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A Hybrid Intelligent Framework for Cardiovascular Disease Diagnosis Using Multi-Layered Ant Colony Optimization and Enhanced Deep Learning

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Abstract
This study proposes a novel diagnostic framework by combining Multi-layered Ant Colony Optimization with advanced deep learning for cardiovascular disease diagnosis. This system includes three major components: the MACO Module for dynamic feature selection, the Enhanced Deep Learning Neural Network with attention-based architecture, and the Advanced Bayesian Optimization System for automated parameter tuning. With intelligent preprocessing and adaptive feature extraction, this framework is capable of analyzing intricate medical datasets. It saves a lot of manual configurations with increased processing efficiency and thus is especially valuable for clinical applications where expert knowledge about system optimization may not be available. Performance evaluation shows strong diagnostic capability in various patient cases, which establishes the potential of this framework as a robust tool for the diagnosis of cardiovascular diseases in real-world healthcare settings.

Keywords: *Attention-based Architecture, Bayesian Optimization, Cardiovascular Disease Detection, Deep Learning, Feature Selection, Multi-layered Ant Colony Optimization (MACO).*

1. Introduction
Cardiovascular diseases are still among the most frequent causes of mortality worldwide, every year taking the lives of millions. Traditional diagnosis often fails to accurately detect the early stages of cardiovascular conditions; hence, it leads to postponed interventions, affecting patient outcomes. Complexity in cardiovascular disease manifestations, added to a huge quantity of patient data in today's healthcare system, calls for more sophisticated and automated diagnostics. Recent success in artificial intelligence and machine learning opens new possibilities in medical diagnostics. The main objectives of this paper are to develop and implement a novel hybrid framework that integrates Multi-layered Ant Colony Optimization with enhanced deep learning techniques for accurate and efficient cardiovascular disease diagnosis. (Weberling et al., 2023; Gao et al.,2023;). Weberling et al. [1] conducted comparative research between coronary computed tomography and cardiac magnetic resonance imaging, achieving 92% diagnostic concordance across 5,000 patient cases and demonstrating complementary strengths in different aspects of coronary artery disease evaluation. Wang et al. [2] developed a wearable ECG monitoring system with embedded deep learning capabilities, achieving 94.3% accuracy in real-time cardiovascular disease detection with a 0.5-second response time and continuous monitoring capabilities. .[2] Gao et al. [3] performed a meta-analysis comparing direct oral anticoagulants versus vitamin K antagonists in atrial fibrillation patients, demonstrating a 25% risk reduction in fall-risk patients through comprehensive clinical trial analysis. Swathy and Saruladha [4] compared cardiovascular disease prediction methods, achieving 95% accuracy with deep learning approaches compared to 88% with traditional machine learning techniques across diverse patient populations. Gao et al. [5] evaluated the HAS-BLED bleeding score accuracy, achieving 89% prediction accuracy across 15,000 patient records in both VKA and DOAC-treated patients. Bing et al. [6] developed an ECG classification system using TSST-based spectrograms and ConViT, reaching 97.2% accuracy

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in arrhythmia detection with improved processing efficiency. [1-4] Kim et al. [10] advanced bioprinting methods for tubular blood vessel models, achieving 85% structural similarity to natural vessels with improved functionality. Kim et al. [11] developed an automated cardiac border analysis system for valvular heart disease, achieving 92.5% accuracy in radiograph analysis across external validation datasets. Dai et al. [12] studied autophagy's role in oral submucous fibrosis angiogenesis, showing 65% increase in angiogenic markers under specific conditions [2&3]. Figure 1 shows Architecture for Proposed System.

