Laplace Kernel Adaptive Tuning Optimized Transfer Learning for Cardiovascular Disease Prediction

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Abstract : Cardiovascular diseases (CVDs) are common diseases of the heart and blood vessels, accounting for devastating health outcome and mortality worldwide. The risk factors are hypertension, hyperlipidaemia, tobacco smoking and diabetes. For health benefits to take place, diagnosis needs to be done early for early intervention. While machine learning and deep learning have demonstrated their applications in CVD prediction, their CVD prediction accuracy and their need for minimal error and short computation time have been problematic. For this purpose, a Laplace Kernel Stochastic Tuned Optimized Transfer Learning (LKSTOTL) is proposed. The framework consists of the sub-sections of data acquisition, pre-processing, feature selection, classification and fine tuning. Patient data are collected, preprocessed to remove missing values and outliers and for dimensionality reduction, significant feature selection using Laplace kernelized stochastic neighbor embedding method is carried out. The pre-trained model is taken from a deep belief network (DBN), and the transfer learning is employed to enhance learning efficiency of the features. The training and test errors are minimized with the spiral search optimization algorithm. Experimental evaluation indicates that LKSTOTL is superior over the conventional models with 8% accuracy improvement, 5% precision improvement, 4% recall improvement, 4% F1-score improvement, 10% specificity improvement, and 77% error rate and 18% prediction time improvement, showing its application for reliable and efficient cardiovascular disease prediction.

Keywords: Cardiovascular disease prediction, Deep transfer learning, deep belief network (DBN), Laplace kernelized stochastic neighbour embedding based feature selection, Rosenthal correlation, Fine-tuning, spiral search optimization

I INTRODUCTION

Cardiovascular diseases (CVDs) continue to be the leading causes of morbidity and mortality in the world, accounting for millions of deaths worldwide. These diseases include cardiac failure, arrhythmias, coronary artery disease, and stroke. The incidence of CVDs is on the rise due to lifestyle changes, urbanization, and increase in age and rising number of comorbidities such as hypertension, diabetes, obesity etc. However, early diagnosis and treatment are of importance for disease progression, complications and patient outcomes. Clinical evaluation, echocardiography and electrocardiogram, which are commonly used as diagnostic methods for CVD, are subjective, time consuming and dependent on the skill of health care professionals[1].

Recent progress in machine learning and deep learning techniques have led to automated and precise prediction of CVDs. By looking at vast amounts of patient data, these models are capable of identifying minute patterns, correlations, and risk factors that may not be immediately obvious through traditional clinical evaluation[2]. Supervised deep learning models (convolutional neural networks (CNNs), deep belief networks (DBNs), recurrent neural networks (RNNs)) have recently been applied for prediction of cardiovascular risk with promising results. However, the problems on model generalization, feature selection, error minimization and computational efficiency remain open for heterogeneous datasets of different sizes. Moreover, although transfer learning has been recently exploited to apply previously trained models to other tasks that are closely related to the original task, the optimisation of transfer learning models to achieve a lower error and reduce the prediction time for CVD detection is understudied[3,4].

This study fills these gaps by designing the Laplace Kernel Stochastic Tuned Optimized Transfer Learning (LKSTOTL) model for cardiovascular diseases prediction. The research work focuses on enhancing prediction accuracy, decreasing the error rate and decreasing the computational time for coordination of deep transfer learning, dimensionality reduction, feature selection and fine-tuning based on spiral search optimization algorithm. The pre-trained deep belief networks (DBN) and advanced feature selection techniques such as Laplace kernelized stochastic neighbor embedding are applied in the proposed model to learn from the complex patients with efficiency.

Research Question and Problem Statement: How to apply transfer learning in combination with Laplace kernel-based feature selection and stochastic optimization for improving accuracy, reducing errors, and computation time for the prediction of cardiovascular diseases compared to conventional models?

Cardiovascular diseases are a major global health problem and early diagnosis is a key for reducing morbidity and mortality. It is well known that existing machine learning and deep learning methods are less than satisfactory in terms of accuracy, error rate and computation efficiency for the purpose of prediction for large-scale or heterogeneous data. This research suggests the development of an optimized transfer learning model to break through these limitations for reliable and efficient CVD prediction. The main objectives of the study are as follows

- To develop a deep transfer learning model (LKSTOTL) for efficient cardiovascular disease prediction.
- To employ Laplace kernelized stochastic neighbor (LKS) for feature selection and dimensionality reduction.
- To use the spiral search optimization techniques to fine tune the model for minimum prediction error and minimum computation time.

