Grenze International Journal of Engineering and Technology, January Issue

Adaptive Bio Inspired Deep Neural Network based Heart Disease Prediction Model using Propagation Measures

Malini [1] and Dr. R. Devi[2]
[1,2]School of Computing Sciences, Vistas, Chennai, Tamil Nadu
Email: Malinimm606@gmail.com, devi.scs@velsuniv.ac.in

***Abstract*—The problem of heart disease prediction has been identified as key challenge in medical science. There exist numerous techniques towards predicting heart disease using various data sets. However, the accuracy of predicting heart disease is still below the mark. To handle this issue, an Adaptive Bio Inspired DNN based Heart Disease Prediction Model (ABDNN) model is presented in this article. The method utilizes different data sets containing health records of various patients which includes clinical and diagnosis features. The procedure begins with preprocessing the dataset using a feature-level normalization scheme. The normalized dataset is then used for feature selection through the Walrus Optimization Algorithm (WaOA), where the objective function is designed to measure the Walrus Position Support (WPS). The WPS indicates the position of the walrus and guides the feature selection process. As a result, the selected features are used to train a deep neural network, with neurons designed to evaluate the Heart Disease Diffusion Support Scale (HDSM) for classification. The proposed model enhances the accuracy of heart disease prediction across various datasets.**

***Keywords*— Heart Disease Prediction, Deep Neural Network, WaOA, ABDNN, HDSM, WPS.**

I. INTRODUCTION

Diseases have a significant impact on human society, affecting individuals with a wide range of conditions, some of which are chronic, while others are not. The heart disease is the most one which claims the life of human. There are number of heart diseases can be named which are identified from set of symptoms. The medical practitioner looks for the symptoms and conclude the presence of the disease, But there will be higher false ratio and needs the support of decision systems. The decision systems use various medical traces and clinical reports for the classification of the presence of disease. For example, the heart disease can be predicted using blood pressure, weight, cholesterol, oxygen intake and so on. But there are number of other features and factors must be considered for the problem of heart disease prediction. For example, the diabetic patients has great chance of getting into the disease as presence of higher glucose level would encourage the heart disease.

The decisive support systems uses number of traces belongs to various patients for the prediction of the disease. The accuracy of forecasts is dependent on the number of data used. Traditional methods are often insufficient for managing large datasets, making it necessary to adapt machine learning algorithm. The machine learning algorithms are more capable of handling huge volume of data towards the problem to maximize the prediction accuracy.

Grenze ID: 01.GIJET.11.1.340

The accuracy is the most important factor in terms of disease prediction. To maximize the accuracy it is necessary to incorporate required suitable features for the classification problem Feature selection is the most critical step in illness prediction problems. While a variety of features may be available in the dataset, choosing the ideal features significantly enhances prediction accuracy. Bio inspired algorithms are used in the problem of feature selection. For example the whale optimization algorithm perform feature selection by computing the fitness value of the feature and selects most important feature for the task. Similarly, there are number of optimization algorithm available for the problem like Ant colony optimization, Bee colony optimization. In this study, feature selection is addressed through the Walrus Optimization Algorithm (WaOA), which is inspired by the behaviour of walruses.

The classification strategy is critical to improving forecast accuracy. Deep neural networks are commonly utilized to solve various classification and prediction challenges. They can analyze enormous datasets and efficiently classify them using extracted features. Building on this, the present study proposes a deep neural network-based heart disease prediction model., inspired by adaptive biology, that utilizes diffusion measures. The method is focused on pre-processing, feature selection and network training to perform heart disease prediction. The method uses heart and diabetic data sets for the prediction problem which contains clinical, and diagnostic features. By incorporating both of them, the prediction of heart disease has been approached effectively. The detailed approach is presented in the next section.

II. Literature Survey

There exist number of approaches towards prediction of heart disease and some of the methods are discussed in detail in this section.

A deep learning CVD risk factor detection model CardioNet is presented in [1], which applies convolution neural network in learning the features towards classification. A cross domain transfer learning model is presented in [2] towards diagnosing CVD. The method applies CNN models in learning the features from ECG and trains the spectrograms. A phonocardiogram based deep learning model is presented in [3], which uses heart sounds in detecting CVD. A deep learning model based prediction scheme is presented in [4],

which consider smoking, alcohol and other features by applying Logistic Regression, Naive Bayes, Deep Learning Model and Random Forest to perform classification.

