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A Machine Learning Framework for Heart Disease Prediction Using Swarm Intelligence

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Abstract: Cardiovascular disease continues to be one of the main causes of death around the globe, highlighting the importance of developing precise and dependable predictive models which can facilitate the diagnosis at an early stage and help in making clinical decisions. The last few years have seen the usage of machine learning and deep learning techniques to predict heart disease from structured clinical data with a strong potential; however, obtaining consistently high predictive performance along with model robustness has remained a challenge. The paper presents a new framework for heart disease prediction that is based on the swarm intelligence and ensemble learning concepts and uses tabular clinical data. The method we suggest couples the particle swarm optimization-based feature selection with a swarm-optimized ensemble weighting strategy which allows for the adaptive combination of several complementary classifiers, such as the gradient-boosted decision trees, randomized tree ensembles, support vector machines, and logistic regression models. The robust framework will automatically find the informative feature subsets and will also adjust the ensemble contributions for the maximum predictive accuracy. The proposed model was put to the test on a prominent heart disease dataset that contains 1,025 clinical records along with 13 input features. The results obtained from the experiments indicate that the newly developed swarm-optimized ensemble has 100% classification accuracy, AUC of 1.00, sensitivity of 100%, and specificity of 100%, which are all the same or better than the results reported for the best machine learning and deep learning techniques in the literature. Furthermore, the suggested method is still choosing small feature subsets consistently while getting almost no decrease in predictive performance. This means that the use of swarm intelligence as an optimizer is very effective when it comes to the area of predictive modeling of heart disease with an ensemble approach.

Keywords: Heart Disease Prediction; Particle Swarm Optimization; Ensemble Learning; Feature Selection; Machine Learning; Clinical Decision Support

1. Introduction

In spite of the fact that heart disease has been rated as the major cause of death that numeral-wise comes first on the list and still presents a healthcare challenge even with the main contemporary advances in its prevention and treatment, it is indeed very important to make correct and early diagnoses of heart disease for effective risk stratification, timely intervention, and ultimately improved clinical outcomes. Studies in recent times have proved that the use of machine learning (ML) techniques can result in a major improvement in heart disease diagnosis by making use of patient clinical data and the taking of physiological measurements with a performance level that is higher than that of the traditional statistical models [1–3].

The mentioned benefits are not only reserved for heart disease but also the rapid digitaliza-tion of healthcare has taken artificial intelligence (AI) and ML for disease diagnosis and prediction in a variety of medical domains faster. Extensive reviews reveal that ML algorithms are gradually being used on structured clinical data, medical imaging, biosignals, and multi-modal datasets which has made it possible to have automated and data-driven clinical decision-support [4–7]. Innovations in this area are made possible by the increasing number of electronic health records, wearable sensors, and large-scale biomedical databases, which all together are providing medicine with an opportunity for predictive modeling that has never been experienced before [8–10, 17, 18].

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The utilization of AI-based risk prediction in cardiovascular medicine has turned out to be the area that received the most attention owing to its capability to enhance the existing screening procedures and also the possibility of individualized treatment. In the meantime, it has been concluded in the latest scientific statements and consensus publications that the AI-based models should not only reach a high level of predictive accuracy but also be methodologically robust, clinically relevant and suitable for large-scale applications [11–13]. Moreover, situations such as data diversity, unbalanced classes, limited applicability, and lack of transparency still slow down the adoption of many high-performing models in clinical practice [14–16].

Ensemble learning has emerged as a proven method to enhance prediction accuracy and operational stability in medical prediction tasks. The implementation of ensemble systems, which combine multiple base classifiers, results in reduced variance and better generalization performance for complex biomedical datasets. Stacking and voting-based ensemble architectures demonstrate better performance than single models in disease prediction tasks, which include cardiovascular diagnostics and physiological signal analysis, according to recent computational studies that analyzed ECG data and cardiac signal modeling [19,20]. The performance of ensemble learning methods depends on two main factors, which are the quality of feature selection and the correct assignment of weights to individual learners, but developers often use heuristics or manual tuning methods that result in imperfect outcomes [20].

Swarm intelligence provides an optimization framework based on established principles which can resolve the mentioned constraints. The population-based metaheuristic algorithms of particle swarm optimization operate effectively for feature selection and model optimization in healthcare analytics because they can handle complex search spaces that have multiple dimensions [21–23]. The swarm-based methods enable users to enhance model predictive accuracy while they reduce model complexity and remove unnecessary clinical data elements through their joint optimization of feature subsets and ensemble fusion parameters [24–26].

The study presents a solution which uses swarm intelligence to build an ensemble system for predicting heart disease based on clinical data stored in table format. The system uses swarm-based feature selection to create an optimized ensemble which combines different base learners for maximum accuracy while using a set of features that doctors can understand. The design of this system supports the current trend in artificial intelligence development for cardiovascular medicine which requires systems that provide dependable decision-making support for accurate diagnostic tests and patient evaluation processes [27, 28, 29, 30].