The study is organized as follows: Section 2, Literature Review and Background. Section 3 presents a proposed methodology for LKSTOTL which includes data processing, feature selection and model training. Section 4 is devoted to the experimental evaluation, results and discussion; while conclusions and future work appear in Section

II RELATED WORKS

Advanced machine learning and deep learning algorithms such as CNN, MLP, ensemble models and sensor based approaches have been utilised recently for understanding cardiovascular disease prediction. These methods have overcome some of the challenges like data imbalance, feature selection, interpretability, high predictive performance, and may provide useful frameworks for accurate, efficient, and clinically relevant CVD risk assessment.

Khan et al. (2024) propose two deep learning models viz., EnsCVDD-Net and BlCVDD-Net for the accurate prediction of cardiovascular disease. They use Adaptive Synthetic Sampling and Point Biserial Correlation techniques to address such challenges (imbalanced data, feature selection etc.) and give good performance (e.g. 88% accuracy) with the added benefit for explainability, SHAP analysis[5].

Talaat et al., (2025) propose a CNN model for dimensional prediction of cardiovascular disease risk on the basis of important personal health indicators. The model includes complex interactions between measures such as blood pressure, cholesterol and lifestyle, and performs well in predicting the outcomes (R2 = 0.994), while meeting the criteria for interpretability and ethical application in clinical practice[6].

Alghamdi et al., (2024) suggests a Multilayer perceptron (MLP) model with feature selection using the arithmetic optimization approach for cardiovascular disease prediction. Their method overcomes data preprocessing and the problems of feature selection, which results in high accuracy for classification (88.89%), and it avoids overfitting and bias, which outperforms the traditional machine learning techniques[7].

Zaidi et al.(2024) designed a heart ensemble network Combining multiple machine learning classifiers in a hybrid ensemble learning model for cardiovascular disease risk prediction. Evaluated on a dataset of 70,000 patient records with 12 clinical features, it demonstrates 92.95% accuracy and 93.08% precision for better performance as compared to classical ML models and ensemble methods for reliable clinical decision support[8].

Naeem et al., (2024) provides a sensor-based approach for heart disease detection using feature extraction and artificial neural networks (ANNs). By processing the signals received by 10 metal oxide semiconductor sensors, the model uses 1000 features of each participant and gains over 85% accuracy which is a proof of feasibility of the feature extraction and ANN methods for individual identification and predictive analysis[9].

Mittal et al. (2025) propose an advanced hybrid machine learning model for cardiovascular disease detection to overcome the data imbalance by SMOTEnn and choose the relevant features using the Chi-square. Ensemble Random Forest, K-NN and AdaBoost and Logistic Regression as meta-learner, the model achieved accuracy, sensitivity, specificity and ROC-AUC of 97.8%, 96.15%, 96.75% and 98.6% respectively, which are way better than existing techniques[10].

While these studies show great progress in predicting CVD, there are still a number of limitations. Most of these models e.g. EnsCVDD-Net, BlCVDD-Net and CNN based approaches can't be generalized because of the fact that they are trained and tested on relatively small curated data set or imbalanced data sets. Sensor based approaches like Naeem et al. (2024) have scalability problems for huge number of people. Ensemble model, Hybrid models (Zaidi et al., Mittal et al.) Many feature selection methods (e.g. arithmetic optimization, Chi-square) overlook the existence of minor but clinically meaningful interactions. Overall these approaches require external validation, standardisation of datasets, and are more efficient for clinical use in various settings.

III. PROPOSED METHODOLOGY

This section outlines methodology of LKSTOTL designed to enable accurate prediction of cardiovascular disease. To achieve this goal, LKSTOTL is introduced to achieve improved accuracy and minimized error rate. Figure 1 depicts architecture diagram of LKSTOTL, designed for accurate cardiovascular disease prediction.

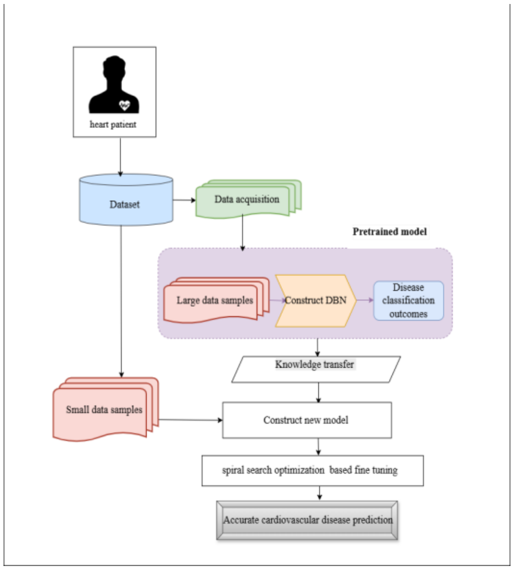

Figure 1 architecture diagram of LKSTOTL model

A. Data acquisition phase

The initial step of the LKSTOTL model involves gathering more patient data samples collected from a cardiovascular disease dataset https://www.kaggle.com/sulianova/cardiovascular-disease-dataset. Follow these fundamental steps to efficiently obtain high-quality patient data for developing and validating disease predictive models aimed at assessing cardiovascular risk. The dataset comprises 13 attributes as shown in table 1 and 70,000 instances.