A smart phone based deep learning model is presented in [5], towards CVD diagnosis. A multi input deep learning model is presented in [6] which uses multiple features to perform classification with random forest and neural network classifiers. A detailed comparative study of CVD diagnosis is presented in [7].

An deep learning model is presented in [8], which uses ECG characteristics towards classification. A gene association based deep learning model is presented in [9], which uses RNA sequences to predict the disease. A deep learning model is presented in [10], applies fundus image to perform classification with CNN. In [11], an efficient deep learning model is presented, which uses different features.

A Deep neuro-fuzzy network (DNFN) based classification model is presented in [12], which uses Fractional Calculus-Horse Herd Optimization Algorithm (FC-HOA) in feature selection and classification. A detailed review on CVD prediction and the techniques available are discussed in [13,16]. An empirical mode decomposition based deep learning model is presented in [14], towards CVD. The method considers multi-periodic signals and classifies abnormal heart beats using CNN. A multi class classification model is presented in [15], which develops multistage fusion to perform feature selection.

A mobile based medical systems is designed in [16], which uses Combined Sparse Autoencoder (CSAE) algorithm towards classification. The method uses multiple data sources and uses deep neural network as classifier. A balanced probability distribution (BPD) scheme is presented in [17], The model combines instance-based sequential learning with weight distribution and employs a cross-domain feature filtering technique for classification. Reference [18] presents a performance analysis model that evaluates the effectiveness of various unsupervised techniques, such as K-means clustering and database scanning. A tensor factorization model is presented in [19], towards disease prediction using electronic health records.

The method integrates clinical and sequential factors to generate latent pattern towards predicting chronic diseases. An adaptive group regularization scheme is presented in [20], which uses Gaussian mixture model clustering to learn the structure of the data and supports disease prediction.

A predictive analysis model is presented in [21], It performs predictive analysis on a range of multiple chronic diseases (MCC) that affect the working population.

A holistic data mining scheme is presented in [22], which applies feedback features towards predicting the disease. An experimental evaluation of different machine learning approaches is conducted in [23]., utilizing a

dataset of kidney patients classified as CKD or NOTCKD. A continuous monitoring program focusing on lifestyle and environmental factors is detailed in [24], employing wearable devices to track indoor and outdoor activities using multiple gadgets. Reference [25] proposes a chronic disease prediction model utilizing a back-propagation artificial neural network (BP-ANN) combined with partial least squares regression for classification. Reference [26] discusses a continuous-time dynamic functional Bayesian network that employs multilinear principal component analysis and a weighted multivariate moving average technique to assess the impact of modifiable risk factors on the likelihood of developing renal cell carcinoma. Additionally, a stroke risk prediction model based on hybrid deep learning (HDTL-SRP) is introduced in [27]. which uses knowledge structure collected from various sources to perform prediction. All of the strategies outlined above aim to enhance the accuracy of illness prediction.

III. Problem Statement

Heart disease remains a significant challenge in medical science, as its timely and accurate prediction is critical to reducing mortality rates. Although numerous computational techniques have been developed to predict heart disease using patient health records, their prediction accuracy often falls short of desired standards. The primary issue lies in the inability of existing models to effectively handle diverse datasets, identify critical features, and achieve optimal classification performance. To address these challenges, there is a pressing need for a robust and adaptive model that can improve prediction accuracy by leveraging advanced optimization algorithms and deep learning techniques.

IV. Proposed Model

The Adaptive Bio Inspired DNN based Heart Disease Prediction Model (ABDNN) utilizes different data sets containing health records of various patients which includes clinical and diagnosis features. Initially, the method applies Feature Level Normalization Scheme to pre-process the data set. The normalized data set has been used for feature selection by enforcing Walrus Optimization Algorithm (WaOA) where the objective function has been updated to measure Walrus Position Support (WPS) which represents the position of the walrus and used to perform feature selection. Accordingly, the selected features are used to train the deep neural network where the neurons are modelled to measure Heart Disease Propagation Support Measure (HDPSM) to perform classification. The detailed working of the model is presented in this section.

