Proceedings of the 3rd International Conference on Self Sustainable Artificial Intelligence Systems (ICSSAS-2025)
DVD Part Number: CFP25DN7-DVD; ISBN: 979-8-3315-3883-5

Optimized DenseNet Model for Heart Disease Prediction from Medical Health Records

R.Sivanathbabu, Research Scholar
Department of Computer Science
School of Computing Sciences
Vels Institute of Science, Technology & Advanced Studies (VISTAS)
Pallavaram, Chennai, India
meet.sivanath@gmail.com

Dr.S.Kamalakkannan, Professor
Department of Computer Science
School of Computing Sciences
Vels Institute of Science, Technology & Advanced Studies (VISTAS)
Pallavaram, Chennai, India
kannan.scs@vistas.ac.in

Abstract— **One of the most well-known and fatal illnesses in the world is Heart Disease (HD) claims the lives of countless people each year. To save lives, this disease must be identified early. Initial identification enables rapid intervention and ongoing clinical monitoring, both of which are crucial but frequently constrained by the incapacity of medical personnel to continuously supervise patients. Specialists can lower fatality rates by detecting cardiac issues early and keeping a close eye on their patients. HD detection is not always reliable, and doctors cannot be in regular contact with their patients. Machine Learning (ML) techniques offer an intriguing method to identifying risk factors because they offer a stronger basis for predicting and making decisions based on data supplied by medical organizations. In order to make accurate predictions about HD, this research work presents a Deep Learning (DL) model that utilizes the DenseNet (DN) architectures. Moreover, this research focused on developing the prototype model of patient likelihood in diagnosing the HD with the availability of medical records using DN model. The dataset of 70,000 cases from Kaggle is used to test the suggested DN model. The model's accuracy is greatly influenced by the DN technique and the features in the dataset that were employed to train the model. The suggested DN model achieves an accuracy of 91.86% over 150 epochs using batch size 1, surpassing all current models.**

Keywords— ***HD, DenseNet model, prediction, DL, Medical Health Record, diagnosis***

I. INTRODUCTION

The phrase "HD" describes a collection of conditions that impact the heart. The World Health Organization (WHO) predicts that HD causes seventeen million mortalities globally, creation it the top reason of mortality at the moment. Ischemic HD and stroke are the two greatest number of disorders that damage the heart and are collectively referred to as HD, or Cardiac Disease (CD). According to the WHO, tobacco use, drinking too much alcohol, a lack of exercise and poor diet are the main behavioural risk factors for CD. Regular exposure with these health risks, which include weight gain, increased blood lipids, hypertension, and high insulin levels, can be the initial indication of HD. The emergence of more than one of the following symptoms is considered a warning indication by the American Heart Association: loss of breath, constant coughing or wheezing, ankle and foot edema, exhaustion, decreased appetite, and cognitive difficulties. Additionally, coronaviruses can cause heart disease. Effective early detection can reduce the risk and global burden of heart disease with prompt initiation of treatment to prevent further health problems. Furthermore, coronary HD diagnosis relies on technology like CT scans and cardiac recordings, which are frequently too expensive and unfeasible for users. CVD can be treated with a variety of techniques, including angiogram. However, there are some limitations to this method. The majority of the primary negatives is the reality that it is expensive since while diagnosing the patient, the physician has to examine numerous aspects, such as cancer, high chorestrol, high blood pressure, kidney and liver disease. The whole process takes a lot of time, and there is no assurance that the illness will be fully treated. The WHO estimates that by 2030, there would be 23.6 million fatalities from HD overall, with HD and stroke accounting for the majority of the deaths.

Predicting the onset of heart illness has become one of the most serious and challenging issues confronting healthcare today. In many developed countries, HD is the leading cause of death. Early identification can be difficult, and medical staff making incorrect predictions owing to a shortage of knowledge might exacerbate patient worry. Due to a lack of trained staff and the additional assets required for accurate diagnosis and managing patients in impoverished nations.

The goal of this study is to determine and evaluate the organizational obstacles that impede medical organizations from adopting an effective approach that offers managers with strategic responses to these difficulties. The development of ML and AI has enabled researchers to utilize greater use of the accessible huge databases.

As a result, ML systems that can predict the possibility of receiving HD based on hazards must be developed. The healthcare areas faced significant challenges as a result of illness prediction's low accuracy. After selecting the appropriate features, classifications and hybrid models can be utilized to predict the chance of sickness recurrence. To develop classifiers and mixture models, researchers explored a wide range of methodologies. Insufficient medical datasets, feature selection, ML process implementations, and a lack of in-depth study are just some of the challenges that may prevent successful HD prediction. The purpose of this work is to fill up some of these gaps in understanding so that we may develop an improved model for predicting HD.

