International Journal of Engineering Trends and Technology
ISSN: 2231 – 5381 / https://doi.org/10.14445/22315381/IJETT-V70I11P238

Volume 70 Issue 11, 364-377, November 2022

Original Article

Prediction of Cardiac Disease using Kernel Extreme Learning Machine Model

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Received: 08 August 2022 Revised: 02 November 2022 Accepted: 16 November 2022 Published: 26 November 2022

Abstract - *Cardiac disease is now a major cause of death for people affected by COVID-19. For the past five years, the death rate of people affected by the cardiac disease has increased a lot. In recent years, many deep learning models have provided prominent results for predicting it from different UCI heart disease data and other ECG data. Cardiac disease can be predicted from medical diagnosis and electrocardiogram data. Even though many types of detection for cardiac disease are available, ECG plays a major role in identifying it accurately. However, still, there is some gap in identifying the correct data, cleaning the unwanted features with popular methods, and optimizing it for better accuracy. In this paper, we propose a deep learning model, such as an Extreme Learning Machine (ELM), for predicting cardiac disease from the benchmark dataset, such as the MIT-BIH Arrhythmia dataset available in the PhysioNet database. The Principal Component Analysis is used to extract and identify the best features. Transfer learning is additionally used with kernel ELM for the improvement of the classification performance of ELM. Finally, the proposed Extreme Learning Machine model classifies cardiac disease with a promising result of 98.50% accuracy. In future research, it can be predicted in various datasets for performance improvement by selecting all other ensemble models.*

Keywords - *Cardiac disease, Deep learning, Extreme Learning Machine, Principal Component Analysis, Prediction.*

1. Introduction

Cardiac disease (also known as cardiovascular disease) is a common disease that has caused a severe burden on human health for the past two decades. It leads to a major death rate worldwide. It has types of heart failure, heart attack, sudden cardiac death, and other problems linked with arrhythmia and hypertrophy cardiomyopathy. From the WHO [1] data, more than 17.9 million people died of cardiac disease in 2019, which will cause more in the upcoming years. Many people were affected by cardiac-related issues due to the COVID-19 lockdown [2]. It is analyzed that around 24 million people per year will die by 2030. The above statistics show that cardiac disease has become a significant problem for humans nowadays. So, it is necessary and necessary to identify it early and diagnose it as soon as predicted since many old and middle-aged people are still unaware of it. Even now, mid-age people are averagely affected by heart-related problems. The main reason for this kind of disease is the adoption of bad diets and lack of physical activities that lead to high blood pressure and high blood cholesterol levels, and some may be affected by their family history (gene). There are different methods used for the prediction or detection of cardiac disease. Many researchers found several models for predicting cardiac disease based on image and categorical data, but only a few have been done in ECG data.

The most widely used tool is the electrocardiogram [3], mainly used for clinical diagnosis in cardiac disease identification. With this ECG classification, the major problem that can be identified, such as heartbeat segmentation, cardiac arrhythmia, and heart rhythms, will be detected or predicted with the support of artificial intelligence, machine learning, and deep learning models. Cardiovascular diseases include hypertensive heart disease, rheumatic heart disease, valvular heart disease, cardiomyopathy, aortic aneurysms, heart arrhythmia, carditis, congenital, myocardial infarction, and heart failure. For patients with heart illnesses, an assortment of cardiovascular irregularities might happen, and these anomalies ordinarily lead to changes in ECG designs. Electrocardiography is the most well-known method for observing heart movement. The examination of ECG signal anomalies can distinguish different heart problems. The electrical sign created by the heart is distinguished by cathodes put on the body's outer layer. The ECG recorder looks at the changes in electrical exercises in the electrodes and makes a purported lead. Today a standard ECG comprises 12 leads, everyone not entirely set in stone by the arrangement and direction of the anodes on the body. This is fundamental because the heart is a 3-layered organ; accordingly, it should be seen from various points to reproduce the entire signal. The electrodes for a 12-lead ECG are spread as follows: 2 on the arms, 2 on the legs, and 6 on the chest, outlining the precordial leads. Essentially, using PC-based techniques for the programmed handling of ECG signs can help cardiologists in their conclusion.

Existing approaches for detecting heart disease in an ECG are based on morphological characteristics of a single or few QRS complexes or beats. Human cardiologists can still not keep up with the increasing demand for ECG data. As a result, processing ECG data automatically and accurately for predicting heart illness has become a prominent study area. Since many companies have developed technology based on ECG data. For example, Apple has launched a new watch that includes an ECG app that records a person's heartbeat and rhythm using the electrical heart sensor, and in Japan, over 63000 ECG data have been used to develop an AI tool for early diagnosis of heart disease. Some studies also demonstrate that ECG is essential in predicting short- and long-term [4] cardiac disease problems. It is crucial to recognize irregular cardiac rhythms in ECG readings. The manual inspection, which is difficult and time-consuming, is necessary to interpret the ECG recording. The ECG recording is stored in the form of categorical data as features which are then utilized in the final model for the prediction or classification based on feature extraction and feature selection. In the proposed work, we used feature extraction to get the right features for heart disease prediction.

Feature extraction changes and simplifies data, whereas feature selection minimises the dataset by deleting worthless features. PCA [5] has recently been employed as a feature extraction approach for categorization in health care in various research. By capturing a large variance, principal component analysis (PCA) develops new components with the most relevant information about the characteristics. Rajagopal et al. [6] used the neural network (PNN) classifier to compare an automated classification of cardiac arrhythmia using five different linear and non-linear unsupervised dimensional reduction strategies. Zhang et al. [7] used the AdaBoost algorithm based on PCA to detect breast cancer. Ivoline C et al. [8] used PCA with CNN-SVM classifier and predicted the prevalence of heart disease. Therefore, in this work, for accurate prediction and time consumption things different machine learning and deep learning models have been employed with PCA and compared with experimental results for the automatic identification of cardiac disease.

