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An Intelligent Hybrid Long Short-Term Memory (LSTM) and Generative Adversarial Networks (GAN) Model for Patient in-House Monitoring

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Abstract: The importance of monitoring patients inside and outside healthcare settings is becoming more critical in enhancing patient safety, identifying diseases at an early stage, and effective healthcare management. Typically, the current systems used in patient monitoring may not offer timely and accurate identification of any abnormalities in the patient's health because the systems operate by manually observing the condition of the patient or raising alerts based on sensors. Intelligent health care monitoring systems have been gaining popularity especially due to their machine learning models that utilize deep learning techniques. In this study, an intelligent patient in-house monitoring a combined deep learning method is used in the development of the system, it comprises Long Short-Term Memory (LSTM) networks and Generative Adversarial Networks (GAN). The modified Principal Component Analysis (HPCA) algorithm is proposed to derive the important features of this technique. Both techniques are incorporated into this hybrid deep learning scheme, where the GAN model helps in generating fake data and making the model resilient, while the LSTM model assesses successive physiological parameters, including body oxygen level, body temperature, and heart rate. Through the application of GAN-based data augmentation techniques, this technology is able to address issues related to small and imbalanced datasets in medicine. The hybrid machine learning model suggested by researchers would increase the reliability and accuracy of patient monitoring in a home-based healthcare setting. Using sophisticated analytical tools and technologies for health monitoring, the solution can contribute to better healthcare provision in terms of remote diagnoses and treatment.

Keywords: Cardiac dysrhythmia, patient monitoring, smart health care, modified Principal Component Analysis (HPCA), Generative adversarial networks (GAN) and Long Short-Term Memory (LSTM) networks.

1. INTRODUCTION

An important issue with current healthcare systems, cardiovascular diseases account for some of the world's leading causes of death [1]. Some of the diseases related to heart which affect the health and lifestyle of humans are heart failure, arrhythmia, cardiovascular disease, and heart infarction. Timely and accurate diagnosis along with regular monitoring and treatment is crucial in order to lower mortality and save lives [2]. Conventional monitoring systems available in hospitals are dependent on constant supervision by medical practitioners, costly healthcare equipment, and lengthy hospitalization periods. As a result, intelligent monitoring systems within hospitals have become highly important in present-day healthcare. The emergence of advanced technologies of remote monitoring of patients' conditions that enable continuous monitoring of patients' health conditions at home settings has been facilitated by recent advances in wearable sensors, cloud computing, artificial intelligence, Internet of Things (IoT) technology, and smart healthcare [3]. In-house monitoring systems record the vital signs of the patient like electrocardiogram (ECG), body temperature, heart rate, and blood pressure, and oxygen saturation level through wearable or wireless medical devices. Such approaches offer real-time analysis of health conditions and identification of any abnormal heart activity.

In intelligent computing technologies, deep learning is especially useful in analyzing medical information and predicting diseases [4]. Deep learning-based algorithms can identify complex patterns in huge amounts of health care data and predicting any abnormalities of the heart. Specifically, when analyzing sequential data related to patient vital signs and electrocardiogram (ECG), Long Short-Term Memory (LSTM) networks achieve great success. In predicting cardiac diseases, LSTM-based models have long-term dependency within dynamic physiological changes [5]. Despite their predictive superiority, medical data sets suffer from a number of weaknesses including insufficient training examples, imbalanced classes, missing values, and noise. This might restrict the model's ability for generalization as well as its predictive accuracy. GAN methods have attracted great interest because of these weaknesses. Within GANs, the discriminator and generator networks compete to produce artificial data samples. GANs find a wide range of application in medicine where their major applications include data augmentation, denoising, image enhancement, filling missing values, and improvement of the robustness of deep learning models [6]. Combination of LSTM and GAN models has become a promising strategy of using hybrid deep learning in intelligent healthcare monitoring systems [7]. For example, in LSTM-GAN architectures, GANs create realistic synthetic data and increase feature diversity, while LSTM networks process time-series data and make predictions on the patient's state.

The use of cardiac monitoring systems that employ a hybrid deep learning approach provides many benefits compared to the conventional healthcare system [8-10]. Such intelligent systems allow for real-time remote monitoring, identification of cardiac anomalies, decreased expenses on hospitalization, and tailored healthcare management. The healthcare personnel can identify critical situations at their very beginning and offer proper medical care to the patients [11]. Additionally, such intelligent monitoring systems increase the comfort level for patients and alleviate the pressure on healthcare facilities. However, there are also several problems with building intelligent systems for cardiac monitoring. Firstly, the information collected by the smart health system is usually very sensitive and should be protected. Furthermore, there could be some noise or even some missing data in the physiological signals recorded by wearables [12]. There is a set of other technical and methodological challenges related to computational issues that need further investigation.

The research work presents an approach known as Intelligent Hybrid LSTM and GAN Models for In-House Patient Monitoring-based Cardiac Disease Diagnosis. The main objective of this intelligent framework is the development of an intelligent system that can remotely monitor patients by processing patient data continuously to detect any cardiac abnormality. The physiological data of the patient in the proposed system gathered using wearable devices will go through preprocessing and feature extraction methods to enhance data quality. GAN Models will be used for generating balanced datasets. Further, the refined data undergoes analysis using LSTM networks that help to detect the temporal relationships and classify cardiac disorders with high accuracy. The designed hybrid approach enables real-time monitoring, detection of any anomalies, and intelligent decision-making for early diagnosis of cardiac diseases. The developed framework provides several advantages, including improved prediction accuracy, ability to deal with imbalanced medical data, real-time monitoring of patients, minimized false alarm rate, and improved healthcare access. In addition to that, the adoption of hybrid deep learning together with the intelligent healthcare monitoring can lead to the creation of advanced personalized medical care systems which would allow building future digital healthcare facilities. In general, the suggested hybrid cardiac monitoring system based on LSTM-GAN is an important step forward in the development of intelligent healthcare systems. Through the use of temporal deep learning models along with generative deep learning approaches, the enhancement of remote patient monitoring becomes the target of the investigation.

The rest of the study is organized as follows: section 2 examines some of the most existing methods for employing sophisticated deep learning algorithms to identify heart diseases. Section 3 shows the process of the proposed technique. The results and comments are shown in Section 4. The conclusion and future work are covered in Section 5.

2. LITERATURE REVIEW

This section examines some of the most existing methods for employing advanced deep learning algorithms to detect heart disease.

Ramkumar et al [13] IoT-capable devices provide data to the proposed framework and integrates electronic medical records associated with patients, which are maintained in cloud storage. These data are subsequently processed using predictive analytics techniques to support disease diagnosis and monitoring. LSTM and Recurrent Neural Network (RNN) models are used by the smart healthcare system to precisely anticipate the emergence of cardiac disease and continually monitor patient health status. The proposed technology outperforms current cardiac disease prediction algorithms and traditional methods with 99.99% accuracy, according to experimental data.

Rajan Jeyaraj et al. [14] introduced an innovative physiological signal monitoring framework based on IoT technology to enhance e-healthcare services. The proposed architecture required a Deep Neural Network (DNN), the technique that has been applied for prediction and estimation of the traffic signals in order to conduct proper analysis of the physiological signals. The architecture has been implemented in a form of an electronic healthcare platform equipped with intelligent sensors and using National Instruments myRIO as the core of the platform. The Smart Monitor System was designed as a consumer-centric device, which uses intelligent sensing technology for continuous monitoring of the physiological signals. Two users' data were used to examine the accuracy of four physiological signal predictions to assess the system's effectiveness. The results indicated that the prototype was capable of delivering an average accuracy of 97.2% in predicting physiological signals. Thus, it is evident from the experiments carried out that the monitoring system will offer reliable assistance in predicting physiological signals.

Alzakari et al. [15] proposed using an XGBoost model-based prediction system to efficiently analyze huge amounts of data and identify key features that help boost the prediction ability of the system. To improve the model's ability for prediction, the complex temporal relationships in the medical health information data were modelled using a Bi-LSTM model. The proposed technique surpassed Naïve Bayes, Decision Trees, and Random Forests with 99.4% prediction precision. This paper can serve as a real-world solution to remote medical monitoring and predicting diseases using the latest deep learning and machine learning technologies with the IoT.

Hemalatha et al. [16] proposed a cloud security model based on an Enhanced Auto Encoder-Based Convolutional Neural Network (EAE-CNN) with the Mdata model to protect smart city infrastructure. The proposed model improves security by detecting cyber threats and protecting data. The results showed that the model performed better than existing methods and provides an effective solution for cloud security in smart cities.

Umer et al. [17] proposed an AI-based IoT heart care monitoring system. By constantly monitoring and reporting patient behavior, IoT may provide real-time health monitoring. The proposed machine learning approach by the authors called ensemble learning model ET-CNN resulted to a heart disease prediction accuracy rating of 0.9524. Results of their study prove the effectiveness of the suggested structure in categorizing and giving timely health information regarding cardiac patients.