The main motivation for the research is forecasting when someone will acquire an illness is a challenging challenge that must be addressed before the disease progresses to a critical stage. People are safer after the illness has been predicted. The cost-effectiveness of early-stage prediction should not be underestimated. The inadequacy of traditional DL models to predict HD in its early stages. To solve the inadequacies of current models, this research introduces the DN model.

Below is a list of the contributions this paper produced.

- The Proximity Weighted Random Affine Shadow Sampling (PWRASS) balancing approach was employed in this research work. In order to render the minority class samples identical to the overall class, this method oversamples them.
- A novel method for predicting HD was put forth. Utilizing pre-trained CNNs known as the DN design, the suggested method concurrently utilizes feature extraction as well as classification capabilities.
- To see model generalizability, proposed model using different performance metrics.

II. Literature Review

HD is still the top cause of death worldwide, which emphasizes how urgently accurate and useful screening and prognostic tools are needed. The promise of ML and DL algorithms to enhance the prediction of HD has garnered significant interest in recent years. This overview of the literature shows the approaches, limitations, and conclusions of several research that use ML and DL to predict HD.

In DL, [1] proposes a Deep CNN for the early detection of HD with an accuracy of 90.12%. The research limited sample size and absence of participation from a varied belonging, however, cast doubt on the CNN algorithm's applicability in other contexts. Shah et al. [2] describes to usage ML algorithm to generate a model for HD prediction. The information utilized for this purpose came from the UCI ML source and was taken from the Cleveland HD dataset, containing seventeen parameters and 303 cases. The researchers used a range of supervised classification methods. According to the research's findings, the KKN model achieved accuracy at 90.8%. Nevertheless, Gunasekaran et al. [3] employed an improved CHIO-based approach that takes cognitive processes into account in order to forecast and assess HD on the Internet of Health Things (IoHT). Although possible problems with dataset integrity and complicated models, their ARDL-AM approach demonstrated promise in accurately predicting CVD in IoHT scenarios, suggesting potential advances in treatment effectiveness. Gjoreski et al. [4] describes ML and DL were the key elements of the suggested approach. Although ML acquired significant attributes, DL acquired from the spatiotemporal representation of signals. This approach outperformed the base model by 9.1% with an accuracy of 89.3% when used on the CHF dataset. During their participation in the 2014 i2b2/UTHealth NLP Challenge, Yang and Garibaldi [5] presented an information extraction approach designed for automatically identifying HD associated risks in medical records. In order to handle the complex medical environments included in a wide range of risk factors, these algorithms rely on a number of Natural Language Processing (NLP) techniques, including ML, dictionary-based keyword and rule-based detection technique.