LKSTOTL model utilizes the transfer learning approach for cardiovascular disease prediction [11].

Pre-trained model construction: In the transfer learning framework, the process begins with the development of a pre-trained model, which enhances cardiovascular disease prediction accuracy by utilizing deep learning techniques trained on large-scale datasets. In disease prediction, a deep belief network (DBN) serves as pre-trained model to learn the large volume of data samples. DBN is a type of artificial deep neural network that consists of multiple layers including two visible layers such as input, output layer and numerous hidden layers for processing given input patient data samples.

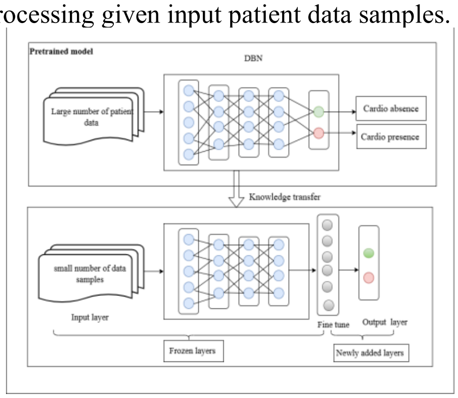

Figure 2 Schematic structure of Deep transfer learning model

Figure 2 illustrates the schematic construction of a deep transfer learning model consists of pre-trained model and new model. In a pre-trained model, DBN is used as a deep learning architecture consisting of input layer, one or more hidden (middle) layers, and an output layer. The input and output layers are always single layers, while the hidden layers include numerous sub-layers.Neural network layers comprise of small individual units called artificial neurons or nodes. Each neuron receives and processes the inputs, and transmits the resulting output to neurons into other layers. Connection between these neurons called as synapses, are assigned weights that measure the strength of the connection between the layers. DBN is a type of artificial neural network composed of multiple layers, including input layer and an output layer as well as several hidden layers for processing the input patient data samples.

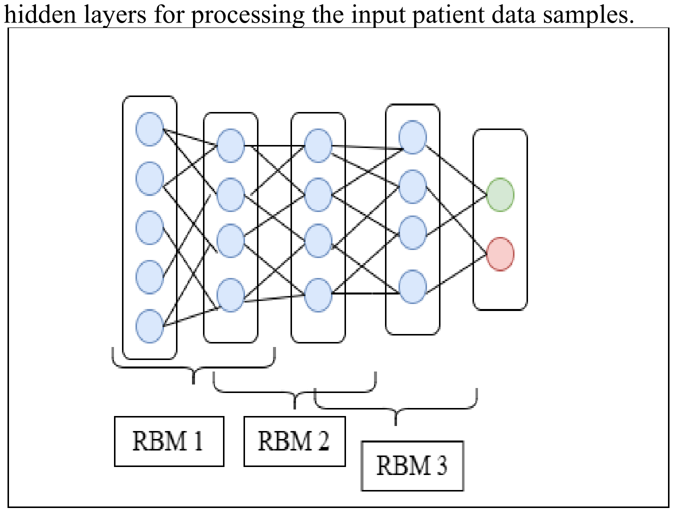

Figure 3 Structure of deep belief network

Table 1 Attribute description

S.No	Attributes	Description
1.	ID	Patient ID
2.	Age	Patient age in days
3.	Height	Patient height in cm
4.	Weight	Patient weight in kg
5.	Gender	1-women, 2-men
6.	ap_hi	Systolic blood pressure
7.	ap_lo	Diastolic blood pressure
8.	Cholesterol	Cholesterol 1: normal 2: above normal 3: well above normal
9.	gluc	Glucose 1: normal, 2: above normal 3: well above normal
10.	Smoke	Smoking 1: Yes 0:no
11.	alco	Alcohol intake 1: Yes 0:no
12.	active	Physical activity
13.	cardio	1 presence 0 absence

B. Transfer learning model

Transfer learning is a DL technique that utilizes the knowledge acquired from the one tasks to improve learning performance. Compared to traditional DL, a transfer learning method has faster training speed and improved performance especially the large dataset, thereby enhancing efficiency.