Machine learning is a subset of AI used to learn a task by some data. It has been used widely for the applications of several diseases' prediction, diagnosis, and detection. However, for large datasets, it is somehow slow in time or low in accuracy for the prediction. It has five important challenges: it does not have enough training data, resulting in poor quality data, irrelevant features, nonrepresentative training data, and finally, it has overfitting and underfitting problem. Overcoming these challenges, the subset models are approached. So, Deep learning (DL) models were invented by researchers to solve the above kind of issues. It has emerged mainly due to the increase in the computational power of GPUs. It has also been used in applying classification, segmentation, natural language processing, disease analysis, prediction, and diagnosis with promising results. Deep learning does not require any explicit feature extraction step using human experts since it can perform automatically. The performance of deep learning is more accurate than other traditional methods on many ECG analysis tasks, for example, in detecting various diseases such as heart, cancer, and acute kidney disorder. The deep learning method can be categorized into various subtypes based on the problem in training the method. The DL models have also been used or combined with other models as an ensemble method for better accuracy in an optimized way. Therefore, deep learning has become very popular in the last few years for classifying various healthcare applications such as cardiac arrhythmia, heartbeat segmentation, heart rhythms identification, cancer diagnosis, and brain tumor.

Many researchers have analyzed ECG to detect cardiac disease with single-lead or multi-lead signals. So, data variations may vary from person to person depending on their age, gender, and lifestyle. Data imbalance problems essentially occurred in the dataset for analyzing ECG data accurately using machine learning models. In addition, solving missing data problems and identifying heartbeats with different rhythms can also provide good results in classifying cardiac arrhythmia. This paper is intended to solve the above-said problems and can accurately predict cardiac disease by deep learning models such as extreme learning machines with an optimized result.

The main contributions of this work are as follows:

- Cardiac disease prediction is performed in this work with the new combination of methodologies.
- The principal component analysis is used for feature extraction from the benchmark dataset MIT-BIH Arrhythmia.
- Then, an Extreme learning machine with the kernel is used as a classification method for predicting cardiac disease.
- Transfer learning embed kernel extreme learning machine is utilized for the better optimal result in identifying cardiac disease.
- The results shown in work are better when compared with other state-of-the-art methods.

The balance concept of this paper is organized as follows. Section 2 explains the survey on deep learning and machine learning models in cardiac disease detection and prediction. The existing model details are discussed in section 3, and the proposed model with the databases used in work is introduced in sections 4 and 5 with deep learning theoretical background. The result and discussion of the proposed deep learning method with their performance are analyzed and presented in section 6. Finally, section 7 draws a brief conclusion with future opportunities for deep learning to embed bio-inspired algorithms in cardiac disease detection on various datasets.

2. Literature Survey

The following survey is based on the various machine learning, and deep learning models that the researchers used for the prediction of cardiac disease by analyzing heartbeat classification, data imbalance, and missing data problems with ECG data which come among the proposed topics analyzed with their dataset details as follows:

Table 1. Related survey on ECG data for the prediction and classification of cardiac disease

Reference	Author / year	Contribution	Techniques / Accuracy
[9]	V. Jahmunah et. al., 2021	They have proposed an AS based on the automated categorization of ECG signals into four different classifications.	CNN and unique GaborCNN models Accuracy: 98.5%
[10]	Ozal Yildirim et. al., 2020	They used a new public ECG dataset with more than 10,000 unique subject data with 12-lead inputs to detect different rhythm classes.	Deep Neural Network Accuracy: 92.24% and 96.13%
[11]	Mohammed Hammad et al., 2021	They have proposed a computer-aided arrhythmia classification (CAAC) system to detect shockable ECG rhythms.	CNN, CNN+RNN, CNN+LSTM: 87.95% without using PCA, and of the proposed method: 91.14%
[12]	Vajihe Mazaheri, and Hamed Khodadadi 2020	The ECG signal is used in this work with the CAD system and classified different cardiac arrhythmias with support from multiobjective optimization.	KNN, FF net, Fit net, RBFNN, and Pat net 98.75% from FF net (highest accuracy)
[13]	Tianyu Liu et. al., 2021	They presented a few-shot learning strategy based on meta-transfer to classify arrhythmia using ECG signals from wearable devices.	A meta-transfer-based few-shot learning method with CNN 2-way task (1 shot=93.3±0.3, 5 shot=96.3±0.8, 10 shot=97.0±0.4) 4-way task (1 shot=90.9±1.8, 5 shot 93.8±0.6, 10 shot 95.6±0.3)
[14]	Georgios Petmezas et. al., 2021	The authors used a unique hybrid neural model with a focal loss to deal with training data imbalance. In their result, a more accurate classification has been done for the four ECG rhythms.	Novel hybrid neural model, CNN, LSTM model. Sensitivity of 97.87%, and specificity of 99.29%
[15]	Adyasha Rath et. al., 2021	The ECG data of the participants were used as essential inputs to the HD detection algorithm in this study. It has been discovered that the detection accuracy of imbalanced HD data is poorer.	GAN model, and LSTM + GAN (ensemble model) MIT-BIH database: Acc - 99.2%, F1- score: 98.7%, and AUC: 98.4% PTB-ECG database: Acc - 99.4%, F1- score: 99.3%, and AUC: 99.5%
[16]	Edward B. Panganiban et. al., 2021	The authors used Convolutional Neural Network (CNN) with images based on spectrograms to develop a classification approach for ECG arrhythmia without performing an identification of R-peak or P-peak. The last layer of CNN was retrained for dataset recognition using Google's Inception V3 model.	Convolutional Neural Network (CNN) Average Accuracy: 98.73%, Specificity: 99.21%, Sensitivity: 96.83%, Positive Predictive value: 96.85%, and F1 score: 96.83%.