At a total micro-averaged the F measurement of 0.915, the entire system demonstrated excellent results on the challenging test data, outperforming the top scheme (F-measure of 0.927) in this encounter job. DL models that could reliably forecast HD were used by Javed et al. [6]. This is due to the fact that DL models have shown promise in the medical field for forecasting a number of infections, counting type 2 diabetes, coronary thrombosis artery disease, lung cancer, and more. By attaining an accuracy 91% and accomplishment time of 1883 s on 30 periods with batch size 32, the suggested DB-Net surpasses all of the previous models. The number of parameters in a DL model is described by Krishnan et al. [7], who also offer an extensive approach for determining if a patient is healthy or not. The suggested method uses pre-trained CNNs called DenseNet121 to extract substantial characteristics from the best data. An additional complex feature set made up of the features obtained from every CNN can help the model. The trained classifiers were rated based on performance metrics. The categorizing outcomes of the proposed models were shown. The efficiency for organizational replicates taught with a lower feature set significantly increased with fewer training sessions than models trained on a full feature set. A novel approach to predicting HD is presented by Alghamdi et al. [8], which makes use of the combined powers of autoencoder and DenseNet topologies. The HD UCI Cleveland dataset, which contains 13 variable quantity including medical and demographic information are served as the basis for our investigation. By precisely identifying and characterizing complex trends in the data, this approach can enhance medical judgment and patient results in cardiovascular treatment. Ordas et al. [9] suggest assessing a patient's likelihood of HD developing by combining DL algorithms with feature increase approaches. The findings of the suggested methods show a considerable enhancement, particularly when it pertains to a disease that disturbs a wide population, outperforming conventional techniques by 4.4% and achieving a 90% precision. Nayak et al. [10] proposes an architecture for predicting HD utilizing primary risk indicators and various classifier methods. The findings show that the suggested unique optimization algorithm may offer an efficient healthcare tracking device for the early detection of HD. The greatest efficiency achieved with the suggested algorithm is 93.3%. Reddy et al. [11] discuss the identification and identification of three essential illnesses: HD, a respiratory infection, and retinopathy from diabetes. Every illness provides unique diagnosing challenges, such as differences in representations of data and the necessity for precise forecasts. To overcome these problems, the proposed system combines many DL architectures to create a comprehensive reliable diagnosing system. Honi and Szathmary [12] suggest designing customized CNN to perform the identification of critical factors using various preparation processes. To address the difficulty of gaining greater precision, we provide a method that use 1D-CNN and rigorous testing to maximize the network structure and improve the accuracy of prediction. The accuracy of the predictions has been estimated to be 99.95% when using a train-test technique, and roughly 98.53% while using K-Fold cross-validation techniques. Rahman et al. [13] use a unique self-attentiveness-based converter framework that incorporates self-cognitive processes and transformer networks to predict CVD risk. When evaluating the suggested model to multiple benchmark techniques, we attained the maximum precision at 96.51%. Chibueze et al. [14] use ML and AI, specifically DL, to improve diagnosing skills. Despite other research, this investigation identified caffeine as a potential threat that is frequently neglected in datasets. The CNN model obtained an impressive accuracy rating of 94% and minimal loss values while classifying cardiac MRI data. Jeyachandra et al. [15] proposes employing a DL algorithm-based CNN to identify heart illness. Clustering with K-means can be used to locate collections of data points across a dataset. Particle swarm optimization (PSO) is a technique for estimating responses to difficult or intractable computational reduction and maximizing issues. CNN maintains a precision of 97.7% and a recall of 94.17%, correspondingly. Xia et al. [16] used feature selection and hyperparameter optimization to identify CVD. The framework uses Bayesian optimization to rebuild the DLENN hyperparameters for CVD identification. The model provides a practical method for increasing CVD classification effectiveness and precision in real-world healthcare environments by using ACO for feature selection, min-max scalability for data pre-processing, and Bayes's optimization for hyperparameter tuning.

III. PROPOSED METHODOLOGY

The study objective is to automated HD identification, the present research seeks to determine the likelihood that patients may experience HD, which could be advantageous for both patients and healthcare providers. DN are suggested in our findings, as Figure 1 illustrates. The input dataset must be pre-processed before being sent to the DL models. This study work plan will clean the data, remove unnecessary details, and equalize the data in order to improve the approach. The dataset is utilizing has the issue of not being balanced. Instances of class 0 are substantially more numerous than those of class 1. This paper used the PWRASS balancing technique to alleviate class imbalance. In order to upsurge the precision and effectiveness of HD prediction, this work uses these data to construct a HD forecasting model using a DN architecture.

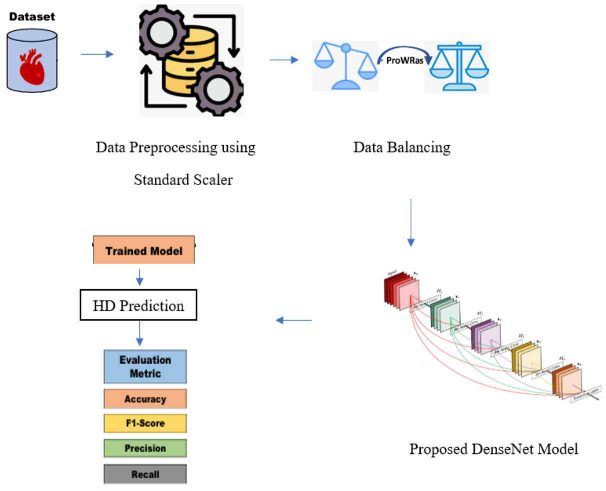

FIGURE 1. PROPOSED SYSTEM MODEL FOR HD PREDICTION

A. Dataset Description

According to [17], the dataset used in this investigation includes 70,000 medical records with 12 distinctive characteristics, as shown in Table 1. The dataset's range of clinical, diagnostic and demographic characteristics makes it appropriate for HD prediction models. Every example in the set represents a patient. These characteristics includes systolic and diastolic blood pressure, age and gender. The target class, "cardio," denotes whether a patient is healthy presented as 0 or at risk of developing HD presented as 1.

