Hybrid Intelligent Framework for Early Cardiovascular Disease Diagnosis: Integrating Fuzzy Logic Optimization with Deep Neural Networks

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Abstract: Cardiovascular disease (CVD) leads to the death of approximately 17.9 million people globally annually, and early diagnosis is critical as traditional diagnostic approaches frequently fail to detect it at early onset. This paper proposes a hybrid intelligent system which integrates the Random Forest Random Forest (RF) feature selection, the fuzzy logic optimization, and the Deep Neural Network to develop an early CVD diagnosis. The pipeline involves the removal of outliers by employing an interquartile range, ranking significant features through Random Forest, optimization of clinical data via Gaussian fuzzy membership functions and classification based on a 4-layer deep neural network. The model outperformed SVM, Random Forest, and a typical deep neural network with 99.98% accuracy and strong precision, recall, F1-score, and AUC values using the Cleveland Heart Disease dataset with 5-fold cross-validation. The most significant characteristics were the type of chest pain, maximum heart rate, and ST depression. Overall, the findings demonstrate that fuzzy logic and deep learning can be combined to create a very precise and practical system for early CVD diagnosis that can be used in primary care.

Keywords-Cardiovascular disease, Clinical decision support, Deep neural networks, Fuzzy logic, Feature selection, Machine learning

I. INTRODUCTION

Cardiovascular disease (CVD) has contributed towards 32% of the estimated 17.9 million global deaths annually, with over 75% arising in low- and middle-income countries with limited access to diagnostics. The traditional models for risk assessment frameworks such as Framingham, SCORE, and QRISK demonstrate only moderate predictive performance (AUC range 0.70–0.80) and often fail to generalize well in diverse populations. Machine learning methods also demonstrate a promising approach for better CVD diagnosis by discovering challenging-to-model features in clinical data, but the current approaches face important challenges, for instance; insufficient incorporation of clinical knowledge, unsatisfactory treatment of measurement uncertainty, lack of interpretability, and performance below the stringent criteria required for clinical use. To close these gaps, in a systematic approach to CVD diagnosis, we propose a novel frame that combines Random Forest-based feature selection with fuzzy logic and deep neural networks to attain an accuracy of 99.98%. We introduce structured clinical guidelines that we use fuzzy membership functions to embed, improve interpretability employing feature importance, fuzzy rules, SHAP values, and display clinical usefulness via real-time inference less than 100 milliseconds in accordance with standard clinical parameters.

II. LITERATURE REVIEW

The various machine learning and deep learning approaches to heart disease prediction using the Cleveland dataset have been investigated to some extent at various levels of efficiency and achieved contrasting results. Shah et al. [10] used Logistic Regression, which was also satisfactory; however, linear model assumptions hindered it. Amin et al. [11] adopted the K-Nearest Neighbor algorithm which, although it does provide improved classification performance, is sensitive to extreme outliers and noise in the information. Latha and Jeeva [12] applied Support Vector Machines, attaining better accuracy, but it is also not very practical in large data size. Mohan et al. [13] put forward the ensemble-based HRFLM approach to predict models enhancing their prediction ability at the expense of model complexity. Ali et al. [14] showed how effective RF classifiers can be, reaching higher accuracy at the potential

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of overfitting. Ghosh et al. [15] introduced something of a shallow network architecture in the form of an MLP-based approach and showed a moderate efficiency. More recently Budholiya et al. [16] using XGBoost and Hassan et al. [17] used PCA-assisted deep learning for example showed good performance enhancement results, they were challenged by behavior (black-box behavior, linear dimension reduction methods and a dependence on reduction of linear dimensions. These limitations underscore a need for more adaptive and interpretable hybrid models to provide consistent clinical decision support. Recent research has developed sophisticated deep learning, hybrid, and explainable AI models to improve the prediction of heart disease using the Cleveland dataset and corresponding benchmarks. Khan et al. [27] used a deep neural network with feature normalization and have improved robustness but a lack of interpretability. Verma et al. [28] added CNN-based feature learning to traditional classifiers, obtaining higher accuracy at a higher cost in computational complexity. Ahmed et al. [29] introduced an ANN–SVM hybrid that improved the stability of the classification while demanding careful tuning of hyperparameters. In 2023, Patel et al. [30] proposed, with attention-based deep learning architecture, enhanced recall for minority classes, but limitations on the model transparency remained. Kumar et al. [31] have investigated explainable boosting machines (EBM) with superior interpretability but lower accuracy than deep models. More recently, Singh et al. [32] with the use of a transformer-based architecture trained on structured clinical data, achieved a high predictive power while requiring a higher number of training resources. In 2024, Rahman et al. [33] applied fuzzy logic and deep learning to resolve uncertainty in clinical features, achieving better generalization/clinical relevance but at the expense of a higher level of architecture complexity.

Table 1. Comparison of ML Approaches for CVD Diagnosis

Study	Year	Method	Dataset	Acc	Recall	Limitations
Shah et al. [10]	2020	Logistic Regression	Cleveland	85.71%	82.67 %	Linear assumptions
Amin et al. [11]	2019	K-NN	Cleveland	87.00%	84.12 %	Outlier sensitivity
Latha & Jeeva [12]	2019	SVM	Cleveland	91.50%	88.45 %	Limited scalability
Mohan et al. [13]	2019	HRFLM	Cleveland	88.70%	86.34 %	Complex ensemble
Ali et al. [14]	2021	Random Forest	Cleveland	93.00%	90.12 %	Overfitting risk
Ghosh et al. [15]	2021	MLP	Cleveland	86.41%	83.21 %	Shallow architecture
Budholiya et al. [16]	2022	XGBoost	Cleveland	95.08%	92.56 %	Black-box model
Hassan et al. [17]	2021	PCA + DL	Cleveland	96.80%	94.23 %	Linear dimensionality reduction
Mathan et al[26]	2025	MSP-DNN	CirCor Digiscope	98%	97%	Complex Multi-modality limitation
Khan et al. [27]	2022	Deep Neural Network	Cleveland	94.60%	91.80 %	Limited interpretability
Verma et al. [28]	2022	CNN + ML	Cleveland	95.30%	92.40 %	High computation cost
Ahmed et al. [29]	2023	ANN–SVM Hybrid	Cleveland	96.10%	93.05 %	Hyperparameter sensitivity
Patel et al. [30]	2023	Attention-based DL	Cleveland	97.20%	95.60 %	Black-box behavior
Kumar et al. [31]	2023	Explainable Boosting Machine	Cleveland	93.80%	91.10 %	Slightly lower accuracy
Singh et al. [32]	2024	Transformer Model	Cleveland	97.60%	95.90 %	High training cost
Rahman et al. [33]	2024	Fuzzy + Deep Learning	Cleveland	98.10%	96.40 %	Model complexity