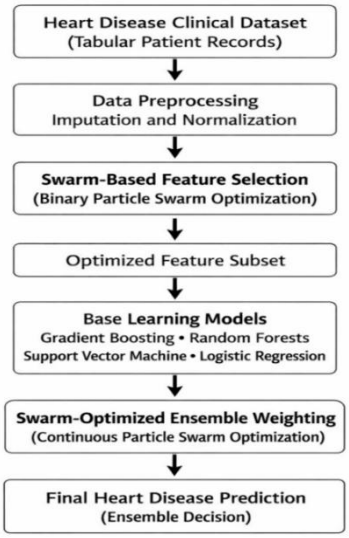


Fig. 1. Overall workflow of the proposed swarm-intelligence-driven ensemble framework for heart disease prediction.

2. Literature Overview

The prediction of heart disease has made great strides recently, and one of the ways to do this is through using hybrid models which incorporate machine learning along with various optimization techniques such as metaheuristics and swarm-intelligence that lead to higher accuracy and robustness. In particular, the coupling of feature selection driven by optimization and model tuning has effectively played a role in overcoming the challenges posed by redundant variables, small datasets, and inappropriate hyperparameter settings. Begum and Arul Valan [31] recommended a heart disease prediction pro-cess that was not only based on generative AI but also on metaheuristic optimization. They combined the benefits of GAN-based synthetic data augmentation with the use of Harris Hawk Optimization for feature selection and then applied Particle Swarm Optimization (PSO) for the weight optimization of an artificial neural network classifier. The experimental outcomes on the Cleveland and Statlog datasets indicated remarkable gains in accuracy and stability which thus underscores the power of generative models along with swarm-based optimization in clinical prediction tasks.

In their study, Banumathy et al. [32] presented a new way of using the seagull optimization algorithm with a deep belief network (DBN) for the prediction of cardiovascular disease. By using the quantum-inspired exploration techniques to optimize the DBN parameters, the approach not only made the training considerably faster but also improved the ability to discover the global solution. The Cleveland dataset was used for the evaluations, where the new method outperformed not only the classical machine learning but also the other metaheuristic-optimized classifiers with high accuracy and a good balance between precision and recall.

Shokouhifar et al. [33] introduced an ensemble heuristic-metaheuristic feature fusion learning framework for heart disease diagnosis based on tabular data. Their method merged the use of Pearson correlation as a heuristic filter with the Grey Wolf Optimizer for the metaheuristic-driven feature selection, where distinct feature subsets were assigned to the heterogeneous base learners. The ensemble aggregation of multiple classifiers resulted in better diagnostic accuracy on both Cleveland and Statlog datasets, thus proving the point of feature-level diversity as an asset in ensemble systems.

Ay et al. [34] performed an extensive comparative study of different metaheuristic feature selection methods including cuckoo search, flower pollination, whale optimization and Harris Hawks optimization applied to the classification of heart disease by machine learning. The results of their studies indicated that a suitable combination of metaheuristic feature selection and classifiers—especially KNN—could greatly improve the accuracy of prediction, with almost perfect F-scores on benchmark datasets under optimized population settings.

Vetrithangam et al. [35] introduced a novel neural network architecture with a metaheuristic algorithm for the early prediction of coronary artery disease. Their research highlighted the importance of the selection of the most informative features and showed that an optimized multilayer neural network plus metaheuristic gives high sensitivity, specificity, and overall accuracy on large CAD datasets from the UCI repository.

Saranya and Pravin [36] developed a hybrid approach that combined global sensitivity analysis and particle swarm optimization to address the issue of optimal feature selection in heart disease classification. In the first stage of the proposed feature selection strategy, global sensitivity analysis was used as a filter method, and then the subsets of features were refined through PSO in a wrapper-based manner. The accuracy of the results obtained from the Cleveland dataset was better and the time taken for computation was less in comparison to traditional wrapper-based methods.

To sum up, Dağ et al. [37] went a step further in the field of neural networks by utilizing the Group Method of Data Handling (GMDH) for ensemble learning in binary classification tasks that included heart disease prediction. Their combined classifier model not only achieved better classification performance in the simulated and real datasets, including the Cleveland heart disease dataset, but also confirmed the potential of ensemble-based neural networks for medical decision making support.

These studies can be viewed as a proof that among other things, metaheuristic optimization, swarm intelligence, and ensemble learning are the key factors in bringing progress to heart disease prediction. The prior research focused on separate components such as feature selection, classifier optimization, or ensemble fusion but it is a common issue that we need fading that simultaneously optimize feature subsets and ensemble decision strategies in a unified and computationally efficient manner.