[17]	Dongdong Zhang et al., 2021	In this work, the authors proposed a deep neural network for automatically classifying cardiac arrhythmias from 12-lead ECG recordings. The deep model outperformed four machine learning approaches based on extracted expert characteristics.	Long short-term memory, Time-incremental CNN, an ensemble model InceptionTime (Inception) Average AUC and Accuracy: 95%, Average F1 score: 81.3%, Average precision: 82.1%, and Average recall: 81.2%
[18]	Junli Gao et. al., 2019	Due to the highly unbalanced nature of ECG beat data, LSTM and RNN with focal loss (FL) are developed in this work. The FL is utilized to fix the category imbalance by down-weighting easily recognizable standard ECG samples, while the LSTM network can detangle the temporal aspects in complex ECG data.	LSTM and RNN model with focal loss (FL) Accuracy: 99.26%, Recall: 99.26%, Precision: 99.30%, Specificity: 99.14%, and F1 score: 99.27%
[19]	Ehab Essa and Xianghua Xie 2021	The classification of electrocardiogram (ECG) data is proposed in this work using a deep learning-based multi-modal system. CNN-LSTM captures local features and temporal dynamics. The RRHOS-LSTM model combines higher-order statistics (HOS) with the LSTM model to effectively pinpoint aberrant heartbeat classes.	CNN-LSTM, RRHOS-LSTM Accuracy: 95.81%
[20]	Hao Dai et al., 2021	Using typical 12-lead ECG readings, the authors proposed a deep CNN to classify CVDs.	Deep convolutional neural network (CNN) ECG signals result in One-Second: Acc - 99.59%, Sen - 99.04%, and Spe - 99.87%. ECG signals result in Two-Seconds: Acc - 99.80%, Sen - 99.48%, and Spe - 99.93%. ECG signals result in Three-Seconds: Acc - 99.84%, Sen - 99.52%, and Spe - 99.95%.
[21]	Xin Zhang et al., 2020	They used a DL method to create a system that automatically recognises and classifies ECG data. An independent test data set of 18,018 ECG signals were used to validate the CNN classification.	Convolutional neural network (CNN) Accuracy: 95%
[22]	A Sheryl Oliver et al., 2021	The authors have proposed an RLNNC method that presents a fully automated technique for categorising HD.	Regressive Learning-Based Neural Network Classifier (RLNNC) Accuracy: 97.5%
[23]	Chaitra Sridhar et. al., 2021	ECGs from 200 people were studied in this study. The suggested technique comprises pre-processing signals, and then they utilized the Pan-Tompkins algorithm to detect R peaks. For separating normal from MI classes, the collected features were scored using the student's t-test and fed into KNN, SVM, PNN, and DT classifiers.	Pan-Tompkin's algorithm, KNN, SVM, PNN, and DT Accuracy: 97.96%
[24]	Saroj Kumar Pandey and Rekh Ram Janghel 2021	In this work, the authors have reduced the size of ECG signal segments by DCEF based on the non-linear compression composition technique. The B-LSTM network classifier receives these encoded features as input.	BLSTM network classifier, ULSTM network, GRU, and MLP. Accuracy: 99.52%

[25]	Jingshan Huang et. al., 2019	Using a 2D-DCNN, this research presents an ECG arrhythmia classification approach. The short-time Fourier transform was used to convert time-domain ECG signals into time-frequency spectrograms for five heartbeat types: NOR, LBB, RBB, PVC, and APC.	2D-CNN MIT-BIH arrhythmia database: Accuracy: 99%
[26]	Yinsheng Ji et. al., 2019	Using the Faster R-CNN technique, this study provides the ECG classification based on faster regions. The initial 1D ECG signals in this experiment include pre-processed patient ECG signals and some ECG recordings from the MIT-BIH database.	Faster R-CNN and compared with OVR SVM algorithm MIT-BIH database: Accuracy: 99.21%,
[27]	Ozal Yildirima et. al., 2018	This work aimed to propose a DL-based method for classifying cardiac arrhythmias efficiently and promptly. The work is based on 1000 ECG signal fragments from 45 people from the MIT - BIH Arrhythmia database for one lead. The design of a novel 1D-Convolutional Neural Network model is the key contribution (1D-CNN).	1D-Convolutional Neural Network model (1D-CNN) MIT-BIH Arrhythmia database: Accuracy: 91.33%

3. Existing Model

From the existing literature survey, much research has been done on the benchmark dataset MIT-BIH Arrhythmia with single lead or multiple leads for detecting cardiac disease or classifying arrhythmia. Most of the findings used CNN for feature extraction since the deep learning model can also be used as both an extractor and a classifier. To extract the right features for the analysis, the principal component analysis method is used to increase the accuracy of the final prediction. In previous research, many findings result in CNN, LSTM, and DNN for classifying cardiac disease using ECG data. The existing concept is enhanced by implementing an extreme learning machine to classify cardiac disease from the ECG data.

4. Proposed Model

The proposed method is exhibited on the well-known MIT-BIH arrhythmia database in this work. The proposed architecture is shown in Figure 1. ECG data is widely spread with imbalanced and missing data. Feature extraction is the most important process, so in the proposed work, principal component analysis is utilized to optimize the best features. So, in data pre-processing of ECG data, the principal component analysis method is utilized for handling the ECG data. The extracted features are passed to the training and testing set for classifying cardiac disease with the DL model, such as an extreme learning machine (ELM).

The following three subsections of the proposed model will explain the description of the dataset, followed by the pre-processing of data with feature extraction of ECG data for cardiac disease prediction. In comparison to other state-of-the-art methodologies, the newly proposed strategy gives significant accuracy increases with minimal expert input, as shown in section 6.

4.1. Dataset Description

In the experiments, the MIT-BIH Arrhythmia Dataset is used, which is the benchmark database for ECG data processing in the identification of Cardiac Disease. It comprises 48 two-lead recordings, each lasting around a half-hour and sampled at 360 Hz. It provides two pieces of independently confirmed information, such as beat class and time. The number of samples is large enough to train a deep learning method such as an extreme machine. This dataset was developed to study heartbeat classification using deep convolutional neural network architectures and to evaluate some transfer learning capabilities. The signals correlate to heartbeats' electrocardiogram (ECG) morphologies for normal cases and cases of different arrhythmias and hypertrophic cardiomyopathy. These signals are segmented and pre-processed, with each segment representing a heartbeat. MIT-BIH Arrhythmia Dataset consists of 109446 samples with 188 attributes. It has a sampling frequency starting from 125Hz to 360Hz. It has 5 different classes: {N - 0, S - 1, V - 2, F - 3, Q – 4}. A series of CSV files constitute the above dataset. Each CSV file includes a matrix, with each row representing one of the dataset's instances. Each row's last element identifies the class to which that instance belongs. The data pre-processing task is explained in the following section.