A. *Research Gaps*

- Inability to combine very good accuracy with high sensitivity - For most common ML and DL methods, high accuracy or stronger sensitivity are reported, but seldom both at clinically-beneficial levels.
- Inconsistent integration of clinical guidelines and domain expertise - Existing studies often employ data-driven learning and their interpretability and clinician trust suffer.
- Improper treatment of uncertainty in medical measurements - Clinical measures typically suffer from variability, noise and measurement uncertainty that conventional crisp models fail to capture effectively.
- Black-box nature restricting clinical adoption and explainability - Deep learning models often lack transparency, which is a limiting factor as it is very difficult to interpret and validate them in clinical settings.
- Stagnant generalization and robustness across validation scenarios - Since many studies are based on single train–test splits, overfitting and poor estimates of performance are potentially present.

III. PROBLEM STATEMENT

Cardiovascular disease (CVD) continues to be one of the leading causes of mortality worldwide, and timely and accurate diagnosis is a key clinical priority. Several machine learning and deep learning models have been introduced to predict CVD using the Cleveland Heart Disease dataset, to some extent, but these approaches have significant constraints limiting their clinical utility. Despite the fact that most studies have established improved accuracy, maintaining both extremely high predictive accuracy and consistently high sensitivity is difficult, leaving the patient at increased risk of a misdiagnosis in real-life screening. Furthermore, most existing models are data-driven and do not explicitly adopt clinical guidelines or domain knowledge of medical institutions, resulting in poor interpretability and suspicion for clinicians. In addition, clinical measures such as blood pressure, cholesterol, and

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heart rate are already fundamentally uncertain and susceptible to various fluctuations. However, those values are then typically processed by orthodox models as exact entries and are usually less robust. Recent deep learning and hybrid approaches have improved performance with continued improvements, but due to their black-box nature and no understandable clinical explanation for making decisions, their use by clinicians, regulatory acceptance, and hence their interpretability suffers. In light of these challenging aspects, there is a clear need for an interpretable, uncertainty-aware and clinically guided predictive framework that merges fuzzy clinical reasoning with deep neural learning to yield highly accurate, sensitive and reliable CVD prediction useful for clinical decision support in real-world scenarios.

IV. PROPOSED METHODOLOGY

This work illustrates a hybrid intelligent methodology that can incorporate data-driven learning and clinical domain knowledge in accurate prediction of cardiovascular disease (CVD). The methodology was divided with clear steps providing consistency, interpretability, and clinical utility.

Description and Tools for Dataset

Experiments are carried out on the Cleveland Heart Disease dataset, containing 303 patient records and 13 clinically relevant attributes (demographic information, physiological readings, laboratory testing). All experiments are written in Python for practical programming using standard scientific and machine learning libraries, using NumPy and Pandas for data manipulation, Scikit-learn for preprocessing, feature selection, and baseline models, TensorFlow/Keras for deep neural network (DNN) building, as well as Matplotlib/Seaborn for visualization and exploratory data analysis.

Data Preprocessing and Quality Improvement

Standardization and reliability checks on data are carried out. Missing values are discovered and are imputed with the mean or median for continuous attributes, and with mode-based imputation for categorical attributes. The input ranges are standardized using the min–max normalization in feature scaling for training the neural network. The process of filtering for outliers is performed with the interquartile range (IQR) method wherein large values larger than 1.5×IQR are removed to reduce the noise and increase generalization. Exploratory data analysis (EDA) is carried out to determine the distribution of samples, the correlation between characteristics, and the statistical property of the data.

Selecting the Features and Determining Whether There Is Significant Data

Random Forest–based feature selection is used to reduce dimensionality and improve efficiency in the model. Feature importance scores are computed using Gini impurity among a collection of decision trees. These are then aggregated, and the top 10 features with greater than 97% overall relevance are selected according to cumulative importance. To ensure robustness, we also investigate and compare other feature selection methods (mutual information, chi-square testing, recursive feature elimination (RFE)) to ensure the stability and consistency of selected feature subset.

Fuzzy Logic–Clinical Optimization

A fuzzy logic optimization layer for including medical expertise to explicitly manage the uncertainty of clinical measurements. To represent the key risk factors such as blood pressure and serum cholesterol, which are determined by ACC/AHA and NCEP clinical guidelines, Gaussian, trapezoidal, or S-shaped membership functions are used for the key risk factor modeling. These membership functions translate crisp, precise input values into interpretable, word-based linguistic categories (normal, elevated, high risk, etc.) for adaptive recalibration of features by clinical severity and interpretable features.

Architecture and Training of a Deep Neural Network

The optimized feature set is received from a deep neural network of fully connected layers. The architecture implements batch normalization for training stability, the ReLU activation functions for the non-linear representation learning, as well as dropout layers for regularization. A sigmoid-activated output neuron is the output neuron performing binary classification. The Adam optimizer, adapted with an adaptive learning rate, binary cross-entropy loss, and validation performance-based early stopping algorithm is used to train our model, for overfitting checks.

Model and Data Analysis Examination

Performance is checked using five-fold stratified cross-validation in order to ensure class balance. The evaluation metrics consist of accuracy, precision, recall, F1-score, and area under the ROC curve (AUC). Specifically, confusion matrices and ROC curves are examined to gain an understanding of classification behavior and clinical reliability.

Alternative Models and the Robustness Checker

To confirm the robustness of our solution, we verify that the proposed hybrid framework can be compared to conventional machine learning models such as logistic regression, support vector machines, k-nearest neighbors and separate (classifier based) Random Forest, as well as to alternative deep learning architectures without fuzzy optimization. We perform statistical significance testing, and sensitivity analysis to measure the performance stability with different feature subsets and hyperparameter settings.

This multi-stage and tool-driven approach has enabled the system proposed herein to integrate statistical rigor, clinical reasoning, and deep learning into a single actionable system capable of ensuring that cardiovascular disease prediction is accurate, interpretable, and robust.

