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Deep Featured Adaptive Dense Net Convolutional Neural Network Based Cardiac Risk Prediction in Big Data Healthcare Environment

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Abstract— In recent days, cardiac vascular disease has been one of the deadliest health-affecting factors causing sudden death. So, the importance of early risk prediction through feature analysis has become a big problem in data analysis because more nonlinear time series data increase the feature dimension. Irrelevant feature dimension scaling affects the prediction accuracy and leads to classification inaccuracy. To resolve this problem, we propose an Enhanced Healthcare data analysis model for cardiac data prediction using an adaptive Deep Featured Adaptive Convolution Neural Network for early risk identification. Initially, the preprocessing was augmented to formalize the time series data collected from the CVD-DS dataset. Then the feature evaluation was carried out with the Relative Subset Clustering (RSC) approach. The Cardiac Deficiency Prediction rate (CDPr) was estimated to identify the relational feature to subset margins. Based on the CDPr weight the feature is extracted using Cross-Over Mutual Scaling Feature Selection Model (CMSFS). The selected features get with a deep neural classifier based on logical neurons. They are then constructed into a Dense Net Convolution Neural Network (DN-CNN) classifier to feed forward the feature values and predict the Disease Affection Rate (DAR) by class category. The proposed system produces high prediction accuracy in classification, precision, and recall rate to support premature treatment for early cardiac disease risk prediction..

Keywords- Cardiac Risk Prediction, Cardiac Deficiency Prediction rate (CDPr), Cross-Over Mutual Scaling Feature Selection Model (CMSFS), Dense Net Convolution Neural Network (DN-CNN), Disease Affection Rate (DAR)

I. INTRODUCTION

Heart disease is one of the leading causes of death worldwide. Generally, heart diseases are known in several types. Heart diseases include heart failure, angina, cardiomyopathy and arrhythmias. Men are more affected by this heart disease than women in middle or old age. Major causes of heart disease include high blood pressure, high blood cholesterol and smoking. It has been reported that more than half of people suffer from heart disease due to these three factors. The causes of the disease and its prevention methods

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have been described in already existing methods. However, no method has yet been predicted to completely prevent them. There are many challenges to be overcome in computerized fields. Each patient's health effects are associated with different aspects. It is difficult to know the cause of the disease by combining the symptoms of one patient with another patient. A classification technique using the machine learning (ML) method is used to detect breast disease. Although the performance of a categorical model must be accurately measured, no model measures performance accurately. So, we're developing an approach that can accurately measure patients' symptoms and performance.

1. Comparing real-time data from large data sets also requires more time and more storage space.
2. It is difficult to accurately and timely predict heart diseases using existing methods.
3. Prescriptive classifiers delay the accurate classification of cardiovascular disease.
4. It is difficult to select the right features while extracting features using the feature selection method.
5. difficult to handle large datasets by using the existing method.

The proposed system process the feature based on a machine-learning decision tree to perform logical decision. This is used to make the class better by highlighting the supportive feature weight selection. This produces highly predictable by training the feature limits into the decision nodes. This creates the successive link between the nodes carrying the successive compare the feature weights to make class by category. By evaluating node decision support to evaluate the information gains for all the attributes. Then the attributes used to obtain the information are specified

The Big data process holds a massive amount of data in the healthcare industry. Also, big data, which represents the huge to collect and process incredibly time series progress. Organizations maintain such big data in various locations of any network, which can be accessed to produce intelligence towards decision-making or analysis.

Significantly, Healthcare data analysis plays an essential approach in Medical care for early disease prediction by analyzing more features. Analyzing more features leads to increasing dimensions to get inaccuracy to classify the prediction. Due to more dimensions of features leads,

- Irrelevance and redundancy are major problems that affect the prediction performance to analyse a large number of records which belongs to the nature of medical weightage values.
- Decisions are carried out by the max value set by mean error rate margins are dependent to categorize the results. This leads to marginal failures in predictions to make inaccurate classes.
- Low precision-recall, f-measure, more time complexity, weightage adjustment, and false classification resembles class preference leads to wrong suggestions in healthcare sectors.
- The health care records contain a collection of time series dataset that leads to more attributes in big data processing which belongs to more dimensions and values to predict treatment.

The main contribution of the research is to improve cardiac prediction based on data cardiac prediction using a machine-learning approach. This improves the data prediction by analyzing the cardiac dataset to recommend early treatment.

1. First, Relative Subgroup Clustering (RSC) is used to solve the problem of feature selection by using feature selection methods through pre-processing techniques. Experiments are carried out to find out whether the feature selection algorithm and classifier give good results for the appropriate subset in terms of accuracy and computational time.
2. Second, For feature identification, the Cardiac Defect Prediction Ratio (CDPr) corresponding to the subset edges is extracted using the cross-over mutual scaling feature selection model (CMSFS). This increases the performance of classifiers and enables computation based on classifications.
3. Finally, our proposed Enhanced Healthcare data analysis model for cardiac data prediction using the adaptive Deep Featured Adaptive Convolution Neural Network (DFA-CNN) method is an excellent method for the early prediction of cardiac disease.