Arivalahan et al. [18] proposed a healthcare monitoring framework, DCSNN-WMA-HCM-IoT-CAA is an IoT-based context-aware architecture that combines a Deep Convolutional Spiking Neural Network (DCSNN) with the Woodpecker Mating Algorithm (WMA). Preprocessing includes data collection, storage, and redundancy removal for real-time healthcare datasets. To remove duplicate and redundant records, a Kernel Correlation-based method is employed, thereby improving data quality for subsequent analysis and monitoring tasks. The feature extraction procedure uses the pre-processing output. The rapid discrete Curvelet transform technique is used to extract the feature. The gathered characteristics are then sent into a DCSNN that has been improved using WMA to categorize the patient's regular, irregular, and critical states. In comparison to current approaches, the proposed DCSNN-WMA-HCM-IoT-CAA methodology achieves high accuracy of 4.08%, 8.17%, 9.32%, and 5.17%, reduced computation time of 14.3%, 15.4%, 19.51%, and 27.81%, and increased AUC of 12.29%, 15.36%, 11.55%, and 13.91%.

Shafi et al. [19] developed a health monitoring framework that combines IoT-based sensors with advanced Deep Learning (DL) techniques to continuously track vital physiological parameters, the proposed system monitors essential physiological parameters, including heart rate, blood pressure, body temperature, and oxygen saturation, to support continuous health assessment and early detection of abnormalities. To efficiently process the large volumes of data generated by IoT devices, deep learning techniques such as Convolutional Neural Networks (CNNs), Recurrent Neural Networks (RNNs), and Artificial Neural Networks (ANNs) are utilized for accurate anomaly identification. Experimental results confirm that the integrated IoT and deep learning framework provides reliable patient monitoring, enhances clinical decision-making, and improves the quality of healthcare services.

Fouad et al. [20] considered an IoT and artificial intelligence (AI) healthcare system. The study revealed that the traditional healthcare assistant systems have been found deficient when it comes to making accurate predictions about patient conditions and personal needs, thus resulting in inefficient clinical assistance. In order to address such issues, the system incorporates sensors associated with IoT technology with the use of AI-based algorithms for collecting and analyzing information about various patients' characteristics, including their level of fitness, medical history, daily activity, BMI (body mass index), body temperature, etc. To collect all required patient information, a healthcare mobile application is used. When all of the data has been gathered, it is saved in the cloud and examined using machine learning algorithms that have been improved. An Iterative Golden Section Optimized Deep Belief Neural Network (IGDBN) is used to handle patient data for healthcare prediction and analysis, which enhances predictive accuracy and decision-making performance. The proposed network analyzes patients' historical health records to accurately assess their current condition and predict future health status. The MATLAB platform was used to assess the IoT sensor's performance in combination with the AI-based healthcare support prediction model. Experiments show that the suggested strategy works well, achieving a precision of 99.87%, a loss error of 0.045, a Simple Matching Coefficient (SMC) of 99.71%, a Matthews Correlation Coefficient (MCC) of 99.10%, and an overall prediction accuracy of 99.86%.

Preetha et al [21] presented a novel five-stage IoT–cloud-based smart healthcare management framework was developed for disease prediction using a Seahorse Optimization-driven Mutated Convolutional Neural Network (SHO-MuCNN). In the first stage, there are several sources of healthcare data. Data standardisation in the second step ensures consistency and analytical capability. Customized Principal Component Analysis (CPCA) extracts the most important characteristics in the third step. Finally, the fourth stage employs the proposed SHO-MuCNN model to predict disease conditions accurately, enabling efficient and intelligent healthcare management. In the fifth stage, doctors give personalized advice to patients according to predicted results in order to reduce possible risks to their health. Our designed intelligent monitoring system for healthcare was evaluated highly, with accuracies of 98.56%, precision of 96.69%, F1-score of 97.86%, recall of 94.59%, and AUC of 95.02%. Moreover, SPSS and t-test were performed to determine statistical significance of the results. The experimental data, the performance of our proposed method is significantly more than that of all other current methods.

Mojjada et al [22] a Hybrid Whale–Grey Wolf Optimization (Hyb-WGWO) algorithm was proposed for the effective selection of the cluster heads for data transmission in IoT healthcare environments. The IoT healthcare devices gather and cluster the healthcare data, and through the proposed Hyb-WGWO algorithm, the best suited cluster head is chosen. The selected cluster head is then used to transmit the data gathered to the cloud server. Deep Ensemble Multitask Classification (DEMC) is applied to classify the patients' diseases into different groups of low, normal, abnormal, and critical. As compared to other algorithms including EDA-ENN and GOPSO-CE, the Hyb-WGWO-DEMC system has proven successful by achieving improvements of 25.98% and 31.86% in accuracy and 28.08% and 26.87% in specificity, respectively.

Nancy et al [23] to increase prediction accuracy, deep learning algorithms using RNN have been used, which are capable of processing sequential time-series data. The proposed approach combines cloud-based electronic health records with real-time data gathered from IoT devices to perform predictive analytics. For heart disease risk prediction with high accuracy, a bi-directional long short-term memory network-based intelligent healthcare monitoring system is used. The proposed intelligent healthcare monitoring system achieved 98.86%, 98.90%, 98.80%, 98.89%, and 98.86% of sensitivity, specificity, accuracy, precision, and F-measure, through experimental evaluations.

Premalatha et al. [24] developed a well-thought-out methodology for predicting illnesses employing the use of CNNs. One of the key strengths of the proposed CNN framework is that it has the ability to learn from oversampling. To address the issues related to class difference, oversampling was done through the XGBoost methodology. Decision trees are used in the ensemble learning technique XGBoost and employs the concept of gradient boosting to improve the classification process by developing strong predictors. Together with artificial neural networks, the framework can transform unstructured data into structured formats. The suggested model was analysed by using the actual IoT data set obtained from heart disease patients of older age groups. The results obtained showed excellent prediction capabilities, with recall, precision, F1 score, and accuracy being 100%, 98%, 94.8%, and 98%, respectively. As compared to traditional ML algorithms, like decision trees, random forest, and SVM, the proposed model has shown better classification accuracy. This result signifies that higher accuracy is provided through CNN-based heart disease detection for older patients with minimum error rates in prediction as compared to other existing methods.

In general, the reviewed literature suggests that intelligent cardiac patient in-house monitoring solutions using IoT technology, cloud computing, deep learning algorithms, and hybrid artificial intelligence have made major contributions to remote healthcare management and improved disease prediction accuracy. Using cutting-edge deep learning methodologies, privacy-preserving mechanisms, and intelligent data analysis plays an important role in creating the next generation of smart healthcare monitoring technologies. Nevertheless, many research gaps persist in the development of intelligent cardiac patient in-house monitoring systems. Current technologies used for intelligent cardiac patients' health monitoring suffer from problems such as real-time processing, healthcare device interoperability, security in communication, computational complexity, and adaptively in prediction of diseases.

3. PROPOSED METHODOLOGY

LSTM-GAN hybrid deep learning architecture, this research suggests an intelligent inside patient monitoring system. To extract the most useful characteristics for further analysis, HPCA is first used. As the GAN creates realistic synthetic data to add to the training set and enhance the prediction model's robustness and generalization ability, the LSTM model records temporal patterns in sequential physiological signals, such as oxygen saturation, heart rate, and body temperature. By incorporating GAN-based data augmentation, the system can effectively handle limited or imbalanced medical datasets and improve predictive performance.

The proposed hybrid deep learning framework aims to improve patient monitoring systems' dependability, precision, and effectiveness in home healthcare environments.