TABLE 1. DETAILS OF DATASETS

S.No	Features	Variable	Min and Max Values
1.	Gender	Gender	2: F, 1:M
2.	Age	AGE	Mn: 9,679 and Mx:24,523
3.	Weight	Weight	Mn:20 and Mx:150
4.	Glucose	Gluc	Values between 1.5(Mn) to 4(Mx)
5.	Height	Height	Mn:45 and Mx:200
6.	Physical activity	Active	Yes-1, No-0
7.	Smoking	Smoke	Yes-1, No-0
8.	Diastolic Blood Pressure	Ap_lo	Mn:-75 and Mx:10,000
9.	Alcohol intake	Alco	Yes-1, No-0
10.	Lipid	Chol	Value between 1.5(Mn) to 4 (Mx)
11.	Systolic Blood Pressure	Ap_hi	Mn: 140 and Mx:15,030
12.	Presence or absence of HD	Cardio	Yes-1, No-0

B. Removing Outliers

An important part of data cleansing is eliminating outliers. Data entry mistakes could have caused these outliers. Our forecasting model's performance could be enhanced by eliminating these outliers. We eliminated all occurrences of height, ap_hi, weight and ap_lo that did not fall within 2.5% and 97.5% in order to solve this problem. Exceptions were manually identified and removed during this process. Following this data cleansing procedure, there were 57,155 rows instead of 70,000. This research work used a standard scaler for scaling. Preprocessing is crucial since the dataset is extremely unbalanced, with class 0 containing 91% occurrences and class 1 containing 9% occurrences.

C. Pre-processing using Standard Scaler

The standard scaler is a widely used scaling of features technique for getting data ready for DL models. An entirely novel probability having an average of one and a mean of zero is produced by transforming every element in the dataset by removing the average of it and multiplying by the standard deviation.

$$X_{scaled} = \frac{X - \mu}{\sigma}$$

where X is the feature's value, μ signifies the mean for every feature, and σ signifies the standard deviation.

D. Data Balancing based on Proximity Weighted Random Affine Shadow Sampling (PWRASS) technique

One of the greatest crucial preprocessing processes is data balance [18]. When the number of instances of single class surpasses the numeral of instances of another class, data imbalancing problems arise. The dataset is unbalanced meanwhile there are more data instances in the majority class than in the minority class. The model will operate poorly and inefficiently if the dataset is not balanced. One of the main problems with authentic datasets is data imbalance. The problem of data imbalance is addressed by two distinct kinds of data balancing methods: under sampling and oversampling. In order to equalize the ratio of minority to majority classes, the research work employed the PWRASS data balancing technique. PWRASS is an oversampling method that groups minority class observations together. The clusters are formed based on the gap among the data points and the dominant class. Each group has a weight assigned to it. A significant weight is given to the group that most closely resembles the majority class. The number of fake specimens from every cluster is determined by weights. In borderline clusters, majority class artificial specimens with low variability are created to prevent overlapping [19]. Based whether or not the model provides four oversampling techniques, two parameters are max-conv and net-conv. Max-conv is used to determine how many shadow samples are used to create a unique fake data point. The purpose of the oversampling technique is to equalize the data for both classes. Findings from many classifiers can be reliable and effective.

E. DenseNet (DN) for HD Prediction

In order to solve the concatenation compactness issues with the suggested models, a DL architecture called DN also known as a tightly coupled convolutional network was created. DN's main concept is the dense connection pattern, in which every layer is feed-forward connected to every other layer. DN provides extensive links whereby data moves through levels progressively by connecting one layer directly to the next, in contrast to traditional architectures. This link architecture promotes differential flow, allows reusing characteristics, and promotes the network-wide distribution of attributes.

DN's connection architecture reduces disappearing gradient issues and promotes feature reuse, which enhances the recognition of intricate patterns in image data. In addition, ablation research would be very helpful in comprehending how well DN works individually, in contrast to CNNs or LSTMs. The effects of each model element would be investigated independently in this study, emphasizing their distinct roles and provide justification for their selection.

Equation (1) may be represented by = concat (0, 1,…, 1) for a Dense Block (DB), where H I denotes the operations carried out on the i-th layer of the DB and X denotes the feature that is being input translations to the DB.

$$Hi=concat(H0,H1,...,Hi1,X) \quad \text{……………………(1)}$$

Concat is the combining method utilized here, and many convolutional layering methods with the appropriate activation variables are employed to calculate each H i. DN uses transition layers to restrict feature map development and reduce their depths. These are usually placed between dense bricks. Equation (2) gives the equation for the transitioning layer.

$$Htrans=BN(1X1Conv(Hdense)) \quad \text{………………………(2)}$$

Here, BN denotes batch normalization, dense H is the outcome of the previous DB, and Conv denotes a convolutional coding process.