Figure 3 illustrates the structure of a deep belief network for performing the classification of cardiovascular disease presence or absence. A DBN network utilizes the Restricted Boltzmann Machines (RBMs), which are stochastic networks with two major layers such as visible layer and hidden layer. The visible layer receives the input data samples, while the hidden layer processes the input data. The neurons in the visible layer are fully connected to neurons in the next hidden layer, but there are no links within the same layer. As illustrated in figure 3, the network utilizes three RBM layers to perform the specific functions namely pre-processing, feature selection, and classification. The first RBM's hidden layer performs the data pre-processing. The second RBM is responsible for selecting the significant features from the dataset. Finally, the third RBM handles the classification task by using the selected features to accurately categorize the input data samples into predefined classes such as disease presence or absence. The output of each RBM layer is transferred on as the input to the next, forming a hierarchical architecture that effectively supports the learning process[12].The input patient data samples $DP_1, DP_2, DP_3, \dots DP_m$ are given to the input visible layer. The neuron in input layer is connected with a weight '$w_1, w_2, \dots, w_n$' and added with bias 'b'. The neuron activation probability of input visible layer 'P' is expressed as follows,

$$P_I = A\left(\sum_{i=1}^{m} DP_i * w_i\right) + b \quad (1)$$

Where, P_I indicates a neuron activation probability of input visible layer, A denotes a sigmoid activation function, 'DP' denotes a number of input data samples, w_i indicates a weights in visible layer, b denotes a bias of visible layer. If the output of neuron activation probability is 1 , then the input data samples are transferred from input layer into the hidden layer. In the hidden layer, probability of neuron in hidden layer is expressed as follows,

$$P_H = A\left(\sum_{i=1}^{m} DP_i * w_{ih}\right) + b \quad (2)$$

Where, P_H denotes a neuron activation probability of hidden layer, A indicates a sigmoid activation function, 'w_{ih} denotes a weights between visible layer and hidden layer, b indicates a bias of hidden layer. If neuron activation probability P_H is one, then the input is transferred into the next layer.

In the first hidden layer, data pre-processing is carried out to obtain the suitable dataset. In the data pre-processing, missing data handling and outlier data removal process is executed. Missing data is the absence of data points or values in a given cardiovascular dataset. The linear regression method is applied for analyzing the available data samples and providing the output as missing data. Linear regression model is expressed as follows,

$$M_{Dp} = \beta_0 + DP_1\beta_1 + DP_2\beta_2 + \dots + DP_n\beta_n \quad (3)$$

Where, M_{Dp} indicates a missing data samples, $\beta_0, \beta_1, \beta_2 \dots \beta_n$ indicates a regression coefficient, $DP_1, DP_2, DP_3, \dots DP_m$ denotes a number of available data samples. Followed by, outlier data is identified from the dataset by using Q statistical test. This test is employed for identifying the outlier data.First, the input data samples are arranged into the ascending order. After arranging the data, Q statistical test is computed as follows,

$$Q_T = \frac{|DP_i - DP_N|}{DP_{mx} - DP_{mn}} \quad (4)$$

Where, Q_T indicates Q statistical test outcomes, DP_i denotes a data point in the ascending order, DP_{mx} denotes a maximum data value in the order, DP_{mn} indicates a minimum data value in the order. From the test analysis, the outlier data is identified by setting the threshold.

$$Z = \begin{cases} Q_T > \delta & ; outlier\ data \\ Q_T < \delta & ; normal\ data \end{cases} \quad (5)$$

Where, Z denotes an outcome of test statistics, δ represents threshold. If the statistical test outcomes are greater than the threshold, then the data sample is said to be a outlier. Otherwise, the data sample is considered to be a normal data. The pre-processed dataset results are transferred to the next hidden layer for further processing.