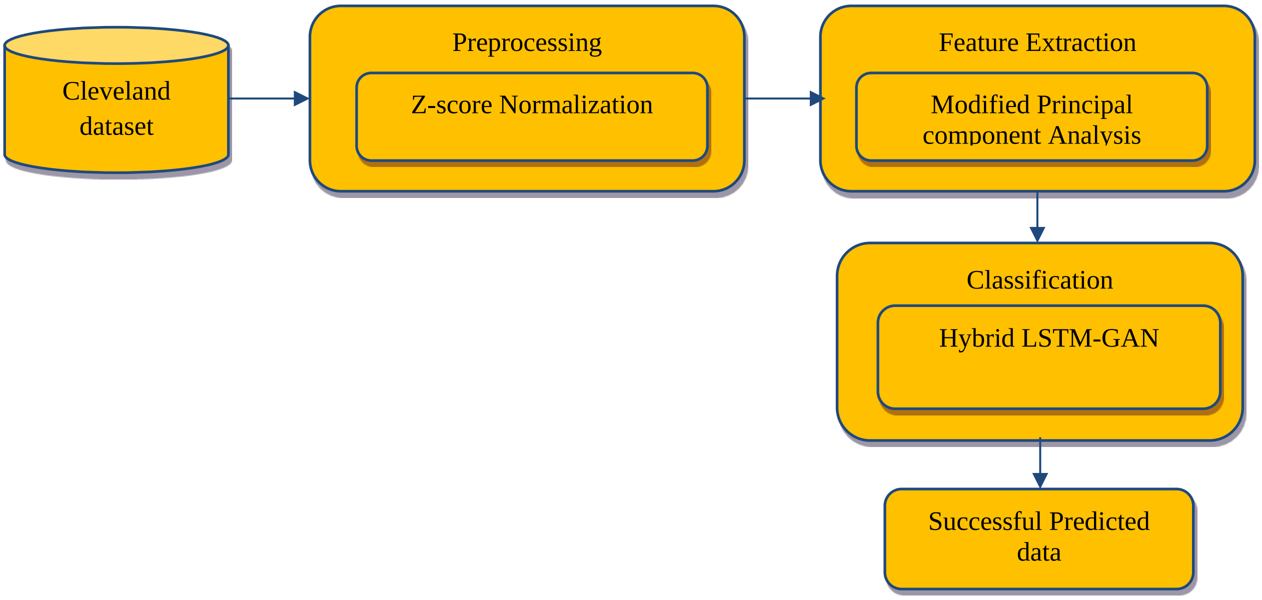
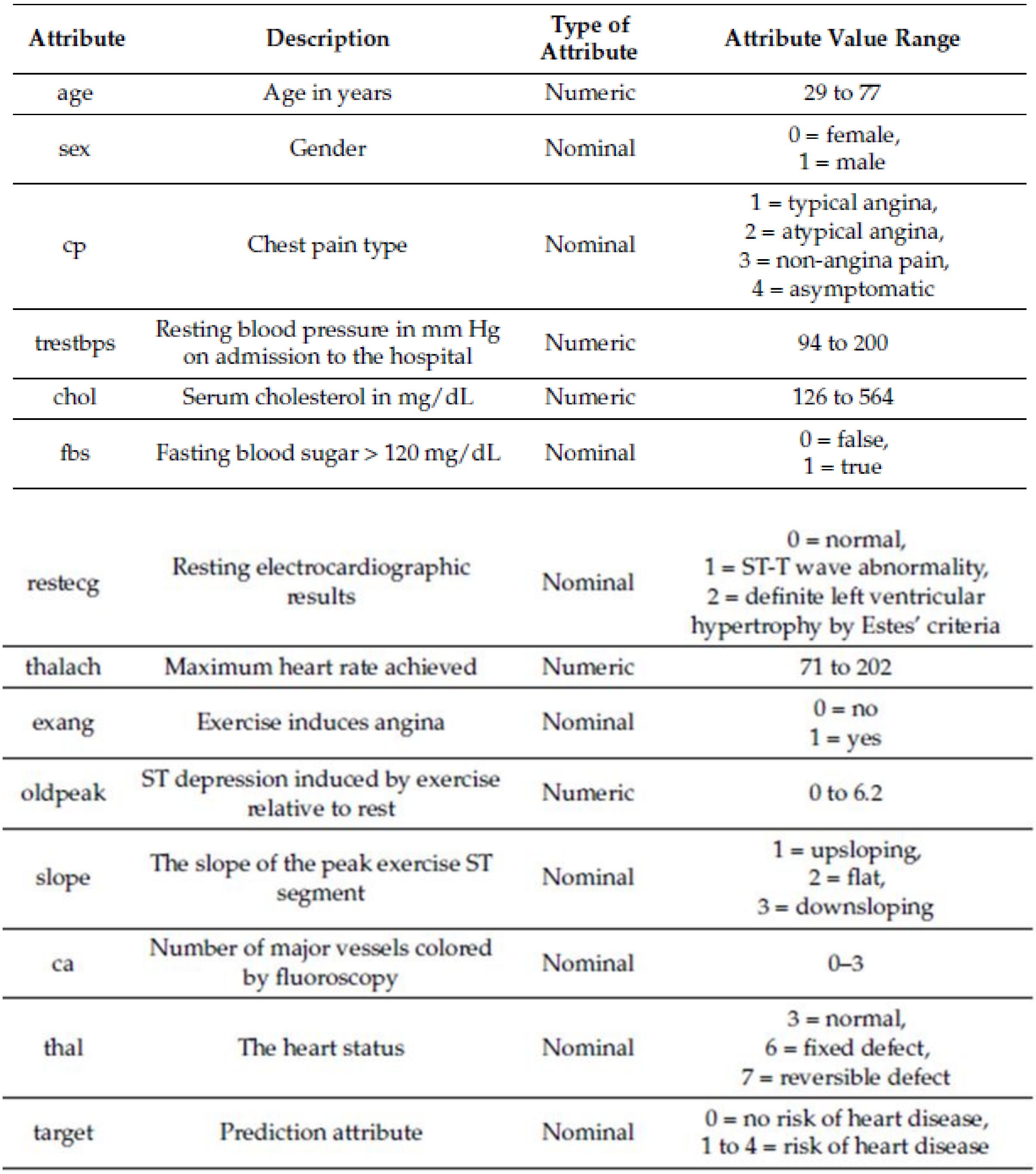


Figure 1. The proposed methodology's overall procedure

3.1. Dataset Description and Statistics

Only 14 of the 76 characteristics in the Cleveland Heart dataset's 303 occurrences are thought to be more appropriate for study and experimentation [21].

Table 1. The UCI machine learning source provides descriptions of the characteristics of the Cleveland Heart dataset.

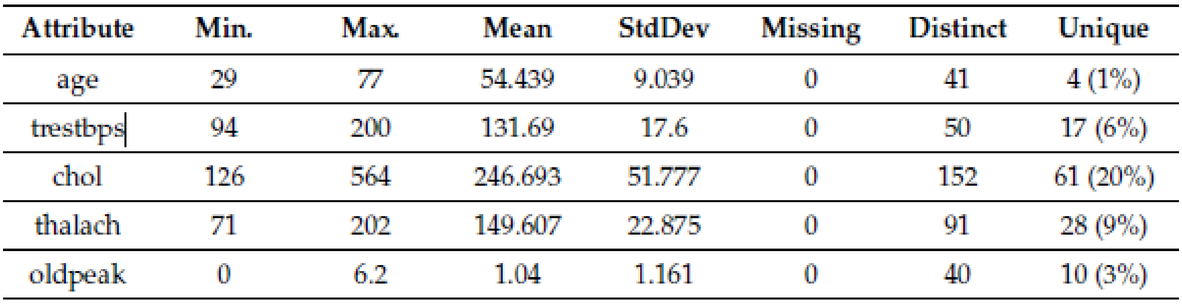


Attribute	Description	Type of Attribute	Attribute Value Range
age	Age in years	Numeric	29 to 77
sex	Gender	Nominal	0 = female, 1 = male
cp	Chest pain type	Nominal	1 = typical angina, 2 = atypical angina, 3 = non-angina pain, 4 = asymptomatic
trestbps	Resting blood pressure in mm Hg on admission to the hospital	Numeric	94 to 200
chol	Serum cholesterol in mg/dL	Numeric	126 to 564
fbs	Fasting blood sugar > 120 mg/dL	Nominal	0 = false, 1 = true
restecg	Resting electrocardiographic results	Nominal	0 = normal, 1 = ST-T wave abnormality, 2 = definite left ventricular hypertrophy by Estes' criteria
thalach	Maximum heart rate achieved	Numeric	71 to 202
exang	Exercise induces angina	Nominal	0 = no 1 = yes
oldpeak	ST depression induced by exercise relative to rest	Numeric	0 to 6.2
slope	The slope of the peak exercise ST segment	Nominal	1 = upsloping, 2 = flat, 3 = downsloping
ca	Number of major vessels colored by fluoroscopy	Nominal	0–3
thal	The heart status	Nominal	3 = normal, 6 = fixed defect, 7 = reversible defect
target	Prediction attribute	Nominal	0 = no risk of heart disease, 1 to 4 = risk of heart disease