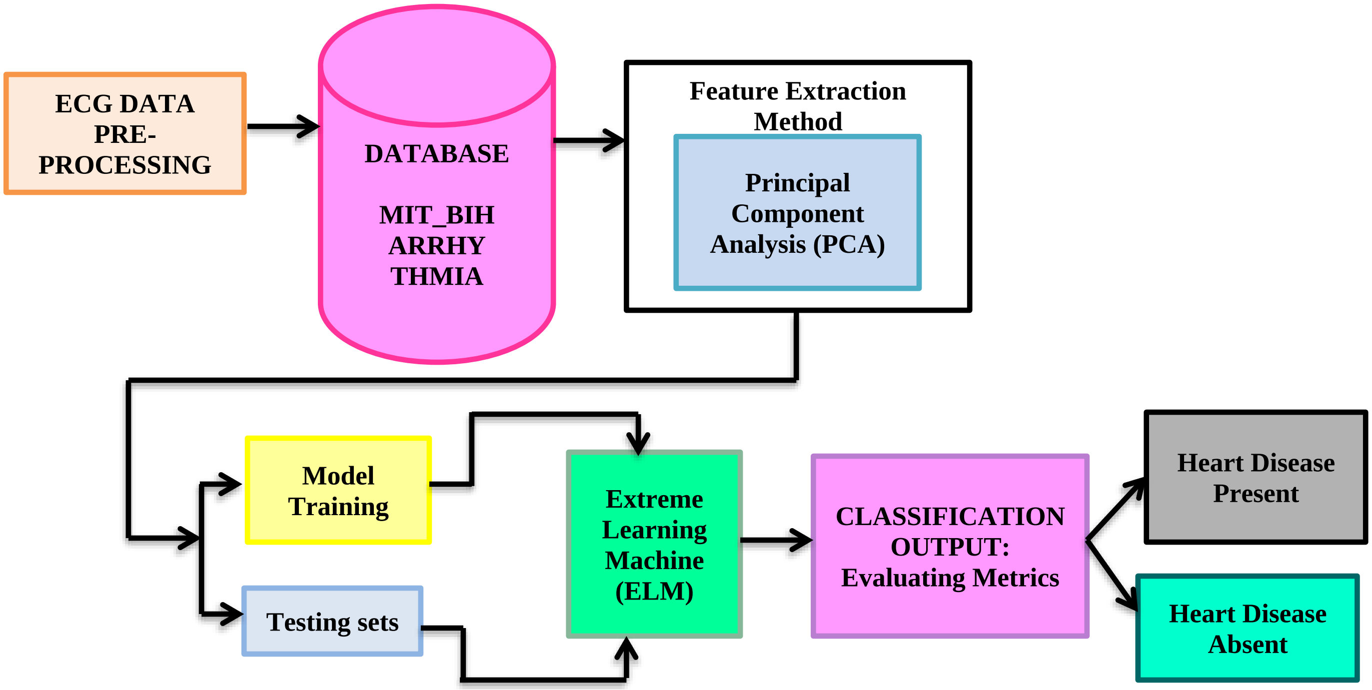

Fig. 1 Proposed architecture for the prediction of heart disease using deep learning models

4.2. Data Pre-processing

The data pre-processing is initiated with the PCA method to clean and identify the missing data. The signal quality assessment (SQA) phase was skipped because the current work focuses on illustrating the DL-based model for heart disease classification using ECG categorical data, except for eliminating missing and false data from the MIT-BIH Arrhythmia dataset. In the proposed work, feature extraction is done by principal component analysis for extracting the right features for the analysis and classification of cardiac disease.

4.2.1. Feature Extraction by Principal Component Analysis

The process of extracting the most pertinent features from a vast collection of features is known as feature extraction. This method simplifies the model by lowering training time and avoiding the problem of overfitting. In the last decade, there have been several real-world issues with the classification challenges in heart disease detection, drawing a big interest in feature extraction because the datasets for those challenges are mingled with a variety of irrelevant and redundant features. Principal Component Analysis feature extraction methods are proposed in work on the MIT-BIT Arrhythmia dataset that is publicly available from the Physionet database. The following section explains the PCA concept in the feature extraction process for heart disease prediction.

A common multivariate data analysis approach is principal component analysis. Principal Component Analysis, or PCA, is a dimensionality-reduction strategy for reducing the dimensionality of big data sets by translating an extensive collection of variables into a smaller one that retains the critical data in the large set. PCA [28] is used in classifying arrhythmia based on the data characteristics for dimensionality reduction of ECG recordings. It decreases the number of space dimensions while maintaining dataset variability and intrinsic correlations. It attempts to explain correlations between variables by utilizing a limited subset of linear combinations of these variables known as the major components. The principal components analysis for dimensionality reduction is supported by the fact that the total variability of a data set with m variables can often be stored for a smaller set of k other variables, mainly composed of linear combinations of primary variables.

The main goal of this technique is to generate smaller subsets of essential features. The PCA hybrid search strategy combines the standardization and feature vector approaches. Using the above two methodologies, PCA constructs the principal component by recasting the data for the final selection.

5. Methodology

Machine learning has been widely used for the past decade in medical diagnosis, prediction, detection, and classification with certain accuracy for the problem statements stated by various researchers worldwide. However, due to the enhancement of data in the medical field, some faults arise in predicting it with good accuracy. So, deep learning has now become a top picker for all researchers around the globe, mainly for the early prediction of certain diseases. Extreme learning machine [29] models can generate good performance and learn many times quicker than other networks. It is more robust with fewer optimization constraints that provide better performance.

Moreover, ELM has a faster convergence speed due to random feature mapping. According to Wang and Cao's [30] study findings, extreme learning machines exhibited several benefits over conventional neural network structures, such as improved accuracy and cheaper training costs. According to the outcomes of their experiments, Zhang and Ding [31] also used deep representation to enhance the extreme learning machine, which showed out to be superior to the DBN approach. So, based on the above literature on ELM, in the proposed work, an extreme learning machine (ELM) is utilized for the prediction of cardiac disease using ECG data.

5.1. Extreme Learning Machine

Extreme Learning Machines [42] is a feedforward neural network that G. Huang invented in the year 2006. As a new technique, ELM reached out for converging, feature selection, and representational learning. ELM has effortlessness of use, snappier speed of learning, more prominent speculation execution, fittingness for a few non-linear piece capacities, and actuation work. ELM has been applied in various spaces, for example, in biomedical designing, Computer vision, framework identification, and control and mechanical technology. It is utilized in classification, clustering, regression, and feature learning using a single layer or several layers of hidden nodes, and no need to tune the hidden node parameters. For better generalisation performance, its learning speed will be faster than other learning algorithms thousands of times, such as the backpropagation (BP) algorithm. It works without using gradient-based backpropagation. It sets its weights using the Moore-Penrose modified inverse. Some of the basic steps in using ELM are (1) combine inputs by weights, (2) add bias, (3) apply the activation function, (4) repeat steps 1–3 number of layers times, and (5) compute output, (6) then backpropagate it and (7) finally repeat everything until solution found. The mathematical model for calculating output in ELM is as follows:

$$f_L(x) = \sum_{i=1}^{L} \beta_i g_i(x) = \sum_{i=1}^{L} \beta_i g(w_i * x_j + b_i),\ j = 1,\dots,N \qquad (1)$$

Where:

- L is a symbol of hidden units
- N is a symbol of training samples
- w is a weight vector between the input and hidden layer
- g is an activation function
- b is a bias vector
- x in an input vector

The beta matrix equation can be written as follows:

$$T = H\beta \qquad (2)$$

Where:

$$H = \begin{bmatrix} g(w_1 * x_1 + b_1) & \cdots & g(w_L * x_1 + b_L) \\ \vdots & \cdots & \vdots \\ g(w_1 * x_N + b_1) & \cdots & g(w_L * x_N + b_L) \end{bmatrix}_{N \times L} \qquad (3)$$

$$\beta = \begin{bmatrix} \beta_1^T \\ \vdots \\ \beta_L^T \end{bmatrix}_{L \times m} \qquad T = \begin{bmatrix} t_1^T \\ \vdots \\ t_N^T \end{bmatrix}_{N \times m} \qquad (4)$$

Where:

- m is a symbol of outputs
- H is the matrix of the output hidden layer
- T is a training matrix for data-target

The learning algorithm details are as follows:

- Assign randomly with weight w_i and bias $b_i, i = 1,\dots L$
- Compute hidden layer output **H**
- Determine output weight matrix $\hat{\beta} = H^{\dagger}T$
- Use $\hat{\beta}$ to predict new data $T = H\,\hat{\beta}$

Algorithm 1: Extreme learning machine

Input: Training set, $\mathcal{N} = \{(x_i, t_i)\} |\ x_i \epsilon\, \mathcal{R}^n, t_i \epsilon\, \mathcal{R}^m, i = 1,2,\dots,N,$ activation function $g(x)$, N_h is the symbol of neurons in the hidden layer

Output: β is the Output weights

A1: For input weights w_i, select random values and bias b_i, $i = 1,2,\dots,N_h$

A2: Determine the output matrix of the hidden layer, H, which is specified as:

$$H = \begin{bmatrix} g(w_1 x_1 + b_1) & \cdots & g(w_{N_h} x_1 + b_{N_h}) \\ \vdots & \cdots & \vdots \\ g(w_1 x_N + b_1) & \cdots & g(w_{N_h} x_N + b_{N_h}) \end{bmatrix}_{N \times N_h} \qquad (5)$$

A3: Calculate output matrix, β as

$$\beta = H^{\dagger}T \qquad (6)$$

where, $H^{\dagger}$ is the Moore-Penrose generalized inverse of H that minimizes the L_2 norm of both $||H\beta - T||$ and $||\beta||$. T is the label matrix of the training set defined as

$$T = \begin{bmatrix} t_1^T \\ \vdots \\ t_N^T \end{bmatrix}_{N \times m} \qquad (7)$$

where m is the label dimension for each training instance

A4: **return** β

5.1.1. Kernel Extreme Learning Machine

Pan et al. initiated a Q learning framework for nonstop spaces developed as a regression problem for an ELM. Rather than including speculation across issue cases, transfer learning stresses exchanging information across jobs, areas, and divisions that are connected but not equivalent. If the two divisions are distinct, then two different transfer learning sub-problems can be detailed reliant on whether the training and testing data cite to a similar domain. In the system of certain field variations, the vast majority of the learning strategies are motivated by the possibility of these two thoughts about areas, even though distinct, being exceptionally related. In this article, the following disputes are analyzed. A transfer learning dependent on the ELM model (TL-ELM) is developed that utilizes a minimum value of destination tag data and a maximum value of source field early data to fabricate an excellent classification model. The model enhances classic ELM and adjusts for traditional ELM's difficulty in presenting the information. In particular, as an extension to the TL-ELM approach for the issues of pattern classification, the TL-KELM is adapted based on the kernel extreme learning machine KELM [33]. The experimental results show the potency of the proposed model.

The ELM can be reformulated as,

$$min : \frac{1}{2} \| \omega_t \|^2 + C_t \sum_{i=1}^{N} \xi_i^t + \frac{1}{2} \mu \|\omega_t - \omega_S \|^2, \quad (8)$$
$$s.t : y_i^t(\omega_t \cdot h(x_i^t)) \geq 1 - \xi_i^t, \quad i = 1,2,\dots,N,$$
$$\xi_i^t \geq 0, \quad i = 1,2,\dots,N,$$

ω_S is source transfer knowledge, ω_t is target transfer knowledge, μ is the penalty parameter. The TL-ELM model framework for predicting cardiac disease is shown in Figure 2.

Then, the corresponding Lagrangian is

$$L = \frac{1}{2} \| \omega_t \|^2 + C_t \sum_{i=1}^{N} \xi_i^t + \frac{1}{2} \mu \|\omega_t - \omega_S \|^2 - \sum_{i=1}^{N} \alpha_i \left(y_i^t(\omega_t \cdot h(x_i^t)) - 1 + \xi_i^t\right) - \sum_{i=1}^{N} \gamma_i \xi_i^t , \quad (9)$$

where $\alpha_i \geq 0$ and $\gamma_i \geq 0$.
To maximize L concerning α_i and γ_i, then minimize it to ω_t and ξ_i^t. The derivatives of the fundamental factors should be 0 at this phase,

$$\frac{\partial L}{\partial \xi_i^t} = 0, \frac{\partial L}{\partial \omega_t} = 0 \quad (10)$$

Then, delete the variables ξ_i^t and ω_t from L using these equations and obtain the dual solution. The next step is to start with the derivative to ξ_i^t,

$$\frac{\partial L}{\partial \xi_i^t} = 0 = C_t - \alpha_i - \omega_i, \; i = 1,2,\dots,N \quad (11)$$

which implies that

$$0 \leq \alpha_i \leq C_t \quad (12)$$

In the case of ω_t,

$$\frac{\partial L}{\partial \xi_t} = 0$$
$$= \omega_t + \mu(\omega_t - \omega_S) - \sum_{i=1}^{N} \alpha_i \left(y_i^t\left(h(x_i^t)\right)\right), \quad (13)$$

which results in

$$\omega_t = \frac{\mu \omega_S}{1+\mu} + \frac{1}{1+\mu} \sum_{i=1}^{N} \alpha_i \left(y_i^t\left(h(x_i^t)\right)\right), \quad (14)$$