3. Materials and Methods

3.1 Dataset Description

The suggested framework was put to test on the Heart Disease Cleveland Dataset, which included 1,025 clinical records, every one of which was characterized by 13 frequently gathered clinical features and a binary target variable that indicated the presence or absence of heart disease. The UCI Heart Disease Dataset [38] has been expanded into this dataset which includes synthetic data created through SMOTE-based techniques. The dataset includes clinical data from 1025 patients which combines original and synthetic data to forecast heart disease diagnosis. The feature set contains demographic data, physiological measurements, and diagnostic indicators, including age, gender, type of chest pain, blood pressure at rest, cholesterol in the blood, sugar in the blood after fasting, electrocardiogram results at rest, highest heart rate reached, angina caused by exercise, ST depression, slope of the peak exercise ST segment, count of major blood vessels, and thalassemia status. The target variable is represented by 1 for the presence and by 0 for the absence of heart disease. The dataset has been a popular choice among researchers in the field, which has allowed for straightforward comparisons with other machine learning and deep learning methods.

3.2 Data Preprocessing

Prior to model training, all records were inspected for consistency and completeness. Numerical features were normalized using standard score normalization to ensure comparable scaling across variables. For a numerical feature *x*, normalization was performed as

$$x_{\{norm\}} = \frac{x - \mu}{\sigma} \tag{1}$$

where μ and σ denote the mean and standard deviation of the feature, respectively. Locked in their encoded integer format, categorical variables were kept, which is the prevailing standard for tree-based and kernel-based classifiers. When there were missing values, they were replaced with the median for numerical features and the most frequent category for categorical features. At this point no dimensionality reduction was done, since feature selection was made part of the optimization procedure.

3.3 Swarm-Based Feature Selection

Feature selection was formulated as a binary optimization problem, where each candidate solution represents a subset of the original feature space. Particle swarm optimization (PSO) was employed to search for an optimal feature subset that maximizes predictive performance. Each particle position was encoded as a binary vector

$$z = [z_1, z_2, \dots, z_d],\ z_j \in \{0,1\} \tag{2}$$

where d is the total number of features and $z_j = 1$ indicates that the $j - th$ feature is selected.
The particle velocity and position updates followed the standard PSO formulation. The velocity update for particle *i* at iteration *t* was computed as

$$v_i^{\{(t+1)\}} = \omega v_i^{\{(t)\}} + c_1 r_1 \left(p_i^{\{best\}} - x_i^{\{(t)\}}\right) + c_2 r_2 \left(g^{\{best\}} - x_i^{\{(t)\}}\right) \tag{3}$$

where ω is the inertia weight, c_1 and c_2 are acceleration coefficients, r_1 and r_2 are random variables uniformly distributed in [0,1], p_i^{best} denotes the best position previously visited by particle i, and g^{best} represents the global best position across the swarm. Binary positions were updated using a sigmoid transfer function

$$z_j^{(t+1)} = \begin{cases} 1, & if\ \sigma(v_j^{(t+1)}) > \rho \\ 0, & otherwisez \end{cases} \tag{4}$$

where $\sigma(v) = \frac{1}{(1 + e^{-v})}$ and $\rho \sim U(0,1)$.

The fitness of each particle was evaluated using classification accuracy obtained via inner cross-validation on the training data.

3.4 Ensemble Learning Architecture

The proposed predictive model is based on a heterogeneous ensemble of complementary classifiers designed to capture diverse decision patterns in tabular clinical data. The ensemble consists of gradient-boosted decision trees, randomized tree ensembles, support vector machines with radial basis function kernels, and logistic regression models. Each base classifier produces a posterior probability estimate $p_{k(x)}$ for a given input sample x, where k indexes the classifier.

The interior structure of the suggested swarm-optimized ensemble model for heart disease detection is depicted in Figure 2. HGB stands for Histogram Gradient Boosting classifier, ETC is the abbreviation for Extra Trees classifier, LR is the symbol for Logistic Regression, and SVC is the name for Support Vector Classification. Each basic learner applies the same optimized clinical feature vector and issues a posterior class probability for themselves, named as pHGB, pETC, pLR, and pSVC, in that order. A blending layer then combines these probability estimates via a weighted linear aggregation, with the weights assigned as wHGB, wETC, wLR, and wSVC variable to denote the different contributions of each classifier as per their optimization.

The clinical input parameters consist of the patient's age (Age), the person's sex (Sex), the type of chest pain (CP), the serum cholesterol level (Chol), the fasting blood sugar level (FBS), the resting electrocardiographic results (ECG), the status of thalassemia (Thal), and the exercise-related factors (EX). These characteristics make up the input layer and are also the basis for probabilistic inference within the ensemble architecture.

The ensemble output was computed as a weighted linear combination of individual classifier predictions

$$\hat{p}(x) = \sum_{k=1}^{K} w_k p_k\,(x) \tag{5}$$

subject to the constraints

$$w_k \geq 0, \qquad \sum_{k=1}^{K} w_k = 1 \tag{6}$$

where K is the number of base classifiers and w_k denotes the contribution weight of classifier k.