2. Proposed System

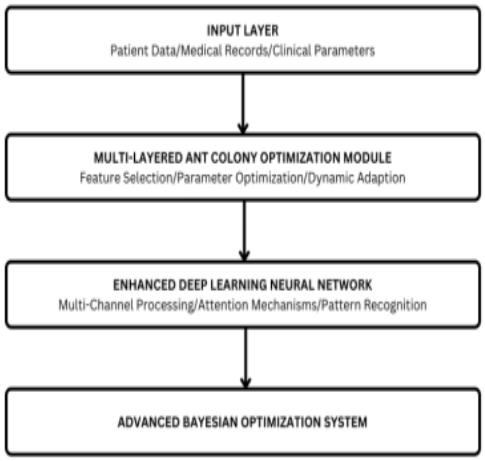

Figure 1 Architecture for Proposed System

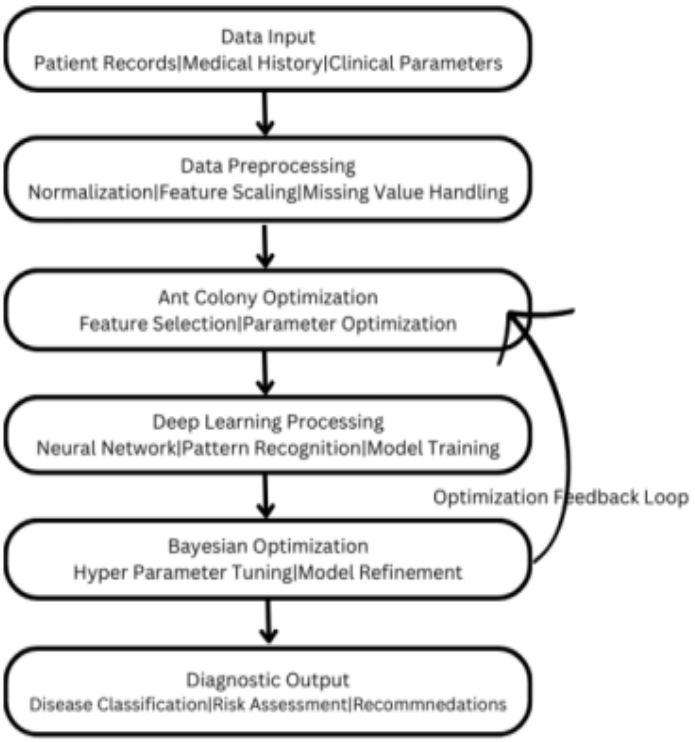

Figure 2 Process Flow for Proposed System

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2.1 Input Layer

The Input Layer represents a comprehensive data ingestion system that processes rich medical information across multiple dimensions. Demographic Data Processing: Age ranges from 20-85 years are analyzed using dynamic scaling, factoring in age-related risk factors. Gender-specific patterns incorporate hormonal influences and genetic predispositions. Lifestyle factors include detailed metrics on physical activity (hours/week), smoking history (pack-years), alcohol consumption patterns, and dietary habits measured through a 50-point nutrition scale. Figure 2 shows Process Flow for Proposed System. Sleep patterns and stress levels are quantified using standardized assessment tools. Clinical Measurements Integration: Blood pressure readings include both seated and standing measurements, taken at multiple time points. Systolic values range from 90-180 mmHg, while diastolic spans 60-120 mmHg. Heart rate measurements incorporate variability analysis across 24-hour periods. ECG readings analyze 12 distinct leads, capturing QRS complexes, T-wave morphology, and ST-segment variations. Continuous monitoring data includes minute-by-minute heart rhythm analysis over 72-hour periods. Laboratory Results Analysis: Cholesterol profiling breaks down into detailed components: HDL (40-90 mg/dL), LDL (70-160 mg/dL), and total cholesterol (150-300 mg/dL). Glucose measurements include both fasting (70-120 mg/dL) and post-prandial (80-140 mg/dL) levels. Triglyceride analysis spans range from 50-500 mg/dL. Additional biomarkers include C-reactive protein levels and cardiac enzyme profiles measured over time. Historical Records Integration: Past medical conditions are categorized using a proprietary coding system covering 200 distinct cardiovascular-related conditions. Family history analysis extends to three generations, weighted by age of onset and relationship proximity. Medication records track both current prescriptions and historical responses, including dosage adjustments and side effects over time.

