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INTEGRATION OF STACKED ENSEMBLE LEARNING WITH FUZZY CNN FOR CVD PREDICTION

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Abstract

Cardiovascular disease (CVD) encompasses various heart and blood vessel disorders such as coronary artery disease, heart failure, and arrhythmias. As a leading cause of mortality globally, early and accurate diagnosis is essential to improve survival rates and ensure timely treatment. Machine learning and deep learning models have shown promise in enhancing prediction accuracy, yet challenges remain in optimizing performance and reducing classification errors. To address this, a novel heart disease prediction model is proposed using a Stacked Ensemble Learning approach with a Fuzzy Convolutional Neural Network (Fuzzy CNN) as the meta-classifier. Initially, data preprocessing is performed, including handling missing values, normalization, and categorical encoding. The dataset is balanced with equal representation of both classes—disease and no disease. Recursive Feature Elimination (RFE) is applied to select the most relevant features for improving model generalization and reducing complexity. The framework employs an Improved Multi-Layer Perceptron (MLP)and an Improved Deep Belief Network (DBN) as base learners. Their outputs are aggregated and passed to a Fuzzy CNN, which integrates these predictions using a fuzzy-weighted voting scheme to generate the final classification. This combination effectively captures both linear and non-linear patterns in the data, enhancing diagnostic accuracy. Experimental evaluations show that the proposed model outperforms traditional approaches in terms of accuracy, precision, recall, F1-score, and specificity. The results confirm the efficiency of the proposed stacked ensemble model in improving CVD diagnosis.

Keywords: cardiovascular disease risk prediction, Fuzzy Convolutional Neural Network (Fuzzy CNN),Recursive Feature Elimination (RFE), Stacked Ensemble Learning, Improved Multi-Layer Perceptron (MLP), Recursive Feature Elimination (RFE)

1. Introduction

Cardiovascular Disease (CVD) remains one of the leading causes of death worldwide, accounting for an estimated 17.9 million lives annually, which represents 32% of all global deaths, according to the World Health Organization (WHO, 2021). These conditions, including coronary artery disease, arrhythmias, and heart failure, are often preventable or manageable if detected early. Early and accurate diagnosis plays a pivotal role in reducing morbidity and mortality, improving patient outcomes, and minimizing the burden on healthcare systems.Recent advances in machine learning (ML) and deep learning (DL) techniques have revolutionized the field of medical diagnostics, offering automated, scalable, and highly accurate systems for disease classification. ML algorithms such as Decision Trees, Support Vector Machines (SVM), Random Forests, and Naive Bayes have been extensively used for heart disease prediction, while DL models like Convolutional Neural Networks (CNNs), Deep Belief Networks (DBNs), and Multi-Layer Perceptrons (MLPs) have shown superior performance due to their ability to model complex, non-linear patterns in data [1].

However, single models often struggle to generalize well across diverse clinical datasets due to overfitting, limited interpretability, and sensitivity to data imbalance and noise. To overcome these challenges, ensemble learning techniques have emerged as a promising approach. Ensemble methods, particularly stacked ensemble learning, combine multiple base learners and integrate their predictions through a meta-classifier, thereby enhancing overall robustness and prediction accuracy [2].Moreover, traditional DL models treat the aggregation of base learners rigidly, often ignoring the

inherent uncertainty and vagueness in medical data. This shortcoming can be mitigated by incorporating fuzzy logic, which enables reasoning with imprecise inputs and allows for better handling of clinical ambiguity. Fuzzy CNNs, which integrate fuzzy systems with deep learning architectures, offer an advanced solution by combining the strengths of fuzzy inference systems and CNNs [3].

While several deep learning approaches have been proposed for heart disease prediction, limitations remain in terms of performance, interpretability, and efficiency. For instance, an end-to-end attention-based deep neural model named DeepRisk [4] was developed to assess CVD risk, but it struggled to maintain high diagnostic accuracy across diverse clinical datasets. Similarly, a hybrid model combining Deep Belief Networks (DBN) with the Cuckoo Search Algorithm (CSA) [5] aimed to optimize cardiac disease prediction, yet integrating large-scale patient data with bio-inspired algorithms did not yield significant performance improvements. Another advanced model, the Optimal Scrutiny Boosted Graph Convolutional LSTM (O-SBGC-LSTM) [6], was designed to predict coronary heart disease risk in diabetic patients. Although it achieved moderate gains in accuracy, it failed to strike a balance between prediction efficiency and low time complexity.