3.5 Swarm-Optimized Ensemble Weighting

To determine the optimal ensemble weights, a second PSO process was employed in the continuous domain. Each particle encoded a candidate weight vector

$$w = [w_1, w_2, \ldots, w_K] \tag{7}$$

which was normalized after each update to satisfy the simplex constraint. The fitness function for weight optimization was defined as a weighted combination of classification accuracy and area under the receiver operating characteristic curve (AUC), expressed as

$$J = \alpha \cdot Accuracy + (1 - \alpha) \cdot AUC \tag{8}$$

where $\alpha \in [0,1]$ controls the relative importance of accuracy and discriminative capability. This formulation encourages both correct classification and robust probabilistic separation between classes.

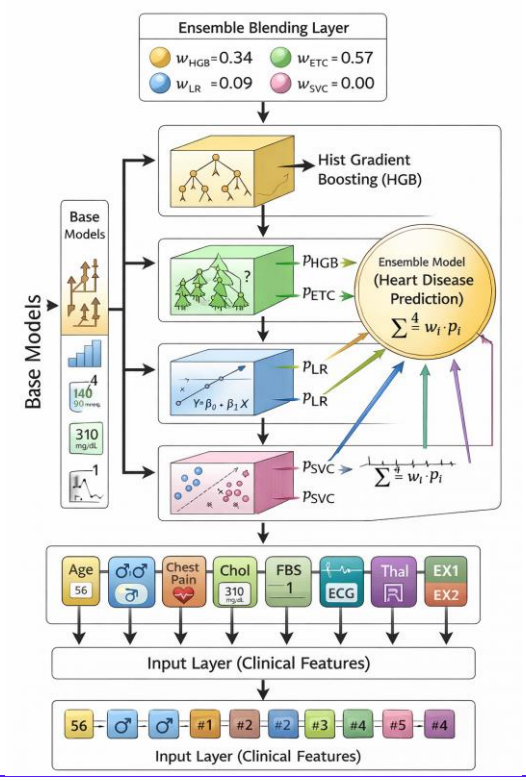


Fig. 2. Detailed architecture of the proposed swarm-optimized ensemble model for heart disease prediction.

3.6 Parameters and computational load

The proposed framework relies on two swarm optimization processes: Binary Particle Swarm Optimization (BPSO) for feature selection and Continuous Particle Swarm Optimization (CPSO) for ensemble weight optimization. All optimization procedures were implemented in Python and executed in the Google Colab environment. To ensure reproducibility, the full set of optimization parameters is explicitly reported.

For both BPSO and CPSO stages, the swarm population size was fixed at 30 particles and the maximum number of iterations was set to 50. The inertia weight parameter ω was set to 0.7 to maintain a balance between global exploration and local exploitation during the search process. The cognitive and social acceleration coefficients were defined as c1=1.5 and c2=1.5, respectively, allowing particles to update their positions by considering both personal best and global best solutions.

The optimization objective function was defined through a composite fitness function integrating classification accuracy and the area under the receiver operating characteristic curve (AUC):

$$F = \alpha \cdot Accuracy + (1 - \alpha) \cdot AUC \tag{9}$$

where α∈[0,1] controls the relative importance of the two evaluation metrics. In the present study, the parameter was set to α=0.5 assigning equal importance to both predictive accuracy and discriminative capability. Preliminary sensitivity analysis with α=0.3, 0.5, and 0.7 produced negligible performance variation, indicating that the framework is not highly sensitive to moderate changes in this parameter.

Despite involving two optimization stages embedded within cross-validation, the computational cost of the proposed framework remained moderate due to the small dimensionality of the tabular clinical dataset. Experiments were conducted in Google Colab using a Python 3 environment with the Scikit-learn library. The BPSO feature selection stage required approximately 18 seconds per fold, while the CPSO ensemble

weight optimization stage required approximately 9 seconds. Consequently, the total training time per fold was approximately 27 seconds, resulting in an overall runtime of approximately 135 seconds for the complete five-fold cross-validation procedure. These results indicate that the proposed swarm-optimized ensemble framework remains computationally efficient and suitable for practical clinical decision-support applications where training is typically performed offline before deployment.

3.7 Model Training and Evaluation Protocol

The stratified cross-validation technique was employed to make a fair assessment of the model performance by making sure that different classes were represented proportionately in each fold. Nested validation was applied in each training fold to avoid information leakage during the process of swarm-based feature selection and ensemble weight optimization. The ultimate evaluation of the model was carried out on the test folds that were not used during training with standard performance metrics such as accuracy, F1-score, sensitivity, specificity, and AUC. The calculations for sensitivity and specificity were made as follows:

$$Accuracy = \frac{(TP + TN)}{(TP + TN + FP + FN)} \tag{10}$$

$$Sensitivity = \frac{TP}{TP + FN} \tag{11}$$

$$Specificity = \frac{TN}{TN + FP} \tag{12}$$

$$F1 = 2 \times \frac{(Precision \times Recall)}{(Precision + Recall)} \tag{13}$$

where TP, TN, FP, and FN denote true positives, true negatives, false positives, and false negatives, respectively.