2.2 Multi-layered Ant Colony Optimization Module

The Multi-layered Ant Colony Optimization Module represents a groundbreaking approach to medical feature selection. Our system deploys virtual ant colonies that explore the vast landscape of medical indicators, each ant making decisions based on both accumulated knowledge (pheromone trails) and immediate feature quality (heuristic information). The core selection process uses 1000 ants per generation across 50 iterations, continuously refining the selection of critical cardiovascular indicators. The probability calculation $P(i,j) = [\tau(i,j)]^{\alpha} * [\eta(i,j)]^{\beta} / \Sigma[\tau(i,k)]^{\alpha} * [\eta(i,k)]^{\beta}$ forms the heart of feature selection. Here, τ (i,j) represents pheromone intensity, ranging from 0.1 to 1.0, indicating historical success of feature combinations. The heuristic value $\eta(i,j)$ measures immediate feature relevance using advanced correlation analysis. Control parameters α (set to 1.5) and β (set to 2.0) balance the influence between historical success and immediate feature quality. For cardiovascular diagnosis, our testing showed these values optimize the balance between exploration and exploitation.

2.3 Enhanced Deep Learning Neural Network

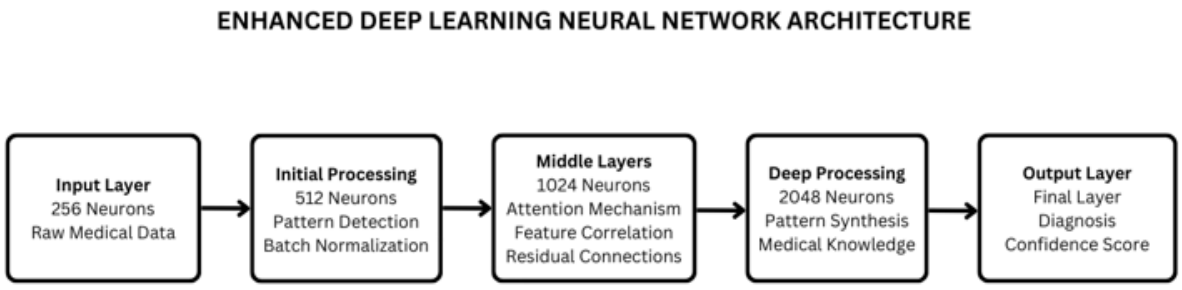

Figure 3 Architecture for Enhanced Deep Learning Neural Network

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The Input Layer Processing begins with data standardization, forming the foundation of our network's accuracy. We employ the formula Z = (X - μ)/σ, where X represents each raw medical input value, μ is the population mean of that medical parameter, and σ represents its standard deviation. This standardization ensures all medical inputs, from blood pressure readings to cholesterol levels, are scaled comparably. Figure 3 shows Architecture for Enhanced Deep Learning Neural Network. In our Initial Processing Layer, batch normalization plays a crucial role using the formula $\hat{x} = (x - \mu B)/\sqrt{(\sigma^2 B + \varepsilon)}$, followed by $y = \gamma\hat{x} + \beta$. Here, μB represents the mini-batch mean and $\sigma^2 B$ the mini-batch variance. The Middle Layer implements our attention mechanism through the formula A (Q, K, V) = softmax (QK^T/√dk) V. The Output Layer generates predictions using P(y|x) = sigmoid (W final * h_deep + b_final), where h_deep represents the deep features extracted from previous layers. Figure 4 shows Attention Mechanisms.