The rate of growth (k) in DN is the quantity of new feature maps generated by each layer in a DB. A DB's layers typically provide k output map features, where k is a pre-training parameter. DN's dense connectivity and growth rate affect its efficiency, enhanced parameter use, and ability to obtain rich hierarchies characteristics from the information being processed. Managing memory usage and algorithmic complexity is essential, though, especially as depths increase and development rates rise. The combination mechanism is a crucial part of DN that makes strong links between layers possible. Given an input attribute map X to the present layer and a set of feature maps H 0, H 1,…, H I 1 from the previous layers, the combination process is defined as follows in equation (3).

$$concat(H0,H1,\cdots,Hi1,X)=[H0,H1,\cdots,Hi1,X] \quad \text{………..(3)}$$

Batch Normalization (BN), an essential part of DN, stabilizes the process of learning and accelerates resolution. The BN equation (4) can be expressed as follows.

$$BN(H)=-H-\mu(\sigma\,2 + \varepsilon\,H)^{1}/2\mu\times\gamma+\beta \quad \text{…………(4)}$$

μ stands for the mean of the mini-mini-batch, σ2 for the variability, epsi for the value of constant that prevents separation by zero, and γ and β for limitations that can be learned. H stands for the input characteristic Maps.

One important procedure is the convolution procedure of a thick difficulties which uses convolutional filters to gather data from the input. For a convolutional layer with filtering F and speed of 1, the subsequent formula is applicable using equation (5).

$$Hi=Conv(Hconcat) \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots(5)$$

Where concatenated takes place, the resulting map of features is called H concat. Because they are essential to the dense connection and effective information flow of the DN design, these foundational equations place special emphasis on concatenated operation, normalizing batches, and convolution function. Each layer's input in a DN design is a concatenation of the feature maps from every layer below it along their channel length. Feature recycling is made possible by the dense feature diagram that this dense link produces. Since it retains all previous characteristics, it avoids the disappearing gradient issue. Additionally, the dense link architecture improves variable efficiency and model homogeneity. Additional DN components include DBs with many densely connected layers, transition layers that control the spatial dimensions, and a minimal number of feature translations. The entire architecture is built by stacking these impenetrable blocks and conversion levels. Improved feature development reduced disappearing gradient problems, greater variable consumption, and the ability to train very deep networks are just a few of the benefits that DN has shown.

F. Model building design

The DN construction, a densely connected CNN designed for reusing features and gradient flow efficacy, serves as the foundation for the DN model design used in our investigation. The design consists of several DBs with transitions layers to regulate the extent of the plots of features across every block's tightly associated convolutional layers. The elaborate layout of the model is displayed here:

Input layer: The input data, that includes a form (1, 1, 13), was created to be accommodated by the first layer of the model. 13 is the number of characteristics linked to this design, which shows that the information being input has been expressed in a 4D manner.

Initial convolution layer: This layer uses sixty-four filters overall, an offset of (2, 2), and a kernel size of (7, 7) for a 2-multidimensional inversion operation. The non-linear is then introduced by using a Rectified Linear Unit (ReLU) activation equation and regularization in batches. Figure 2 shows the suggested design the building's design.

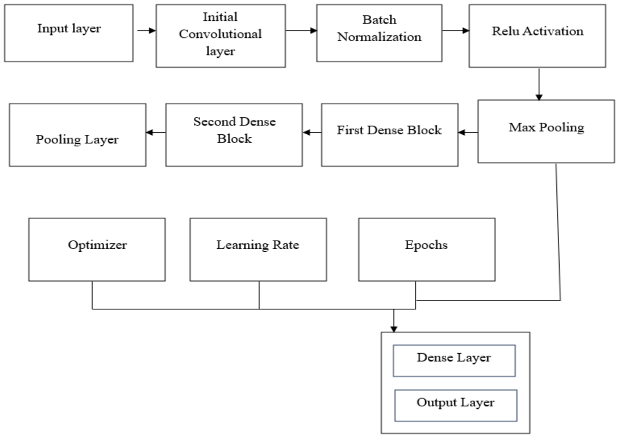

FIGURE 2 BLOCK DIAGRAM FOR PROPOSED DN MODEL

Pooling layer: While keeping the features' depth, the use of a maximum-pooling layer with a pool dimension of (3, 3) and an offset of (2, 2) minimizes the sizes of the space.
DB: The first DB It consists of six densely populated units. Every unit follows this sequence.

1. Normalization of batches and ReLU activation.
2. To cut down on the number of pathways, use 1x1 convolution, often known as the limit layer.
3. Normalization of batches and ReLU activation.
4. 3x3 convolution.
5. The final result and the original input are concatenated.

