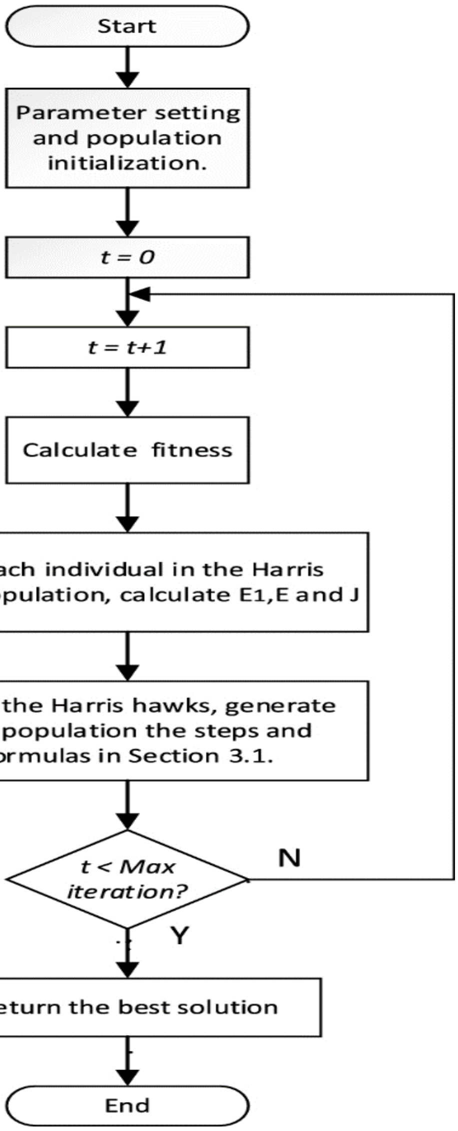


Figure 3: Flowchart of IHHO.

3.4 Proposed CCNN

The ECG data was categorized according to cardiac arrhythmia via the development of a multi-layer deep convolutional network. Figure 4 shows the proposed CCNN model enables automatic input ECG classification without requiring any manual feature extraction or selection. The suggested CNN model for classifying cardiac arrhythmias makes use of a specialized architecture, ECG signal processing, convolutional layers, pooling, non-linearity, regularisation, optimization, tuning hyperparameters, early stopping validation, Class Activation Mapping, and interpretability metrics. This is feasible because of the holistic design. The CCNN structure is at the heart of the deep network model, which is built on the layers of a CCNN. Input, convolutional, and activation functions are used in the construction of CCNN layers, which are impacted by the properties of the input data, the needs of the issue, and the selection of the hyperparameters. Feature maps, which are representations of ECG segments, are concatenated using weights of varying sizes in multi-dimensional convolution layers. A convolution with 128 weight vectors is used on the ECG data in the first layer of the model. To avoid gradient problems, assist with uniform weight initialization, promote faster convergence, and improve generalization, normalizing activation outputs is an essential preprocessing step in deep learning. Before processing each batch, the activation outputs of this layer are normalized by the batch normalization layer. By preventing division by zero, batch normalization improves training, regularisation, and neural network efficiency by ensuring uniform allocation of activating responses within every batch. The max pooling layer takes the maximum value from each region specified on the feature maps gathered in the layers below it to generate new feature maps. To make better use of the available feature space, the feature maps from the previous layer have been reduced in size in this one. Reducing the size of feature maps is a crucial step in making DL systems faster and more resource-friendly. Decreased feature map size in deep learning methods increases computational speed, resilience, and efficiency, making models more scalable, deployable, and quick on devices with limited resources. To achieve this, we use methods like averaging the max pooling layer's maximum values. In the fourth layer, the convolution technique is repeated many times on the input feature maps using weights that are 32 by 7. With the pooling approach applied to the layer, the feature maps with a region width of two are decreased by a factor of half. This is done by completing yet another round of batch normalization. The next layer is a convolution, and the layer after that is a max pooling, both of which are repeats of the prior layers' algorithms. The feature maps collected at the previous layer will be downscaled in this step so that they may be used as input at higher network levels. When dealing with multidimensional feature vectors, we "flatten" them into a single dimension. Following their transit through the flattened layer, the features are sent onto a 512-unit, strongly linked neural network layer. A SoftMax layer serves as the network's last layer. This layer determines the total number of output classes. For multi-class classification problems, the Softmax layer is an essential last layer in neural networks. It generates normalized probability distributions, facilitates training, stable optimization, and understanding, handles one-hot encoded labels, and supports model assessment and inference. To forecast what category, the input data belongs to, the SoftMax layer is used. To prevent the network from becoming too specialized as it learns, several layers have a dropout parameter. Because of this, the layer's precision is limited to prevent problems. By periodically deactivating neurons during training, increasing resilience, and limiting co-adaptation, the dropout parameter is a regularisation strategy for neural networks that reduces overfitting and improves generalization.