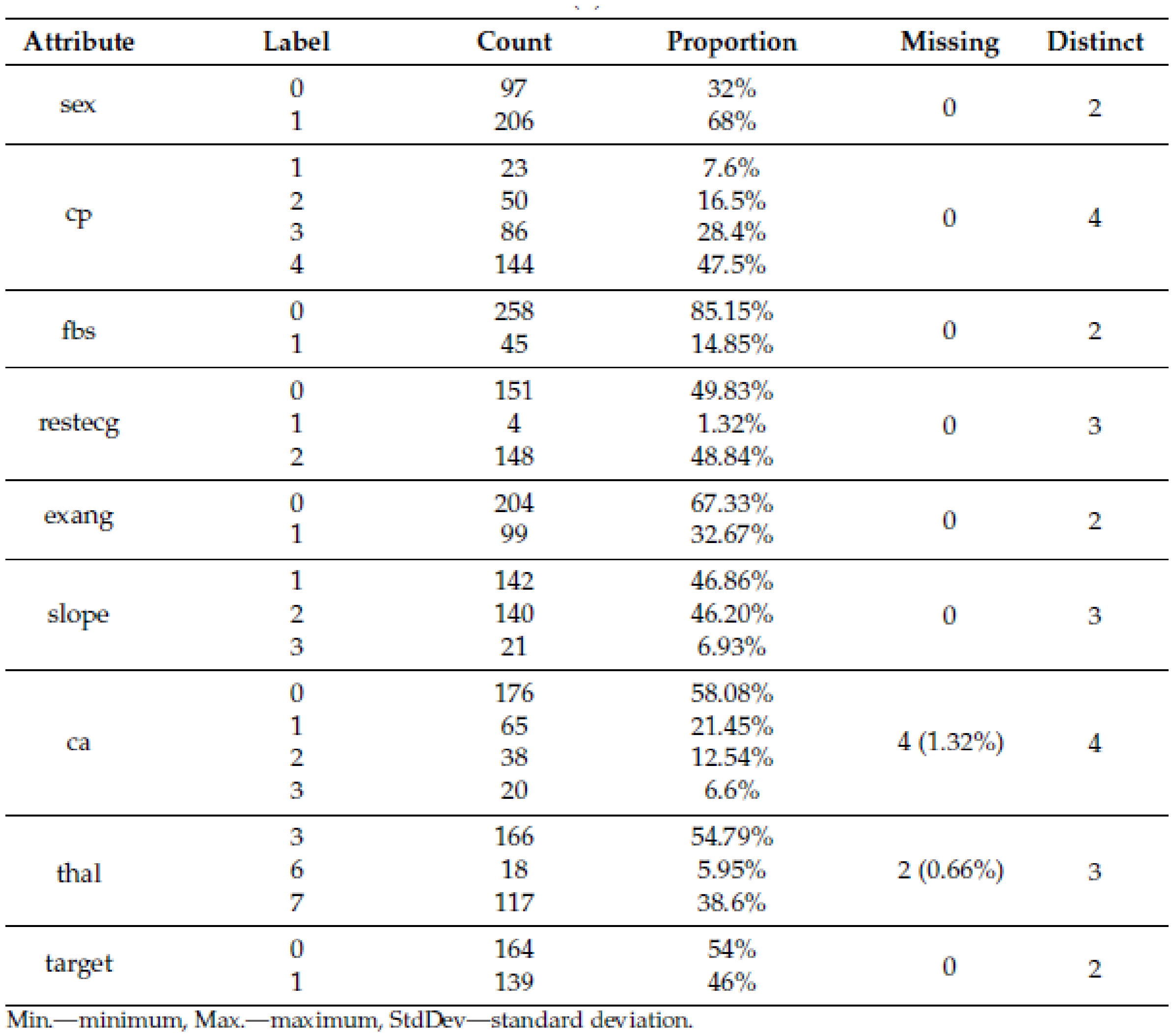
Features with less than ten classes are categorical or nominal types. Gender-based classes make up the property "sex", with 1 denoting male and 0 denoting female. Four types of chest pain are included in the characteristic "cp": traditional angina, atypical angina, non-angina pain, and undiagnosed. Based on whether the fasting blood sugar is more than 120 mg/dL, the attribute "fbs" has two classes: 1 = true and 0 = false. Resting ECG data is categorized by the property "restecg" as 0 = normal, 1 = aberrant ST-T wave, and 2 = obvious left ventricular hypertension. Based on exercise-induced angina, the characteristic "exang" is divided into two classes: 1 = yes and 0 = no. The attribute "slope" includes upslope, flat, and downslope peak training ST segment elevations. The characteristic "ca." has four classes based on the number of fluoroscopy-colored major vessels (0–3). Three levels of heart status are included in the attribute "thal": normal (3), fixed (6), and reversible (7). Five prediction classes make up the attribute "target": The numbers 1 through 4 indicate heart disease risk at different phases, whereas 0 indicates no risk at all. The results in the range of 1 to 4 were converted to 1 since the finding determining whether a patient was at risk of developing heart disease was the primary objective of this investigation. Consequently, there were only two classes in the "target" attribute: 0 and 1. Attributes of the numeric/integer type include "age," "trestbps," "chol," "thalach," and "oldpeak".

Table 2(a) presents the statistical features of the numerical properties, comprising the values that are missing, distinct, unique, mean, minimum, maximum, and standard deviation. The Cleveland dataset's numerical properties have no missing values.

Table 2. (a) The numerical characteristics' statistical outline. (a) The statistical overview of the nominal attributes.



Attribute	Min.	Max.	Mean	StdDev	Missing	Distinct	Unique
age	29	77	54.439	9.039	0	41	4 (1%)
trestbps	94	200	131.69	17.6	0	50	17 (6%)
chol	126	564	246.693	51.777	0	152	61 (20%)
thalach	71	202	149.607	22.875	0	91	28 (9%)
oldpeak	0	6.2	1.04	1.161	0	40	10 (3%)



Attribute	Label	Count	Proportion	Missing	Distinct
sex	0 1	97 206	32% 68%	0	2
cp	1 2 3 4	23 50 86 144	7.6% 16.5% 28.4% 47.5%	0	4
fbs	0 1	258 45	85.15% 14.85%	0	2
restecg	0 1 2	151 4 148	49.83% 1.32% 48.84%	0	3
exang	0 1	204 99	67.33% 32.67%	0	2
slope	1 2 3	142 140 21	46.86% 46.20% 6.93%	0	3
ca	0 1 2 3	176 65 38 20	58.08% 21.45% 12.54% 6.6%	4 (1.32%)	4
thal	3 6 7	166 18 117	54.79% 5.95% 38.6%	2 (0.66%)	3
target	0 1	164 139	54% 46%	0	2

Min.—minimum, Max.—maximum, StdDev—standard deviation.

Table 2(b) presents the nominal attributes' label, count, missing, and different values, among other statistical characteristics. Two (2) occurrences from the "thal" element and four (4) from the "ca" attribute were among the six (6) occurrences out of 303, or 2% of the whole dataset, that were found to contain missing values. Labels 139 (heart disease risk) and 0 (no risk of heart disease) comprised 164 and 46% of the dataset, respectively, for the target class labels.

3.3.2. Data pre-processing

The process of transforming unstructured data into an appropriate format for analysis is referred to as data preparation. Raw data is a crucial phase in data mining and machine learning because it often includes errors, noise, and missing values that might affect model performance. Quality assurance for data prior to algorithmic analysis leads to more dependable and accurate results. Moreover, pre-processing decreases the complexity and dimensionality of data, thus increasing the efficiency of the analysis process, but maintaining important data intact. The decreased size of the processed data decreases costs associated with its storage and processing as well. A comprehensive data set used for analysis is constructed using many data sources. Because quality and amount of data influence the analytical results, this process is very important. Quality and abundant data sets will produce more accurate results. In the proposed methodology, Z-Score normalization is employed to standardize the data set and put its characteristics into a standard range.

- **Z-Score Normalization**

The raw intensity values gathered in each experiment were first normalized to maintain consistency among all the gathered data sets. The first step in normalization was determining the mean intensity for each data set. The mean for all the mean intensities was calculated next. This mean acted as the standard for calculating the normalization factors that were then used to normalize the other data sets such that their means equalled the overall mean. In order to standardize the data sets, the z-score technique was used. A z-score is the position of a certain value within a normal distribution and is measured in standard deviations away from the mean. Z-scores normally vary between −3 and +3. The computation of a z-score requires the population mean (μ) and standard deviation (σ).

The i-th component of each feature vector x ∈ R D is represented by xi (i = 1, 2, · · ·, D). First, these D components' mean and standard deviation are determined:

$$\mu_x = \frac{1}{D}\sum_{i=1}^{D} x_i, \sigma_x = \sqrt{\frac{1}{D}\sum_{i=1}^{D} (x_i - \mu_x)^2} \qquad (1)$$

The following step is Z-score normalization as

$$x^{(zn)} = ZN(x) = \frac{x - \mu_x 1}{\sigma_x} \qquad (2)$$

From these calculations that z-score normalization first projects a hyperplane perpendicular to √ 1 comprises the origin and the original feature vectors along the 1 vector. The length of normalized vectors is equal to D, resulting in a hypersphere with a radius of √ D. After preprocessing the given data and then feature selection process is carriedon which is described in the below section.