The remaining section of this paper is given in the following. In section 2 the related work and problems are discussed. In section 3 we describe the methods and algorithms, and also discussed the feature selection methods, classifier algorithms, and datasets. In section 4 we describe the experimental result and analysis. At last, we explain the conclusion and future direction of research work in the section

II. Related Work

S. Mohan et al, (2019), The author propose a hybrid random forest with a linear model (HRFLM) method to accurately predict cardiovascular disease using machine learning techniques to detect significant features. This system is developed with several known classifications and combinations of different features. It helps to improve the accuracy of the performance level of the prediction model for heart disease.

N. L. Fitriyani et al, (2020), The author proposes a heart disease prediction model (HDPM) model for the clinical decision support system (CDSS). Density-Based Spatial Clustering of Applications with Noise (DBSCAN) helps detect

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outliers in noisy applications. It enables XGBoost to predict heart disease and equate Synthetic Minority Over-sampling Technique-Edited Nearest Neighbor (SMOTE-ENN) training data.

G. Joo et al, (2020), The author developed various ML-based predictive models using logistic regression, deep neural networks, random forests, and LightGBM. It compares and validates cardiac arrhythmias with receiver operating characteristic curves, precision-recall curves, sensitivity, specificity and F1 score.

D. R. Krithika et al, (2021), The author proposes a method to predict Cardiovascular Disease (CVD) using Extreme Gradient Boost, DD, KNN, SVM, Naive Base, Random Forest, ANN, Hyperparameter Dense Random Forest algorithm. It should be noted that using these does not give correct and accurate results.

G. Wang et al, (2022), The author introduces the minimum Redundancy - Maximum Relevance (mRMR) method to Principal Component Analysis (PCA), Linear Discriminant Analysis (LDA), Kendall, Random Forest and other research tasks in multi-scale. It analyzes and presents its results to improve the performance of the unprocessed dataset.

G. N. Ahmad et al, (2022), The author explains the model with techniques for various feature selection applications. Developed to guide activity that can be optimized appropriately in real-world situations to create a unique and novel model.

Wiharto et al, (2022), The author defines an intelligent system for diagnosing coronary heart disease to develop a model using a feature selection model considering the cost of the test. A genetic algorithm and support vector machine is developed using feature selection.

J. P. Li et al, (2020), The author discusses an efficient and accurate system based on machine learning techniques for diagnosing heart disease. This method has features of classification methods including multi-method support vector machine, logistic regression, artificial neural network, k-nearest neighbour, naive bays and decision tree. This is a great way to remove unwanted features.

P. Ghosh et al, (2021), The author develops a system that incorporates different methods to effectively predict heart disease. The model is specially developed to generate accurate information for the training model using efficient data collection, data pre-processing and data transformation methods.

A. Abdellatif et al, (2022), The author proposes a method to predict heart disease and patient survival. It focuses on solving the problems of existing heart patients. Improved Weighted Random Forest (IWRF) and infinite feature selection (Inf-FSs) are required to track important features.

M. Alkhodari et al, (2021), The author proposes a Support vector regression (SVR) method to estimate the optimal fit of Left Ventricle Ejection Fraction (LVEF) from 24-hour ECG recordings at hourly intervals. Support vector regression (SVR) models were developed to estimate heart rate variability (HRV) from ECG-derived data.

A. Javeed et al, (2019), The author develops a dog recognition method using a random search algorithm (RSA) for feature selection and a random forest model for heart failure prediction. A grid search algorithm can be used to estimate the accuracy of feature selection. First, the random forest model is generated and then the RSA-based random forest model is generated.S. Mohan et al, (2019), The author proposes a method using machine learning techniques to detect significant features. Cardiovascular symptoms can be accurately predicted by using this method. Any method is made up of combinations of various features and many known classifications.S. A. Ali et al., (2020), The author propose an optimally configured and improved deep belief network (OCI-DBN). It optimizes computer performance to explain redundant features and develops the Ruzzo-Tompa model.

A. Rahim et al, (2021), The author has developed a Machine Learning based Cardiovascular Disease Diagnosis (MaLCaDD) framework for the effective prediction of cardiovascular diseases. Rasari replacement technique is also developed to handle missing values and equality of data in a model.A. Gupta et al, (2020), The author describes a machine intelligence framework for heart disease diagnosis (MIFH) method to extract features from datasets. Factor analysis of mixed data (FAMD) is a method that aims to develop a machine learning predictive model for analysis.

S. E. A. Ashri et al, (2021), The author focus on developing a framework to accurately predict and improve hypertensive cardiovascular disease through a hybrid classification. It is based on a genetic algorithm and preprocessing methods to extract features.S. Li et al, (2021), The author describe a lightweight automatic heart sound classification (LAHSC) method for simple preprocessing of heart sound data. A neural network model is developed to extract time-frequency features of heart sound data.G. N. Ahmad et al, (2022), The author develops a method that combines machine learning algorithms LR, KNN, SVM and GBC with GridSearchCV to predict heart disease. Analysis of training and testing and GridSearchCV detection from the XGBoost classifier dataset.