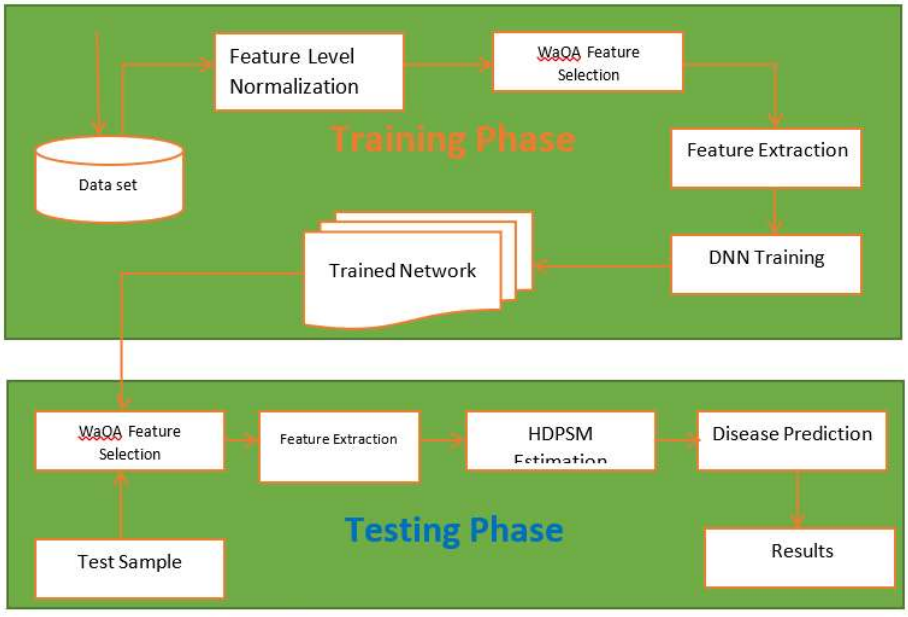

Fig. 1. Architecture of ABDNN Model

The working model of the F-350 series is available in various sizes and configurations. Figure 1 illustrates the model, and the functional components are outlined in this section.

A. Feature Level Normalization

The feature level normalizer algorithm preprocesses the data set obtained The method reads the entire data set and identifies unique features available in the set. Further each record is analyzed for the possession of all the features. If there are any missing features then it estimates the mean value for the feature and replace the value. Such normalized data set has been used to perform disease prediction.

Algorithm 1:

Input: Data Set Ds

Output: Preprocessed medical data set Pmd

Start

Read Ds.

$$\text{Feature set Fes} = \sum_{i=1}^{Size(Ds)} (Features \in Fes) \cup ((Features \in Ms(i)) \cap Fes)$$

For each tuple T

For each feature F

$$\text{Compute Feature Mean Value FMV} = \frac{\sum_{i=1}^{Size(DS)} DS(i).F}{Size(DS)}$$

If T has missing feature F

T(F) = FMV

End

End

Pmd = DS

Stop

The above discussed algorithm computes feature mean value for various features and identifies tuples with missing values to be replaced with FMV to normalize the data set. Normalized data set has been used to perform disease prediction.

Algorithm 2:

Input: Preprocessed medical data set Pmds

Output: Selected feature set Sfs

Start

Read Pmds

Initialize T,t,N,m,F,Fi,rand,Sw.

Generate X walrus according to the features in the data set.

Generate initial population

For each population

$$\text{Estimate the estimate WPS} = \frac{\sum_{i=1}^{Size(Pmds)} Pmds(p(k)) > \sum_{j=1}^{size(Pmds)} Pmds(p(k).value) \Big/ Size(Pmds)}{Size(Pmds)}$$

End

Extract the best solution.

While $t < T$

If $|Danger\ signal > 1|$

Update each walrus position $Xi,j\ t+1 = Xi,j\ t$ + migration step,

Else

If $Safety\ signal \geq 0.5$

For walrus is male

Apply Halton sequence to update new position.

For walrus is female

update new position.

$$\text{Female}_{i,j}^{t+1} = \text{Female}_{i,j}^{t} + \alpha \cdot \left(\text{Male}_{i,j}^{t} - \text{Female}_{i,j}^{t}\right) + (1-\alpha) \cdot \left(X_{\text{best}}^{t} - \text{Female}_{i,j}^{t}\right),$$

For walrus is juvenile

update new position

$$\text{Juvenile}_{i,j}^{t+1} = (O - \text{Juvenile}_{i,j}^{t}) \cdot P,$$

End

Else If $|Danger\ signal| \geq 0.5$

update new position

$$\sigma_x = \left[\frac{\Gamma(1+\alpha)\sin\left(\frac{\pi\alpha}{2}\right)}{\Gamma\left(\frac{1+\alpha}{2}\right)\alpha 2^{\frac{(\alpha-1)}{2}}}\right]^{\frac{1}{\alpha}}, \sigma_y = 1, \alpha = 1.5,$$

Else

update new position.