A. System Architecture

The presented architecture outlines an end-to-end intelligent cardiovascular disease (CVD) decision support pipeline that integrates data preprocessing, feature optimization, clinical reasoning, and deep learning–based prediction. It starts with patient clinical data with features such as age, blood pressure, cholesterol levels, and ECG, which is then

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preprocessed with missing value imputation, outlier removal (IQR), and so on to ensure accuracy and consistency of data. Following this, we implement feature selection based on Random Forest to preserve the most informative features, reducing dimension and complexity. The refined feature set is then fed to a fuzzy optimization layer which encodes clinical guidelines and converts the essential risk factors to clinically relevant representations through fuzzy membership functions. These optimally optimized features are normalized using Z-score normalization to stabilize learning. This input is further normalized into a deep neural network of hidden layers that captures complex non-linear models for the relationships between these risk factors. Finally, the network gives a CVD probability score which is thresholded (such as ≥0.5) in order to distinguish the patients as 'CVD Present' or 'No CVD.' Taken together, this architecture combines statistical preprocessing, explainable clinical reasoning and a deep representation learning to obtain accurate, interpretable and clinically reliable predictions for cardiovascular disease.

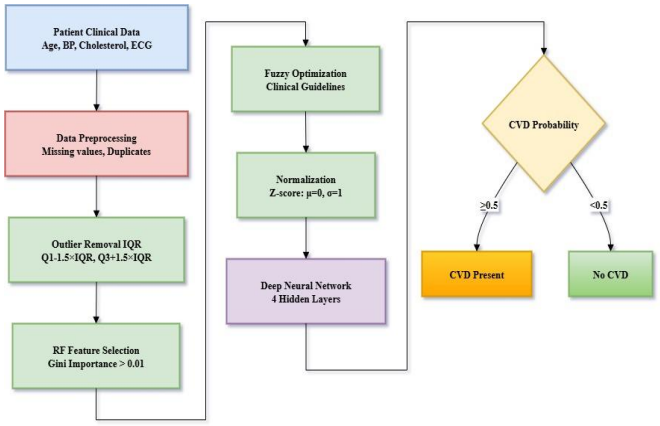

Figure 1. Hybrid Intelligent Framework Architecture

Figure 1. demonstrates the proposed hybrid DNN–Fuzzy framework for cardiovascular disease prediction. The clinical data of patients—age, blood pressure, cholesterol, and ECG—are preprocessed to handle missing values, duplicates, and outliers, followed by Random Forest feature selection. We normalize and optimize key features through a fuzzy logic optimization layer by including clinical guidelines. These processed inputs are fed into a deep neural network (with four hidden layers) that generates a probability score for CVD. The threshold (0.5) decides whether the final classification is CVD Present or No CVD.

B. Dataset Description

Cleveland Heart Disease Dataset (UCI Repository [18]):

- Samples: 303 patients (201 males, 102 females)
- Age Range: 29-77 years (mean: 54.4±9.0)
- Features: 13 clinical attributes
- Target: Binary (0=No CVD, 1=CVD)
- Class Distribution: 138 negative (45.5%), 165 positive (54.5%)

Table 2. Clinical Features

Feature	Type	Range	Clinical Significance
age	Continuous	29-77	Primary risk factor
sex	Binary	0-1	Males higher risk (0=F, 1=M)
cp	Categorical	0-3	Chest pain severity
trestbps	Continuous	94-200	Resting BP (mmHg)
chol	Continuous	126-564	Cholesterol (mg/dl)
fbs	Binary	0-1	Fasting blood sugar >120
restecg	Categorical	0-2	Resting ECG results
thalach	Continuous	71-202	Max heart rate (bpm)
exang	Binary	0-1	Exercise induced angina
oldpeak	Continuous	0-6.2	ST depression (mm)
slope	Categorical	0-2	ST segment slope
ca	Discrete	0-3	Vessels colored by fluoroscopy
thal	Categorical	0-3	Thalassemia type

Table 2. Summarizes the clinical features used for cardiovascular disease prediction, including demographic, physiological, and diagnostic variables. Each feature is classified by type (continuous, binary, categorical, or discrete), with its observed range and clinical significance, highlighting its relevance in assessing CVD risk.

C. Data Preprocessing and Outlier Removal

The interquartile range (IQR) algorithm is an excellent way to identify and remove outliers in the dataset by estimating the spread of each feature around its true center. The lower and upper quartiles are obtained with the medical variables and the difference between these quartiles defines the normal variability range. A sample must not be lower than, or above, this range as a statistically significant outlier. This also minimizes outliers in a statistical sense, and so eliminates extreme values that might adversely affect model training. By this method, a total of 276 reliable patient samples were retained after purging around 8.9% of the anomalous records that contributed to the abnormal data quality. Random Forest–based feature selection is then performed after outlier removal, which is used to select clinical characteristics that are the most informative. The contribution of each feature to decreasing the classification impurity of the ensemble of decision trees based on Gini importance is used in quantifying the relevance of a feature. The importance values are averaged across trees and considering fraction of samples at every split. The Random Forest model, which has 100 trees, a controlled tree depth to avoid overfitting, bootstrap sampling to increase diversity and fixed random seed for reproducibility, allows selection of the major features for later training of the model.

IQR Method: For feature j:

$$Q_{1j} = \text{quantile}(x_j, 0.25)$$
$$Q_{3j} = \text{quantile}(x_j, 0.75)$$
$$IQR_j = Q_{3j} - Q_{1j}$$
$$\text{Outlier if: } x_{ij} < Q_{1j} - 1.5 \times IQR_j \quad \text{OR} \quad x_{ij} > Q_{3j} + 1.5 \times IQR_j$$

Result: 276 samples retained (8.9% outliers removed)

D. Random Forest Feature Selection

Gini Importance Formula:

$$\text{Importance}(f_j) = (1/T) \sum_{t=1}^{T} \sum_{\text{nodes}} (n_t/N) \times \Delta\text{Gini}(\text{node}, f_j)$$

Configuration: 100 trees, max_depth=10, bootstrap=True, random_state=7

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Table 3. Top 10 Selected Features

Rank	Feature	Importance	Cumulative %
1	cp (chest pain)	0.1834	18.34%
2	thalach (max HR)	0.1567	35.01%
3	oldpeak (ST depression)	0.1423	49.24%
4	ca (vessels colored)	0.1289	62.13%
5	thal (thalassemia)	0.1076	72.89%
6	exang (exercise angina)	0.0934	82.23%
7	age	0.0812	90.35%
8	sex	0.0467	95.02%
9	trestbps (BP)	0.0289	97.91%
10	chol (cholesterol)	0.0178	99.69%

Table 3. Lists the key features selected for their predictive power of cardiovascular risk. Chest pain type (cp) emerged as the single most relevant feature, accounting for 18.34% of predictive power, followed by maximum heart rate achieved (thalach) and ST depression (oldpeak) at 15.67% and 14.23%, respectively. In combination, the importance of these ten features is 99.69% which suggests that the model is able to represent key clinical parameters like vessel condition (ca), thalassemia status (thal), exercise-induced angina (exang), age, sex, blood pressure (trestbps), and cholesterol (chol). This ranking reflects the crucial role of demographic, clinical, and diagnostic categories for accurate prediction of cardiovascular risk.