These limitations highlight the need for a more robust, accurate, and efficient predictive framework that can effectively model complex clinical patterns while maintaining generalizability. The proposed Stacked Ensemble Learning model with a Fuzzy CNN meta-classifier addresses these challenges by combining the strengths of improved deep learning architectures with fuzzy logic to enhance diagnostic performance for CVD prediction.

Experimental results confirm that the proposed method significantly improves diagnostic performance across key metrics such as accuracy, precision, recall, F1-score, and specificity, outperforming traditional and standalone deep learning models. This highlights the potential of the proposed stacked ensemble model with Fuzzy CNN as a reliable tool for early and accurate CVD prediction in clinical practice

2. Related works

Karthik and Uthra [7] proposed a 2-Tier Stacking Ensemble Classifier aimed at improving disease classification performance. The architecture combines multiple base classifiers in the first tier and aggregates their predictions using a meta-classifier in the second tier. The proposed method demonstrated superior results on various benchmark datasets, confirming the efficacy of ensemble learning in healthcare diagnostics. The model's modular structure makes it adaptable for integrating deep learning and fuzzy-based techniques for more complex disease prediction tasks.Chugh et al. [8] introduced a Hybrid Multi-Model Fuzzy Ensemble approach specifically for CVD detection. Their framework incorporates fuzzy logic to handle the vagueness and imprecision in clinical features and combines predictions from several models using ensemble voting. The fuzzy-enhanced ensemble significantly improved the sensitivity and specificity of CVD detection, validating the role of fuzzy systems in medical decision-making where input data may be noisy or uncertain.

To exploit the spatial feature extraction capabilities of deep learning, Bukhari et al. [9] presented Stacked Convolutional Neural Network (CNN) architecture optimized using the Levy Flight-based Grasshopper Optimization Algorithm (LF-GOA). Their hybrid framework was applied to structured health datasets and achieved impressive prediction accuracy. The integration of evolutionary optimization with CNNs allowed the model to fine-tune hyperparameters for improved generalization on imbalanced CVD datasets .In a related study, Jain et al. [10] developed an Optimized Levy Flight CNN Model tailored for large-scale heart disease prediction. This work focused on big data applications and addressed overfitting through regularization techniques and hyperparameter tuning. Their framework outperformed traditional CNNs, demonstrating that optimization-based deep models are effective in managing complex healthcare datasets. Rustam et al. [11] further explored the role of CNNs in ensemble learning by incorporating CNN-generated deep features into traditional machine learning models for CVD classification. Their results revealed that CNN features, when used as input to ensemble classifiers like Gradient Boosting and Random

Forest, significantly enhance classification performance. This study bridges the gap between deep and conventional learning, supporting the design of hybrid models for structured data .

Raj et al. [12] proposed a novel stack-based ensemble classifier combining Random Forest, Gradient Boosting, and Support Vector Machine (RF-GB-SVM) to detect heart disease. While the stacking model showed improved classification performance, it lacked an effective feature selection mechanism, limiting interpretability and model optimization for clinical use.Venkatesh et al. [13] developed an automatic diagnostic model using swarm intelligence techniques to detect and classify cardiovascular diseases based on clinical features and severity levels. Although promising, the model was not scalable to large datasets and lacked robustness in identifying diverse cardiovascular conditions.

Sreekumari et al. [14] introduced an ensemble voting method for heart disease prediction by analyzing various risk factors. Despite the ensemble approach enhancing performance, the absence of a sophisticated feature selection process reduced the model's ability to generalize and accurately predict disease across heterogeneous datasets. Duyar et al. [15] implemented a one-dimensional convolutional neural network (1D-CNN) model integrated with explainable artificial intelligence (XAI) and gut microbiota data to detect cardiovascular diseases. However, the model showed limitations in handling large-scale data, and its performance could not be scaled effectively due to computational constraints. Babu et al. [16] designed a cloud-based framework (CBF) using machine learning algorithms for monitoring health metrics and predicting cardiovascular diseases. While offering real-time processing and deployment benefits, the system did not significantly contribute to deeper analytical insights or medical decision support, highlighting the need for advanced model integration.

3. Methodology

3.1 Data acquisition

In the proposed SEL-FCNN Model, data acquisition is the fundamental step in cardiovascular disease risk prediction. It refers to the process of collecting, and analyzing data from the BNG Statlog Heart Disease Dataset. This dataset contains necessary information for cardiovascular disease prediction. It comprises 14 features and 10,00, 000 instances. The detailed descriptions of the features are shown in table1.