3.3.3. Feature Extraction using modified principal component analysis

A common statistical method for reducing dimensionality is principle Component Analysis (PCA), it reduces correlated data into principle components based on orthogonal and uncorrelated variables. The first principal component of the transformation is intended to represent the greatest amount of variation in the original data. While staying orthogonal to all previously derived components, each succeeding component explains the maximum amount of residual variation. In this case, data can be reduced to lower dimensions with a preservation of only the essential data information, thereby making it more useful when applied to machine learning applications. This process entails combining the original variables using a linear combination method to create the principal components created through the use of PCA, which create an orthogonal and uncorrelated feature set. Because PCA is scale-dependent on the original input features, normalization is done prior to PCA implementation. PCA has numerous applications in exploratory data analysis, data mining, feature extraction, and modeling by decreasing dimensions with retaining important information. Another use of PCA includes representing the connection or similarity between various populations or datasets through visual representation. In general, PCA computations involve singular value decomposition (SVD) performed on the normalized matrix data or eigenvalue decomposition of the covariance (correlation) matrix. Before performing the computations for PCA, standardization is performed where each attribute is subtracted with their respective mean values leading to mean-centered attributes with an average of zero. Normalizing each attribute with unit variance can help to have uniform contribution of all attributes. The output of PCA is generally interpreted through component scores and loadings. Component scores represent the transformed coordinates of individual observations in the reduced-dimensional feature space, in contrast, loadings measure each standardized variable's contribution to the associated main component. When component scores are normalized to unit variance, the loadings reflect the components' explanation of the variance and are associated with the corresponding eigenvalues. Alternatively, if the component scores retain their original variance, the loadings are normalized to unit length and correspond to eigenvectors, which define the orthogonal transformation between the original feature space and the principal component space.

PCA is a popular multivariate statistical method for reducing dimensionality that is based on eigenvectors. Its primary objective is to uncover the underlying structure of a dataset by identifying directions that capture the maximum variance. By reducing the number of primary components in high-dimensional data, PCA provides a compact representation while retaining the most significant information. This reduced-dimensional projection facilitates data visualization, interpretation, and analysis without substantial loss of information. Owing to its ability to extract latent patterns, PCA is also closely associated with factor analysis and other feature extraction methods. PCA resembles Canonical Correlation Analysis. CCA optimizes cross-covariance across two datasets, whereas PCA optimizes variance in a single dataset using a new orthogonal coordinate system.

Consider V = {vi, 1 ≤ i ≤ s} be a set of s nodes in the distributed structure that are all able to interact with a central coordinator v_0. Pi is the local data matrix. On each node vi, there is Rni×d with nidata points in d dimension (ni>d). The global data P∈$R^{n\times d}$ is then produced by concatenating the local data matrix, $P^T = [P_1^T, P_2^T, \ldots \ldots\ P_s^T]$ and $n = \sum_{i=1}^{s} n_i$. Pi represents the i-th row of P. In this instance, consider that there is a zero mean since the data points are equal, therefore $\sum_{i=1}^{s} p_i = 0$. The algorithms, which are dominated by those in the previous stages in terms of communication and computation costs, must be modified rank-one for uncentered data.

- **Constructing the Kernel Matrix**

Let $\phi(x)$ be a nonlinear transition from D-dimensional to M-dimensional, where M≫D. Each data point x_i is then projected to a point $\phi(x_i)$. In the new feature space, do normal PCA, however this may be very expensive and ineffective. Luckily, the computation may be made simplified by using kernel approaches.

First, assume a zero mean for the anticipated new features,

$$\frac{1}{N}\sum_{i=1}^{N} \phi(x_i) = 0. \tag{3}$$

The projected features' covariance matrix, M × M, is determined by

$$C = \frac{1}{N}\sum_{i=1}^{N} \phi(x_i)\phi(x_i)^T. \tag{4}$$

The eigenvectors and eigenvalues of it are provided by

$$Cv_k = \lambda_k v_{k.} \tag{5}$$

with k = 1, 2, · ·— The M. Equations (4) and (5) have

$$\frac{1}{N}\sum_{i=1}^{N} \phi(x_i)\{\phi(x_i)^T v_k\} = \lambda_k v_k, \tag{6}$$

which may be changed to

$$v_k = a_{ki}\phi(x_i) \qquad .(7)$$

Now, by changing vk in Equation (6) with Equation (7), have

$$\frac{1}{N}\sum_{i=1}^{N} \phi(x_i)\phi(x_i)^T \sum_{j=1}^{N} a_{kj}\phi(x_j) = \lambda_k \sum_{i=1}^{N} a_{ki}\phi(x_i). \tag{8}$$

The kernel function's definition is,

$$k(x_i, x_j) = \phi(x_i)^T\phi(x_j), \tag{9}$$

Equation (9) may be multiplied on both sides by $(x_l)^{\,T}$.

$$\frac{1}{N}\sum_{i=1}^{N} k(X_l, X_i)\sum_{j=1}^{N} a_{kj}k(X_i, X_j) = \lambda_k \sum_{i=1}^{N} a_{ki}k(X_l, X_i) \tag{10}$$

In this case, using the notation for matrices as,

$$K^2 a_k = \lambda_k N K a_k \tag{11}$$

where

$$K_{i,j} = k(X_i, X_j) \qquad (12)$$

a_k is the column vector of a_{ki} in N dimensions:

$$a_k = [a_{k1} a_{k2} \dots a_{kN}]^T \qquad (13)$$

a_k is resolvable by

$$K a_k = \lambda_k N a_{k,} \qquad (14)$$

the main elements of the resultant kernel may be computed using

$$y_k(X) = \phi(X)^T v_k = \sum_{i=1}^{N} a_{ki} k(X, X_i). \qquad (15)$$

Kernel techniques are effective because they eliminate the need for explicit computation of ϕ(x_i). Using the training data set {xi}, directly create the kernel matrix. Two popular kernels are the polynomial kernel and $\phi(x_i)$

$$k(x, y) = (x^T y)^d \qquad (16)$$

$$\text{or } k(x, y) = (x^T y + c)^d, \qquad (17)$$

where the Gaussian kernel and the constant c>0

$$k(x, y) = exp\,(-\frac{\|x-y\|^2}{2\sigma^2}) \qquad (18)$$

Compute PCA and l_2-Error Fitting with parameter σ. For a matrix A = [a_{ij}], the ith singular value of A is denoted by σ_i(A), and the Frobenius norm of A = [aij] is represented by $\|A\|_F^2 = \sum_{i,j} a_{ij}^2$ [26]. Let the matrix containing the first t columns of A be represented by $A^{(t)}$. X's columns span a linear subspace is represented by L_X. Let π_L(p) be the projection of a point p onto subspace L, and πX(p) be the abbreviation for π_{LX} (p). The squared distance between a point p ∈ R^d and a subspace L ⊆ R^d is represented by

$$d^2(p, L) := \frac{min}{q \epsilon L} \|p - q\|_2^2 = \|p - \pi_L(p)\|_2^2. \qquad (19)$$

Explanation 1. The r-Subspace k-Clustering on P ∈$R^{n\times d}$ is linear (or affine).

$$P_L^{d^2(P,L) := \sum_{i=1}^{n} \frac{min\, d^2(p_i,L)}{L \epsilon L}} \qquad (20)$$

where $L = \{L_j\}_{j=1}^{k}$ is a set of r-dimensional linear (or affine) subdomains, each with k centers, and P is a n × d matrix whose rows are $p_1, \dots, p_n$.

When k = 1 and the center is an r-dimensional subspace, PCA is a unique case. The Singular Value Decomposition (SVD) may be used to determine this ideal r-dimensional subspace, this is performed by the primary components, or top r right singular vectors of P. Point-based k-means clustering is another such instance. Focus on relative-error approximation techniques, finding a set L' of k centers with $d^2\,(P, L') \leq (1 + \epsilon)\, min_L d^2\,(P, L)$.

The approximation distributed PCA method is implied in [28]: each server i determines and transmits to the coordinator its top $O(r/\epsilon)$ principal elements Y_i of P_i. The coordinator produces an $O(sr/\epsilon) \times d$ matrix Y by layering the $O(r/\epsilon) \times d$ matrices Yi on top of one another. Select and return the top r main Y components to the servers. The PCA issue is therefore approximated in terms of relative error.

- **Improved Communication:** Distributed PCA-based K-means clustering and l_2-fitting communication cost reduction. To achieve a (1+)ϵ - project the rows onto the top of a data matrix P as an approximation $O(k/\epsilon^2)$ main elements and solve the k-means problem this way. In a distributed situation, Algorithm IDK-PCA with parameter $r = O(k/\epsilon^2)$ is needed to calculate global principal components, which requires at least $O(skd/\epsilon^3)$ communications. In this subspace, solve a distributed K-Means problem, then utilize an α-approximation to estimate the overall α(1 + ϵ) estimate.