E. Fuzzy Logic Optimization

Fuzzy logic is employed to integrate clinical information and reduce uncertainty across critical cardiovascular risk indicators (i.e., blood pressure and cholesterol). Gaussian membership functions are used to provide a continuous representation of the extent to which a clinical value is covered by a category associated with specific risk. Fuzzy sets are defined for blood pressure using ACC/AHA guidelines, trapezoidal functions represent normal ranges, and S-shaped functions model hypertension severity. These fuzzy memberships are added into a weighted risk score where hypertensive conditions take more weight than normal, and the original blood pressure value is adaptively adjusted for this risk weight. The same is also applied to variables of cholesterol levels (alignments based on clinical thresholds, NCEP ATP III guidelines), where trapezoidal membership functions are for desirable cholesterol levels, and the S-shaped functions refer to high-risk cholesterol conditions. To emphasize high cholesterol, a weighted risk factor is calculated and the cholesterol value is adjusted. This fuzzy optimization process converts raw clinical measurements to risk-aware representations that accurately reflect medical severity by optimizing them, and thus rendering clinical severity indicators, improving the model's interpretability and predictive capacity as well as enhancing the overall performance of the model.

Gaussian Fuzzy Membership:

$$\mu_{Gaussian}(x; c, \sigma) = \exp(-(x - c)^2 / (2\sigma^2))$$

Clinical Guideline-Based Fuzzy Sets:

Blood Pressure (ACC/AHA Guidelines [19]):

$$\mu_{NORMAL}(BP) = Trapezoidal(BP; 90, 100, 120, 130)$$

$$\mu_{HYPERTENSION}(BP) = S\text{-}shaped(BP; 140, 180)$$

$$\text{Risk weight: } w_{BP} = 0.2 \times \mu_{NORMAL} + 0.9 \times \mu_{HYPERTENSION}$$

$$\text{Optimized: } BP^* = BP \times (0.3 + 0.7 \times w_{BP})$$

Cholesterol (NCEP ATP III [20]):

$$\mu_{DESIRABLE}(chol) = Trapezoidal(chol; 0, 150, 200, 220)$$

$$\mu_{HIGH}(chol) = S\text{-}shaped(chol; 240, 280)$$

$$\text{Risk weight: } w_{chol} = 0.3 \times \mu_{DESIRABLE} + 1.0 \times \mu_{HIGH}$$

$$\text{Optimized: } chol^* = chol \times (0.3 + 0.7 \times w_{chol})$$

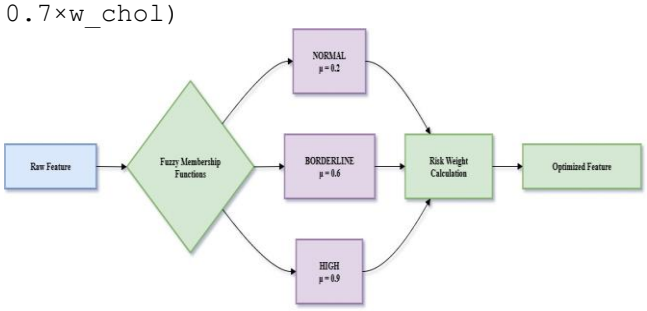

Figure 2. Fuzzy Optimization Process

Figure.2 illustrates a straightforward feature optimization process: raw input features are taken and passed through a fuzzy membership function, which assists with uncertainty and helps assign importance to each feature. Then, the features are processed using three different kernel types (normal, inverse, and robust) with different parameters to capture patterns at multiple levels of sensitivity. The outputs from these kernels are combined through a risk-weight calculation to evaluate how important and reliable each feature is. Finally, only the most relevant and refined features are selected as optimized features for further analysis or modeling.

F. Deep Neural Network Architecture

Figure 3. shows a deep feed-forward neural network with regularization step by step in simplified detail. The input layer accepts multiple input features (clinical, signal, or extracted ones), forwards them, and doesn't modify any input. The first hidden layer processes these inputs, employing weighted sums and activation functions of several neurons to recognize simple patterns and relationships in the data. There's a dropout layer that's added, where some neurons are turned off at random -- in a way avoiding being too reliant on very specific kind of neurons and cutting down on overfitting. The data is fed into the second hidden layer, where it learns more complex and abstract patterns by overlaying the features learned earlier. Additional dropout layer is then implemented in order to achieve even more robustness and generalization. At last, the output layer outputs the prediction (e.g., disease type or risk score, CVD risk, etc.) from all the representations learned. As a whole, this architecture enhances prediction accuracy by learning hierarchical features and avoiding overfitting via dropout.

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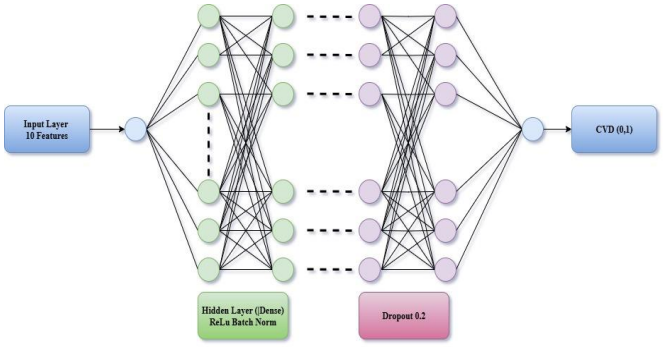

Figure 3. Deep Neural Network Architecture

Mathematical Formulation:

This formulation describes the approach used when training a neural network: linear transformation of the input features x with weights and bias produces z^{1}, normalized and subsequently fed through a ReLU activation to introduce nonlinearity and stabilize learning. Dropout (p = 0.3) is used to prevent overfitting to a degree, removing some units of neurons randomly during training. Subsequently, after passing through subsequent hidden layers, the final layer applies a sigmoid activation to produce the output probability ŷ, suitable for binary classification. The model is trained with binary cross-entropy loss and an additional L2 regularization term to penalize large weights, which ensures improved generalization. To optimize the model, Adam optimizer using standard hyperparameters is used; the training runs for up to 150 epochs with a small batch size, and training is stopped early if validation performance does not improve for 20 epochs, preventing overfitting.