A. Abdellatif et al, (2022), The author has developed a method based on hyperparameter optimization (HPO) to deal with the imbalanced distribution problem by detecting the patient's condition through Artificial Minority Optimization Technique (SMOTE). They used features extracted from common datasets to build this model.T. Amarbayasgalan et al,

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(2021), The author presents an efficient approach for the early prediction of coronary heart disease risk on well-sorted and trained datasets based on two deep neural networks. This approach is generally based on two stages.

S. B. Shuvo, S. N et al, (2021), The author has developed a lightweight end-to-end CRNN architecture to detect five types of cardiac auscultations with CardioXnet. It is developed through the involvement of both auto-transformed representation learning and sequential residual learning.X. Yuan et al, (2022), The author focuses on a machine learning-based predictive model for the simultaneous detection of binary and multi-classification heart disease predictors. Fuzzy logic and Gradient Boosting Decision Tree (GBDT) has been developed to be used to reduce data complexity.

D. Bertsimas et al, (2021), The author also proposes a method to extract ECG-related features to predict the type of recorded ECG in real-time. The model is trained using the XGPOST algorithm, a leading machine learning method.A. S. B et al, (2022), The author introduces a hybrid CNN-Naive Bayes classifier for heart failure from the MIT-BIH arrhythmia database. A continuous wavelet transform is used to convert one-dimensional ECG signals into two-dimensional scalogram images.R. T. Selvi et al, (2021), The author introduces a large health application system for heart disease diagnosis based on optimal artificial neural network (OANN). The removal of misclassified instances (DBMIR) and (TLBO-ANN) distance-based teaching and learning-based optimization (TLBO) algorithms include performance packages.

A. U. Haq et al, (2018), The author develops a machine learning-based diagnosis method for heart disease prediction using a heart disease dataset. Seven popular machine learning algorithms, and three feature selection algorithms are used to evaluate the performance.H. Wang et al, (2020), The author develops a method to identify intravenous immunoglobulin-resistant patients for prompt and optimal treatment of Kawasaki disease by enabling the prediction of intravenous immunoglobulin resistance to overcome the shortcomings of machine learning models' lack of interpretation.Y. Pan et al, (2020), The author proposes an improved deep learning-assisted convolutional neural network (EDCNN) to help predict patient heart disease. The EDCNN model incorporated with regulatory learning approaches is developed to model a multi-layer perceptron focusing on deep structure.M. A. Khan et al, (2020), The author proposes a method using Modified Swarm Swarm Optimization (MSSO) and Adaptive Neuro-Fuzzy Inference System (ANFIS) to improve the prediction accuracy of IOMD framework for heart disease diagnosis.

III. PROPOSED IMPLEMENTATION

Towards the development of cardiac disease prediction, the Enhanced Healthcare data analysis model for Deep Featured Adaptive Dense Net Convolution Neural Network Based Cardiac Risk Prediction is implemented for early risk identification. First, the time series data collected from the CVD-DS dataset are normalized to increase the prior processing. The features are then evaluated by Relative Subset Clustering (RSC). The Cardiac Defect Prediction Ratio (CDPr) was used to identify the corresponding feature for subgroup edges to identify the relative cardiac disease feature margins.

Then the feature evaluation was carried out with the Relative Subset Clustering (RSC) approach to reduce the dimension. The Cardiac Deficiency Prediction rate (CDPr) was estimated to identify the relational feature to subset margins through cumulative feature margin. Figure 1 shows the proposed architecture diagram (CMSFS-DNCNN). Based on the CDPr weight the feature is extracted using Cross-Over Mutual Scaling Feature Selection Model (CMSFS). The selected features get with a deep neural classifier based on logical neurons with a gated ReLU unit. They are then constructed into a Dense Net Convolution Neural Network (DN-CNN) classifier to feed forward the feature values and predict the Disease Affection Rate (DAR) by class category