Second DB: There are twelve compressed units in the building. These compact block components are arranged similarly to the initial DB.

Layer of global average pooling: The spatial dimensions are compressed via global average pooling into a single vector, that is then fed into completely interconnected layers.

Layers that are fully connected: 512 units in a dense layer that is triggered by ReLU. output layer with multiple components equal to the total number of programs and a sigmoid activation function.

Model Hyper-parameters: The Adam optimization algorithm with a rate of learning of 0.0001 is used to build the DN model, which has been designed for binary categorization.

Using the supplied training data, x_train_4d and y_train, the framework is trained across 150 epochs. The hyperparameters that are utilized in the suggested model are shown in Table 2. This specific design enables effective feature sharing and utilization across the network by using the dense connection pattern. Binary classification is one of the many tasks for which DN is an extremely useful tool. DN deep and compact architecture is used in this study to forecast heart disease. DN compact and deep architecture makes it possible to effectively separate complicated details from the incoming data.

TABLE.2 HYPER-PARAMETERS FOR DN MODEL

S.No	Hyperparameters	value
1.	Learning rate	1e-5
2.	Optimizer	Adam
3.	Loss Function	sigmoid
4.	Epochs	150

IV. RESULTS AND DISCUSSIONS

This research work Python has been employed to implement the suggested system. Using the PyTorch framework, DN and other ML and DL models were created. The tests were then carried out to access a faster GPU utilizing Google Colab Pro. The DN-weights and biases were also optimized using the Adam optimizer, with a velocity of 0.9 and a learning rate of 0.001. The number of epochs was set to 150 and the batch size to 64. The following is the mathematical formula (6), (7) and (8) for updating weights based on the Adam optimizer.

$\theta_{t+1} = \theta_t + \Delta\theta_t$ ………………………..(6)

$v_t = \mu_1 * v_{t-1} - (1 - \mu_1) * g_t$ ……………………(7)

$s_t = \mu_2 * s_{t-1} - (1 - \mu_2) * g_t^2$ ……………………….(8)

v_t represents the first moment estimate,
g_t represents gradient with respect to θ
μ_1 and μ_2 are the two hyperparameters
s_t is the second moment

After preprocessing and sanitation, the dataset's 70,000 rows and 12 attributes decreased to about 59,000 rows and 11 attributes. Outliers were eliminated to upsurge the effectiveness of the model because all of the attributes were categorical. This study included a number of effectiveness metrics. The dataset was divided into two sections: 20% was utilized for model testing, while the remaining 80% was used for model training. Using a range of performance metrics, such as accuracy, F1-score, precision, recall, sensitivity, and specificity, this section examines the suggested model's presentation. A CM can be used to explain how a classification model is presented. A table that displays the discrepancy between the actual and expected classes is called a CM. In the CM, an instance in the real class is represented by each column, and an example in the anticipated class by every row (and vice-versa). The following formula is used to determine these assessment criteria, which are frequently applied to binary classification.

$Accuracy = (TP+TN)\ (TP+FP+FN+TN)$

The average harmonic of recall is the F1-Score.

$Precision = TP/(TP+FP)$

$Recall = TP/(TP+FN)$

Sensitivity = TP/(TP+FN)

Specificity = TN/(TN+FP)

After applying the suggested DN approach to the test data, the outcomes were contrasted with those of other ML and DL techniques, including ANN, AlexNet, DecisionTree, ResNet and VGGNet.

TABLE.3 PERFORMANCE EVALUATION OF SUGGESTED DN APPROACH WITH ML AND DL MODELS

Methods	Accuracy (%)	Precision (%)	Recall (%)	F1 score (%)	Sensitivity (%)	Specificity (%)
ANN	82.46	82.36	85.34	81.32	82.89	82.31
Decision Tree	83.87	83.87	84.57	84.52	83.92	83.45
ResNet	89.52	88.61	87.56	86.48	88.64	88.61
VGGNet	90.92	89.89	88.52	87.23	89.87	90.58
AlexNet	90.93	89.52	90.78	89.61	88.56	90.67
Proposed DN Model	91.86	90.94	91.02	89.89	91.54	91.45

The accuracy investigation showed that the suggested model obtained 91.86%, while the current models, including ANN, AlexNet, Decision Tree, ResNet and VGGNet achieved between 82% and 90%. Existing methods including AlexNet, ANN, Decision Tree, ResNet and VGGNet achieved between 81% and 90% when the models were tested. In contrast, the suggested model achieved 90.94% precision, 91.02% recall, and 89.89% F1-score. Table 3 displays the results of the performance evaluation of the current model using the suggested DN.