According to the above equation, the dual representation of the foremost issue is represented as,

$$min \frac{1}{1+\mu} \sum_{i=1}^{N} \sum_{j=1}^{N} \alpha_i \alpha_j \, y_i^t y_j^t \left(h(x_i^t) \cdot h(x_j^t)\right) + \sum_{i=1}^{N} \left(\frac{\mu y_i^t (h(x_i^t) \cdot w_S)}{\mu+1} - 1\right) \beta_i \frac{1}{1+\mu} \|\omega_S\|^2 \quad (15)$$
$$\text{s.t } 0 \leq \beta_i \leq C_t, \; i = 1,2,\dots,N$$

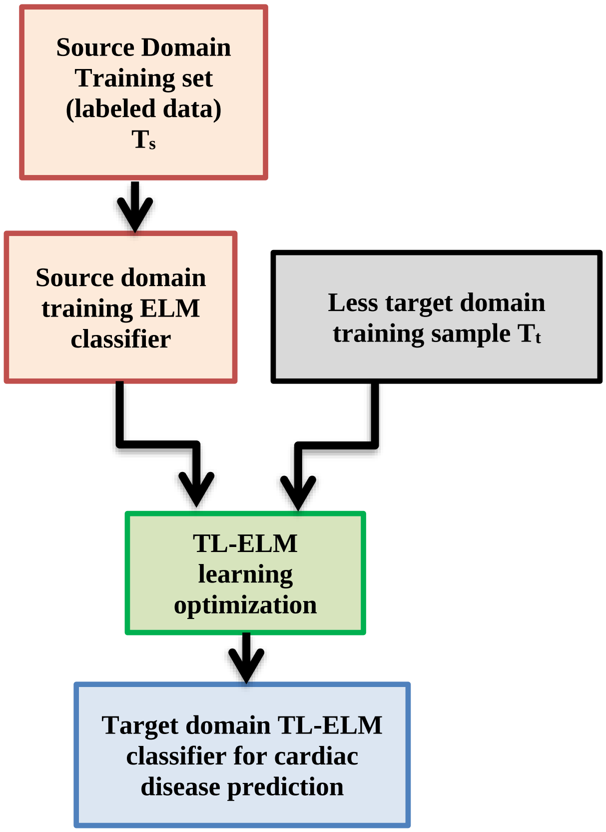

Fig. 2 The TL-ELM framework (Xiaodong Li et al.)

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Algorithm 2: TL-ELM
A1: Attain the basic information of $\omega_S$, and choose the suitable variables $C_t$, $\mu$;
A2: For the given $C_t$, discover the best vector $\alpha^* = (\alpha_1^*, \dots, \alpha_N^*)^T$ by using Equation 15.
A3: Acquire $w_t^*$, confessing to Equation 14;
A4: Output the decision function
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6. Results and Discussion

This section explains the experimental results of ECG data analysis with its description for predicting cardiac disease. For the automatic classification of cardiac disease, the MIT-BIH dataset was used for the performance evaluation with an optimized extreme learning machine model. The proposed ELM method is trained sequentially with validation for each optimised feature. The standard evaluation criteria are used to evaluate the prediction model's performance. They are precision and overall accuracy. The schematic diagram of the proposed work is shown in Figure 3.

First, the input is transferred to the next stage after performing it with the feature extraction method. This work uses principal component analysis (PCA) to extract the right features. Using PCA, the optimized features are selected by the dimensionality reduction concept.

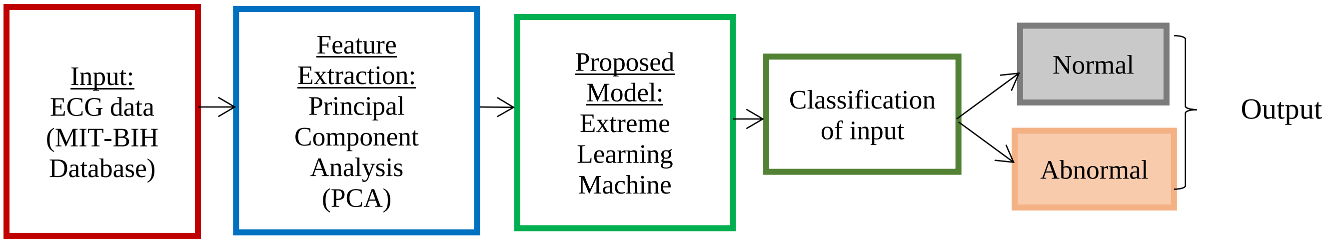

Fig. 3 Schematic diagram of the proposed work

The proposed model is trained using transfer learning combined with a powerful learning machine optimizer with its decision function to minimize cross-entropy. Then the selected features are split into two sets, namely training and testing sets. This work divides the dataset into an 80% - 20% ratio for training and testing the model's classification performances. Dropout is used to reduce over-fitting risk by applying a 10% ratio. The training process is initiated by selecting epochs of 5, 10, and 15 with kernel sizes of 32, 64, and 128, respectively. Behind each training epoch, 20% of the entire training dataset is used to validate the proposed work. When the finest cohort of the method is assessed, it tends to be utilized straightforwardly in the testing dataset to estimate its classification performance. The performance of the proposed ELM model is assessed from the MIT-BIH Arrhythmia Database. The proposed method's classification accuracy is assessed with the help of the cross-validation technique. As previously stated, the dataset is divided merely into the ratio of 80% and 20%, respectively, and the validation technique is repeated with 9 trials on the test data. Table 2 shows the performance metrics of the proposed model, and Figure 4, Figure 5, Figure 6, Figure 7, Figure 8 and Figure 9 show the visual representation of the lowest and the highest average of it. The result shows that the proposed model outperforms all other models with precision, recall, f1-score and accuracy values.

Table 2. Average Values of Performance Metrics of the Proposed model (ELM)

Execution / Performance Metrics	Precision	Recall	F1-Score	Accuracy
1	0.928	0.882	0.902	0.983
2	0.942	0.882	0.910	0.974
3	0.932	0.874	0.900	0.981
4	0.914	0.842	0.874	0.984
5	0.900	0.914	0.908	0.982
6	0.898	0.890	0.892	0.983
7	0.914	0.882	0.892	0.981
8	0.940	0.884	0.908	0.981
9	0.938	0.898	0.896	0.985