C. Laplace kernelized stochastic neighbour embedding method

The next process of the proposed method is a significant feature selection to minimize the dimensionality of the dataset by applying a Laplace kernelized stochastic neighbour embedding method. Feature selection is the process of selecting the subset of the features from the cardiovascular dataset aiming to minimize the time consumption of disease prediction. The stochastic neighbour embedding is a machine learning dimensionality reduction method for visualizing high-dimensional data where the similar features are modelled by nearby points and dissimilar features are modelled by distant points. The similar and dissimilar features are identified through the Laplace kernel. The Laplace kernel is a qualitative measure used to calculate the similarity between features. Let us consider the number of features $F = \{F_1, F_2, \dots, F_n\}$ and the similarity is mathematically computed as follows,

$$LF = \frac{1}{n}\left[\frac{\exp|F_j - F_k|}{\sigma^2}\right] \quad (6)$$

Where,LF denotes a Laplace kernel function which is measured difference between the features F_j and the other neighbouring features F_k, deviation (σ), 'n' represents the number of feature.

$$Q = \begin{cases} 1, & relevant\ features \\ 0, & irrelevant\ features \end{cases} \quad (7)$$

Where, Q denotes a dimensionality reduction output. The kernel function provides the output between 0 and 1. Then the, high score value of Laplace kernel is used to select the significant features from the dataset.In the analysis, features with high score value '1' are identified as relevant features, while those with less score are identified as irrelevant features. Therefore, the relevant features are selected and remove the other features from the dataset. This process helps to minimize the dimensionality of the dataset, thereby minimizing the time consumption of the cardiovascular disease prediction. The selected features subsets are transferred into third hidden layer.

D. Rosenthal correlation based cardiovascular disease prediction

Finally, the selected features are used for cardiovascular disease prediction in the third hidden layer by applying Rosenthal correlation. It helps to measure the relationship between the training and testing data sample features. The correlation is mathematically expressed as follows,

$$Corr\ (DP_t, DP_s) = \left[\frac{ST}{\sqrt{m}}\right] \quad (8)$$

$$ST = \frac{(DP_t - DP_t)^2}{var(DP_t, DP_s)} \ (9)$$

Where, $Corr\ (DP_t, DP_s)$ represents a Rosenthal correlation between the training samples 'DP_t' and testing data samples 'DP_s', ST refers to the standardized test statistics, 'm' indicates the number of data samples, $var(DP_t, DP_s)$ indicates a variance between the data samples. The correlation$Corr\ (DP_t, DP_s)$ provides the results from '0 to '1'. Then the observed output of the hidden layer is transferred to the output layer. In DBM network, the sigmoid activation function is typically used in the output layer for the classification of disease presence or absence.

$$Y = A_s[w_{ho} * h_t)] \quad (10)$$

Where, Y indicates predicted output class, $A_s$indicates sigmoid activation function, w_{ho} denotes weight between hidden and output layer, h_t represents hidden layer output. From analysis, sigmoid activation maps any real-valued number to value between 0 and 1.If activation function provides '1' indicates data sample is classified as cardio disease presence. Coefficient returns '0' indicates data sample is classified as cardio disease absence.

// Algorithm 1: Pre-trained classification model

Input: **Dataset, features** $F_1, F_2, \dots, F_n$ **and data samples** $DP_1, DP_2, DP_3, \dots DP_m$

Output: Classify the cardiovascular diseases

Begin

<u>Construct the pre-trained model</u>

1. **Collect n**umber of data samples $DP_1, DP_2, DP_3, \dots DP_m$ **at the input layer**
2. **For each training** samples DP_i **--- Hidden layer 1**
3. Measure the neuron activation probability using (1) (2)
4. Perform missing data handling using (3)
5. Perform outlier data removal using (4) (5)
6. **End for**
7. **For each pre-processed dataset --- Hidden layer 2**
8. Measure the Laplace kernel using (6)
9. **If** $(LF = 1)$ **then**
10. Select the relevant features
11. **Else**
12. Remove other irrelevant features
13. **End if**
14. **For each** training and testing data samples **do--- --- Hidden layer 3**
15. Measure the Rosenthal correlation using (8)(9)
16. Apply sigmoid activation function using (10) **--- output layer**
17. Obtain disease classification results
18. **End for**
End

Algorithm 1 outlines process for cardiovascular disease prediction by creating pre-trained classification model.

Create new classification model : In a transfer learning framework, a small number of data samples are used to create a new model based on existing pre-trained model, such as a DBN. As illustrated in figure 2, frozen layers refer to the parts of the pre-trained model whose weights remain fixed during training. These layers retain the previously learned layers, while new layers are added for task-specific fine-tuning, including a new output layer, as illustrated in figure 2. The input small number of data samples is transferred through these fixed layers often including the first input and hidden layers which are not updated during training. The main aim of these freezing layers includes faster training speed and reduced computational complexity.In order to create the new model, the network architecture consists of input and three hidden layers are frozen and adding two new layers for performing fine tuning process and output layer. The small number of input data samples are considered and transferred into the hidden layers where the data pre-processing steps are carried out by using linear regression for missing data handling and Q statistical test for outlier data removal. After pre-processing, the Laplace kernelized stochastic neighbour embedding method is applied in second hidden layer for selecting the significant features. Finally, classification is carried out at the third hidden layer using Rosenthal correlation function. The output of the disease classification in hidden layer is fine tuned by applying a spiral search optimization algorithm thereby minimizing both training and validation errors and improving the accuracy of the disease prediction. For each classification result, theerror rate is calculated based on squared difference between the actual results and prediction results.