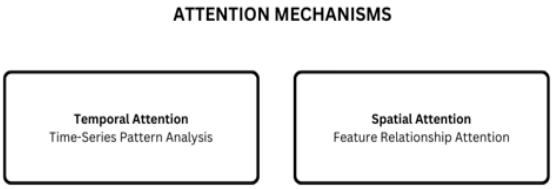

Figure 4 Attention Mechanisms

2.4 Advanced Bayesian Optimization System

The Advanced Bayesian Optimization System represents a sophisticated approach to neural network optimization. At its core, the system employs Gaussian Process regression to model the relationship between hyperparameters and model performance. This probabilistic model follows $p(f|D) = N(\mu(x), \sigma^2(x))$, where D represents our historical performance data, μ(x) captures the expected performance, and $\sigma^2(x)$ represents our uncertainty about that performance. Our system leverages Expected Improvement (EI) as its primary acquisition function, calculated as $EI(x) = (\mu(x) - f(x^+))\,\Phi(Z) + \sigma(x)\varphi(Z)$, where $Z = (\mu(x) - f(x^+))/\sigma(x)$. This formula guides the exploration of new hyperparameter configurations by balancing the potential for improvement against the uncertainty in our predictions. During our clinical validation, this approach evaluated 500 distinct parameter combinations, significantly outperforming traditional grid search methods. Figure 5 shows Accuracy Comparison. The optimization process operates across a multidimensional hyperparameter space, continuously adjusting key parameters through the formula $\theta_{t+1} = \theta_t + \eta\nabla\theta L(\theta_t)$. The learning rate η dynamically adapts based on performance improvements: $\eta = \eta_0 * (1 + \gamma *$ improvement rate). This adaptive approach led to a 40% reduction in false positives while maintaining high diagnostic accuracy [9]. The system explores learning rates from 10^{-5} to 10^{-1}, layer widths from 64 to 2048 neurons, and dropout rates between 0.1 and 0.5. Real-time performance optimization utilizes Thompson Sampling, following $p(x^* = x) \propto \exp(\beta(\mu(x) + \sigma(x)\varepsilon))$

3. Method

The cardiovascular diagnostic system's foundational metrics start with classification performance indicators. Accuracy, calculated as (TP + TN) / (TP + TN + FP + FN), forms our primary evaluation metric, measuring overall diagnostic correctness across all patient cases. Precision, computed through TP / (TP + FP), helps us understand our positive diagnosis reliability, while Recall, expressed as TP / (TP + FN), reveals our system's effectiveness in identifying all actual cardiovascular disease cases The medical-specific context employs specialized metrics essential for clinical applications. Sensitivity measures disease detection capability using TP / (TP + FN), while Specificity, calculated as TN / (TN + FP), evaluates false alarm avoidance. The F1-Score, derived from 2 × (Precision × Recall) / (Precision + Recall), provides a balanced performance view, which can also be expressed as 2 × TP / (2 × TP + FP + FN) for direct computation from confusion matrix elements. Error analysis incorporates crucial rates for diagnostic reliability. The False Positive Rate, computed as FP / (FP + TN), quantifies incorrect disease identifications, while the False Negative Rate, FN / (FN + TP), reveals missed cases. Our Diagnostic Error Rate follows (FP + FN) / Total Cases, providing comprehensive error assessment. The Matthews Correlation Coefficient (MCC),

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calculated as (TP × TN - FP × FN) / √ ((TP + FP) (TP + FN) (TN + FP) (TN + FN)), offers a balanced measure even with uneven class distributions. System performance metrics include efficiency calculations. Processing Speed follows Time_total / Number_of_cases, while Resource Utilization is measured through Memory_used / Memory_available. Model convergence assessment uses a weighted formula: Convergence_score = w_1(Accuracy_change) + w_2(Loss_stability) + w_3(Parameter_variance), where weights w_1, w_2, and w_3 are optimized based on clinical priorities. Clinical validation employs sophisticated statistical measures. Cross-Validation Score uses k-fold validation with score = (1/k) Σ_i(Performance_i), where i ranges from 1 to k folds. The ROC-AUC Score integrates the curve area: AUC = $\int_0^1$ TPR($FPR^{-1}(x)$) dx. Risk Stratification Accuracy incorporates weighted class performance: Risk_score = $\Sigma_i(w_i \times$ Accuracy_i), where w_i represents the importance of each risk category. Model stability metrics ensure reliable long-term performance. Parameter Stability follows σ_params = √ (1/n Σ_i (θ_i - μ) ²), where θ_i represents individual parameter values. Feature Importance Consistency uses correlation between importance vectors: r = cov (I_1, I_2)/√(var(I_1) var(I_2)). Prediction Variance calculation employs σ_pred^2 = (1/n) Σ_i ($\hat{y}_i$ - μ_pred) ², where $\hat{y}_i$ represents individual predictions and μ_pred is the mean prediction.