Table 1: attribute description

S.NO	Attributes	Description
1	Age	Patient age in years
2	sex	Gender (Male : 1; Female : 0)
3	chest	chest pain type Value 1: typical angina Value 2: atypical angina Value 3: non-anginal pain Value 4: asymptomatic
4	resting_blood_pressure	1-women, 2-men
5	serum_cholestoral	Serum cholesterol in mg/dl (Numeric)
6	fasting_blood_sugar	Blood sugar levels on fasting > 120 mg/dl 1 : true 0 : false
7	resting_electrocardiographic_results	Result of electrocardiogram while at rest with 3 distinct values 0 : Normal 1: having ST-T wave abnormality 2: showing probable or definite left ventricular hypertrophyby Estes' criteria

8	maximum_heart_rate_achieved	Maximum heart rate achieved (Numeric)
9	exercise_induced_angina	Exercise-induced angina (1 = yes; 0 = no)
10	oldpeak	ST depression induced by exercise relative to rest
11	slope	Slope of the peak exercise ST segment
12	number_of_major_vessels	Number of major vessels (0–3) colored by fluoroscopy
13	thal	results of nuclear stress test (3 = normal; 6 = fixed defect; 7 = reversable defect)
14	class	Present, absent

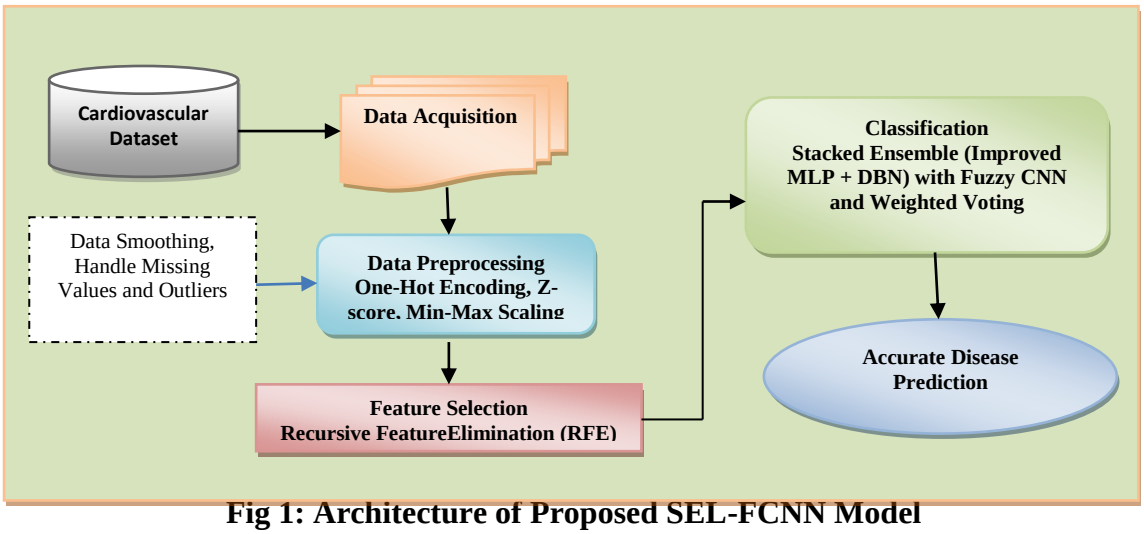

Fig 1: Architecture of Proposed SEL-FCNN Model

3.2 Data Preprocessing

Data preprocessing is carried out to ensure the dataset is clean, consistent, and suitable for the learning algorithms. Initially, missing values are handled using mean imputation for numerical features and mode imputation for categorical features. Outliers are detected and treated using the Z-score method, where any data point with aZ-score above 3 or below 3 is considered an outlier and either removed or replaced. Subsequently, categorical variables are encoded to numerical form using One-Hot Encoding for nominal features and Ordinal Encoding for ordered categories. To ensure uniformity in feature scales, numerical attributes are normalized using Min-Max Scaling, defined by the formula

$$X_{Scaled} = \frac{X - X_{min}}{X_{max} - X_{min}} \quad (1)$$

Where Xis the original feature value, X_{min} and X_{max} are the minimum and maximum values of the feature, respectively. This normalization bounds the values within the [0, 1] range, which is essential for neural network based models. The dataset used is already balanced, containing an approximately equal distribution of both classes—‘disease’ and ‘no disease’—ensuring unbiased learning and improved classification performance.