- **Improved Computation**: SVD of its point set Pi is a substantial bottleneck, taking $min(n_i d^2, n_i^2 d)$ time. Try Algorithm IDK-PCA with each server sampling an Oblivious Subspace Embedding (OSE) matrix first. Use H_iP_i rows to run the algorithm on. H_iP_i may be computed in $nnz(P_i)$ time by selecting Hi to have each column have one non-zero item using known OSEs. Moreover, H_i row count is $O(\frac{d^2}{\epsilon^2})$, which may be much smaller than the initial number. For $O(nnz(P_i)\, log^{O(1)}\, d/\epsilon)$ time, this number of rows may be lowered to O(d). The number of non-zero elements in H_iP_i is equal to P_i. Algorithm 1. describes MDK-PCA.

```
Algorithm 1. Modified Distributed Kernel based Principal Component Analysis (MDK-PCA)
Input: Number of Attributes
Output: Optimal features
Step 1: Initialization
Step 2: Find the feature vector's mean.
    $\mu = \frac{1}{p}\sum_{k=1}^{p} x_k,$
    where x is the feature matrix, p is the number of patterns, and $x_k$ is a pattern (k = 1 to p).
Step 3: Find the matrix of covariance $C = \frac{1}{p}\sum_{k=1}^{p} \{x_k - \mu\}\{x_k - \mu\}^T$
    where matrix transposition is represented by T.
Step 4: Determine the covariance matrix's Eigen values $\lambda_i$ and Eigen vectors $v_i$.
    $Cv_i = \lambda_i v_i$    (i=1,2,3,…,q), q = number of features
Step 5: High valued eigen vector estimation
    (i)   Set each eigenvalue $\lambda_i$ in decreasing order.
    (ii)  Select a threshold value $\theta$
    (iii) To achieve the connection, the number of high-valued $\lambda_i$ may be selected.
    $[\sum_{i=1}^{s} \lambda_i][\sum_{i=1}^{q} \lambda_j]^{-1} \geq \theta$, where s = number of high valued $\lambda_i$ chosen
    $(iv)$ Determine the eigen vectors that match selected high-valued $\lambda_i$.
Step 6: Computation of global particles // Modified distributed kernel
    Compute the kernel that has the similarity value $r = O(k/\epsilon^2)$ of the attributes.
    If the covariance value of the attribute and kernel value is higher, the classification accuracy is high
Step 7: From the updated feature matrix $p = v^T x$, using x as the feature vector and v as the principal component matrix, extract low dimensional feature vectors (principal components).
Step 8: Return top k principal components.
Step 9: End
```

3.3.4. Classification using Hybrid deep learning

The hybrid approach leverages the strengths of both models, where LSTM is used to analyze sequential physiological signals GAN generates realistic synthetic data and improves model resilience, while body temperature, oxygen saturation, and heart rate are used. By incorporating GAN-based data augmentation, the system can effectively handle limited or imbalanced medical datasets and improve predictive performance.

a) LSTM based Deep Learning

DL uses a backpropagation algorithm to automatically refine the interior parameters of computational models with many layers of data processing to detect recurrent structures from a large amount of training data [29]. To improve the representation's selectivity and invariance, each network layer nonlinearly modifies the signal. The network may produce a hierarchy of representations with enough layers to make the model both sensitive to minute details and insensitive to significant alterations. Since it focuses on determining which predetermined sample category a new sample belongs to base on a train set that contains a certain number of previous samples, the classification problem is a crucial part of deep learning. As each sample in the train set has a label and each category is predetermined, the classification issue is also referred to as supervised classification. The following formula in (21) defines the output:

$$Y = f(\sum_{j} w_j + b) \qquad (21)$$

When f is a designated activation function, b is a bias value, and w_j is the network weights. Several neurons are combined to create a so-called hidden layer, which is a natural extension of this basic paradigm. This research presents deep learning using the LSTM model for predictability of heart diseases.

A deep learning artificial RNN architecture is identified as LSTM. LSTM has feedback connections, resemble feedforward neural networks in general. Time series requires a model that can handle data sequentially as they enhance the intricacy of the input variables' sequence dependence. Sequential processing power is a feature of MLP and other vanilla neural networks. Considering the current time and the hidden state from the previous timestamp, recurrent neural networks predict at each step. The LSTM model structure is shown in Figure 2.

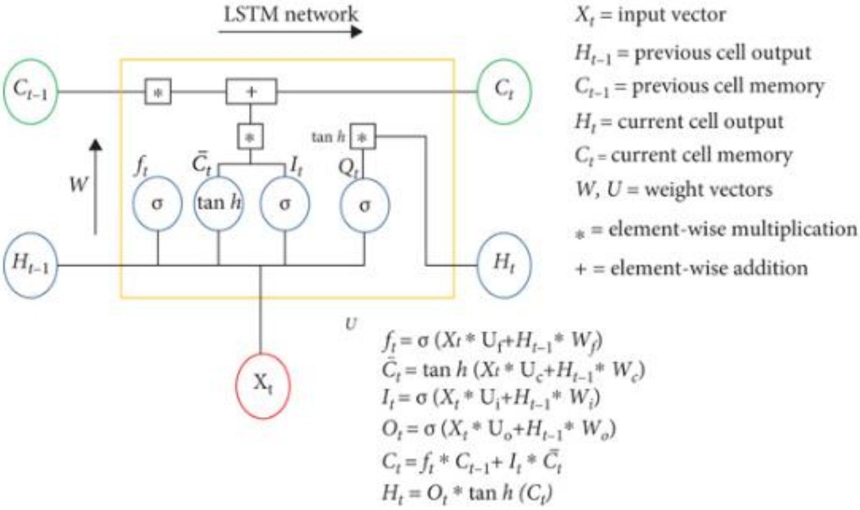


Figure 2. The overall structure of the LSTM model.

To prevent LSTMs from overfitting, the dropout strategy is challenging. During network training, a dropout occurs when input and recurrent connections to LSTM units are probabilistically excluded from activation and weight updates. To address the aforementioned issue, this paper proposed a generative adversarial network (GAN).

b) Generative Adversarial Network (GAN)

GAN is a framework for producing comparable samples by learning from an unknown data distribution. A GAN is mostly composed of the generator and discriminator. The generator's primary purpose is to produce samples with distributions that are as similar to the actual data as feasible [30]. The discriminator is used to separate the genuine and fraudulent data from the combined data of the produced and original samples. Independent alternating iterative training maximizes discrimination model D and generation model G, both of which are completely independent. For the whole network, the loss function may be written as follows:

$$L(D,G) = E_{x\sim P_r}\left[log\, log\, \left(D(x)\right)\right] + \; E_{x\sim P_g}\left[log\, log\, \left(D(x')\right)\right] \tag{22}$$

x is actual data and x′ is generator G's deceptive sample data. Pr and Pg are real and created data distributions, respectively. It is challenging for D to determine whether the samples are authentic or fraudulent when P_r and P_g have the same distribution, meaning that the generator can produce a sufficient number of realistic instances.

The advantages of ACGAN combines conditional generative adversarial networks (CGAN), semi-supervised producing adversarial networks (SGAN), and information maximizing generative adversarial networks (infoGAN). Each produced sample has a matching class label in the ACGAN framework. To differentiate between various produced samples, one-hot encoding is used to determine the category label of the generated samples. Sample Xfake = G(z, c) is created by generator G using noise z and class label c, and discriminator D delivers the probability of both actual and fake samples as well as the class label.

$$D(X) = P(X).P(C|X) \tag{23}$$

P(S|X) represents the probability that D will be able to determine if the sample is actual data, and P(C|X) represents a probability that D will be able to recognize the sample's class label. Whereas CGAN, ACGAN's discriminator can differentiate not only between other sample categories but also between "real and fake" samples. Instead than giving the discriminator the class information, the ACGAN approach assigns the discriminator the task of reconstructing the label information. Log probability L_s of accurate source and L_c of correct class comprises the ACGAN discriminator's objective function.

$$L_s = E[logp(X_{real})] + E\left[logp\left(X_{fake}\right)\right] \tag{24}$$

$$L_c = E[logp(X_{real})] + E\left[logp\left(X_{fake}\right)\right] \tag{25}$$

Discriminator D's training objective is to maximize $L_s + L_c$, whereas generator G's training objective is to maximize $L_s - L_c$. Fig. 8 depicts the suggested ACGAN model's structure.