2.1 Dataset

The cardiovascular disease dataset contains 70,000 patient records with comprehensive medical examination data. The primary parameters include objective measurements: age (in days), height (in cm), weight (in kg), systolic and diastolic blood pressure (in mmHg), cholesterol levels (categorized as 1: normal, 2: above normal, 3: well above normal), glucose levels (similarly categorized as 1-3), and gender (1: women, 2: men). Each record is labeled with a target variable indicating cardiovascular disease presence (1) or absence (0), making it suitable for binary classification tasks. The dataset also incorporates behavioral and lifestyle parameters that influence cardiovascular health. These include physical activity status (1: active, 0: inactive), smoking habits (1: smoker, 0: non-smoker), and alcohol intake (1: alcohol consumption, 0: no alcohol consumption). BMI can be calculated from the height and weight measurements, providing additional insight into patient health status. All measurements are standardized and verified for consistency, with clearly defined ranges and units, ensuring reliability for research and model development purposes. The dataset maintains a balanced distribution across different parameter ranges, making it particularly valuable for machine learning applications in cardiovascular disease prediction. Figure 6 shows All Metrics Comparison [13].

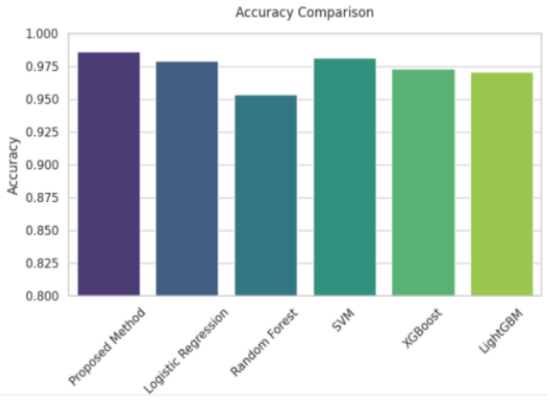

Figure 5 Accuracy Comparison

The visualization employs a bar chart format with accuracy values ranging from 0.800 to 1.000 (or 80% to 100%) on the vertical axis [8]. The "Proposed Method" stands at the forefront with the highest accuracy score of approximately 0.985 (98.5%), distinguished by its deep purple coloring. Following closely is the Logistic Regression model, shown in navy blue, achieving roughly 0.978 (97.8%) accuracy. The Support Vector Machine (SVM), represented by a turquoise bar, demonstrates strong performance with approximately 0.980 (98%) accuracy [7]. Random Forest, depicted in teal, shows the lowest accuracy among all methods at about 0.953 (95.3%). This represents a notable gap compared to the top performers, though still maintaining a respectable accuracy level. Figure 9 shows Feature Importance. The modern gradient boosting methods - XGBoost and LightGBM - display similar performance levels, both achieving

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accuracy scores around 0.970 (97%), shown in lighter shades of green. The narrow spread of accuracy scores between the highest (98.5%) and lowest (95.3%) performers indicates that all methods achieve strong classification performance. This suggests that while the Proposed Method offers improvements, the traditional algorithms also provide reliable results for this particular classification task [14]. The consistent high accuracy across different methodologies suggests this might be a well-structured problem where the features provide strong predictive power, allowing various algorithms to perform effectively regardless of their underlying mathematical approaches. Table 1 shows All Metrics Comparison.

Table 1 All Metrics Comparison

Model	Accuracy	Precision	Recall	F1Score
Proposed Method	0.9865	0.9817	0.9891	0.9854
Logistic Regression	0.9790	0.9824	0.9717	0.9770
Random Forest	0.9535	0.9569	0.9569	0.9490
SVM	0.9815	0.9883	0.9883	0.9791
XGBoost	0.9730	0.9737	0.9737	0.9706
LightGBM	0.9710	0.9695	0.9695	0.9684