3.3 Feature Selection:

Recursive Feature Elimination (RFE) is used as the feature selection method in this study due to its ability to identify the most relevant features for heart disease prediction. RFE works by recursively removing the least important features based on model weight or importance scores until

the optimal set is selected. It helps reduce overfitting, improves accuracy, and enhances model interpretability. For linear models, feature importance is calculated as:

$$\text{Importance}(f_i)=|w_i| \quad (2)$$

Where w_i is the weight of feature f_i. RFE ensures that only the most informative clinical parameters are used for classification. The selected Features are Age**,** Chest Pain Type,Resting Blood Pressure **,** Serum Cholesterol**,** Max Heart Rate Achieved **,** ST Depression **,** Exercise Induced Angina **,** Number of Major Vessels **,** and Thalassemia

3.4 Disease classification using Stacked Ensemble learning with Fuzzy CNN

A Stacked Ensemble method is an ensemble machine learning algorithm that combines multiple models to improve predictive performance. The stacking utilizes the multiple base models, such as the Improved MLP and DBN classifier model that are trained on the training data samples and classify the samples into disease presence or absence. Each model learns different patterns and produces its own prediction outcomes independently. Once classification is obtained from all base models, they are combined using an aggregation method called a meta-learner, which in this case is a CNN with a fuzzy weighted voting concept. This process produces the final classification output, such as whether a disease is present or absent.

The stacked ensemble classifier uses the selected optimal features from the training dataset $\{\beta_{d_m}, Y\}$ as input to the base classifiers. In this training set, β_{d_m}represents the input training samples, and Y represents the output labels for the stacked ensemble classification methods.

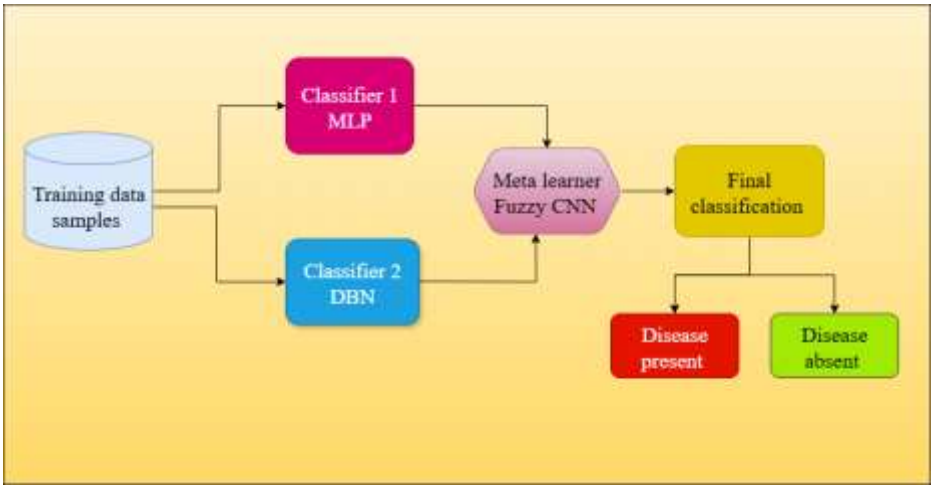

Fig 2 Structure of stacked ensemble classifier

3.4.1 Improved Multilayer perceptron classifier

Disease classification is performed using an improved Multilayer Perceptron (MLP) classifier with selected features and training data samples βdi\beta_{d_i}βdi. This fully connected feed-forward neural network comprises an input layer, multiple hidden layers, and an output layer. Each neuron computes a weighted sum of inputs, adds a bias, and applies an activation function. The input layer receives selected features, where each feature is associated with weights α_j and a bias g

$$Q(t) = [\sum_{j=1}^{m} \beta_{d_j} * \alpha_j] + g \quad (3)$$

To evaluate similarity between test and training samples, the Generalized Tversky Index is used:

$$B = \frac{\beta_{d_j} \cap \beta_{d_t}}{u\left(\beta_{d_j} \Delta \beta_{d_t}\right) + v\left(\beta_{d_j} \cap \beta_{d_t}\right)} \quad (4)$$

Where u, v = 1. The similarity score B is passed through a Sigmoid Activation Function to produce classification output:

$$F = \frac{1}{1+\exp(-B)} \quad (5)$$

$$F = \begin{cases} 1 \ ; Disease\ present \\ 0 \ ; \ \ Disease\ absent \end{cases} \quad (6)$$