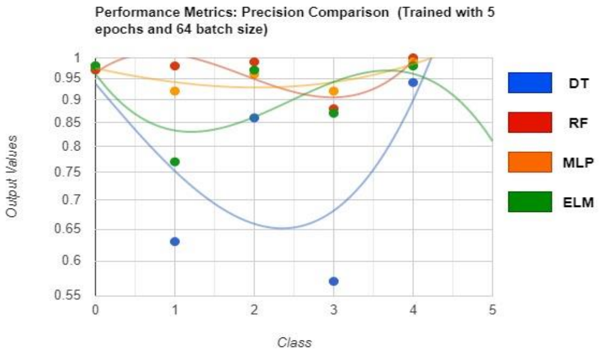

Fig. 4 Comparison of Average Low Precision with other models

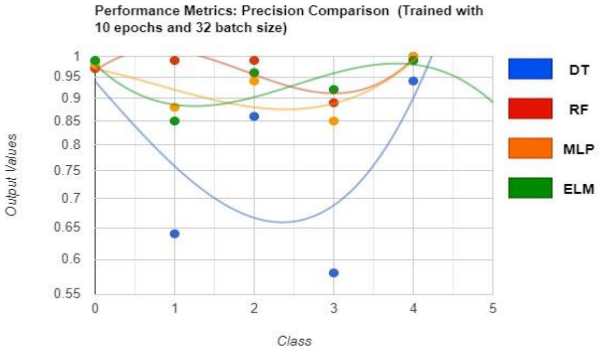

Fig. 5 Comparison of Average High Precision with other models

Fig. 6 Comparison of Average Low Recall with other models

Fig. 7 Comparison of Average High Recall with other models

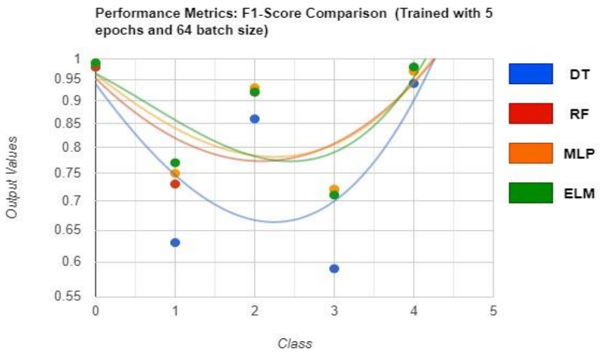

Fig. 8 Comparison of Average Low F1-Score with other models

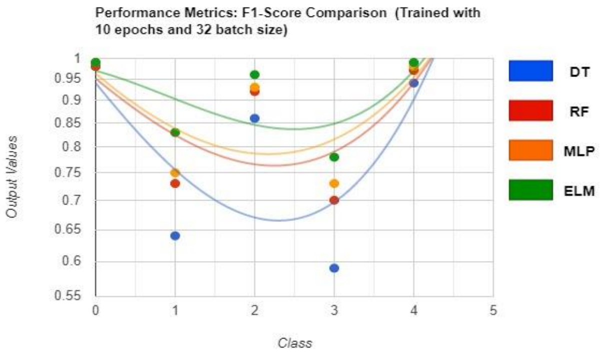

Fig. 9 Comparison of Average High F1-Score with other models

The average accuracy is then taken from the overall trials for the cardiac disease classification. Figure 10 shows the proposed model's precision, recall, f1-score and accuracy after execution. From table 3, the accuracy of the proposed model increases and decreases slightly based on the different epochs and batch sizes, such as while executing with 5 epochs, attained an accuracy of 98.30%, 97.41%, and 98.15% for the batch sizes of 32, 64 and 128 respectively. Similarly, for 10 epochs, obtained an accuracy of 98.41%, 98.27%, and 98.36% for the batch sizes 32, 64, and 128, respectively. Finally, for 15 epochs, achieved an accuracy of 98.19%, 98.10%, and 98.50% for the batch sizes 32, 64, and 128, respectively. From these results, the best accuracy of the proposed work is gained from epochs 15 for the batch size of 128 with 98.50%, respectively. The proposed model ELM outperforms all other classifiers such as DT, RF, and MLP. Figure 11, Figure 12, and Figure 13 show the accuracy of the classical ELM with different epochs and batch sizes. This figure also shows that the proposed DL models converge quickly and obtain stable performances on 15 epochs. No over-fitting issues were observed during the learning phase of all models.

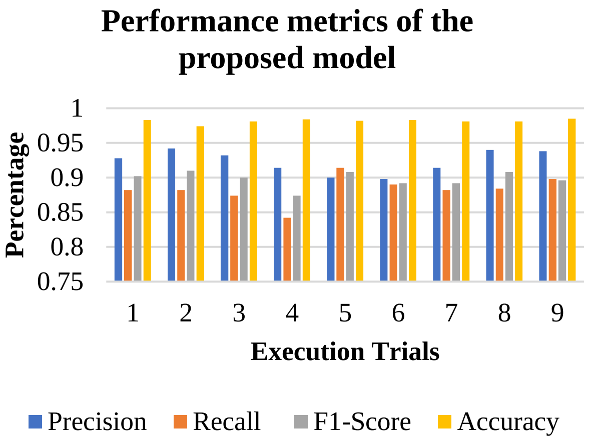

Fig. 10 Performance metrics of the proposed model: Precision, Recall, F1-Score and Accuracy

Table 3. Comparison of proposed model accuracy result with other classifiers for cardiac disease prediction

Epochs	Batch size	Accuracy – Proposed Model (ELM)	Other Classifiers - Accuracy		
			DT	RF	MLP
5	32	98.30	95	97	97
5	64	97.41	95	97	98
5	128	98.15	95	97	98
10	32	98.41	95	97	98
10	64	98.27	95	97	98
10	128	98.36	95	97	98
15	32	98.19	95	97	98
15	64	98.10	95	97	98
15	128	98.50	95	97	98

Predicting and classifying heart disease is a difficult task that has sparked much interest in recent decades. This study used PCA with ELM to predict cardiac disease classification. The proposed method is tested on various ECG data from the MIT-BIH dataset. The performance of the various designed DL architectures is examined. Figure 14 shows the comparison of the proposed work with other works.