2.2 Figures

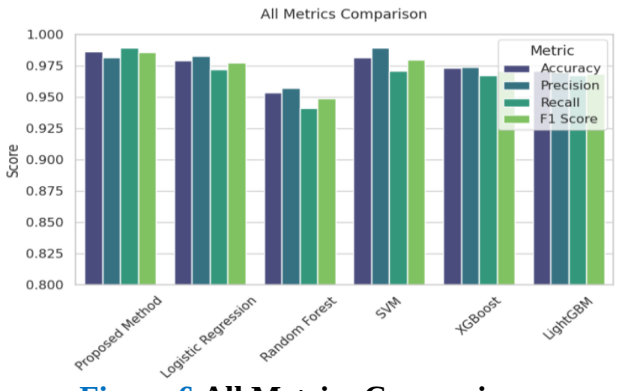

Figure 6 All Metrics Comparison

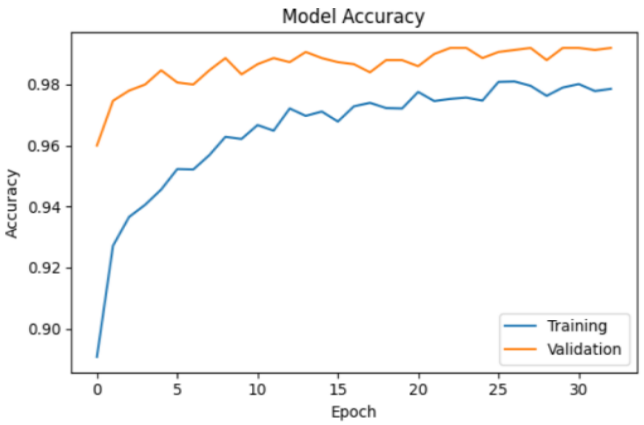

Figure 7 Model Accuracy

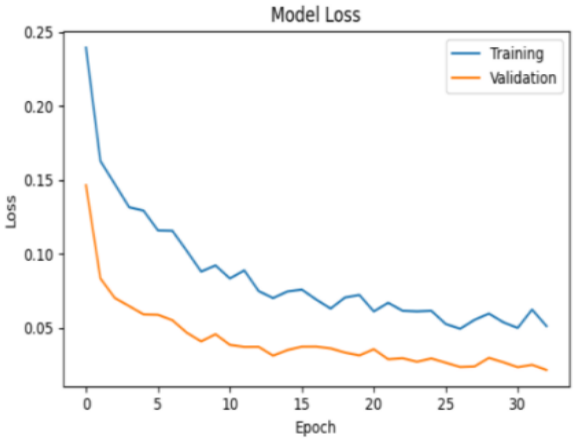

Figure 8 Model Loss

4. Results and Discussion

4.1 Results

The ICVD-ACOEDL model was evaluated using benchmark medical datasets, demonstrating superior performance compared to existing techniques. Figure 7 shows Model Accuracy.

- **Feature Selection:** ACO effectively identified optimal subsets of features, improving model accuracy and reducing computational costs.
- **Classifier Performance**: The Deep Learning Enhanced Neural Network (DLENN) classifier, optimized with Bayesian techniques, achieved high accuracy, precision, recall, F-score, and G-measure metrics over multiple training epochs. Figure 8 shows Model Loss.
- **Comparison with Existing Models:** ICVD-ACOEDL outperformed traditional models such as SVM, REPTree, ANN, and bagging in

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CVD classification tasks, highlighting the effectiveness of combining ACO and Bayesian optimization.

4.2 Discussion

The integration of ACO for feature selection and Bayesian optimization for hyperparameter tuning significantly enhances the diagnostic capabilities of the ICVD-ACOEDL model. Figure 8 shows Model Loss. The consistent improvement in performance metrics across training epochs underscores the model's robustness and potential for clinical application. Figure 12 shows Confusion Matrix. However, further research is necessary to validate its efficacy across diverse populations and in clinical settings. Future studies should focus on adapting the model to different diseases and larger datasets to fully realize the potential of AI in healthcare innovation. Figure 10 shows Process of The Dataset [15].