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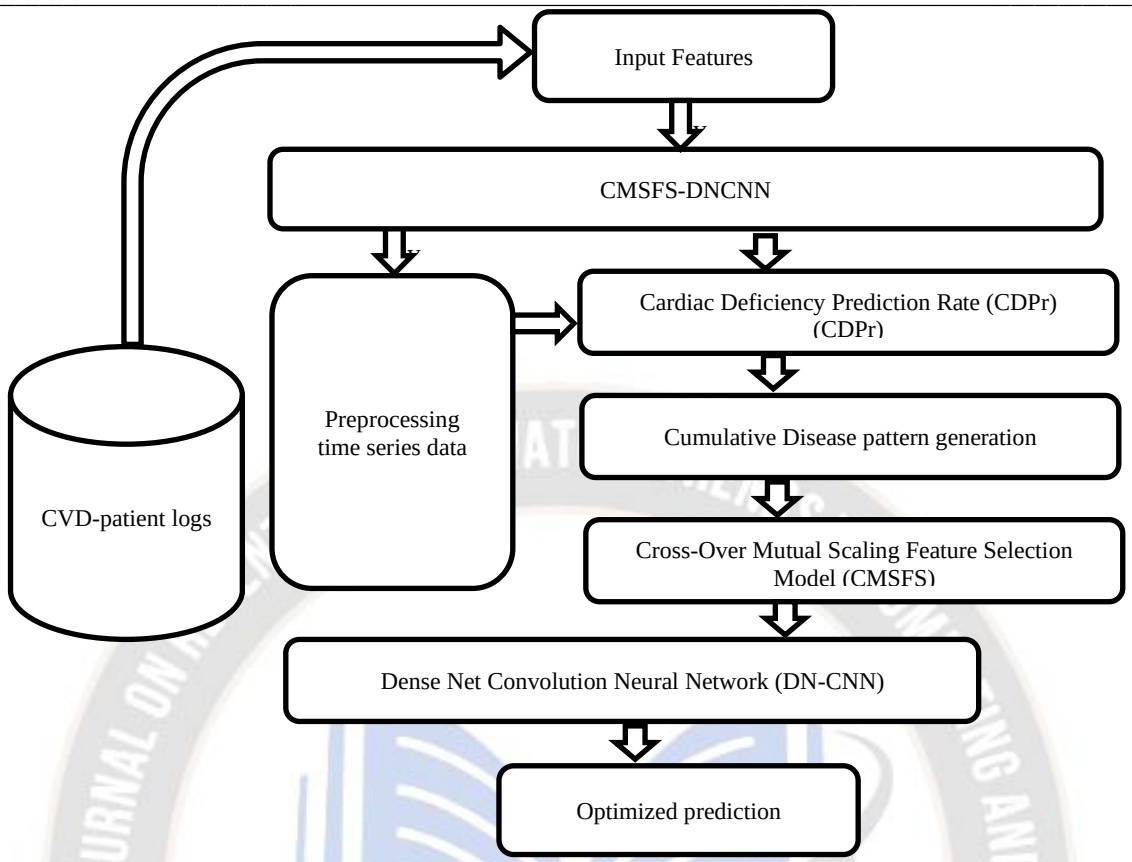

Figure 1 Proposed architecture diagram (CMSFS-DNCNN)

3.1 Pre-processing and splitting

First, preprocessing is performed to reduce the feature dimensionality based on subset cardiac filters. This verifies the cardiac medical margins to Check for equal, null, and null properties against sorted numeric index values. This checks all the features in all dimensions to make the filing, removing the non-residual values to formalize the records. Preprocessed datasets collect various patient characteristics, including temperature, immune status, cold, cough, Erythrocyte Sedimentation Rate (ESR), C - reactive protein (CRP), and Computed Tomography (CT) screening.

So the proposed subset clustering Z-score medical feature margins scaling was generated to index range and compared with the active feature dataset which is used to remove unwanted, inconsistent, incomplete, outlier, and redundant data based on the mean and median from the collected dataset.

$$Z_{score} = \frac{O_i - M_n}{S_d} \quad (1)$$

In above expression is used to identify the missing values and redundant data from the collected dataset O_i. Let us assume , that S_d refer to mean and standard deviation, respectively.

$$M_n = \frac{\sum O_i}{T_n} \quad (2)$$

$$S_d = \sqrt{\frac{\sum O_i - M_n}{T_n}} \quad (3)$$

The above expressions (2) and (3) are used to identify the M_n & S_d values to analyze the Z_{score}. An outlier is an abnormal value in the dataset.

$$D_O = \frac{Z_{score} - Q_{l1}(O_i)}{Q_{l3}(O_i) - Q_{l1}(O_i)} \quad (4)$$

Equation (4) is used to calculate outlier detection (D_O) in the dataset using interquartile range difference among Q_{l1}, Q_{l3} refers 1st quartile, and 3rd quartile to decrease the impact of outliers.

$$P(N_d) = \frac{O_i - M_{im}(D_O)}{M_{ax}(D_O) - M_{im}(D_O)} \quad (5)$$

Formula (5) can be used to sort the pre-processed data $P(N_d)$ based on minimum outlier $M_{im}(D_O)$ and maximum outlier $M_{ax}(D_O)$. This section efficiently analysis the pre-processing dataset using the Z-score method based on mean, median, and outlier to minimize the error in the dataset. Then sorts the data to reduce the dimensionality of the collected dataset. The preprocessing level is explained in the above algorithm that reduces dimensionality based on attributes by filtering values. Every record contains multiple attributes representing information about a single patient related to the group on a subset representation of cardiac feature margins.

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3.2 Cardiac Deficiency Prediction Rate (CDPr)

In this stage, preprocessed data is marginalized into risk rate to evaluate the CVD feature affection rate from the time series data. This splits the subset group based on the centroid margins to create a deficiency of feature affection limits. This chooses maximum risk values of the medical margins which are relatively averaged into disease deficiency factor from each record whether what the data present relatively on risk levels.