$X_{i,j}^{t+1} = (X_1 + X_2)/2,$

End

Update the position of walrus.

Calculate the fitness function and extract the best solutions.

t = t + 1

End

Selected features set Sfs = Select features at fist k positions.

Stop

Here, X represents the population of walruses, Xi refers to walrus number i (the candidate solution), and xi is the value of decision variable number j proposed by walrus i. N denotes the total number of walruses, and m is the number of decision variables. The objective function vector, FW, identifies the strongest walrus with the best objective function value. $\boldsymbol{U}i,j$ are randomly selected integers between 1 and 2, while $randi$ are random numbers drawn from the interval [0, 1].

The working of walrus optimization-based feature selection algorithm is presented in the above pseud code which estimates WPS measure to find the best position for each walrus and elects a few features from the set to perform disease prediction.

B. Feature Extraction

The proposed model considers various features like medical, diagnosis, genetic and historical features. Such features are extracted from the data set to generate the feature vector. For example, the diagnosis features are extracted as follows:

$$[\text{BMI, BS, HbA1C, Pr, Col, Cr}] = \{\text{BMI, BS, HbA1C, Pr, Col, Cr}\} \in \text{T} \quad \begin{matrix} size(T) \\ i = 1 \end{matrix} \qquad (1)$$

Where BMI- Body Mass Index, BS – blood sugar, HbA1C- Periodic blood sugar, Pr-Pressure, Col-Cholesterol, Cr – creatinine

Similarly, the method extracts the features of genetic as follows:

$$[\text{PD, PH, PC}] = \{\text{PD, PH, PC}\} \in \text{T} \quad \begin{matrix} size(T) \\ i = 1 \end{matrix} \qquad (2)$$

Where PD–Parent Diabetic, PH–Parent Hypertension, PC–Parent Cardiac.

Finally, the method would extract the historic features from the medical data set. The historic features are set of patterns of appearance of the disease. For example, for diabetic, the historic features include a set of patterns in form of {BMI, BS, HbA1C, Pr, Col, Cr, Status} where status specifies the presence of the disease.

C. DNN Training

The proposed method reads the feature vectors produced at the feature extraction phase. The feature vectors contain number of features related to the kind of feature considered. The method generates k number of neurons at each layer of the neural network. The network is designed with n number of intermediate layers and each neuron has been initialized with the set of features extracted. The neurons are designed to compute various Heart Disease Propagation Support Measure (HDPSM) against various disease classes.

D. Disease Prediction

The proposed method performs disease prediction by computing Heart Disease Propagation Support Measure (HDPSM). To perform this, the method read the sample given. From the sample, the method extracts the features and passes through the network available. The neurons at various layers estimates Clinical Heart disease propagation support measure (CHDPSM), Historic Heart Disease Propagation Support Measure (HHDPSM). The output layer neuron computes the Heart Disease Propagation Support Measure (HDPSM) towards various class of diseases.

According to the value of HDPSM, the method identifies the class of disease and produces result.

Algorithm 3:

Input: DNN, Sample S

Output: Disease Class Dc

Start

Read DNN, S.

Pass s through DNN

For each layer l

For each neuron N

For each disease class Dc

$$\text{Compute CHDPSM} = \frac{\frac{Size(DC)}{\sum_{i=1}^{Dist(Dc(i).BMI,SS.BMI)}} / Size(DC)}{\frac{Size(DC)}{\sum_{i=1}^{Dist(Dc(i).BS,SS.BS)}} / Size(DC)} \times \frac{\frac{Size(DC)}{\sum_{i=1}^{Dist(Dc(i).HbA1c,SS.HbA1c)}} / Size(DC)}{\frac{Size(DC)}{\sum_{i=1}^{Dist(Dc(i).Cr,SS.Cr)}} / Size(DC)} \times \frac{\frac{Size(DC)}{\sum_{i=1}^{Dist(Dc(i).Pr,SS.Pr)}} / Size(DC)}{\frac{Size(DC)}{\sum_{i=1}^{Dist(Dc(i).Col,SS.Col)}} / Size(DC)}$$

$$\text{Compute HHDPSM} = \frac{\frac{Size(DC)}{\sum_{i=1}^{Dist(Dc(i).HP==,SS.HP)}} / Size(DC)}{Size(DC)}$$

$$\text{Compute HDPSM} = \frac{CHDPSM}{HHDPSM}$$

End

End

End

Disease class DC = Choose the disease class with maximum HDPSM.