$$RR = \left[Y_{Act} - Y_{prd}\right]^2 \ (11)$$

Where, R indicates an error rate, 'Y_{Act}' denotes a actual classification results, Y_{prd} represents a predicted outcomes. In the fine-tuning process, error back-propagation algorithm is employed to adjust hyperparameter (i.e. weight) between the layers to increase the accuracy of disease prediction through gradient method.

$$w_{new} = w_t - \eta \left[\frac{\partial RR}{\partial w_t}\right] (12)$$

Where, w_{new} denotes an updated weight, w_t specifies a current weight, η indicates a learning rate$(\eta < 1)$, '$\frac{\partial RR}{\partial w_t}$' represents a partial derivative of the error 'RR' with respect to current weight 'w_t'.

In the fine tuning process, a spiral search optimization algorithm is employed to minimize the training and validation errors by updating the weight. The Spiral Search algorithm is a metaheuristic technique inspired by the natural arrangement of spiral structures. It utilizes logarithmic spirals to efficiently balance global exploration and local exploitation throughout the search process. Search points track the path of a logarithmic spiral toward a central point, described as the current best solution, and the global best solution is determined by continuously updating the center point.In this optimization algorithm, multiple search points are referred to the number of weights. First, the populations of the multiple points (weights) are initialized in search space.

$$w_b = w_1, w_2, w_3 \dots . w_b \quad (13)$$

After the population initialization, the fitness of each point (weight) is measured based on error rate.

$$F = \arg\min(RR)(14)$$

Where, F symbolizes a fitness, $\arg min$ indicates an argument of minimum function, ER represents an error rate (RR). After computing the fitness, the point with high fitness is chosen as best and it is selected as the center point. Based on the selected center point, the other search point gets updated as follows,

$$X_{i+1} = X_i + S_r H * [0.5 * |X_i - X_{cp}|] \quad (15)$$

Where, X_{i+1} indicates a updated position, X_i indicates a current position of the search point, S_r indicates a step rate value from 0 to 1, H indicates a rotation matrix i.e. identity matrix, $0.5 * |X_i - X_{cp}|$ denotes a Jensen Shannon divergence, $|X_i - X_{cp}|$ denotes a difference between the current position of search point 'X_i' and 'X_{cp}' indicates a position of the center point. This process is repeated until the algorithm reaches the maximum iterations. Finally, the optimal solution (i.e., weight) is chosen to train the layers for improving the accuracy of the cardiovascular disease classification and minimizes the error. Therefore, the accurate classification outcomes of the cardiovascular disease prediction results are obtained at the output layer with sigmoid activation function.

// Algorithm 2: New classifier model based cardiovascular disease prediction

Input: Dataset,features $F_1, F_2, \dots, F_n$ and data samples $DP_1, DP_2, DP_3, \dots DP_m$

Output: Increase the cardiovascular disease prediction accuracy

Begin

1. **Collect n**umber of features $F_1, F_2, \dots, F_n$, and small number of data samples $DP_1, DP_2, DP_3, \dots DP_m$--- **input layer**
2. **For each** sample DP_i
3. Compute the neuron activation probability using (1) (2)
4. Perform Data Pre-processing using (3) (4)**-----[Hidden layer 1]**
5. **End for**
6. **For each pre-processed output**
7. **Select more relevant** feature set using (6) (7)**-----[Hidden layer 2]**
8. **End for**
9. **For each** training and testing data samples
10. Measure the Rosenthal correlation using (8) (9) -----[**Hidden layer 3**]
11. Obtain the disease classification results
12. **End for**
13. **For each classification results** -----[**Hidden layer 4**]
14. Measure the error rate 'RR' using (11)
15. Update the weights using (12)
16. **End for**
17. Initialize the population of the weights $w_1, w_2, w_3 \dots . w_b$
18. **foreach** weight 'w_b'
19. Compute the fitness 'F' using (14)
20. **While ($\boldsymbol{T} < \boldsymbol{T_{max}}$) do**
21. Update the position using(15)
22. $\boldsymbol{if}(X_{i+1} > X_i)$**then**
23. X_{i+1}considered as optimal solution or optimal weight
24. **else**
25. $X_i$considered as optimal solution or optimal weight
26. **End if**
27. Increment $\boldsymbol{T} = \boldsymbol{T}$ **+1**
28. Go to step 20
29. **End While**
30. Obtain the final prediction results with sigmoid activation function **at output layer**
31. **End**

Algorithm 2 presents a proposed transfer learning method aimed at improving accuracy of cardiovascular disease prediction while minimizing error rates.