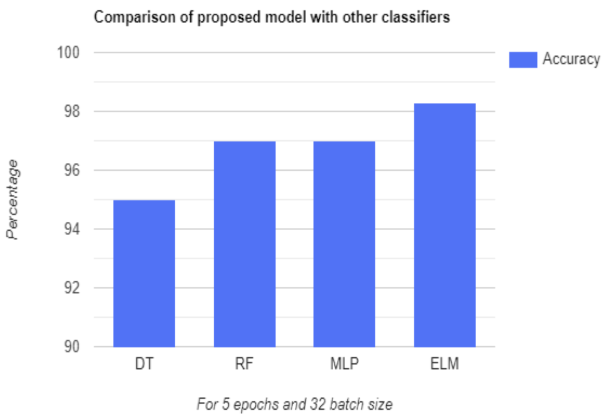

Fig. 11 Accuracy of the proposed model with 5 epochs and 32 batch size

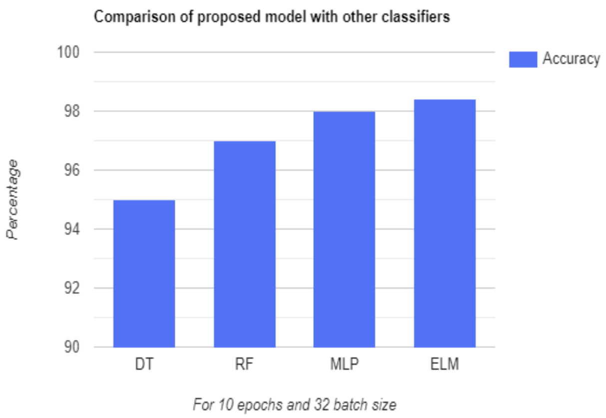

Fig. 12 Accuracy of the proposed model with 10 epochs and 32 batch size

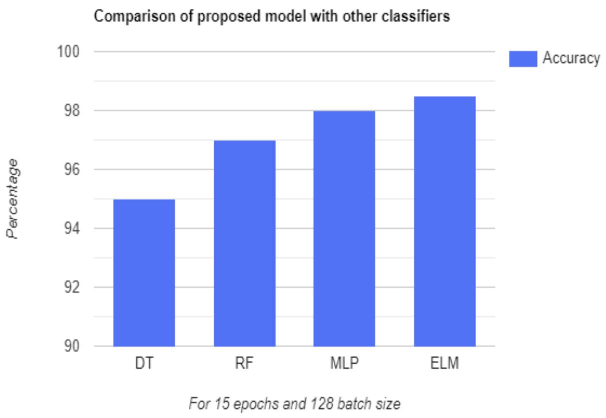

Fig. 13 Accuracy of the proposed model with 15 epochs and 128 batch size

In recent years, various deep learning models [34], [35], and [36] for disease classification and prediction have been proposed. The powerful model CNN, RNN, and LSTM architectures are used in many of these approaches. The comparison of the proposed work with earlier research is shown in table 4. The proposed method can classify efficiently with a maximum overall accuracy of 98.50%, as per the obtained evaluation results. The notations used in this article are shown in table 5.

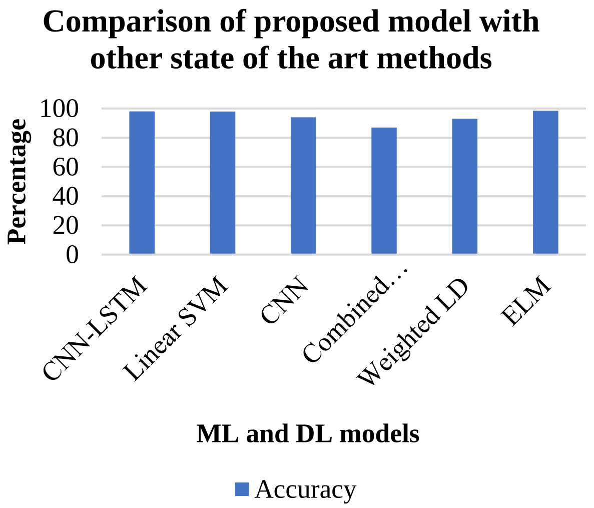

Fig. 14 Comparison of proposed work with other works

Table 4. Comparison of the proposed models to existing state-of-the-art models

References	Classifiers	Number of Classes	Accuracy
[37]	CNN-LSTM	5	98.10%
[38]	Linear SVM	5	97.94%
[39]	CNN	5	94.03%
[40]	Combined SVM	5	87%
[41]	Weighted LD	5	93%
Proposed Model:	**ELM**	**5**	**98.50%**

Table 5. Notations used in this article

Notations	Description
$\boldsymbol{w}$	Input weights of ELM
β	Output weights of ELM
$\boldsymbol{X}$	Input matrix of hidden layers
$\boldsymbol{H}$	Output matrix of hidden layers
$\boldsymbol{b}$	Bias
$\boldsymbol{I}$	Identity matrix
$\boldsymbol{K}$	Kernel matrix
$\boldsymbol{C}, \boldsymbol{C1}, \boldsymbol{C2} \ldots \boldsymbol{etc}$	Regularization matrix
$\boldsymbol{T}$	Label Matrix
$\boldsymbol{\xi}$	Prediction error ($\xi = \boldsymbol{H}\beta - \boldsymbol{T}$)
$\boldsymbol{S}$	Source domain (subscript)
$\boldsymbol{T}$	Target domain (subscript)
$\boldsymbol{O}$	The output of the Extreme learning machine (ELM) ($i.e. O = \boldsymbol{H}\beta$)

The summary of this work is:

- On the publicly available benchmarked MIT-BIH Arrhythmia ECG dataset, the performance of DL architectures for predicting cardiac diseases.
- Principal Component Analysis (PCA) is utilized to extract and select optimized features in ECG data to predict cardiac disease.
- Transfer learning is used with kernel ELM to improve the robustness of ELM classification.
- For classification, the powerful deep learning model, such as an extreme learning machine, is used, which is not done by earlier research.
- The proposed ELM model has performed well, with an accuracy of 98.50%.

7. Conclusion

Cardiac disease is a primary global concern that needs to be screened earlier. Deep learning methods such as the Extreme Learning Machine are adopted in this work to predict cardiac disease. The benchmark ECG data from the PhysioNet database, such as MIT-BIH Arrhythmia, is used for the analysis. PCA initiates the process with data pre-processing with its cleaning and missing data identification. Then, the features are extracted via the Principal Component Analysis. Transfer learning is used with kernel ELM to improve classification performance with more robustness. Finally, ELM classifies the cardiac disease and predicts it with an accuracy of 98.50%, outperforming all other state-of-the-art models. In the future, the deep learning model can be utilized with other hybrid models to improve performance metrics by enhancing several metaheuristics' bio-inspired algorithms for the large heart disease datasets to be useful for the many lives in the world.

Conflicts of Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper. Compliance with Ethical Standards: This article does not contain any studies with human participants performed by authors.

Acknowledgments

We thank our university Vellore Institute of Technology, for the resources they have provided for this research. Author 1 performed data collection, performed the analysis, and wrote the manuscript, and Author 2 performed the review and supervision.

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