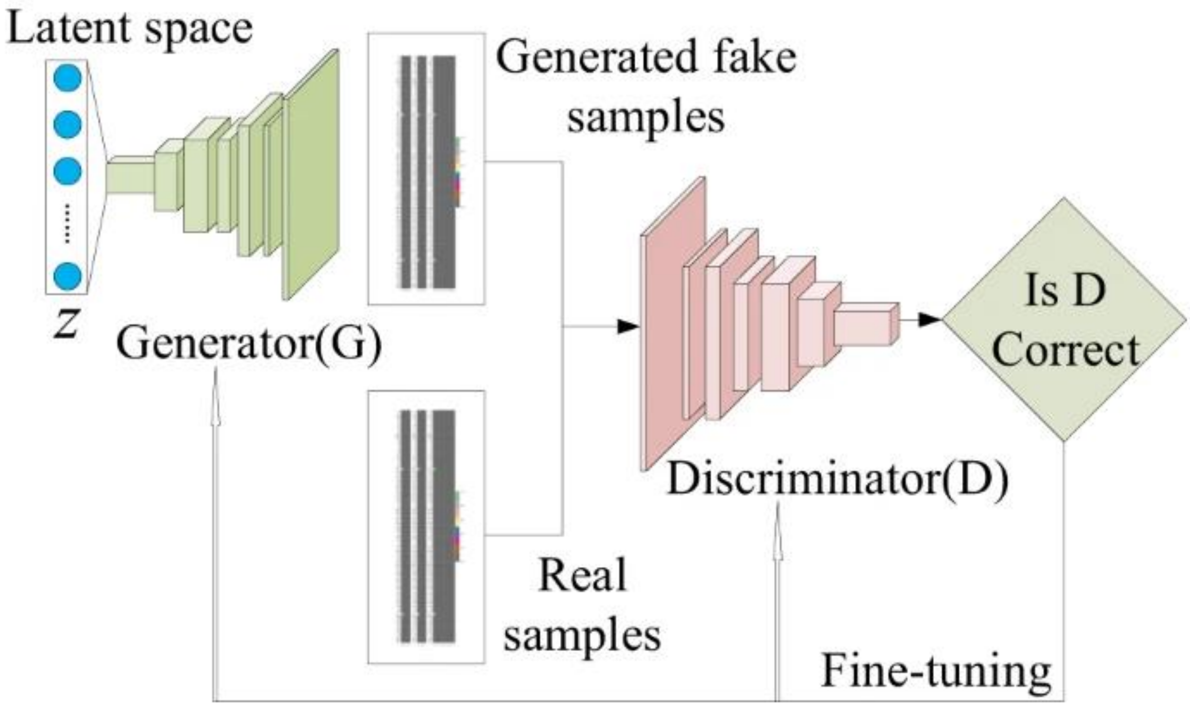


Figure 3. the structure of ACGAN

To improve the generation of high-quality tabular data, an additional generator objective, referred to as the information loss, is introduced. As illustrated in Fig. 3, the feature extraction module, which comes before the discriminator's classification layer, is represented by the neural network in the red box. This intermediate (virtual) network is designed to capture informative data representations prior to the final classification stage. The extracted features enable the output layer to perform both authenticity detection (real or generated data) and class label classification. Consequently, the hidden layers capture the most informative characteristics of the input samples. Leveraging these feature representations, a new loss function is formulated to evaluate and preserve the essential feature information during the training process. The resulting data distribution is encouraged to closely resemble the original dataset by the information loss, which acts as a regularization term. To formulate this loss, the discrepancy between real and generated samples is quantified using both distance- and similarity-based measures. Accordingly, the distance loss component is expressed as follows:

$$L_{dis} = \|E(f_x)_{x\sim p_r(x)} - E(f_{x'})_{x'\sim p_r(x')}\|_2 \qquad (26)$$

where E(·) denotes the average features of all samples from a batch, and fx and fx ′ indicate the high-dimensional features of the original samples and the samples produced by the generator, respectively. The Euclidean norm, also referred to as the L-2 norm, is used to determine the feature distance between the two types of data. The first-order statistics between the original data and the generated data features are therefore measured by L_{dis}. Furthermore, describe how the similarity measure between two types of data works. In this research, the degree to which the produced data resembles the original data is determined using cosine similarity.

4. RESULTS AND DISCUSSION

This section provides a detailed study of the proposed model. The HLSTM-GAN system is evaluated using the Cleveland heart disease dataset from the UCI Machine Learning Repository, which is implemented in MATLAB. Its performance is compared with conventional CNN and LSTM models using precision, recall, accuracy, and F-measure as evaluation metrics. The dataset is multivariate in nature, containing multiple clinical and physiological variables for analysis. The number of major vessels, thalassemia-related data, exercise-induced angina, ST-segment depression (oldpeak), resting blood pressure, serum cholesterol, fasting blood glucose, maximum heart rate, and peak exercise ST segment slope are among its 14 features. The Cleveland heart disease dataset has 920 entries. Table 1 shows the models' comparative performance results.

1) Precisions

Precisions are determined using percentages of pertinent results.

$$\text{Precision}=\frac{Truepositive}{truepositive+falsepositive} \tag{27}$$

2) Recalls

Recalls are defined as the proportion of all relevant results that the proposed algorithm correctly classifies.

$$\text{Recall}=\frac{Truepositive}{truepositive+FalseNegative} \tag{28}$$

3) Accuracies

The percentages of predictions that models correctly produce represent accuracy, and they are described as:

$$\text{Accuracy}=\frac{Truepositive+TrueNegative}{Total} \tag{29}$$

4) F measures

F-scores are determined as the harmonic mean of a system's accuracy and recall.

$$2 \text{ x } [(\text{Precision x Recall}) / (\text{Precision + Recall})] \tag{30}$$

5) Error rates

Prediction errors of models with respect to models are assessed and computed as error rates.

$$\text{Error rate} = 100 – \text{Accuracy} \tag{31}$$

Table.1. Performance comparison results

Metrics	Methods		
	LSTM	**CNN**	**HLSTM-GAN**
Accuracy (%)	85	87	89
Precision (%)	82	85	88
Recall (%)	86	87	90
F –measure (%)	87	89	92
Error rate (%)	15	13	11

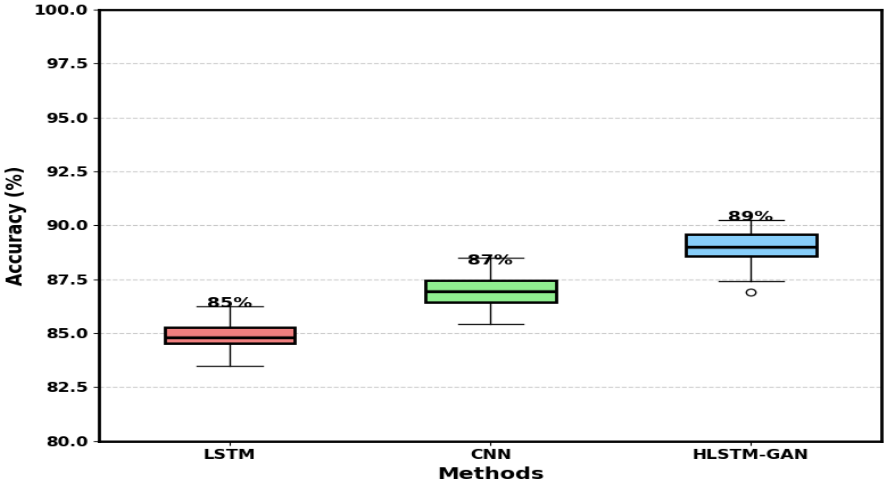


Figure.4. Accuracy results

Figure 4 demonstrates that the proposed HLSTM-GAN model surpasses the comparable techniques in terms of accuracy, indicating its effectiveness in identifying heart disease-related patterns. By learning feature representations from the training data and feature space, the model efficiently captures relevant characteristics and accurately detects variations in the input features. Furthermore, the model utilizes relevant features selected through PCA. By employing covariance matrices for feature transformation, PCA effectively reduces data dimensionality and minimizes redundancy. As a result, the proposed HLSTM-GAN achieves a heart disease recognition accuracy of 89%, outperforming the LSTM and CNN models, which attain accuracies of 85% and 87%, respectively.

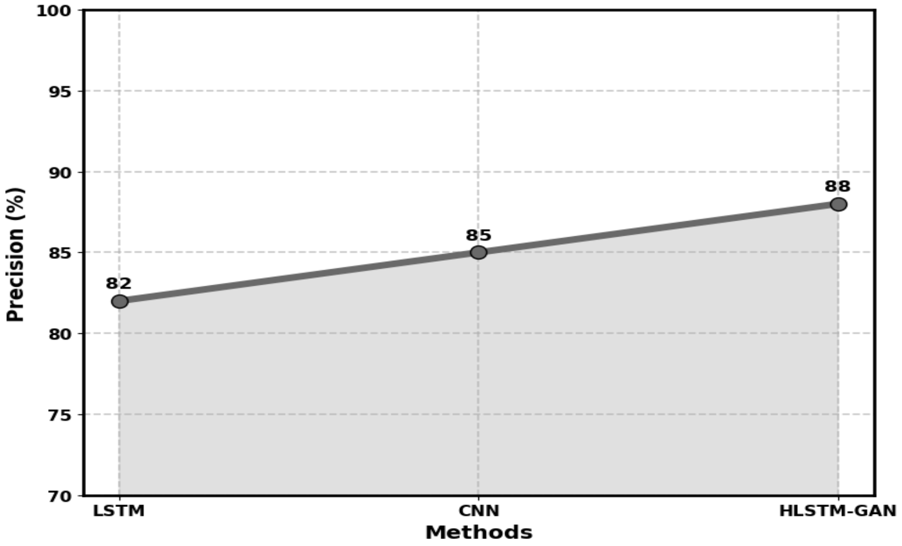


Figure.5. Precision results

The proposed HLSTM-GAN model's performance is compared to that of existing CNN and LSTM methods. The proposed approach's comparative performance is shown graphically. The various classification techniques are shown on the x-axis of the image, and their associated performance values are shown on the y-axis, demonstrating the superior effectiveness of the HLSTM-GAN model. In the proposed framework, the min–max normalization method is used to normalize input characteristics, which enhances the performance and accuracy of the HLSTM-GAN model. Based on experimental results, the suggested method produces an accuracy of 88%, outperforming the existing LSTM and CNN models, which attain precisions of 82% and 85%, respectively.