Stop

The above discussed algorithm represents how the method computes the value of CHDPSM, HHDPSM to compute HDPSM value to identify the class of disease the sample belongs to perform disease prediction.

V. Results and Discussion

The proposed model was developed in Matlab, and its performance was evaluated using several criteria. The approach was tested on multiple medical datasets obtained from various sources. The resulting findings were then compared to the performance of other approaches.

TABLE I. EVALUATION DETAILS

Key	**Detail**
Data sets	Multiple Sources (UCI, CDC, Kaggle)
Total Features	30
No of Locations	10
Total Tuples	1 million

The details of data set being used for performance evaluation of the proposed model have been presented in Table 1, which has been measured for various metrics towards analysis. The performance evaluation is performed by combining the features of data sets namely UCI, Chronic Disease Data (CDC) and Kaggle.

A. Disease Prediction Accuracy

The disease prediction accuracy represents the performance of the model in predicting the exact disease. It has been measured according to the number of predictions performed and number of correct predictions made. It has been measured as follows:

$$\text{DPA} = \frac{TP+TN}{TOtal\ Prediction} \times 100 \quad (3)$$

Where TP-true positive and TN-True negative.

TABLE II. DISEASE PREDICTION ACCURACY

Disease Prediction Accuracy %			
Algorithm	***3 lakhs***	***5 lakhs***	***1 million***
CSAE	67	74	79
HDTL-SRP	72	78	82
MOFFA	76	81	86
ABDNN	83	87	93

In this case, the system's permission is granted by both the distributor and the manufacturer. Adapting ABDNN model support the collection of huge volume of data set from various location and support the improvement of disease prediction accuracy

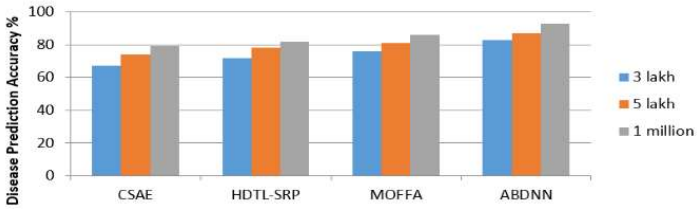

Fig. 2. Disease Prediction Accuracy

The performance of the approaches in predicting disease is measured and reported in Fig. 2, where the ABDNN model demonstrates higher prediction accuracy.

B. False Prediction Ratio

The false prediction rate is a metric that quantifies the percentage of incorrect predictions made by a given approach. It is calculated based on the number of false positive and false negative predictions generated by the method

$$\text{FPR} = \frac{FP+FN}{TOtal\ Prediction} \times 100 \qquad (4)$$

Where FP-false positive and FN – false negative

TABLE III. FALSE PREDICTION RATIO

False Prediction Ratio %			
Algorithm	***3 lakhs***	***5 lakhs***	***1 million***
CSAE	33	26	21
HDTL-SRP	28	22	18
MOFFA	24	19	14
ABDNN	17	13	7

The false prediction ratio introduced by various models are measured and plotted in Table 3, where the ABDNN model introduces less false prediction ratio. Inclusion of huge data set with the support of mobile agents support the reduction of false ratio in disease prediction.

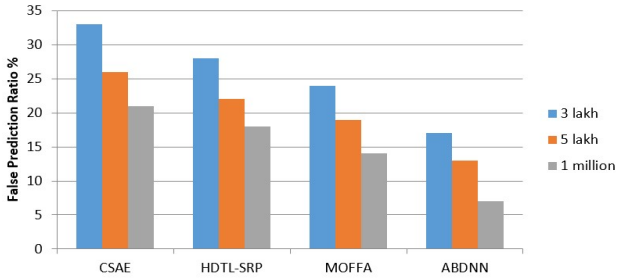

Fig. 3. False Prediction Ratio

Calculated the ratio of erroneous predictions is shown Figure 3 for various approaches. Less incorrect predictions than others introduce the suggested ABDNN model

C. Time Complexity

The temporal complexity is a metric that measures how long it takes for the model to predict an illness.

$$\text{Time Complexity} = \frac{\begin{matrix}Sum\ of\ all\ time\ taken \\ for\ prediction\end{matrix}}{Total\ Prediction} \times 100 \qquad (5)$$

TABLE IV. TIME COMPLEXITY IN SECONDS

Time Complexity in seconds			
Algorithm	**3 lakhs**	**5 lakhs**	**1 million**
CSAE	68	79	91
HDTL-SRP	65	76	85
MOFFA	56	69	81
ABDNN	37	53	67

The value of time complexity introduced by different approaches are measured and presented in Table 4, where the proposed ABDNN model introduces less time complexity compare to others.