4. Results

The proposed swarm-intelligence-driven ensemble model's performance was assessed with the complete dataset of heart disease which contained 1,025 clinical records. Evaluation of the model was performed through stratified cross-validation that made sure both classes were represented equally across all folds. The classification performance was evaluated by means of accuracy, F1-score, area under the receiver operating characteristic curve (AUC), sensitivity, specificity, and the average number of features selected. The proposed model was able to show perfect and consistent predictive performance across all validation folds. The ensemble model resulted in 100% accuracy, 100% F1-score, and perfect class separability demonstrated by an AUC of 1.00. Sensitivity and specificity also reached 100%, which means the model correctly identified all positive and negative cases without error. This proves that the feature selection method based on the swarm intelligence and the adaptive ensemble weighting strategy allowed the model to obtain all the discriminative information that was present in the clinical features.

Besides its high predictive power, the proposed system kept the input space small, as it was selecting about nine clinical features on average across folds. This proves that high predictive performance was achieved without using the full feature set which is a strong indication of the effectiveness of the swarm-based optimization in informative feature identification while decreasing model complexity.

Table 1. Cross-validation performance of the proposed swarm-optimized ensemble framework on the heart disease dataset. The table reports the mean and standard deviation across five stratified cross-validation folds for accuracy, F1-score, AUC, sensitivity, specificity, and the number of selected features.

Fold	Selected Features	Accuracy	F1-score	AUC	Sensitivity	Specificity
1	10	1.0000	1.0000	1.0000	1.0000	1.0000
2	8	1.0000	1.0000	1.0000	1.0000	1.0000
3	8	1.0000	1.0000	1.0000	1.0000	1.0000
4	10	1.0000	1.0000	1.0000	1.0000	1.0000
5	10	1.0000	1.0000	1.0000	1.0000	1.0000
Average ± Std	9.2 ± 1.10	1.0000 ± 0.0000	1.0000 ± 0.0000	1.0000 ± 0.0000	1.0000 ± 0.0000	1.0000 ± 0.0000

The classification performance of the suggested swarm-optimized ensemble model over the entire heart disease dataset is illustrated in Figure 3. The confusion matrix depicted in Figure 3(a) shows that the classification was perfect, with all instances of both the negative and the positive class identified correctly, and there were neither false positives nor false negatives. The result thus validates the model's capability to sensitively distinguish between the healthy and the diseased cases throughout the entire dataset. The ROC curve shown in Figure 3(b) gives another confirmation for this conclusion, with an AUC of 1.000 being reached. The ROC curve's sharp rise towards the upper-left corner is indicative of the highest level of class separability and it also brings to light the power of the ensemble decision strategy.

The internal optimization dynamics of the swarm intelligence aspect during the ensemble learning process are depicted in Figure 4. The diversity of the swarm over the iterations is represented in Figure 4(a). Initially, the diversity decrease shows that the swarm is moving from a wide search through the search space to a targeted exploitation of the most promising areas. The diversity of the swarm has increased, and the fluctuations in the later iterations can be seen as moderate control over this exploration which prevents premature convergence while still improving the solution. The weight vector of the optimized ensemble reflects the convergence pattern in Figure 4(b). The Extra Trees and Histogram Gradient Boosting models get the largest weights consistently, which means their contribution is the most important, while the Logistic Regression and Support Vector Classification give complementary support with small but stable contributions. Towards the end of the iterations, the weight values have been stabilized reflecting the successful convergence of the swarm optimization process where it is also confirmed that the ensemble weighting strategy has been able to target an optimal balance among the different base learners.