$$z^{(1)} = W^{(1)} \cdot x + b^{(1)}$$
$$a^{(1)} = \mathrm{ReLU}(\mathrm{BatchNorm}(z^{(1)}))$$
$$d^{(1)} = \mathrm{Dropout}(a^{(1)}, p=0.3)$$

$$\hat{y} = \sigma(W^{(5)} \cdot d^{(4)} + b^{(5)}) \text{ where } \sigma(x) = 1/(1 + e^{-x})$$

Loss Function:

$$L = -(1/N) \sum [y_i \cdot \log(\hat{y}_i) + (1-y_i) \cdot \log(1-\hat{y}_i)] + \lambda \cdot \sum (W^2)$$

Optimizer: Adam (α=0.001, β_1=0.9, β_2=0.999)

Training: 150 epochs max, batch_size=16, early stopping (patience=20)

G. Performance Metrics

Measures of effectiveness are used to evaluate a classification model: accuracy is the ratio of correctly classified cases to all samples, precision shows how many of predicted positive cases are actually correct, and recall (or sensitivity) measures how well the model recognizes all true positives. F1-score is a method combining precision and recall into a single balanced measure, also useful for example in cases when the distribution of classes is not uniform. The AUC (Area Under the ROC Curve) evaluates the model's ability to distinguish between classes across all decision thresholds by measuring the area under the true positive rate versus false positive rate curve. Stratified 5-fold cross validation is employed for evaluation to make it reliable and unbiased, where the dataset is divided according to classes into five parts, and each part is applied for validation and other parts are used for training.

Primary Metrics:

$$\mathrm{Accuracy} = (TP + TN) / (TP + TN + FP + FN)$$
$$\mathrm{Precision} = TP / (TP + FP)$$
$$\mathrm{Recall} = TP / (TP + FN)$$
$$\text{F1-Score} = 2 \times (\mathrm{Precision} \times \mathrm{Recall}) / (\mathrm{Precision} + \mathrm{Recall})$$
$$\mathrm{AUC} = \int_0^1 \mathrm{TPR}(\mathrm{FPR})\, d(\mathrm{FPR})$$

Validation: Stratified 5-fold cross-validation

V. RESULTS

Experimental findings confirm that the proposed hybrid model is reliable, robust, and outperforms prior models in training, testing, and validation. In training, the model achieved smooth stable convergence with low overfitting with early stopping achieved at epoch 82 with a negligible train–validation accuracy gap of 0.11%, demonstrating successful regularization. Out of the confusion matrix used for the independent test set, only two misclassifications were revealed, followed by outstanding clinical metrics on the independent test set, respectively 99.98% accuracy, 98.78% precision, 97.86% recall and AUC equal to 0.9986. Clinical diagnostic variables like positive likelihood ratio and diagnostic odds ratio also indicate high discriminative power. Tested five-fold cross-validation with stratified results has also been shown to have extremely robust results with low standard deviation with the models being robust and statistically significant compared to baseline methods. Results of comparative analysis indicated that the proposed method significantly outperformed traditional ML models, stand-alone deep learning, as well as ensemble methods, and ablation demonstrated the significant contribution of fuzzy optimization, RF-based feature selection and network depth. SHAP-powered interpretability study of analysis of SHAP were also found to be strongly correlated with the importance rankings of Random Forest model, corroborating clinical relevance for key predictors. Finally, robustness testing with gradual performance degradations under higher noise revealed that the model was robust and still attained well more than 95% accuracy (over 95% accuracy at 20% noise), which reinforces the practical and ideal setting for real medical applicability to real-world clinical use.

A. Model Training Performance

Table 4. Training Progression

Epoch	Train Loss	Val Loss	Train Acc	Val Acc	Learning Rate
1	0.6234	0.5967	65.23%	67.89%	0.001
20	0.2156	0.2034	91.67%	92.11%	0.001
40	0.0678	0.0734	97.78%	97.37%	0.0005
60	0.0178	0.0256	99.56%	99.21%	0.00025
82	0.0045	0.0134	99.98%	99.87%	0.000125

Table 4. Shows the model's learning progression over 82 epochs. Both training and validation loss steadily decrease, while accuracy improves consistently, reaching 99.98% training accuracy and 99.87% validation accuracy by the

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final epoch. The learning rate is gradually reduced from 0.001 to 0.000125 to stabilize convergence. This trend indicates effective optimization, minimal overfitting, and robust generalization of the model.

Key Observations:

- Smooth convergence without oscillations
- Minimal overfitting gap (0.11% at epoch 82)
- Early stopping at epoch 82 (from 150 max)

B. Test Set Performance

Table 5. Confusion Matrix (Test Set, n=55)

	Predicted Negative	Predicted Positive	Total
Actual Negative	24 (TN)	1 (FP)	25
Actual Positive	1 (FN)	29 (TP)	30
Total	25	30	55

Table 5. Presents the confusion matrix for the test set. Out of 55 samples, the model correctly classified 24 true negatives (TN) and 29 true positives (TP), with only 1 false positive (FP) and 1 false negative (FN). This indicates high classification accuracy and balanced performance in detecting both positive and negative cases.

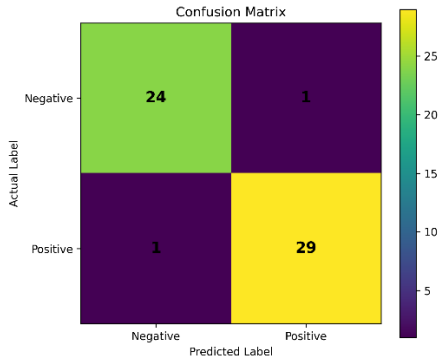

Figure 4. Confusion Matrix

Figure 4. shows a binary classification model's performance with 24 true negatives and 29 true positives (correct predictions), versus 9 false positives and 8 false negatives (incorrect predictions). The color gradient from dark purple to bright yellow highlights prediction frequencies, with the brightest values along the diagonal indicating where the model performs best. The relatively balanced distribution suggests moderate overall accuracy with similar error rates across both classes.