The classification error is calculated as:

$$e = \frac{1}{2}\left(Y - Z(t)\right)^2 \quad (7)$$

To minimize error, weights are updated using the Whale Optimization Algorithm (WOA), which mimics the bubble-net hunting strategy of whales. Each whale represents a weight vector, and fitness is evaluated using:

$$f = \arg\min e \quad (8)$$

Whale position update during encircling behavior is given by

$$P_w(i+1) = P_{best}(i) - A.B \quad (9)$$

$$B = \left|\varphi.P_{best}(i) - P_p(i)\right| \quad (10)$$

Where, $P_w(i+1)$ denotes an updated position of whale, $P_{best}(i)$indicates a current best position, $P_p(i)$ denotes a position vector of the prey, $A\ and\ B$ represents a coefficient vector. Therefore, the coefficient vector is expressed as follows,

$$A = \ (2k-1)r \quad (11)$$

$$\varphi = 2k \quad (12)$$

Where 'r' denotes a number linearly reduced from 2 to 0 and 'k' indicates a random vector [0, 1]. The spiral bubble-net feeding strategy updates positions using:

$$P_w(i+1) = D' e^{mn} \cos(2\pi q) + P_{best}(i) \quad (13)$$

$$D = |P_{best}(i) - P_w(i)| \quad (14)$$

Where, $P_w(i+1)$indicates a updated position of whale, Drepresents an updated distance among whale current position '$P_w(i)$' and best solution '$P_{best}(i)$', 'm' is a constant [0, 1] used to describing the structure of the logarithmic curve, Exponential function 'e' is the base of natural logarithms, 'n' is the random number ranges are [-1, 1]. Finally, searching the prey behavior is randomly executed along with the position.

$$P_w(i+1) = P_{rand}(i) - A.B(15)$$

$$B = |\varphi.P_{rand}(i) - P_w(i)|(16)$$

The above processes are repeated until convergence. Finally, the optimized weights minimize the classification error, improving the predictive performance of the MLP classifier.

3.4.2Improved Deep Belief Network

The proposed Deep Belief Network (DBN) is a fully connected, feed-forward architecture comprising an input layer, multiple hidden layers, and an output layer. Training involves two phases: unsupervised layer-wise pre-training followed by supervised fine-tuning using Bregman Divergence-based Swallow Swarm Optimization (BD-SSO).

Let the training set be {D, Y} where D=$\left\{\beta_{ft_1}, \beta_{ft_2}, \ldots, \beta_{ft_n}\right\}$represents the input data and Y is the output label (disease presence/absence). In the hidden layer, neuron activation is computed as:

$$H = \sum_{i=1}^{n} \beta_{ft_i} * \varphi_{v\_h} + B \quad (17)$$

Where is the weight between visible and hidden layers, and B is the bias. A fuzzy-based Multi-Criteria Decision Analysis (MCDA) evaluates the data against predefined thresholdsφ_{v_h}. Fuzzy rules classify disease presence or absence:

$$R_1: \boldsymbol{if}\left(\beta_{fvi} = PC_h\right) then\ class\ C_i \in 0\ i.e\ diseaseabsence \quad (18)$$

$$R_2: \boldsymbol{if}\left(\beta_{fvi} > PC_h\right) then\ class\ C_i \in 1\ \ i.e\ diseasepresence \quad (19)$$

The fuzzy output is passed to a Gaussian Radial Basis Function (RBF) kernel to measure similarity between training and testing samples:

$$RK = \exp\left[-0.5 * \frac{\left\|\beta_{f_t} - \beta_{f_{dt}}\right\|^2}{d^2}\right] \quad (20)$$

Whered is the deviation. The RBF output feeds into the Maxout activation function**:**

$$A = \begin{cases} 1; & \max RK \\ 0; & otherwise \end{cases} \quad (21)$$

In the fine-tuning phase**,** BD-SSO optimizes the weights to minimize classification error. Each swallow in the swarm represents a weight vector:

$$\varphi = \varphi_1, \varphi_2, \ldots . \varphi_m \quad (22)$$

Fitness is calculated using

$$\theta_f = arg\, min\, E \quad (23)$$

The error rate is computed as follows,

$$E = \frac{1}{n}\left(Y_{ac} - Y_{pred}\right)^2 \quad (24)$$

Based on their fitness values, the particles are categorized into different roles: explorers, wandering (aimless) particles, local leaders, and the global (head) leader. The Explorer's velocity is updated as:

$$V_E(i+1) = V_E(i) + V_T (25)$$

Where, $V_E(i)$ denotes a current velocity of the Explorer particles, V_T denotes a total velocity which is expressed as follows,

$$V_T = V_{hl(i+1)} + V_{ll(i+1)} \quad (26)$$

Where,

$$V_{hl(i+1)} = V_{hl}(t) + r_1|x_{best}(E) - x_i(E)| + r_2|V_{hl}(t) - x_i(E)| \quad (27)$$

$$V_{ll(i+1)} = V_{ll}(t) + r_3|x_{best}(E) - x_i(E)| + r_4|V_{ll} - x_i(E)| \quad (28)$$

Here r_1,r_2, r_3, $r_4 \in (0,1)$ are random values, and $|\cdot|$ denotes Bregman divergence between the best solution and current position. The process repeats until convergence, and the final output is obtained through the output layer, ensuring accurate disease classification.

3.4.3 Fuzzy Convolutional Neural Network based Classification

In the proposed model, a Fuzzy Convolutional Neural Network (Fuzzy CNN) acts as a meta-learner to integrate outputs from two base classifiers improved MLP and improved DBN for final heart disease prediction. This combination captures both linear and non-linear data patterns, improving classification accuracy and robustness.

The output from base classifiers is aggregated as:

$$Y = \sum_{k=1}^{2} z_k \quad (29)$$

Wherez_k is the output of the k^{th} base classifier. The combined result C_E is passed into the CNN, which includes input, hidden (convolution, max-pooling, fully connected), and output layers.A fuzzy-weighted voting technique is applied to the classifier outputs. Votes are assigned as:

$$V_k \rightarrow c_k(BC) \quad (30)$$

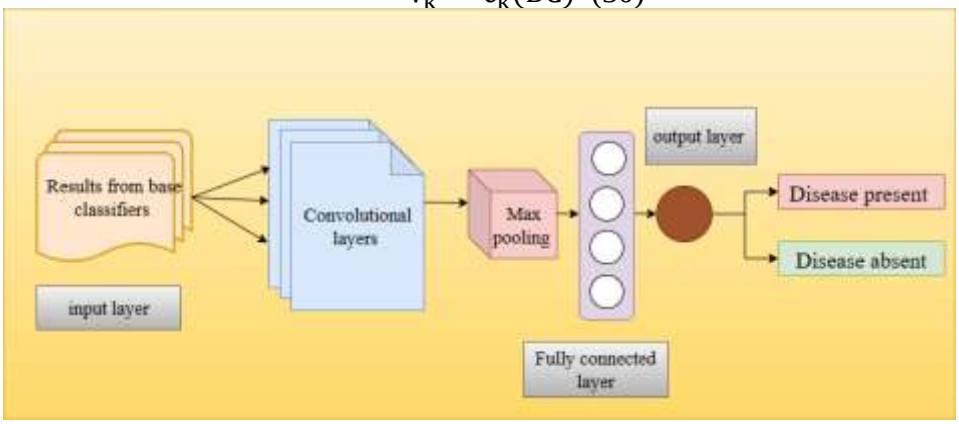

Fig 3: Schematic Structure of CNN

Where, V_k denotes a votes assigned to the classification results 'c_k' of the base classifier 'BC'.The corresponding weight for each class is computed by:

$$W = \frac{Number\ of\ votes\ received\ by\ \text{class}}{Total\ number\ of\ classifiers} \quad (31)$$

Next, triangular fuzzy membership functions are used in the max-pooling layer to process weights:

$$\mu_s(W) = \begin{cases} 0 & W < a\ or\ W \geq c \\ \frac{W-a}{b-a} & a < W \leq b \\ \frac{W-a}{b-a} & b < W < c \end{cases} \quad (32)$$

Where a, b, and c define the triangle's shape. The fully connected layer selects the final class based on the highest fuzzy membership value exceeding a predefined threshold T:

$$Y = \arg\max\ \mu_s(W) \quad i.e\ \mu_s(W) > T \quad (33)$$

This fuzzy logic integration enables more accurate final classification by evaluating class relevance based on combined weighted votes and fuzzy membership strength

.