Algorithm

Start

Step 1: Initialize the collected CVD-DS dataset (C_d)

For each Medical margin (Read ←Cardiac id)

Step 2: For All features A_c from C_d

//A_c cardiac features

Find the threshold closest terms T_c value

Max term value (max variable count → confidence)

Rearrange the Cardiac Id

Create links between the term Cardiac id→cd1, and cd2.

Step 3: Calculate the key feature relation F_r

//F_r feature relation

For each Cardiac attribute F_r from C_d

For each Cardiac term F_r from C_d

If F_r € maximum term then do

Find the maximum count relative to other features.

Relative Set S_r = ∑(Concepts€F_r)+ C_d.

Estimate the relative subset relative cluster margin

F_r = ∑ Relative feature €Gi equaling margin limit

Estimate support feature value max ($Value$)

$Value$ = ∑feature Links (M_{value})<-∑ $M_{value}(F_r)$ (7)

Generate link F_r recognized relation attribute links

Relation link L_r←F_r+A_c; (8)

End if

End for

End for

Step 5: Calculate the max disease deficiency feature margins→CF_l.

For each feature←CF_l

CF_l = = ∑Concept (Links (F_r))) € ∑Concept (A_c)!= C_d (9)

Calculate relation feature→RLK

RLK = $(F_r + A_c) + NIL$

Append feature group into clusters Cfi ←RLK;

End for

Stop.

The disease deficiency is related to risk levels represented in medical margins by selecting maximum margin values of cardiac disease properties through the Cardiac Deficiency Prediction Rate (CDPr). This scales the deficiency levels of the patient's values and compared them to risk factors from medical margins. Then the affected factors are averaged into the absolute mean rate to get the cardiac Prediction rate.

3.3 Cumulative Disease pattern generation (CDPG)

In this stage, each cardiac deficient rate is within feature limits disease levels are marginalized to form a pattern margin. Depending on the medical margin pattern rate of features, the features get influenced to get the maximum level of margins. These weights are attained into the decision tree node traversal rule to create equivalent and relative margins to form the patterns.

Input: CDPr feature, adapted margin Apt

Output: Cumulative pattern CpM

Step 1 Initialize to read cumulative margins limits of relative features.

For each fed layer class Pc

Step 2 Constrict decision tree node medical margin

Mm as pattern =

$$\int_{i=1}^{size(Apt)} \sum Apt(i).class = c \quad (10)$$

Step 3 Choose the relative feature margin correlation To make an intersection to get maximum support.

Max Feature Mp← each pattern p

Step 4 computes each similarity feature are classified it as a category based on the risk of Max cancer affected rate.

Disease Proficient feature selection DPfs=

$$\frac{\int_{i=1}^{size(p)} \sum P(i)==Scs(i)}{size(p)} * Mp \quad \ldots \quad (11)$$

End

Step 5: compute the cumulative rate of cardiac influence rate.

Compute cumulative rate DPFS =

$$\frac{\sum_{i=1}^{size(pps)} Pfs}{size(pps)} \quad \ldots. \quad (12)$$

End

Return max cumulative pattern margin (CpM← DPFS)

Stop

The cumulative pattern set similar to relative subset groups having relational values depends on cardiac disease margins. This integrity chooses the feature limits from the deficiency rate. This actively forms the decision tree support system for proficient level weights compared to active levels. These features are grouped into relative groups for cross-check validation through a mutual feature selection process.

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3.4 Cross-Over Mutual Scaling Feature Selection Model (CMSFS).

The mutual features are selected based on disease margins to choose the relevant risk by class. These factors verify the scaling range between the margins contains the difference between risks and non-risk levels**.**

Start

Read Cumulative pattern Cp

Find the mean feature transition margin FTs = Cfi $size(Cpm)$
$\cup (\sum_{i=1} Tst(i).Type = Cp)$

Compute disease Impact Factor DIF = Dist(T.Temp,$\frac{\sum_{i=1}^{size(PTS)} FTS(i).Crp)}{size(FTS)}$)× Dist(T.Humidity,$\frac{\sum_{i=1}^{size(PTS)} PTS(i)ESR)}{size(Fts)}$)× $\frac{1}{\sum_{i=}^{size(PTS)} PTS(i).\ Cpm / size(Fts)}$

Compute Relative feature support Rfs = Dist(T.AC,$\frac{\sum_{i=1}^{size(PTS)} PTS(i).Cfi)}{size(PTS)}$)× Dist(T.NoI,$\frac{\sum_{i=1}^{size(PTS)} PTS(i).NOI)}{size(PTS)}$) × $\frac{1}{\sum_{i=}^{size(PTS)} PTS(i).Fts / size(Fts)}$

Compute Scaling feature limits SFl = Fts×DIF×Rfs/Pc

Stop

This algorithm chooses the essential class of feature margins to integrate support to the relative margin rate. This reduces the feature dimension to choose the disease or class level importance to group the features for further classification.

3.5 Soft max Logical activation

This creates a logical representation based on the weightage of features trained into the neurons. The Weight 'w' at 'i 'and 'j' remains the max limit of the weight of the feature to predict the category. However, the function 'y' remains the training level from the feature of 'x'. Neurons are shown constructing a fully integrated feedforward network.