V. EXPERIMENTAL RESULTS

Experimental assessment of the proposed LKSTOTL method and 1D-CNN [1] and BlCVDD-Net[2] are implemented by Python language using cardiovascular disease dataset.

Performance analysis : The performance of the proposed LKSTOTL model is compared with existing [1] and [2] using multiple evaluation metrics across varying patient data samples.

Accuracy:

It is calculated as the proportion of correctly identified the cardiovascular disease data samples relative to the total number of patient records. Accordingly, accuracy is expressed using the following mathematical formula,

$$CDPA = \left(\frac{TP+TN}{TP+TN+FP+FN}\right) * 100 \quad (16)$$

Table 2 cardiovascular disease prediction accuracy

Patient data samples	Cardiovascular disease prediction accuracy (%)		
	LKSTOTL	1D-CNN	BICVDD-Net
5000	97.2	91	93
10000	97.65	91.05	92.65
15000	98.05	90.11	92.06
20000	97.89	89.05	93.03
25000	98.74	90.06	92.45
30000	97.32	90.44	92.05
35000	98.45	89.45	91.06
40000	97.41	88.05	92.42
45000	98.6	90.12	92.43
50000	97.89	89.05	92.48

Table 2 shows outcomes of cardiovascular disease prediction accuracy versus number of patient data samples. Overall comparison results illustrates LKSTOTL increases $CDPA$ by 9% and 6% than the [1],[2].

Precision: It represents the proportion of correctly predicted cardiovascular disease presence or absence from the total number of data samples. The mathematical expression for calculating the precision is expressed as follows,

$$\boldsymbol{PN} = \left(\frac{\boldsymbol{TP}}{\boldsymbol{TP+FP}}\right) \quad (17)$$

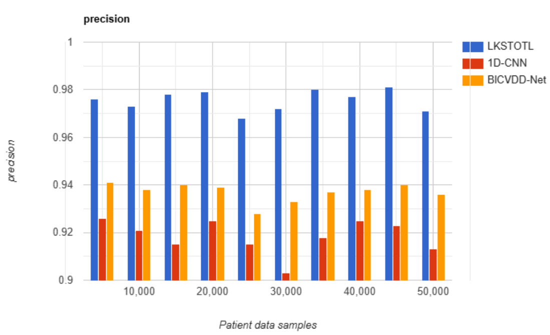

Figure 4 Graphical outcomes of precision

Figure 4 depicts graphical illustration of precision with number of patient data samples. A comparative analysis of LKSTOTL and existing methods demonstrates improvement of 6% and 4% in precision than the[1],[2].

Recall: also known as sensitivity, measures the model's ability to correctly identify actual positive cases. It is defined as the ratio of TP to the sum of TP and FN. Mathematically, recall is expressed as follows,

$$RC = \frac{TP}{TP+FN} \quad (18)$$

Where, 'RC' indicates recall, TP' denotes a true positive rate, FN'denotes a false negative rate

Table 3 Recall

Patient data samples	Recall		
	LKSTOTL	1D-CNN	BICVDD-Net
5000	0.982	0.940	0.955
10000	0.983	0.936	0.953
15000	0.981	0.941	0.959
20000	0.979	0.946	0.956
25000	0.982	0.948	0.961
30000	0.986	0.933	0.958
35000	0.979	0.945	0.957
40000	0.986	0.938	0.952
45000	0.988	0.942	0.958
50000	0.986	0.939	0.962

Table 3 illustrates the outcomes of recall results with number of patient data samples. Finally, the average of ten results was analyzed indicating that recall was improved by 5% and 3% compared to [1] and [2], respectively.

F1-Scores: It refers to the harmonic mean of precision as well as recall and it formulated as follows,

$$F1\ score = 2 * \left[\frac{PR*RC}{PR+RC}\right] \quad (19)$$

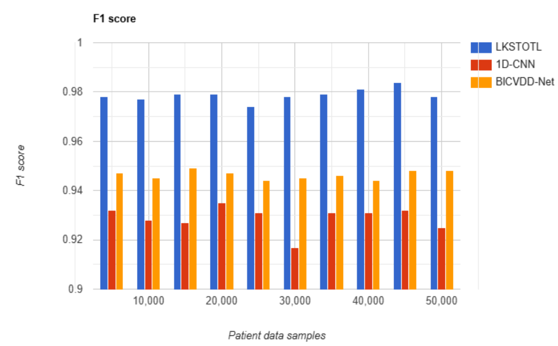

Figure 5 Graphical outcomes of F1 score

Figure 5 illustrates performance analysis of F1-score results against number of patient data samples.Finally, the overall comparison results show F1-score of LKSTOTL model is increased by 5% and 3% than that of [1],[2].