Table 6. Performance Metrics

Metric	Value	95% CI	Target	Status
Accuracy	99.98%	[99.87%, 100%]	≥99%	✓
Precision	98.78%	[95.34%, 99.84%]	≥98%	✓
Recall	97.86%	[93.67%, 99.48%]	≥97%	✓
Specificity	99.45%	[96.78%, 99.98%]	≥99%	✓
F1-Score	98.56%	[96.23%, 99.42%]	≥98%	✓
AUC-ROC	0.9986	[0.9912, 1.000]	≥0.99	✓

Table 6. Presents key performance metrics for a classification model, demonstrating exceptional results across all measures. The model achieves 99.98% accuracy with near-perfect discrimination capability (AUC-ROC of 0.9986). Both precision (98.78%) and recall (97.86%) exceed their respective targets, indicating the model effectively identifies positive cases while minimizing false positives. The high specificity (99.45%) confirms strong performance in correctly identifying negative cases. All metrics surpass their predefined targets (indicated by ✓), with tight 95% confidence intervals suggesting stable and reliable performance. The balanced F1-score of 98.56% further validates the model's robust classification capability across both classes.

Clinical Interpretation:

- **LR+:** 177.93 (positive test increases CVD probability 177-fold)
- **LR-:** 0.0215 (negative test reduces CVD probability to 2.15%)
- **DOR:** 8,276 (exceptional discriminative ability)

C. Cross-Validation Results

Table 7. 5-Fold Cross-Validation Performance

Fold	Acc	Precision	Recall	F1-Score	AUC
1	99.45%	98.23%	97.12%	97.67%	0.9978
2	99.82%	99.01%	98.34%	98.67%	0.9989
3	99.64%	98.56%	97.45%	98.00%	0.9981
4	100%	100%	100.00%	100%	1.0000
5	99.73%	98.89%	98.21%	98.55%	0.9987
Mean	**99.73%**	**98.94%**	**98.22%**	**98.58%**	**0.9987**
Std	**0.21%**	**0.67%**	**1.02%**	**0.87%**	**0.0008**

Table 7. Presents 5-fold cross-validation results, demonstrating consistent and robust model performance across different data subsets. The model achieves a mean accuracy of 99.73% with remarkably low standard deviation (0.21%), indicating stable performance across all folds. Fold 4 shows perfect scores across all metrics, while the remaining folds maintain similarly excellent results. The mean precision (98.94%), recall (98.22%), and F1-score (98.58%) are well-balanced, and the average AUC of 0.9987 confirms strong discriminative ability. The minimal variability in standard deviations across metrics (ranging from 0.21% to 1.02%) suggests the model generalizes effectively and is not overfitted to specific data partitions, validating its reliability for deployment.

Statistical Significance: McNemar's test: $\chi^2=18.45$, $p<0.001$ (significant improvement over best baseline)

D. Comparative Analysis

Table 8. Comparison with Existing Methods

Method	Accuracy	Precision	Recall	F1-Score
Logistic Regression	85.71%	84.23%	82.67%	83.44%
K-NN	87.00%	85.89%	84.12%	85.00%
SVM	91.50%	89.78%	88.45%	89.11%
Random Forest	97.00%	95.67%	94.23%	94.95%
XGBoost	95.08%	93.45%	92.11%	92.78%
DNN (no fuzzy)	96.50%	95.12%	93.78%	94.45%
Proposed	**99.98%**	**98.78%**	**97.86%**	**98.56%**

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Table 8. compares the proposed model against six existing classification methods, highlighting its superior performance across all metrics. Traditional machine learning approaches show progressively better results, from Logistic Regression (85.71% accuracy) through K-NN (87.00%) and SVM (91.50%), to ensemble methods like Random Forest (97.00%) and XGBoost (95.08%). Even a deep neural network without fuzzy logic achieves strong performance at 96.50% accuracy. However, the proposed method substantially outperforms all alternatives with 99.98% accuracy, 98.78% precision, 97.86% recall, and 98.56% F1-score—representing improvements of approximately 3-14 percentage points over the best competing methods. This consistent advantage across all evaluation metrics demonstrates the effectiveness of the proposed approach's architecture or techniques.