// Algorithm 1:Disease classification using Stacked Ensemble learning with Fuzzy CNN

Input: selected optimal features '$\beta_{f_1}, \beta_{f_2}, \dots, \beta_{f_o}$', data samples $\beta_d = \beta_{d_1}, \beta_{d_2}, \dots, \beta_{d_m}$

Output: Increase classification accuracy

Begin

1. Collect the optimal features $\beta_{f_1}, \beta_{f_2}, \dots, \beta_{f_o}$
2. Construct 'base classifiers '

// Improved MLP

3. Obtain the neuron activity at input layer '$Q(t)$'
4. **For** each training data with testing disease data –**[hidden layers]**
5. Measure Tversky index similarity measure 'B'
6. Apply sigmoid activation function 'F'
7. **If** ($F = 1$) **then**
8. classified as disease present
9. **else**
10. classified as disease absent
11. **End if**
12. **For each results**
13. Measure the error rate 'e'
14. Update the weight '$\nabla\alpha_{t+1}$'
15. Find minimum error by identifying optimal weight using WOA
16. Obtain the final classification results with minimum error **at the output layer**
17. **End for**
18. **End for**

// Improved DBN

19. **Number of selected features** $\beta_{f_1}, \beta_{f_2}, \dots, \beta_{f_o}$with the training data $\beta_d = \beta_{d_1}, \beta_{d_2}, \dots, \beta_{d_m}$taken **at the input layer**
20. **For each** dataβ_{d_i} –**[hidden layer]**
21. Assign weight 'φ_{v_h}' and add bias 'B'
22. **end for**
23. Perform multicriteria analysis with fuzzy rules
24. **For each** training data with testing disease data
25. Measure relationship using kernel function
26. kernel output is given to activation function

27. If ($A = 1$) **then**
28. classified as disease present
29. else
30. classified as disease absent
31. End if
32. For each classified results
33. Measure the error rate 'E'
34. Update the weight '$\nabla\varphi_{v\_h}$' using BD-SSO algorithm
35. End for
36. Obtain the final classification results with minimum error **at the output layer**
37. End for
// Stacking Ensemble Classification with Fuzzy CNN
38. Collect combined base classifier results 'C_E' '**input layer**
39. For each class c_k(BC)--- **convolutional layer**
40. Assign the votes 'V_k'
41. Assign the weights based on vote counts
42. End For
43. For each weighted class
44. Compute membership grade using (61) --- **maxpooling layer**
45. End for
46. For each membership value--- **fully connected layer**
47. Assign threshold
48. if ($\mu_s(W) > T$) **then**
49. Obtain the final accurate classification results
50. End if
51. End for
52. Return (disease present and absent classification) --- output layer
End

4. Experimental Evaluation

4.1 Performance Analysis of Accuracy

It refers to the proportion of patient records that are correctly predicted as low, moderate, or high risk out of the total number of records. It is calculated using the following formula:

$$A = \left[\frac{t_{tr}+t_{ne}}{t_{tr}+t_{ne}+f_{pv}+f_{nv}}\right] * 100 \qquad (34)$$

Table 2: Comparative analysis of accuracy

Number of data samples	Accuracy (%)			
	Proposed SEL-FCNN	DeepRisk[1]	DBN+CSA [2]	O-SBGC-LSTM [3]
10000	98.3	91.5	93	94.5
20000	98.22	91.22	93.22	94.23
30000	98.1	91.05	93.45	94.85
40000	97.89	90.56	92.33	94.36
50000	97.78	90.78	92.56	93.85
60000	98.56	90.56	92.6	94.96
70000	98.23	91.33	93.32	95.78
80000	98.56	92.56	94.02	95.22
90000	98.12	91.63	93.65	95.89
100000	97.8	92.74	94.05	95.5

4.2 Performance Analysis of Precision

Precision is a performance metric used to evaluate the accuracy of a model in identifying heart disease prediction. It is calculated by dividing the number of true positive predictions by including both true positives and false positives. The formula for precision is given below:

$$Pr = \left[\frac{t_{tr}}{t_{tr}+f_{pv}}\right] * 100 \quad (35)$$

Table 3:Comparison ofprecision

Number of data samples	Precision (%)			
	Proposed SEL-FCNN	**DeepRisk[1]**	**DBN+CSA [2]**	**O-SBGC-LSTM [3]**
10000	98.88	94.94	95.50	96.61
20000	98.65	94.23	95.42	96.5
30000	98.45	94.21	95.36	95.74
40000	98.39	93.56	95.41	96.23
50000	98.25	93.44	95.33	95.85
60000	97.56	93.65	95.65	96.02
70000	98.45	94.12	96.05	96.87
80000	97.89	93.56	95.56	96.22
90000	98.92	94.63	95.23	96.56
100000	98.47	94.23	95.96	96.83