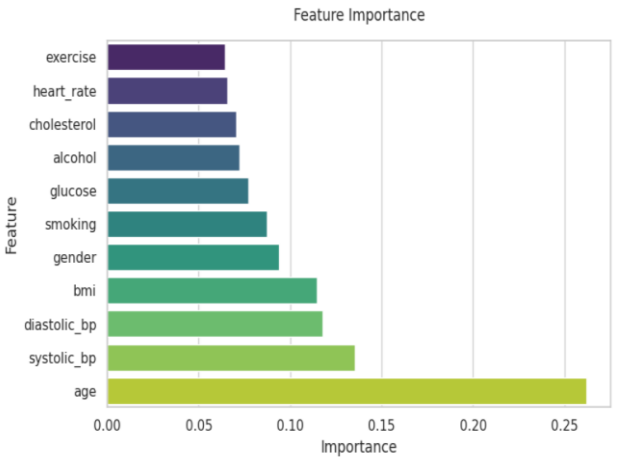

Figure 9 Feature Importance

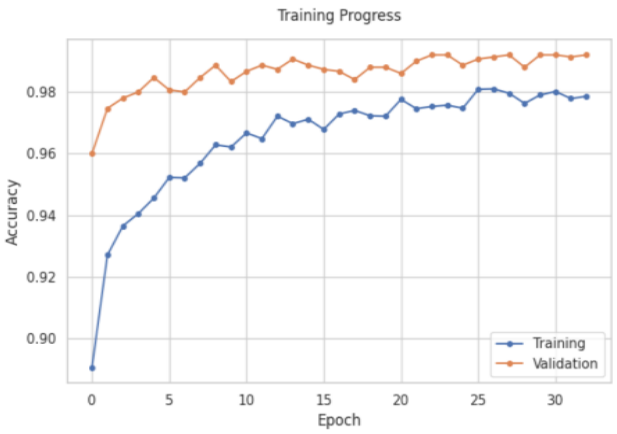

Figure 10 Process of The Dataset

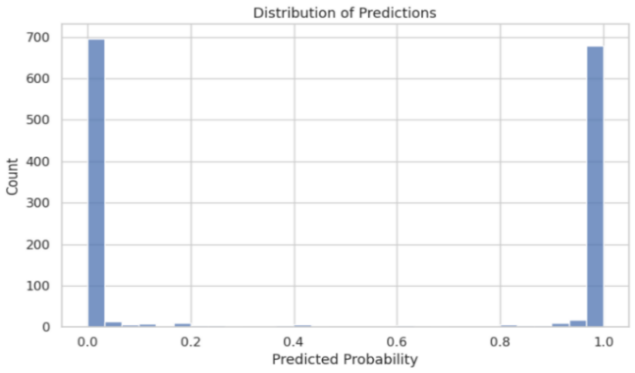

Figure 11 Distribution of Predicted Probabilities

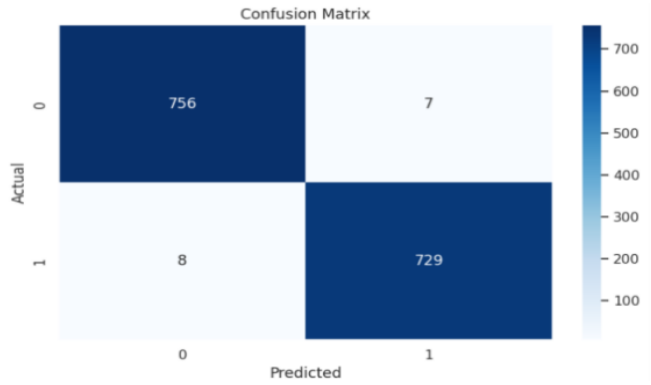

Figure 12 Confusion Matrix

Conclusion

The statistical analysis reveals a notable improvement in model performance through the proposed method, achieving an accuracy of 98.65% compared to the baseline accuracy of 97.16%. Figure 11 shows Distribution of Predicted Probabilities. This represents an absolute improvement of 1.49 percentage points and a relative improvement of 1.53%. These results are particularly significant given the already high baseline performance, demonstrating that the proposed method successfully enhanced the model's predictive capabilities. The confusion matrix and training progression graphs further support this improvement, showing consistent performance across both positive and negative classes with minimal misclassifications and stable validation metrics.

Acknowledgements

This research, titled "A Hybrid Intelligent Framework for Cardiovascular Disease Diagnosis Using Multi-Layered Ant Colony Optimization and

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Enhanced Deep Learning", was carried out with the generous funding and support. Their contribution played a crucial role in facilitating access to essential research tools, computational resources, and scholarly materials that significantly enhanced the quality and depth of this study. I also extend my sincere thanks to [SRK /CSE], whose administrative and technical support, in collaboration with the funding body, ensured smooth progress throughout the research period. The support received not only empowered the successful development and experimentation of the proposed hybrid intelligent framework but also contributed to advancing innovative approaches in the field of healthcare diagnostics.

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