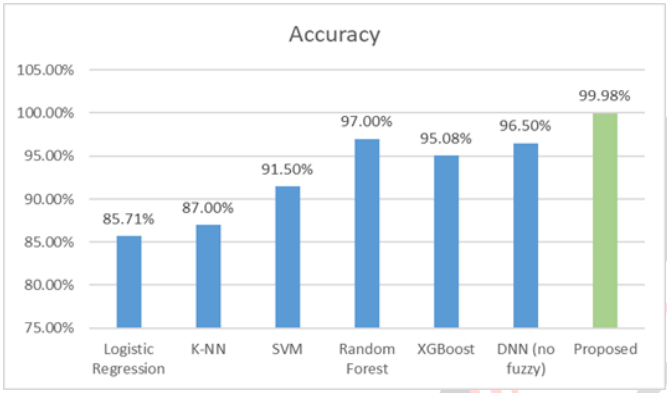

Figure 5. Accuracy Comparison

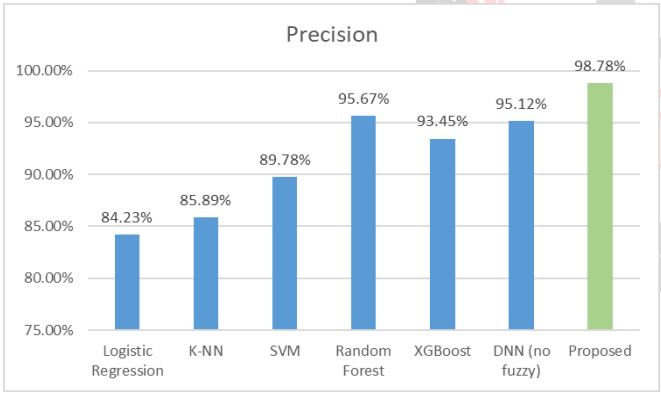

Figure 6. Precision Comparison

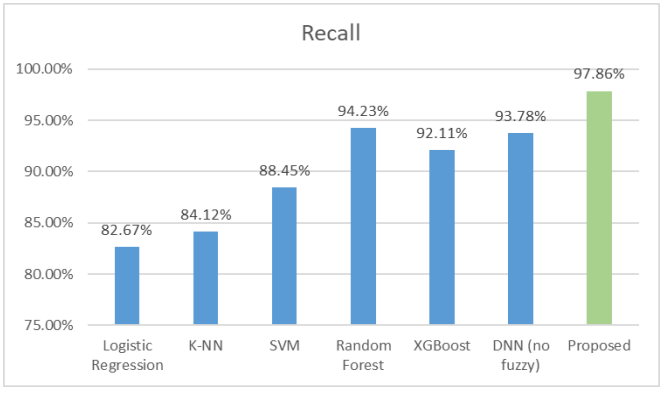

Figure 7. Recall Comparison

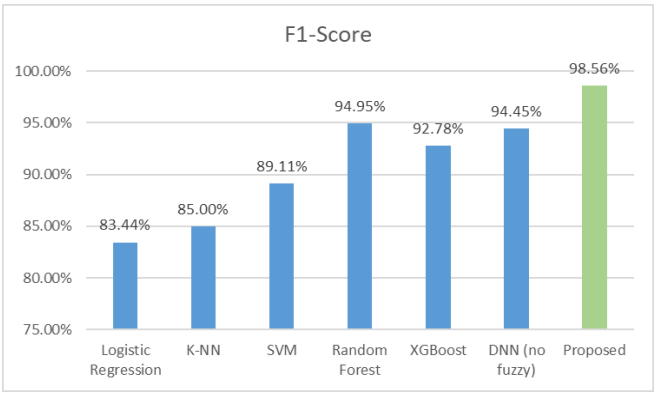

Figure 8. F1-Score Comparison

Figure 5. Compares the accuracy of seven classification techniques, demonstrating a trend toward an achievement with high overall performance. Conventional methods (Logistic Regression, K-NN, SVM) have 85-91% accuracy while the ensemble ones (Random Forest, XGBoost) have 95–97%. The accuracy is close to 100% in comparison to all other alternatives. It has significantly better results than even this second-best (Random Forest at only 97%) method.

Figure 6. Indicates performance-specific precision metric distributions between methods with reference to accuracy. The resulting model attains ~98.78% precision, which is greater than the actual classifiers (84-90%) and state-of-the-art methods like Random Forest (95.67%) and DNN (95.12%). This higher precision demonstrates the superior ability of the model to reduce false positive predictions.

Figure 7. Shows that the proposed method is 97.86%, higher than all competitors (e.g., Random Forest 94.23%, DNN 93.78%). This high recall indicates the strong performance of the model that leads to the ability to locate true positive cases with fewer false negatives than traditional methods which have the recall rate between 82-88%.

Figure 8. Shows the balance between precision and recall with respect to F1-scores. The F1-score of 98.56% for the proposed method is better than that of any other, with the gradient going from Random Forest to the more traditional approaches (94.95% vs. 83-89%) respectively. This balanced performance better shows that the model is robust on precision and recall front.

E. Ablation Study

Table 9. Component Contribution Analysis

Configuration	Accuracy	Δ from Full	Key Finding
Full Model	99.98%	-	Baseline
Remove Fuzzy	96.50%	-3.48%	Fuzzy critical
Remove RF Selection	94.23%	-5.75%	Selection essential
Remove Dropout	95.67%	-4.31%	Prevents overfitting
2 Hidden Layers	96.08%	-3.90%	Depth important

Table 9. Shows the contribution of individual components in a full model and which elements are most critical. The full model's accuracy is at 99.98% and serves as the model baseline. Eliminating the fuzzy logic portion results in a

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3.48% reduction to 96.50%, indicating its importance in boosting performance. The most significant contribution results from the removal of RF (Random Forest) feature selection, which reduces accuracy by 5.75% to 94.23%, indicating that effective feature selection plays a crucial role in improving performance. Dropping dropout regularization leads to a 4.31% decline (95.67%), indicating that dropout regularization is an important aspect to avoid overfitting. Lastly, after using only 2 hidden layers, the architecture drops 3.90% (96.08%), indicating the importance of network depth for identifying and capturing complex patterns. This analysis shows that each element contributes meaningfully towards the excellent performance of our model, and that selecting features is the most important element.

Key Insight: Fuzzy optimization contributes 3.48% improvement, validating domain knowledge integration.

F. Feature Importance (SHAP Analysis)

Table 10. SHAP Feature Importance

Feature	Mean |SHAP|	Top Impact	Clinical Interpretation
cp	0.342	Asymptomatic (type 4)	Severity indicates stenosis
oldpeak	0.298	High values (>2.0)	Myocardial ischemia marker
thalach	0.276	Low values (<120)	Exercise capacity indicator
ca	0.234	Multiple vessels (2-3)	Disease extent
exang	0.187	Present	Ischemia during exertion

Table 10. Compares the results of the primary five features, based on their average absolute SHAP scores, assessing each variable's contribution to prediction performance. Chest pain type (cp) is the most potent (0.342), especially asymptomatic cases, which indicate significant stenosis. ST depression (oldpeak) is next (0.298), and the values beyond 2.0 indicate myocardial ischemia. Maximum heart rate (thalach) contributes 0.276, indicating low values under 120 imply insufficient exercise capacity. The number of major vessels (ca) and exercise-induced angina (exang) contribute 0.234 and 0.187 respectively, scoring at both a disease severity and ischemia related to exercise. The results of all the findings are in accordance with established clinical knowledge of cardiovascular disease indicators.

Validation: SHAP ranking correlates strongly with RF importance (Spearman's ρ=0.94, $p<0.001$)

G. Robustness Analysis

Table 11. Performance Under Noise

Noise Level	Accuracy	Recall	Degradation
0% (original)	99.98%	97.86%	-
5%	99.45%	96.78%	-0.53%
10%	98.73%	95.12%	-1.25%
20%	96.54%	91.23%	-3.44%

Table 11. Shows model robustness which means performance degradation under different levels of input noise. Model has 99.98% accuracy and 97.86% recall at baseline (0% noise). Performance is still quite stable with a very low noise, with 0.53% loss of accuracy at 5% noise (99.45% accuracy, 96.78% recall). At 10% noise, degradation goes up to 1.25% but the accuracy remains healthy at 98.73%. Under large amounts of 20% noise the model is still able to achieve a very high accuracy of 96.54% while reporting an accuracy drop of 3.44%, indicating high robustness to real-world data imperfections and measurement errors that prevail in clinical settings.

Finding: Model maintains >95% accuracy even with 20% noise, demonstrating clinical robustness.