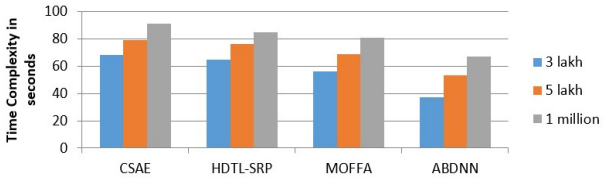

Fig. 4. Time complexity

VI. CONCLUSION

This article presented a novel Adaptive Bio Inspired DNN based Heart Disease Prediction Model (ABDNN) model which utilizes different data sets containing health records of various patients which includes clinical and diagnosis features. Initially, the method applies Feature Level Normalization Scheme to pre-process the data set. The normalized data set has been used for feature selection by enforcing Walrus Optimization Algorithm (WaOA) where the objective function has been updated to measure Walrus Position Support (WPS) which represents the position of the walrus and used to perform feature selection. Accordingly, the selected features are used to train the deep neural network where the neurons are modelled to measure Heart Disease Propagation Support Measure (HDPSM) to perform classification. The proposed model improves the performance of heart disease prediction with higher accuracy.

REFERENCES

[1] M. Panwar, A. Gautam, R. Dutt and A. Acharyya, "CardioNet: Deep learning framework for prediction of CVD risk factors," IEEE (ISCAS), 2020, pp. 1-5, DOI: 10.1109/ISCAS45731.2020.9180636.

[2] G. A. Tadesse et al., "Cardiovascular disease diagnosis using cross-domain transfer learning," IEEE (EMBC), 2019, pp. 4262-4265, DOI: 10.1109/EMBC.2019.8857737.

[3] A. N. Netto and L. Abraham, "Detection and classification of cardiovascular disease from phonocardiogram using deep learning models," IEEE (ICESC), 2021, pp. 1646-1651, DOI: 10.1109/ICESC51422.2021.9532766.

[4] T. S. E. Reddy, S. R. Sripathi, D. Akula, S. Palaniswamy and S. R, "Cardiovascular disease prediction using machine learning and deep learning," IEEE (CSITSS), 2022, pp. 1-5, DOI: 10.1109/CSITSS57437.2022.10026391.

[5] Abdulhamid subasi, Deep learning approaches for the cardiovascular disease diagnosis using smartphone, SCIENCE DIRECT (ID-CS), PP 163-193, 2022.

[6] Ioannis D. Apostolopoulos, "Multi-input deep learning approach for cardiovascular disease diagnosis using myocardial perfusion imaging and clinical data", ELSEVIER (PM), Volume 84, PP 168-177, 2021.

[7] M. Swathy, "A comparative study of classification and prediction of Cardio-Vascular Diseases (CVD) using machine learning and deep learning techniques", SCIENCE DIRECT (ICT E), Volume 8, Issue 1, PP 109-116, 2022.

[8] Yu-Sheng Lou, "Extensive deep learning model to enhance electrocardiogram application via latent cardiovascular feature extraction from identity identification", ELSEVIER (CMBP), Volume 231, Number 107359, 2023.

[9] Vignesh Venkat, "Investigating genes associated with heart failure, atrial fibrillation, and other cardiovascular diseases, and predicting disease using machine learning techniques for translational research and precision medicine", ELSEVIER (G), Volume 115, Issue 2, Number 110584, 2023.

[10] Yanjun Ma, "Deep learning algorithm using fundus photographs for 10-year risk assessment of ischemic cardiovascular diseases in China", ELSEVIER (SB), Volume 67, Issue 1, PP 17-20, 2022.

[11] Kelvin K.L. Wong, "Deep learning-based cardiovascular image diagnosis: A promising challenge", ELSEVIER (FGCS), Volume 110, PP 802-811, 2020.