$net_{i(t)} = \sum_{j=1}^{j} w_{ij} y_{j(t)} + x_{i(t)}, i = 1 \ldots j$and

$Ti \frac{dy(t)}{dt} = -yi(t) + \varphi(net_i) + x_{i(t)}, i = 1 \ldots j \ldots.$ (10)

The weightages are optimized to get each neural layer $net_{i(t)}$ from function 'x' to be the features trained at logical 'y' functions. The frequent neuron weights are constant at Ti be trained from x(i) and y(i) from the average mean weight w(i).

3.6 Dense Net Convolution Neural Network-Based Cardiac

In this stage dense net neural network was constructed to predict the cardiac risk. This defends the risk categories into dense layers optimization modulated in CNN. The feed-forward layers are logically trained with medical margins in the ReLU-softmax activator. CNN processes data by passing it through multiple layers and extracting features to expose convolutional operations. Convolutional layers consist of modified linear units (ReLUs) that have longer lifetimes when modifying feature maps. Pooling layers are used to fix these feature maps into the next feed. Pooling is typically a down-sampling algorithm that reduces the dimensionality of feature maps. Later, the resulting result consists of a single long continuous linear vector two-dimensional array flattened in the map. The next layer, called the fully connected layer, takes as input the flattened matrix or 2D array extracted from the pooling layer and classifies it to class by disease risks.

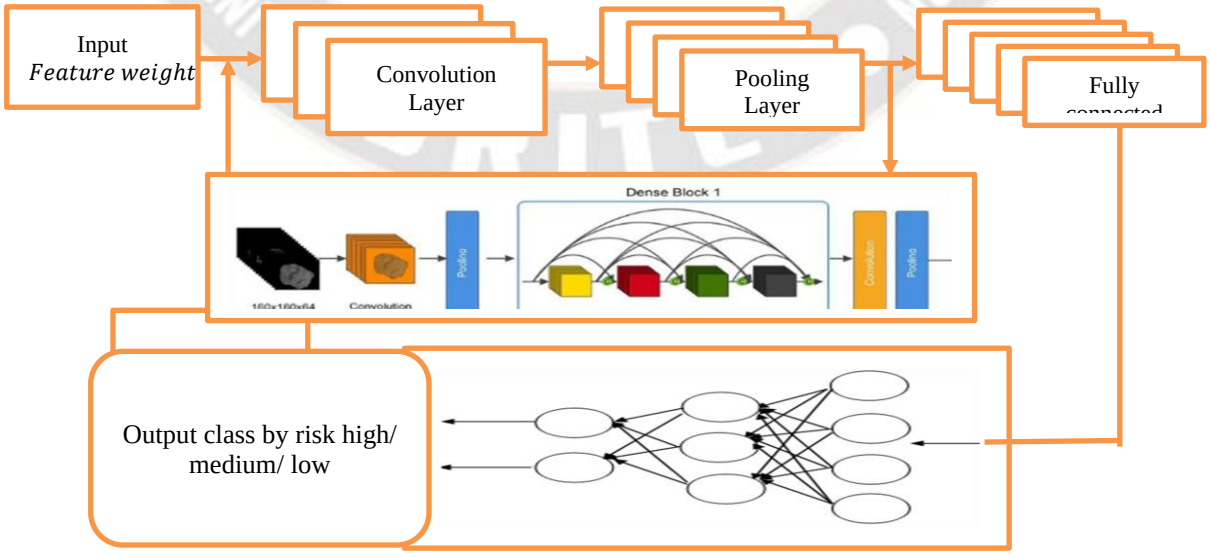

Figure: 2 Proposed dense net CNN

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The selected feature margins are input to Dense net convoluted layer into training and testing layers based on 120 layer feedforward layer which is a 16 *16 polling layer. Figure 2 shows the Proposed dense net CNN This stakes the pooling layer X_{inp}→ { X_{f1}, X_{f2}, $X_{f3...}$ } as testing and training Y_{ts}→{ Y_{f1}, Y_{f2}, Y_{f3} }

First, list the threshold margin values defined in the equation,

$$Thre_{margi} = \{Thre_{margi1}, Thre_{margi2} \dots Thre_{margin}\} \quad (11($$

$$Conv_{impo} = \sum_{i=0}^{n} P_{imp}\left(1 - Thre_{margi}\right) = 1 - \sum_{i=0}^{n} Thre_{margi}^{2} \quad (12)$$

In expression (12), calculate the Convolution layer of important features $Conv_{impo}$ from threshold values$Thre_{margi}$. Where P refers to the probability of important features P_{imp}, I refers to the iteration of the number of terms n.

$$Pol_{lay} = D\left(\sum_{i=1}^{n} w_{ei} * Conv_{impo}\right) + net_{i(t)} \quad (13)$$

In expression is used to calculate the pooling layer important feature dimension factor Pol_{lay}, D refers to the dimension of input vectors, $and\ w_{ei}$ refers to the weight function.