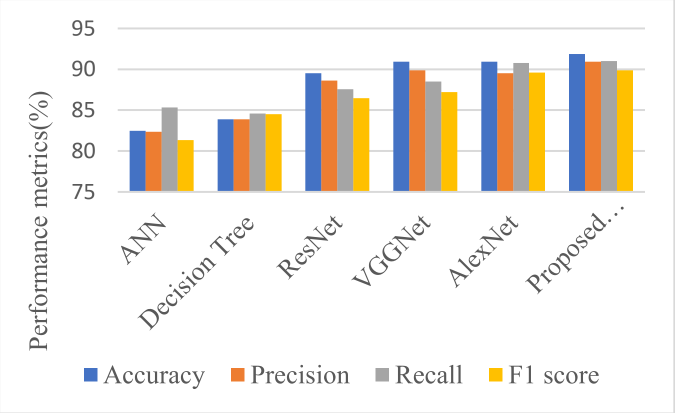

FIGURE 3 GRAPHICAL REPRESENTATION OF PERFORMANCE EVALUATION RESULTS OF EXISTING MODEL WITH PROPOSED MODEL

Comparing the suggested DN classifier to the other methods that were already in use, the accuracy increased to 91.86%. Figure 3 displays the results as graphical representations.

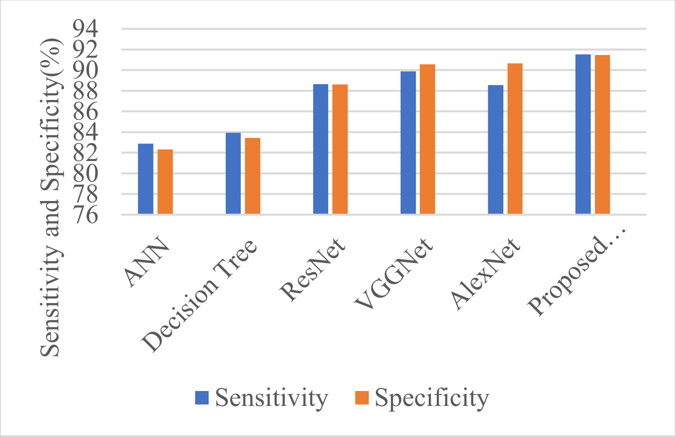

FIGURE 4 SENSITIVITY AND SPECIFICITY EVALUATION RESULTS OF EXISTING MODEL WITH PROPOSED MODEL

The Sensitivity and specificity analysis, the proposed model achieved 91.54% and 91.45%. The existing models such as ANN, Decision Tree, ResNet, VGGNet and AlexNet achieved nearly 82% to 90%. The sensitivity and specificity of graphical illustrations are shown in Figure 4.

V CONCLUSION

HD is one of the foremost causes of death universal, and its incidence is increasing quickly. Early identification and treatment can lessen the severity of this condition's symptoms. In order to predict cardiac issues in a collection of patient records, this paper offers DL-based techniques for classification tasks. This study has demonstrated the considerable potential of DN, a sophisticated neural network architecture, for HD forecasting accuracy. We have tuned DN to achieve outstanding predictions by using strict dataset filtering and advanced pre-processing techniques, as demonstrated by its astounding accuracy rate of 91.86%. The findings highlight the model's robustness and imply that it is ready to function effectively in real-world clinical contexts. The model's capability to differentiate between cases of HD and non-heart illness has been demonstrated by the thorough evaluation using precision, recall, F1 score, sensitivity, and specificity, making it an incredibly reliable tool for early identification. In the future, we may predict HD more accurately by employing feature selection techniques. Because the models' performance is evaluated on a particular dataset, its applicability to other datasets with distinct properties may be limited. To assess a model's generality. and durability, it can be evaluated on various datasets with distinct properties. Furthermore, no methods of hyperparameter-tuning were applied. We can reduce model complexity and execution time by using various hyperparameter-tuning strategies and optimization algorithms to improve model performance.

References

[1] Arooj S, ur Rehman S, Imran A, Almuhaimeed A, Alzahrani AK, Alzahrani A. A deep convolutional neural network for the early detection of heart disease. Biomedicines 2022;10(11):2796. https://doi.org/10.3390/biomedicines10112796.

[2] Shah, D.; Patel, S.; Bharti, S.K. Heart Disease Prediction using Machine Learning Techniques. SN Comput. Sci. 2020, 1, 345.

[3] Gunasekaran K, Kumar VDA, Jayashree K. Prediction and risk analysis of Cardio Vascular diseases in IoHT by enhanced CHIO-based Residual and dilated gated network with Attention Mechanism. Biomed Signal Process Control 2024;94: 106222. https://doi.org/10.1016/j.bspc.2024.106222.