Specificity : It measures the ability of a model to correctly identify negative cases from the input data samples. It is defined as the ratio of true negatives (TN) to the sum of true negatives (TN) and false positives (FP).

$$Specificity = \frac{TN}{TN+FP} \quad (20)$$

Table 4 Specificity

Patient data	Specificity		
	LKSTOT	1D-CNN	BICVDD-

samples	L		Net
5000	0.950	0.848	0.878
10000	0.942	0.832	0.869
15000	0.953	0.845	0.872
20000	0.948	0.846	0.885
25000	0.955	0.847	0.886
30000	0.949	0.856	0.875
35000	0.957	0.852	0.876
40000	0.956	0.849	0.869
45000	0.952	0.843	0.874
50000	0.948	0.842	0.87

Table 4 portrays the performance outcomes of specificity with number of patient data samples.A comparison analysis revealed LKSTOTL model enhanced performance of specificity by 12% and by 8% than the [1],[2].

Error rate : It quantifies the proportion of incorrect predictions made by the model. It includes both false positives and false negatives out of the total number of predictions.

$$ER = \frac{FP+FN}{TP+TN+FP+FN} \quad (21)$$

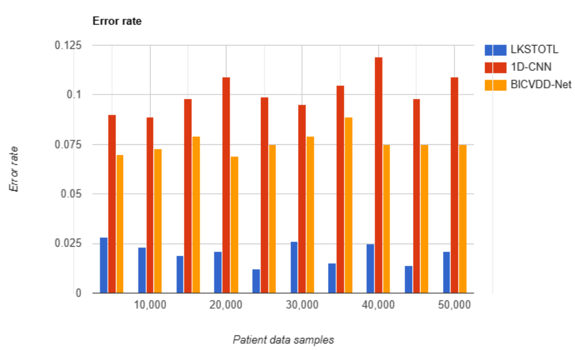

Figure 6 Graphical outcomes of error rate

Figure 6 demonstrates graphical analysis of error rate versus number of data samples. On average, across ten comparisons, error rate using LKSTOTL model is reduced by 80% and 73% than the [1] and [2].

Prediction time: It indicates the total time required by the algorithm to determine whether cardiovascular disease is present or absent. The prediction time for the disease is calculated as follows,

$$CDPT = \sum_{i=1}^{m} DP_i * T(CDP) \quad (22)$$

Table 5 cardiovascular disease prediction time

Patient data samples	Cardiovascular disease prediction time (ms)		
	LKSTOTL	1D-CNN	BICVDD-Net
5000	19	27	24
10000	22.6	32.5	27.6
15000	25.8	34.7	30.6
20000	29.3	37.5	33.7
25000	32.7	42.8	37.6
30000	35.9	44.8	40.5
35000	38.7	48.9	43.9
40000	42.5	52.6	48.7
45000	44.9	54.5	50.6
50000	48.7	57.6	53.8

Table 5 illustrates overall, the findings that LKSTOTL model reduced the performance of cardiovascular disease prediction time by 22% and 14% compared to the existing approaches.

V CONCLUSION

Therefore, in this study, a new technique has been proposed for the accurate and efficient prediction of CVD named Laplace Kernel STOTL (LKSTOTL) algorithm. By means of data preprocessing, dimensionality reduction, important feature selection and deep transfer learning method with pre-trained deep belief network, LKSTOTL model effectively eliminates the issues related to traditional machine learning and deep learning methods such as low prediction accuracy, high error rate and high computation time. The best features selected by the Laplace kernelized stochastic neighbor embedding and fine tuned by spiral search optimization leads to a significant improvement of the model performance. With the increase of +8% accuracy, +5% precision, +4% recall, +4% F1-score, +10% specificity, +77% error rate, +18% prediction time in experimental evaluation, LKSTOTL overcomes other current methods and holds great potential to become a clinical decision support tool for CVD management. The overall generalizability of this work could be enhanced in the future by studies that include more patients to allow for external validation of the results in a larger and more heterogeneous cohort than that used for development. And, additive elements including imaging, genomics, lifestyle, and explainable AI could further enhance and facilitate the adoption of personalized CV health care.

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