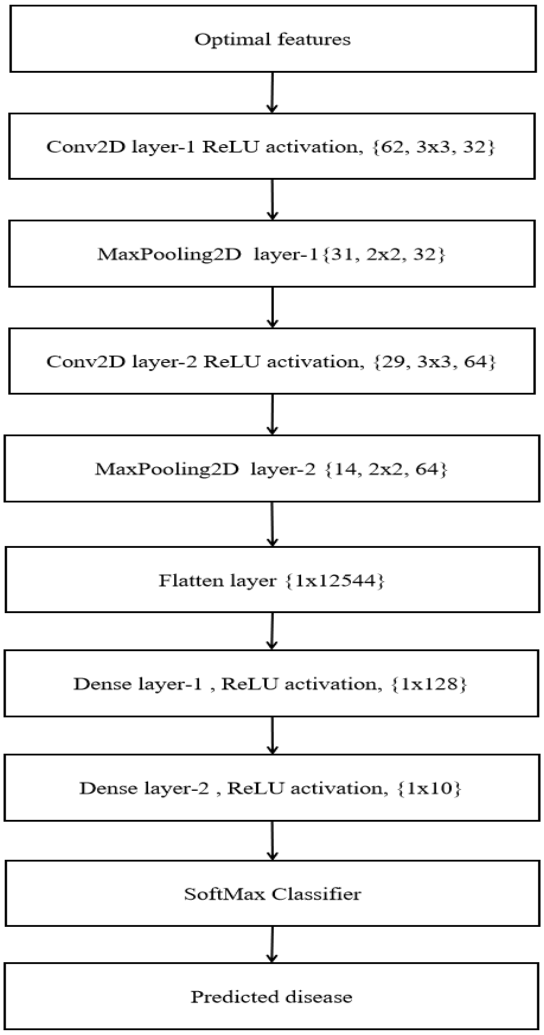


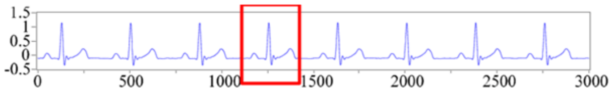
Figure 4: Block diagram of the proposed CCNN model.

4 Results and discussion

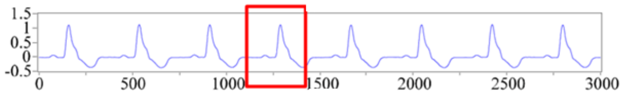
This section gives a detailed performance analysis of the proposed CardiacNet. The performance of the proposed method is measured using several performance metrics, such as accuracy, sensitivity, specificity, F-measure, precision, MCC, dice, and Jaccard. All these metrics are measured for proposed methods as well as existing methods. Then, all the methods use the same MIT-BIH dataset for performance estimations.