[4] Gjoreski, M.; Gradišek, A.; Budna, B.; Gams, M.; Poglajen, G. Machine learning and end-to-end deep learning for the detection of chronic heart failure from heart sounds. IEEE Access 2020, 8, 20313–20324.

[5] Hui Yang and Jonathan M. Garibaldi, “A hybrid model for automatic identification of risk factors for heart disease”, Journal of Biomedical Informatics, 58, September 2015, Pages: s171-s182.

[6] Aymin Javed, Nadeem Javaid, Nabil Alrajeh and Muhammad Aslam, “DB-Net and DVR-Net: Optimized New DeepLearning Models for Efficient Cardiovascular Disease Prediction”, Appl. Sci. 2024, 14, 10516. https://doi.org/10.3390/app142210516.

[7] V. Gokula Krishnan, Dr. M. V. Vijaya Saradhi, Dr. S. Sai Kumar, G. Dhanalakshmi, P. Pushpa and Dr. V. Vijayaraja, “Hybrid Optimization based Feature Selection with DenseNet Model for Heart Disease Prediction”, International Journal of Electrical and Electronics Research (IJEER), Volume 11, Issue 2, Pages 253-261, e-ISSN: 2347-470X.

[8] Norah Saleh Alghamdi, Wattana Viriyasitavat, Mohammed Zakariah, Achyut Shankar, “Heart disease prediction using autoencoder and DenseNet architecture”, Egyptian Informatics Journal, 28,2024.

[9] Marıa Teresa Garcıa-Ordas, Martın Bay onGutierrez, Carmen Benavides, Jose Aveleira-Mata and Jose Alberto Benıtez-Andrades, “heart disease risk prediction using deep learning techniques with feature augmentation”, Multimedia Tools and Applications (2023) 82:31759– 31773.

[10] Gouri Sankar Nayak, Sibo prasad patro and Neelamadhab padhy, “Heart disease prediction by using novel optimization algorithm: A supervised learning prospective”, Informatics in Medicine Unlocked, 2021, 26(2–4):100696.

[11] B Venkateswara Reddy, SK Aashaq Basha, P Naga Lakshmi, P Shesank and V Mahesh, “Deep Learning Framework for the Multi-Disease Diagnosis of Heart Disease, Pneumonia, and Diabetic Retinopathy Using ResNet, MobileNet and DenseNet”, IJARCCE, Vol. 14, Issue 2, February 2025, DOI: 10.17148/IJARCCE.2025.14271.

[12] Dhafer G. Honi and Laszlo Szathmary, “A one-dimensional convolutional neural network-based deep learning approach for predicting cardiovascular diseases”, Informatics in Medicine, 49, 2024, 101535.

[13] Atta Ur Rahman, Yousef Alsenani, Adeel Zafar, Kalim Ullah, Khaled Rabie and Thokozani Shongwe, “Enhancing heart disease prediction using a self-attention-based transformer model”, Scientific Reports, 2024, 14:514, https://doi.org/10.1038/s41598-024-51184-7.

[14] K.I. Chibueze, A.F. Didiugwu, N.G. Ezeji, and N.V. Ugwu, “A CNN Based Model for Heart Disease Detection”, Scientia Africana, Vol. 23 (No. 3), August, 2024. Pp 429-442.

[15] R. Jeyachandra, R. Jeya Malar, G. Kharmega Sundararaj, T. Geetha and S. Renuka, “Heart Disease Prediction using CNN Based on Deep Learning Algorithm”, IJATEM, Vol. 3(01), January 2024, pp. 13-27.

[16] Biao Xia, Nisreen Innab, Venkatachalam Kandasamy and Ali Ahmadian Massimiliano Ferrara, “Intelligent cardiovascular disease diagnosis using deep learning enhanced neural network with ant colony optimization”, Scientific Reports, 2024, 14:21777 https://doi.org/10.1038/s41598-024-71932-z

[17] Kaggle Cardiovascular Disease Dataset. Available online: https://www.kaggle.com/datasets/sulianova/cardiovascular-disease dataset (accessed on 1 November 2022).

[18] Ammar,M.;Javaid, N.; Alrajeh, N.; Shafiq, M.; Aslam, M. A Novel Blending Approach for Smoking Status Prediction in Hidden Smokers to Reduce Cardiovascular Disease Risk. IEEE Access 2024, 12, 2169–3536.

[19] Kim,M.; Hwang, K.B. An empirical evaluation of sampling methods for the classification of imbalanced data. PloS ONE 2022, 17, e0271260.