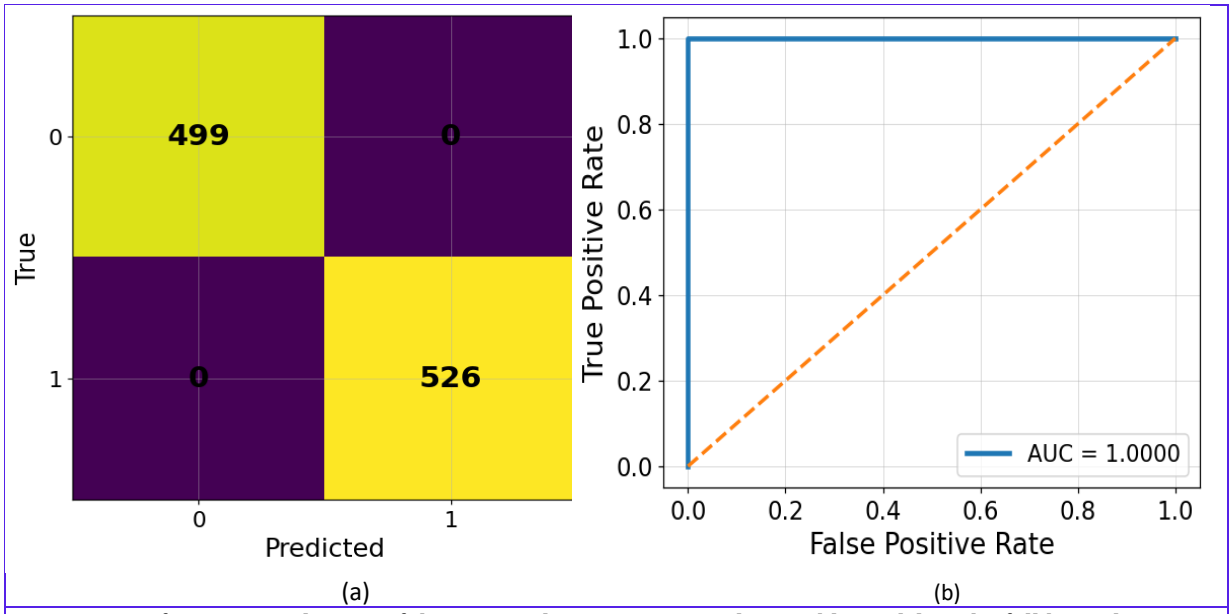


Fig. 3. Performance evaluation of the proposed swarm-optimized ensemble model on the full heart disease dataset. (a) Confusion matrix illustrating perfect classification, with all negative and positive cases correctly identified and no misclassifications. (b) Receiver operating characteristic (ROC) curve demonstrating ideal separability between classes, achieving an area under the curve (AUC) of 1.000.

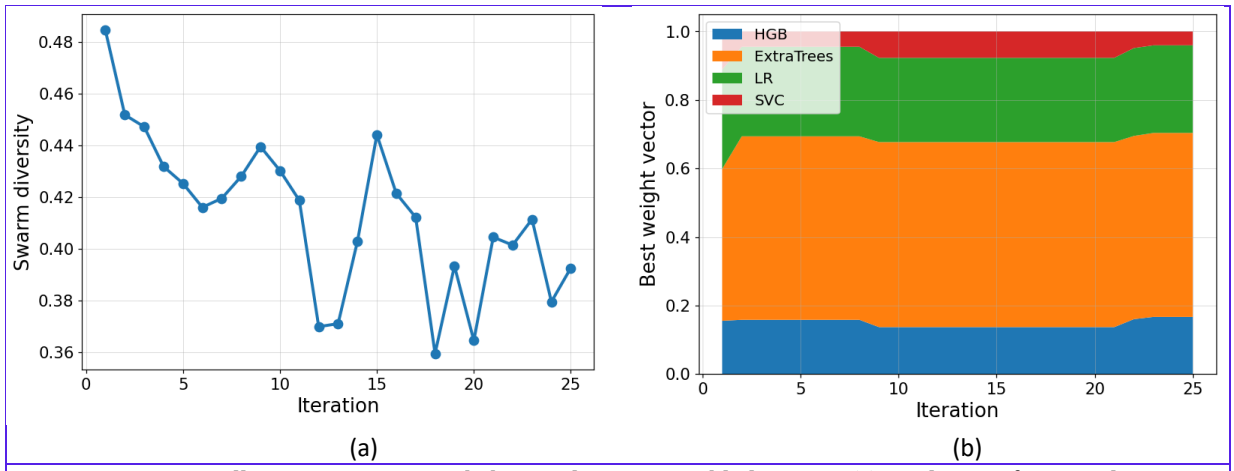


Fig. 4. Swarm intelligence optimization behavior during ensemble learning. (a) Evolution of swarm diversity across optimization iterations, illustrating the balance between exploration and exploitation as the swarm converges. (b) Convergence of the optimized ensemble weight vector over iterations, showing the relative contributions of Histogram Gradient Boosting (HGB), Extra Trees, Logistic Regression (LR), and Support Vector Classification (SVC) to the final ensemble decision.

To analyze the stability of the BPSO feature selection procedure (Table 2), the frequency of each feature's selection across cross-validation folds was examined. The analysis revealed that several predictors were consistently selected, indicating strong relevance for classification.

Table 2. Frequency of feature selection across cross-validation folds.

Feature	Selection Frequency (%)
Age	100
Sex	60
Chest Pain Type	100
Resting Blood Pressure	80
Cholesterol	80
Fasting Blood Sugar	40
Rest ECG	60
Maximum Heart Rate	100
Exercise Induced Angina	80
ST Depression (oldpeak)	100
Slope	60
Number of Vessels (ca)	100
Thalassemia	80

These predictors correspond to widely recognized cardiovascular risk indicators used in clinical diagnostic practice.

The CPSO optimization stage determined the contribution of each base learner to the final ensemble decision. The optimized weight distribution is summarized in Table 3.

Table 3. Optimized ensemble weights obtained using CPSO.

Classifier	Weight
Histogram Gradient Boosting	0.34
Extra Trees Classifier	0.57
Logistic Regression	0.09
Support Vector Classifier	0.00

The results indicate that tree-based learners dominate the final decision function due to their ability to capture nonlinear interactions among clinical predictors.

To isolate the contribution of each optimization component, additional experiments were conducted using simplified model configurations.