4.1 Subjective analysis

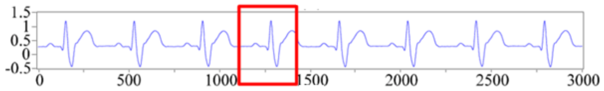
Figure 5 shows the classified outcomes using CardiacNet. The test input is considered several ECG signals, and its data is converted into a binary domain. Now, the CardiacNet analyses these binary signals, yielding a classification result. Here, the red-colored box shows the optimal feature zone. Figure 5(a) shows the classified outcome as sinus bradycardia; Figure 5(b) shows the classified outcome as right bundle branch block; Figure 5(c) shows the classified outcome as anterior myocardial infarction; Figure 5(d) shows the classified outcome as ischemic changes; Figure 5(e) shows the classified outcome as coronary artery diseases; and Figure 5(f) shows the classified outcome as a normal heart.



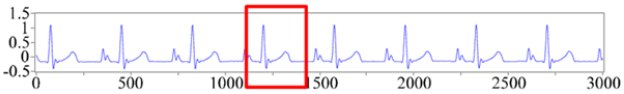
(a) sinus bradycardy



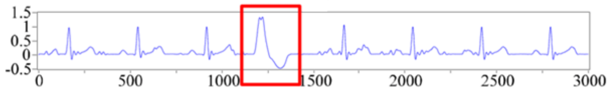
(b) Right bundle branch block



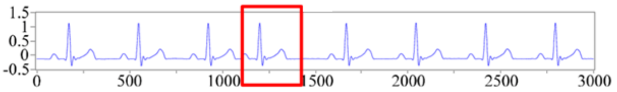
(c) Old Anterior Myocardial Infarction



(d) Ischemic changes



(e) Coronary artery diseases



(f) normal heart

Figure 5: Classification results from CardiacNet

4.2 Performance comparison

Table 1 compares the classification performance of various approaches to the proposed CardiacNet. The first column contains performance metrics. The second column contains the performance estimation during the SVM [17] method. The third column contains the estimated performance of the PNN [20] method. For assessing the generalization, model selection, hyperparameter tweaking, overfitting identification, prediction confidence, task applicability, and iterative improvements of the PNN approach, performance is essential. In the fourth column, the performance estimation during GRU [23] is presented. Here, the proposed CardiacNet resulted in improved classification performance as compared to SVM [17], PNN [20], and GRU [23].

Table 2 presents the percentage of improvements over Table 1. Here, the CardiacNet has increased accuracy by 4.21%, sensitivity by 6.38%, specificity by 2.24%, F-measure by 4.88%, precision by 6.08%, MCC by 2.37%, dice by 3.79%, and Jaccard by 3.77% as compared to the SVM [17]. In the third column, CardiacNet increased accuracy by 4.21%, sensitivity by 6.38%, specificity by 2.24%, F-measure by 4.88%, precision by 6.08%, MCC by 4.52%, dice by 3.79%, and Jaccard by 3.77% as compared to PNN [20]. In the last column, CardiacNet increased accuracy by 3.66%, sensitivity by 6.20%, specificity by 3.70%, F-measure by 5.45%, precision by 7.82%, MCC by 7.59%, dice by 4.48%, Jaccard by 1.55% as compared to GRU [23].

Table 1: Performance comparison of various methods.

Metric	**SVM [17]**	**PNN [20]**	**GRU [23]**	**Proposed CardiacNet**
Accuracy (%)	93.62	93.62	94.12	97.57
Sensitivity (%)	92.39	92.39	92.55	98.29
Specificity (%)	95.82	95.82	94.47	97.97
F-measure (%)	92.86	92.86	92.36	97.40
Precision (%)	93.00	93.00	91.50	98.66
MCC (%)	95.89	93.92	91.24	98.17
Dice (%)	95.34	95.34	94.71	98.96
Jaccard (%)	93.59	93.59	95.63	97.12

Table 3 presents the ablation study for the proposed CardiacNet. Here, the first column contains the different performance metrics. The second column contains the performance estimation using only CCNN, where UML-PCA and IHHO are absent. Then, the third column contains the performance estimation during UML-PCA with the CCNN method, where IHHO feature selection is absent. Finally, the last column contains the performance of CardiacNet with all modules presented. Here, the performance of the proposed method is improved when all modules are present in comparison to the absence of any individual module. So, this ablation study shows the significance of UML-PCA feature extraction and IHHO feature selection.