Therefore extract the important target features Tar_{impo} can calculate as the equation.

$$Tar_{impo} = \varepsilon . Pol_{lay} + b(net_{i(t)}) \quad (14)$$

Let's assume $\varepsilon and b$ refers to the learning vector. The above two expressions are used to analyze the essential target values from the convolution layer.

$$F_{con} = M_{axi \in Tar_{impo}} \quad (15)$$

$$ReLu(f_x) = M_{ax}(0, x) \quad (16)$$

The ReLu activation function converts the positive values for efficient result analysis. Then calculated denseness layer is used to estimate the output of green algae prediction following equations.

$$I_{gate} = ReLu(f_x)(w_{ei})F_{con} + bias \quad (17)$$

Let us assume I_p input of the denseness layer, F_{alcon} fully connected layer values.

$$Hidden_{gate} = ReLu(f_x)\left(A_{w1} I_{gate} + A_{w2} P_{T-1} + bias\right) \quad (18)$$

The above equation is used to calculate the hidden layer process$Hidden_{gate}$. A_{w1} and A_{w2} refer to adjustable weights, P_{T-1} refers to the previous state at time T and bias vector for coefficients.

$$Pre_{out} = ReLu(f_x)\left(I_{gate} + Hidden_{gate} + bias\right) \quad (19)$$

Expression is used to predict the green algae using DenseNet. Pre_{out} denotes output.

The prosed system predicts the risks by class by reference based on the mean weight categorized into the disease margin rate levels. During the test and training phase, the feature gets limits to marginalize the medical margins which are compared to get the actual mean rate margin class. The training filed depends on the logical activation function to compare the conditional fields depending on the weight and its feature importance to predict the class.

IV. Experimental Results And Discussion

In the experimental system, we used the UCI database to test the performance of various classifiers. Softmax- ReLU gated logical Rules to be followed to understand the performance of the model are training and testing. Table 2 shows the classification marks for three different classifiers. for the various features used in the calculation had similar classification scores. DL-based classifiers detect linear kernel models that deliver better results than other kernel models. From the test results, the best choice for developing a method to predict heart disease.

The proposed approach is implemented under various parameters and performance is evaluated. This method measures efficiency in the prognosis of a disease based on various functions and their values. The results of the evaluation are analyzed in conjunction with the performance of other approaches. The results will be displayed in this section.

Table 1 Environment and parameter processed

Parameter	Value
Cloud Environment	AWS (Amazon web service)
Storage	EBS
Configuration	Txlarge core2
Language and Tool	Python, Jupiter notebook.
Dataset name	Cardiac CVD-DS
Attributes count	30 from a cardiac dataset

Table 1 shows the details used to evaluate the performance generated in different ways. Accordingly, the method measures performance by various limits. The consequences got are given in detail in this section.

Table 2 Analysis of Precision and recall rate performance

Precision and recall rate in %						
Number of records/Methods	50 Records		100 Records		200 Records	
	Precision	Recall	Precision	Recall	Precision	Recall
HMLT	65.7	61.3	70.9	72.1	77.4	82.4
ANFIS	70.2	89.1	74.3	78.9	83.2	85.1
HDPM-CDSS	74.6	75.7	80.1	84.3	86.6	87.7
CMSFS-DNCNN	83.4	84.6	85.3	87.9	93.8	94.2

The performance of the Precision and recall rate generated by the various methods was measured and shown in Table 2. Here, the proposed CMSFS-DNCNN algorithm produces higher Precision and recall rate efficiency than other approaches.

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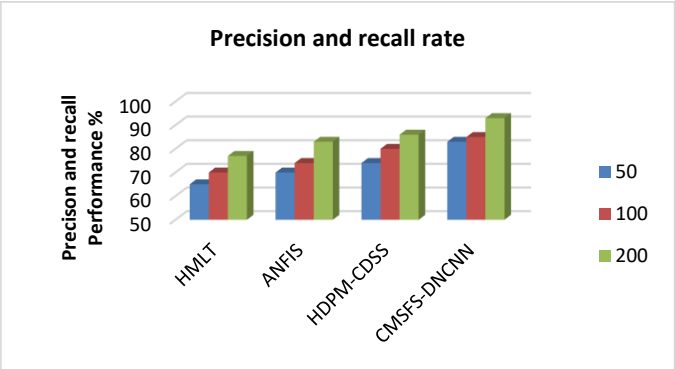

Figure 3 Performance in Precision and recall rate

Precision and recall rate performance is shown in figure 3 with different approaches. The proposed CMSFS-DNCNN method has a higher Precision and recall rate efficiency than other methods at all levels.

Table 3: Accuracy in Clustering

Cluster Accuracy vs No of Patients			
Number of Records /methods	50 Records	100 Records	200 Records
HMLT	75.2	80.5	86.3
ANFIS	81.9	85.7	90.9
HDPM-CDSS	84.1	88.2	92.1
CMSFS-DNCNN	87.6	91.4	96.3

Table 3 shows the accuracy of clustering large data for disease prognosis. Here, the proposed CMSFS-DNCNN approach provides greater clustering accuracy than other methods.