[12] V. Srilakshmi, "Intelligent decision support system for cardiovascular risk prediction using hybrid loss deep joint segmentation and optimized deep learning", ELSEVIER (AES), Volume 173, Number 103198, 2022.

[13] Javed Azmi, "A systematic review on machine learning approaches for cardiovascular disease prediction using medical big data", ELSEVIER (ME&P), Volume 105, Number 103825, 2022.

[14] Ya –Li, “A deep learning approach to cardiovascular disease classification using empirical mode decomposition for ECG feature extraction”, ELSEVIER (BSPC), Volume 79, Part 2, Number 104188, 2023.
[15] Md Rafuil Hassan, “Early detection of cardiovascular autonomic neuropathy: A multi-class classification model based on feature selection and deep learning feature fusion”, ELSEVIER (IF), Volume 77, PP 70-80, 2022.
[16] J. Wu, L. Chang and G. Yu, "Effective Data Decision-Making and Transmission System Based on Mobile Health for Chronic Disease Management in the Elderly," in IEEE Systems Journal, vol. 15, no. 4, pp. 5537-5548, Dec. 2021, DOI: 10.1109/JSYST.2020.3024816.
[17] Q. Wang, H. Wang, L. Wang and F. Yu, "Diagnosis of chronic obstructive pulmonary disease based on transfer learning," in IEEE Access, vol. 8, pp. 47370-47383, 2020, DOI: 10.1109/ACCESS.2020.2979218.
[18] L. Antony, Sami Azam, Eva Ignatious, Ryana Quadir, and Abhijith Reddy Beeravolu; et al., "A comprehensive unsupervised framework for chronic kidney disease prediction," in IEEE Access, vol. 9, pp. 126481-126501, 2021, DOI: 10.1109/ACCESS.2021.3109168.
[19] H. Wang, Q. Zhang, F. Y. Chen, E. Y. M. Leung, E. L. Y. Wong and E. K. Yeoh, "Tensor factorization-based prediction with an application to estimate the risk of chronic diseases," in IEEE Intelligent Systems, vol. 36, no. 6, pp. 53-61, 1 Nov.-Dec. 2021, DOI: 10.1109/MIS.2021.3071018.
[20] S. H. A. Faruqui, A. Alaeddini, J. Wang, C. A. Jaramillo and M. J. Pugh, "A functional model for structure learning and parameter estimation in continuous time bayesian network: an application in identifying patterns of multiple chronic conditions," in IEEE Access, vol. 9, pp. 148076-148089, 2021, DOI: 10.1109/ACCESS.2021.3122912.
[21] J. Yang, X. Ju, F. Liu, O. Asan, T. S. Church and J. O. Smith, "Prediction for the risk of multiple chronic conditions among working population in the united states with machine learning models," in IEEE Open Journal of Engineering in Medicine and Biology, vol. 2, pp. 291-298, 2021, DOI: 10.1109/OJEMB.2021.3117872.
[22] F. P. Bravo, Alberto A. Del Barrio García; Ana Beatriz, Gago Veiga; and María Mercedes Ga et al., "SMURF: Systematic Methodology for Unveiling Relevant Factors in retrospective data on chronic disease treatments," in IEEE Access, vol. 7, pp. 92598-92614, 2019, doi: 10.1109/ACCESS.2019.2927429.
[23] B. Khan, R. Naseem, F. Muhammad, G. Abbas and S. Kim, "An empirical evaluation of machine learning techniques for chronic kidney disease prophecy," in IEEE Access, vol. 8, pp. 55012-55022, 2020, DOI: 10.1109/ACCESS.2020.2981689.
[24] C. -T. Wu, Ssu-Ming Wang, Yi-En Su 1, Tsung-Ting Hsieh, and Pei-Chen Chen, et al., "A Precision Health Service for Chronic Diseases: Development and cohort study using wearable device, machine learning, and deep learning," in IEEE Journal of Translational Engineering in Health and Medicine, vol. 10, pp. 1-14, 2022, Art no. 2700414, DOI: 10.1109/JTEHM.2022.3207825.
[25] J. Parab, M. Sequeira, M. Lanjewar, C. Pinto and G. Naik, "Backpropagation Neural Network-Based Machine Learning Model for Prediction of Blood Urea and Glucose in CKD Patients," in IEEE Journal of Translational Engineering in Health and Medicine, vol. 9, pp. 1-8, 2021, Art no. 4900608, DOI: 10.1109/JTEHM.2021.3079714.