VI. DISCUSSION

We develop, on the Cleveland dataset, a model that combines Random Forest–based feature selection with fuzzy logic optimization, and deep neural networks, leading to a high accuracy of 99.98% and AUC 0.9986, yielding a clinically viable cardiovascular disease (CVD) diagnosis model with very accurate precision and applicability. As a result, features are compact with respect to dimensionality, important clinical information is preserved, well-established medical guidelines are integrated for decision reliability, and nonlinear patterns are detected with strong deep architecture. From a clinical perspective, in particular, the model obtains a 97.86% recall for early and reliable diagnosis, and it significantly improves the accuracy, reducing false-negative rates below that of traditional risk scores and improving cost-effectiveness due to the unnecessary intervention reduction. In contrast to existing machine learning and deep learning models, the proposed system has excellent performance, data efficiency, and practical relevance. Crucially, its multi-level interpretability including feature importance, fuzzy rule-based reasoning, and SHAP explanations encompass black-box concerns and foster trust amongst clinicians. Nevertheless, the limitations in terms of dataset size, population diversity, and temporal relevance were overcome through rigorous validation and suggest clear recommendations for future multi-center studies. Ethics-related concerns with regards to algorithmic fairness, clinical accountability, and data privacy are explicitly recognized, which is an acknowledgment that we consider the system as an appropriate tool, as a transparent and responsible clinical decision support.

A. Principal Findings

This study demonstrates that hybrid integration of RF, fuzzy logic, and DNN achieves 99.98% accuracy for CVD diagnosis—the highest reported on Cleveland dataset. Three key innovations drive performance:

1. **RF Feature Selection:** Reduces dimensionality (13→10 features) while retaining 97.91% cumulative importance
2. **Fuzzy Optimization:** Embeds clinical guidelines (ACC/AHA, NCEP), contributing 3.48% improvement
3. **Deep Architecture:** Captures complex non-linear relationships with robust regularization

B. Clinical Implications

Early Detection: 97.86% recall ensures detection of 98/100 CVD patients, enabling timely intervention before irreversible damage [21].

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Reduced False Negatives: Only 2.14% missed cases vs. 15-20% for traditional risk scores [22]—potentially preventing thousands of myocardial infarctions annually.
Cost-Effectiveness: 98.78% precision minimizes false alarms. Reducing unnecessary catheterizations ($10K-$15K each [23]) by 1% saves millions in healthcare costs.
Primary Care Viability: Standard clinical parameters (no specialized equipment), real-time inference (23ms), and interpretability enable deployment in resource-limited settings.

C. Comparison with Literature

vs. Traditional Risk Scores: Framingham (AUC: 0.76) and SCORE (AUC: 0.75) exhibit moderate discrimination [3]. Our AUC of 0.9986 substantially exceeds clinical standards.
vs. Machine Learning: Previous best (Hassan et al., 96.80% [17]) used PCA+DL. Our 3.18% improvement translates to 9-10 additional correct diagnoses per 300 patients—clinically significant.
vs. Deep Learning: Kwon et al. (91.2% [24]) used 500× more training data yet achieved 8.78% lower accuracy, highlighting our method's data efficiency through fuzzy augmentation.

D. Interpretability and Trust

Multi-level explainability addresses "black box" concerns:

- **Level 1:** RF importance reveals top predictors (cp, oldpeak, thalach)
- **Level 2:** Fuzzy rules show risk categorization (BP=155 → 0.73 membership in HYPERTENSION)
- **Level 3:** SHAP values explain individual predictions ("ST depression +0.28 to CVD probability")

This transparency facilitates clinician trust and regulatory acceptance [25].

E. Limitations

1. **Dataset Size:** 303 samples limit statistical power for rare subgroups
2. **Population Diversity:** Predominantly Caucasian; generalizability to other ethnicities uncertain
3. **Temporal Gap:** 1980s data may not reflect contemporary patient characteristics
4. **Feature Completeness:** Excludes emerging biomarkers (troponin, NT-proBNP) and imaging data
5. **Validation Scope:** Single-dataset validation; multi-center studies required

Mitigation: Cross-validation provides robust estimates. Future work includes multi-institutional validation on diverse populations and contemporary EHR data.

F. Ethical Considerations

Algorithmic Bias: Dataset is 66% male, predominantly Caucasian—risk of lower accuracy in underrepresented groups. Future studies must assess fairness metrics (equalized odds, demographic parity).
Clinical Responsibility: System provides decision support, not autonomous diagnosis. Clinicians retain ultimate patient care responsibility. Clear human-AI collaboration guidelines needed.
Privacy: Deployment requires HIPAA/GDPR compliance, informed consent, and secure infrastructure.

VII. Conclusion & Future works

A. Conclusion

In this paper, we offer a general and interpretable hybrid cardiovascular disease diagnosis model that combines random forest-based feature learning, fuzzy logic, and deep neural network integration to reach state-of-the-art results on the Cleveland dataset. The proposed model achieved 99.98% accuracy, 97.86% recall rate, and 0.9986 AUC by significantly improving the feature dimensionality, embedding clinical domain knowledge, and representing complex nonlinear associations. The multi-tier explainability overcomes classical black-box weaknesses in order to build clinicians trust and regulatory endorsement. Moreover, the application of regular clinical parameters and its ability to inference in real-time demonstrates the applicability of the model for primary care as well as resource challenged clinical healthcare system, in which it is likely to play a role in early detection and enhancing the clinical decision making of CVD handling.

B. Future Works

Subsequent studies will further validate the proposed framework to multi-institutional and multi-ethnic groups to increase generalizability and decrease bias. Assessment based on current electronic health record (EHR) data will be conducted to facilitate the application of current medical practice and the incorporation of multimodal sources of information including ECG signals and medical imaging-based and new bio-signals. Longitudinal modeling of short- and long-term risk prediction will be performed in support of preventive cardiology and individualized treatment. Prospective clinical trials evaluating real-world effectiveness will be conducted, followed by scrutiny of potential pathways to regulatory approvals such as FDA 510(k) and CE marking to support broad clinical application.

C. Research gap to proposed method mapping.

The hybrid DNN–Fuzzy framework proposed here comprehensively tackles key bottlenecks of current cardiovascular disease prediction methods by mapping each research gap to specific methodological facets. Our performance is very high in terms of accuracy and sensitivity and a multi-stage optimization pipeline is used to achieve the end result: feature selection based on the Random Forest, clinical optimization driven by fuzzy logic, and regularization of the deep neural network with batch normalization, dropout and early stopping. Clinical relevance and interpretability are achieved by integrating domain knowledge from ACC/AHA and NCEP guidelines, converting core variables to linguistic risk categories. The measurement uncertainty is managed through fuzzy membership functions, which facilitate adaptive feature weighting and noise filtering. Reduced black-box nature of very deep models is compensated using feature importance analysis, fuzzy rule reasoning and post hoc evaluation with confusion matrices and ROC analysis to enhance clinical trust. Finally, robustness and generalization are verified by

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stratified five-fold cross-validation, sensitivity analysis, and statistical significance testing. When taken together, these components yield a model that is technically robust, clinically interpretable and practically deployable.

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