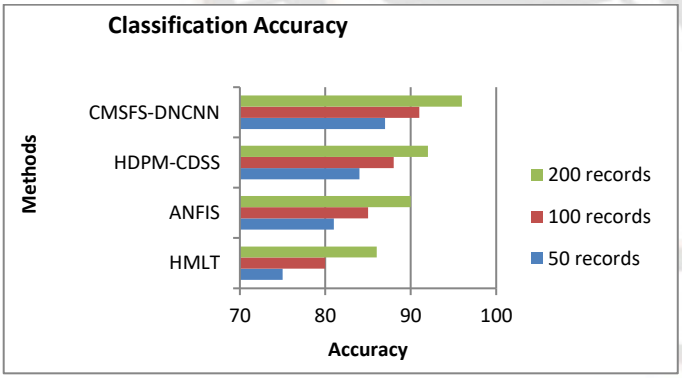

Figure 4: Accuracy in Classifying risks

Figure 4 shows the clustering performance generated by different methods. The proposed CMSFS-DNCNN approach has developed high clustering accuracy under several different diseases.

Table 4: Analysis of Disease Prediction

Disease Prediction Accuracy vs No of Diseases			
Number of Records /methods	50 Records	100 Records	200 Records
HMLT	64.5	70.7	76.9
ANFIS	65.3	72.1	75.3
HDPM-CDSS	66.7	75.2	80.5
CMSFS-DNCNN	70.2	78.8	82.2

The prognostic performance of the disease and its accuracy are measured by considering different disease classes. The results obtained are shown in Table 4.

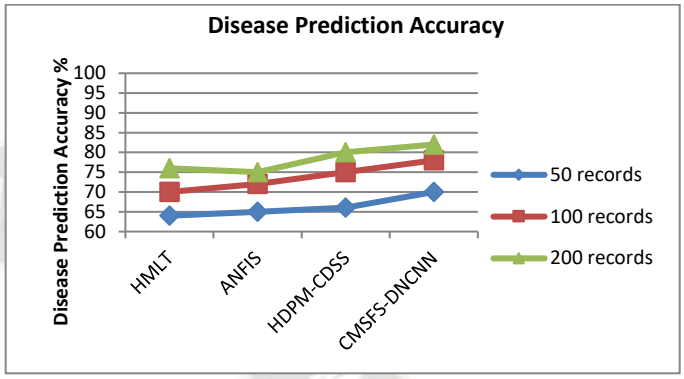

Figure 5: Analysis of disease prediction accuracy

The accuracy of the prognosis generated by the various methods was measured and is shown in Figure 5. The proposed Hybrid approach resulted in a higher disease prognosis than other approaches in each class.

Table 5: Analysis of False Ratio

False Classification Ratio			
Number of Records /methods	50 Records	100 Records	200 Records
HMLT	30.6	25.6	20.3
ANFIS	34.7	27.1	22.1
HDPM-CDSS	30.9	23.4	18.4
CMSFS-DNCNN	28.1	20.2	16.2

The percentage of misclassifications present in different methods is measured and shown in Table 5. Here, the proposed CMSFS-DNCNN technique has lower error rates than other methods.

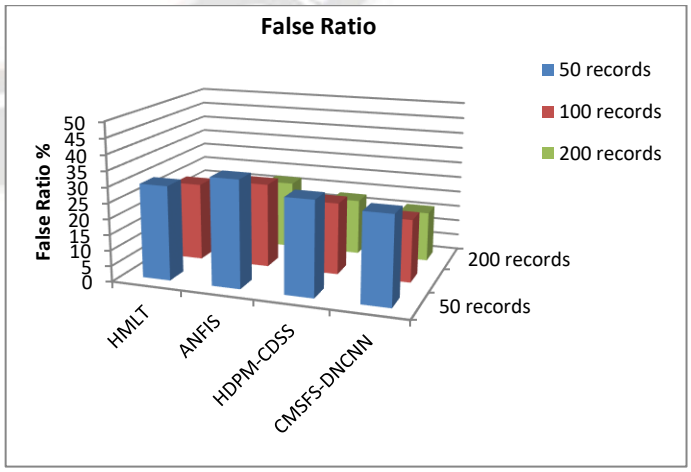

Figure 6 Analysis of False Classification Ratio

The accuracy of disease prognosis made by different methods is measured and shown in Figure 6. The proposed

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CMSFS-DNCNN approach resulted in a higher disease prognosis than other approaches in each class.

V. CONCLUSION

To conclude the proposed system focuses on identifying cardiac risk levels based on Deep Featured Adaptive Dense Net Convolution Neural Network by obtaining cardiological parameters from the person under observation. Temperature, blood pressure, and oxygen levels Oxygen features are derived from temperature, blood pressure, and pulses and tested with a trained classifier model for databases associated with the cardiac database. Various classification algorithms were analyzed, trained for the cardiovascular database and tested in the real-time database, used for classification, and the accuracy and precision derived from them were tested. The results show that the classification performance of the proposed DNCNN achieves high performance compared to the other systems.

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