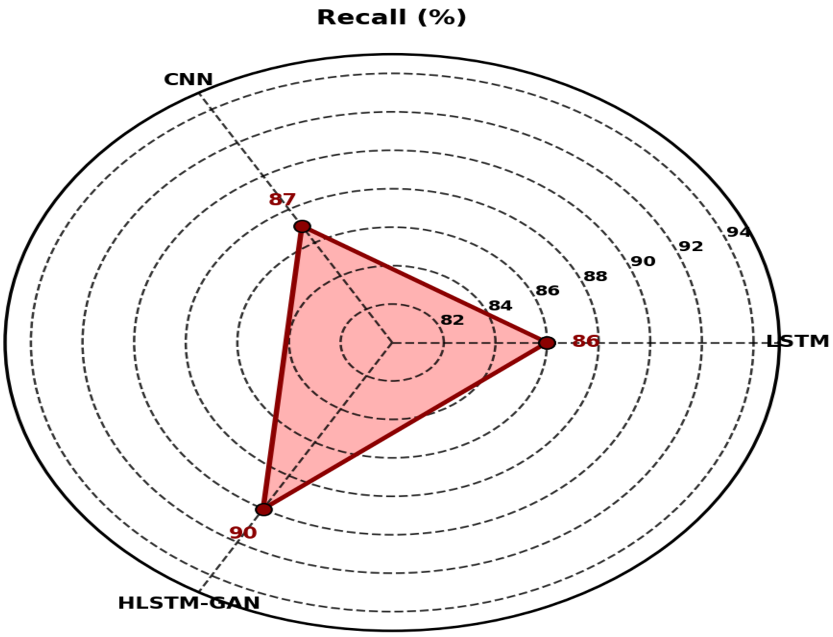


Figure 6. Recall results

Figure 6 presents the recall performance of the LSTM, CNN, and proposed HLSTM-GAN models for heart disease classification. The proposed approach effectively learns discriminative feature representations from the training data, enabling accurate classification of normal and abnormal cases. Owing to its enhanced feature extraction capability, the HLSTM-GAN model achieves a higher recall of 90%, outperforming the LSTM and CNN models, which achieve 86% and 87% recall rates, respectively.

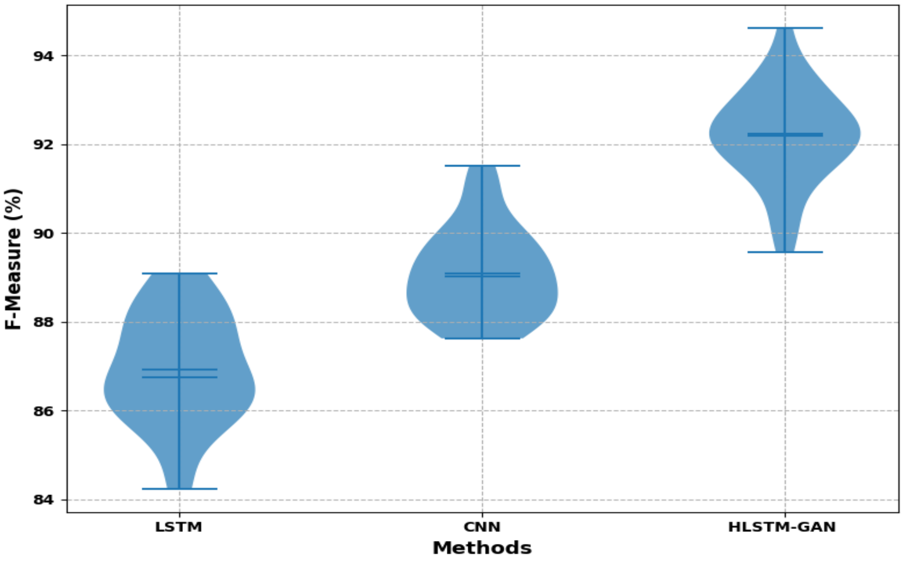


Figure 7. F-measure results

Figure 7 illustrates the F-measure performance of the proposed HLSTM-GAN model in comparison with the existing CNN and LSTM approaches. After training, the HLSTM-GAN effectively identifies disease-related patterns and delivers reliable classification performance. The obtained results demonstrate its potential applicability in intelligent medical data mining and healthcare decision-support systems. To assess the ability to discriminate of several machine learning models, a comparison study was conducted. The proposed HLSTM-GAN achieved an F-measure of 92%, surpassing the LSTM and CNN models, which recorded 87% and 89%, respectively. These results show that the proposed HLSTM-GAN strategy surpasses existing techniques in classification.

Figure 8 illustrates that the proposed HLSTM-GAN model achieves the lowest error rate of 11%, outperforming the CNN and LSTM models, which exhibit error rates of 13% and 15%, respectively. The reduced error rate is attributed to the effective optimization of network weights, biases, and learning parameters during training. Consequently, the model attains improved heart disease prediction performance, as reflected by its enhanced precision and recall values. Table 1 summarizes the obtained results. During training, the input data are processed through multiple feature representations to learn meaningful patterns, which are subsequently used for accurate classification of the test samples. Effective training enhances the model's learning capability and contributes to a lower classification error rate.

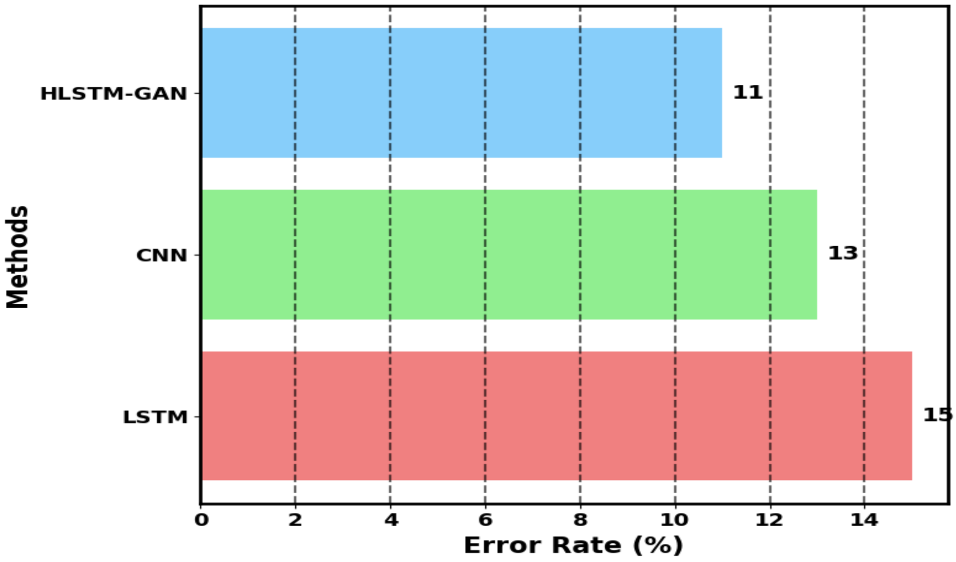


Figure 8. Error rate results

5. CONCLUSION

This research presented an intelligent hybrid Long Short-Term Memory and Generative Adversarial Network (HLSTM-GAN) framework for patient in-house monitoring and cardiac disease prediction. The proposed hybrid framework successfully integrated GAN-based data augmentation with LSTM-based temporal analysis to improve cardiac disease prediction performance. GAN techniques helped improve data quality with the creation of realistic synthetic health care data and solving problems of inadequate and unbalanced medical data sets. On the other hand, LSTM neural networks were able to identify long-term temporal relationships of ECG readings, heart rate, blood pressure, and other physiological signals as well as other health parameters of patients. The combination of both deep learning techniques led to the improvement of accuracy, reliability of predictions, and robustness of the system. Real-time analysis of patient health data provided by wearables and smart health care devices became possible through the proposed intelligent system. The framework supported early detection of abnormal cardiac conditions, reduced false alarm rates, and enhanced decision-making for healthcare professionals. Furthermore, the intelligent in-house monitoring architecture improved patient convenience, minimized unnecessary hospital visits, and contributed to efficient healthcare resource utilization. In terms of classifications precision, sensitivity, sensitivity, and prediction accuracy, the proposed hybrid LSTM-GAN model surpassed both individual deep learning and traditional machine learning techniques, according to experimental assessment. The framework also showed strong adaptability in handling noisy, incomplete, and heterogeneous healthcare data generated in real-world home monitoring environments.

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