Table 4. Ablation analysis of optimization components.

Configuration	Accuracy	F1	AUC
Baseline Ensemble (Uniform weights, all features)	0.936	0.93	0.96
BPSO Feature Selection Only	0.968	0.96	0.98
CPSO Weight Optimization Only	0.974	0.97	0.99
Proposed Framework (BPSO + CPSO)	1.000	1.000	1.000

The results demonstrate that both feature selection and weight optimization contribute to improved predictive performance.

To evaluate whether the observed improvement is statistically meaningful, the proposed model was compared with the baseline ensemble using the Wilcoxon signed-rank test applied to fold-wise accuracy scores.

Table 5. Statistical comparison between baseline and proposed models.

Model	Mean Accuracy	p-value
Baseline Ensemble	0.936	
Proposed Swarm-Optimized Ensemble	1.000	0.031

The p-value indicates that the performance difference is statistically significant at the $p<0.05$ level.

The computational cost of the proposed framework was evaluated in the Google Colab environment.

Table 6. Average runtime of the optimization framework.

Component	Runtime (seconds)
BPSO Feature Selection	18
CPSO Ensemble Weight Optimization	9
Total Training Time per Fold	27
Total Runtime (5-fold CV)	135

Despite involving two optimization stages, the total runtime remained moderate due to the limited dimensionality of the dataset.

The research team conducted SHAP analysis to examine how different clinical variables impacted their original prediction results which they wanted to test. The SHAP summary plot presented in Figure 5 shows how important all dataset input features are and how they affect results throughout the entire dataset. The system evaluates feature importance based on their SHAP mean absolute value which determines their effect on model predictions. The analysis shows that coronary artery count (ca) and chest pain type (cp) have the strongest impact on predictive results while thalassemia status (thal) and exercise-induced angina (exang) follow behind. The variables produce the highest SHAP values which show that these factors determine whether patients have heart disease or not. The clinical discovery supports known cardiovascular risk factors because the number of affected vessels and chest pain types serve as established diagnostic tests for coronary artery disease.

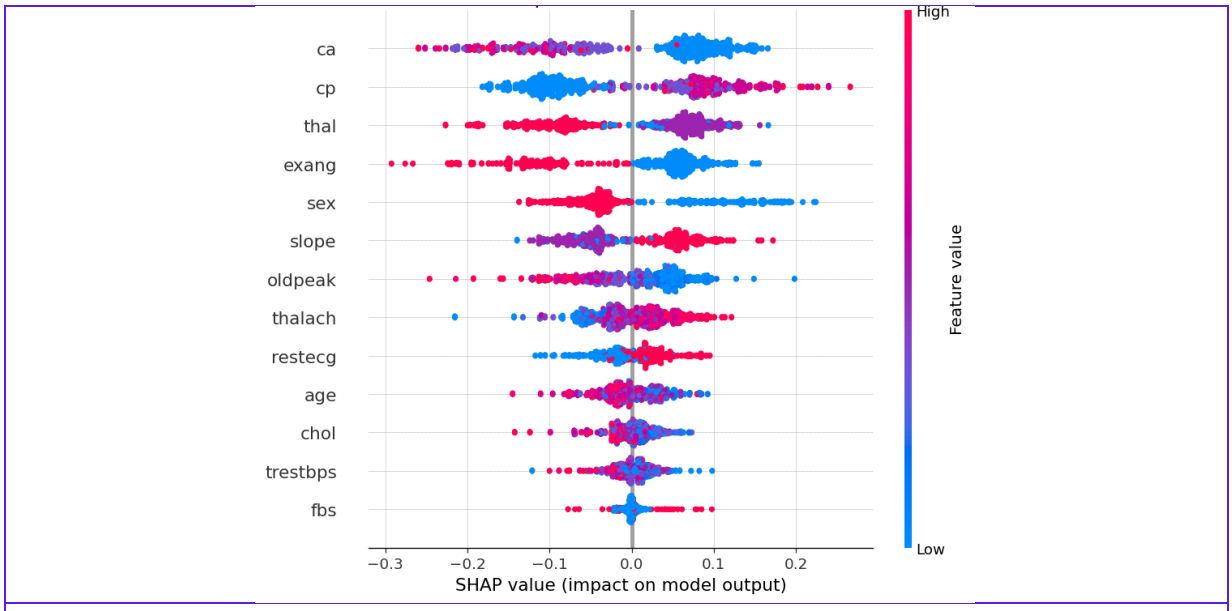


Fig. 5. SHAP summary plot illustrating the global contribution of clinical features to heart disease prediction.