Table 2: Percentage of improvement in proposed CadiacNet model as compared to state-of-the-art methods.

Metric	**SVM [17]**	**PNN [20]**	**GRU [23]**
Accuracy (%)	4.219184	4.219184	3.665533
Sensitivity (%)	6.385973	6.385973	6.202053
Specificity (%)	2.24379	2.24379	3.70488
F-measure (%)	4.88908	4.88908	5.456908
Precision (%)	6.086022	6.086022	7.825137
MCC (%)	2.377724	4.525128	7.595353
Dice (%)	3.796937	3.796937	4.487383
Jaccard (%)	3.77177	3.77177	1.558088

Table 4 presents the percentage of improvements over Table 3. Here, the CardiacNet has increased accuracy by 5.34%, sensitivity by 6.32%, specificity by 4.60%, F-measure by 2.18%, precision by 5.76%, MCC by 1.76%, dice by 1.39%, and Jaccard by 4.25% as compared to the only CCNN case. Performance measures such as accuracy of 5.04%, sensitivity of 3.46%, specificity of 1.70%, F-measure of 4.78%, precision of 4.68%, MCC of 2.23%, dice of 5.23%, and Jaccard of 5.53% are compared to the UML-PCA+ CCNN presented case in the third column. In the final column, accuracy by 6.50%, sensitivity by 2.79%, specificity by 6.33%, F-measure by 4.69%, precision by 6.82%, MCC by 5.14%, dice by 5.99%, and Jaccard by 2.81% are compared to the IHHO+ CCNN presented case.

Table 3: Ablation study of the proposed method.

Metric	**CCNN**	**UML-PCA+ CCNN**	**IHHO + CCNN**	**Proposed CardiacNet**
Accuracy (%)	92.65	92.91	91.64	97.57
Sensitivity (%)	91.54	94.07	94.68	98.29
Specificity (%)	93.97	96.65	92.44	97.97
F-measure (%)	96.43	94.04	94.12	97.40
Precision	92.90	93.86	91.98	98.66

(%)				
MCC (%)	96.40	95.96	93.30	98.17
Dice (%)	96.01	92.51	91.84	98.96
Jaccard (%)	94.89	93.74	96.22	97.12

Table 4: Percentage of improvements in ablation study as compared to state-of-the-art methods.

Metric	CCNN	UML-PCA+ CCNN	IHHO+ CCNN
Accuracy (%)	5.342688	5.047896	6.50371
Sensitivity (%)	6.325104	3.465504	2.798902
Specificity (%)	4.607854	1.707191	6.339247
F-measure (%)	2.188116	4.785198	4.696133
Precision (%)	5.769645	4.687833	6.827571
MCC (%)	1.763485	2.230096	5.144695
Dice (%)	1.395688	5.231867	5.999564
Jaccard (%)	4.257561	5.536591	2.816462

5 Conclusion

This work effort developed CardiacNet, which is an AI tool for identifying cardiac arrhythmias using a dataset based on MIT and BIH. To begin, a pre-processing procedure is carried out on the dataset to eliminate any non-linearities that it may include. After that, UML-PCA is applied to the pre-processed dataset to extract its features. In addition, the IHHO model, which is inspired by nature, is used in the process of carrying out the optimum feature selection operation. In addition, the CCNN model can categorize the many different cardiac arrhythmia illnesses by using IHHO properties. Finally, CardiacNet classifies sinus bradycardia, right bundle branch block, old anterior myocardial infarction, ischemic changes, coronary artery diseases, and the normal heart. Here, the CardiacNet has increased accuracy by 4.21%, sensitivity by 6.38%, specificity by 2.24%, F-measure by 4.88%, precision by 6.08%, MCC by 2.37%, dice by 3.79%, and Jaccard by 3.77% as compared to existing methods. Further, this work can be extended with improved transfer learning methods and class-specific performance estimation.

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