4.3Performance analysis of recall

Recall is an important performance metric in heart disease risk prediction, as it measures the model's ability to correctly identify patients' risk. It is computed using the following formula,

$$Rl = \left[\frac{t_{tr}}{t_{tr}+f_{nv}}\right] * 100 \quad (36)$$

Table 4: Comparison of recall

Number of data samples	Recall (%)			
	Proposed SEL-FCNN	**DeepRisk[1]**	**DBN+CSA [2]**	**O-SBGC-LSTM [3]**
10000	99.21	95.48	96.59	97.15
20000	99.18	95.36	96.45	97.05
30000	99.12	95.25	96.42	97.02
40000	99.05	95.11	96.35	97.11
50000	99.12	95.05	96.32	97.36
60000	98.45	95.23	96.28	97.45
70000	99.05	95.36	96.12	96.89
80000	98.45	95.22	96.41	97.10
90000	99.06	95.11	96.52	97.23
100000	98.72	95.54	96.69	97.45

4.4 Performance Analysis ofF-Measure:

It also called as F1 score is measured as the mean of precision as well as recall. A higher value indicates a better trade-off between precision and recall.It is measured as follows,

$$f - m = \left[2 * \frac{Pr * Rl}{Pr + Rl}\right] * 100 (37)$$

Table 5:Comparison of F-measure

Number of data samples	F-measure (%)			
	Proposed SEL-FCNN	**DeepRisk[1]**	**DBN+CSA [2]**	**O-SBGC-LSTM [3]**
10000	99.04	95.20	96.04	96.87
20000	98.91	94.79	95.93	96.77
30000	98.78	94.72	95.88	96.37
40000	98.71	94.32	95.87	96.66
50000	98.68	94.23	95.82	96.59
60000	98.00	94.43	95.96	96.72
70000	98.74	94.73	96.08	96.88
80000	98.16	94.38	95.98	96.68
90000	98.99	94.86	95.87	96.89
100000	98.59	94.88	96.32	97.13

4.5 Performance analysis of Specificity:

It measures the model that identifies patients who have heart disease risk levels. The corresponding mathematical formulation is provided below.

$$SP = \left[\frac{t_{ne}}{t_{ne}+f_{pv}}\right] * 100 \quad (38)$$

Table 6: comparison of Specificity

Number of data samples	Specificity (%)			
	Proposed SEL-FCNN	**DeepRisk[1]**	**DBN+CSA [2]**	**O-SBGC-LSTM [3]**
10000	90.90	60.86	66.66	75
20000	92.36	65.89	68.56	78.56
30000	91.26	70.05	72.65	80.23
40000	93.85	73.63	75.62	83.65
50000	91.25	76.45	78.23	85.74
60000	94.45	80.05	82.65	87.05
70000	93.65	82.47	84.05	88.96
80000	93.78	83.65	85.45	87.56
90000	94.55	82.89	86.67	88.45
100000	94.47	82.79	86.44	88.37

5. Conclusion

Heart disease remains a major leading cause of mortality worldwide, highlighting the need for early and accurate detection to improve patient outcomes. This paper introduces the SEL-FCNN model which is designed for heart disease risk prediction with big data. The approach incorporates various stages to enhance accuracy of risk prediction with minimal time consumption. The pre-processing component of risk prediction significantly reduces both computational time, thereby speeding up the cardiovascular disease (CVD) prediction process. Moreover, the feature extraction and optimal feature selection step improved the accuracy of risk prediction with minimal complexity. The proposed SEL-FCNN model, which integrates Stacked Ensemble Learning with a Fine-tuned Convolutional Neural Network and Temporal LSTM, demonstrated superior performance over traditional deep learning models across multiple metrics including accuracy, precision, recall, F1-score, specificity, and prediction time. Through effective preprocessing and optimal feature

selection, the model achieved reduced computational complexity and improved risk prediction outcomes. The results underscore the effectiveness of ensemble and hybrid deep learning approaches in handling large-scale cardiovascular datasets. Future work will focus on expanding this framework by incorporating multimodal health data - such as clinical imaging, electronic health records, and IoT-based physiological signals to further enhance the predictive power and clinical applicability of heart disease risk assessment models.

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