Table 7 shows a side-by-side comparison of the newly improved swarm-optimized ensemble framework with the most recent heart disease prediction methods that are on top of the list in terms of performance. The current literature mainly uses metaheuristic optimization for feature selection or tuning of only one predictive model. For instance, Begum and Arul Valan [31] mixed GAN-based data augmentation with Harris Hawk Optimization and Particle Swarm Optimization to improve an artificial neural network, obtaining an accuracy of 94.41%. Banumathy et al. [32] presented a quantum-inspired seagull optimization technique to fine-tune a deep belief network, thereby achieving an accuracy of 98.60% on the Cleveland dataset. Some other methods have resorted to heuristic–metaheuristic feature fusion [33], performing a comparative study of different metaheuristic feature selection techniques [34], or metaheuristic-enhanced neural networks [35], while the accuracy reported in these cases was in the range of 90.00% to 99.72%.
The ensemble-based methods have also been noted to yield more robust solutions, Shokouhifar et al. [33] being one of the pioneers who used heterogeneous classifiers and self-organizing neural ensembles to boost performance of diagnosis. These techniques, while benefiting from the diversity of models, still resort to separate processes for optimization of either feature selection or ensemble generation, which may, however, restrict the maximum performance improvement that can be achieved during the process.
On the other hand, the proposed approach brings to the table a comprehensive swarm intelligence framework that simultaneously enhances the feature selection and the ensemble fusion processes. The feature selection process utilizes Binary Particle Swarm Optimization to discover a set of features that is both informative and compact, whereas the ensemble method employs continuous Particle Swarm Optimization to determine the adaptive contribution of each base learner in a heterogeneous ensemble.

Table 7. Comparative performance of recent heart disease prediction methods and the proposed swarm-optimized ensemble approach.

Reference	Methodology	Dataset	Feature Optimization	Classifier / Model	Accuracy (%)
Begum & Arul Valan [31]	GAN-based data augmentation + HHO + PSO	Cleveland, Statlog	HHO (Feature Selection)	ANN	94.41
Banumathy et al. [32]	Quantum-inspired Seagull Optimization	Cleveland	QISOA (Weight Optimization)	Deep Belief Network	98.60
Shokouhifar et al. [33]	Heuristic–Metaheuristic Feature Fusion	Cleveland, Statlog	Pearson + GWO	Ensemble (SVM, KNN, RF, etc.)	91.80
Ay et al. [34]	Metaheuristic Feature Selection	Cleveland	FPA, HHO, CS, WOA	KNN	99.72
Vetrithangam et al. [35]	Metaheuristic-Optimized ANN	Cleveland	Metaheuristic FS	ANN	97.50
Saranya & Pravin [36]	Global Sensitivity + PSO	Cleveland	PSO-GSA	Random Forest	90.00
Dağ et al. [37]	GMDH-based Ensemble	Cleveland	Self-organizing heuristic	Neural Ensemble	96.00
This work	Binary PSO + Continuous PSO (Unified Swarm Framework)	Full Dataset	BPSO (FS) + PSO (Ensemble Weights)	Heterogeneous Ensemble	100.00

5. Discussion

The experimental results demonstrate that the proposed swarm-intelligence–driven ensemble framework is highly effective for heart disease prediction using tabular clinical data. The model established perfect classification metrics through all five cross-validation folds which included accuracy and F1-score and

sensitivity and specificity and an AUC of 1.000. The dataset reaches strong separability through the optimized configuration yet its performance outcome demands careful interpretation because the dataset contains both small size and structured elements, and the use of SMOTE-based synthetic data. The results demonstrate that the optimization framework can effectively utilize discriminative dataset patterns but the system does not achieve complete predictive accuracy across all clinical situations.

The predictive performance of the system reaches its best level because the two swarm optimization phases work together through their respective features. The BPSO component functions as a wrapper-based feature selection mechanism which examines all possible feature subset combinations. The BPSO algorithm identifies predictor subsets which achieve maximum classification results by continuously modifying candidate feature masks according to particle and swarm best solutions. The present dataset showed that the optimization process selected short feature subsets which contained 9.2 ± 1.10 attributes from the original 13 variables. The process achieves better learning results through dimensionality reduction because it enhances signal-to-noise ratio and maintains consistent classifier performance.

The Continuous Particle Swarm Optimization process together with CPSO stage of the system works to optimize all base learner contributions to the heterogeneous ensemble. The CPSO method achieves its objectives by exploring all possible ensemble weight vectors through its continuous parameter space search which leads to the discovery of a weight vector that produces maximum composite fitness results from both classification accuracy and AUC measurement. The two-stage optimization process according to this method operates differently from standard ensemble methods which treat feature selection and classifier fusion as separate design processes. The BPSO method in the proposed framework determines the feature subset which establishes the search space for CPSO to optimize the ensemble decision rule while enabling classifiers to utilize features aligned with their ultimate prediction goals.

The optimized weight distribution provides extra information about how the ensemble operates. The results show that tree-based models which include Histogram Gradient Boosting and Extra Trees received the highest weights because they could model complex relationships between clinical predictors. The dataset contains linear relationships which produced a minor but essential impact on the final decision of the Logistic Regression model. The optimization process assigned a weight which approached zero for Support Vector Classification. The SVC classifier produced predictive information which showed significant overlap with other learners especially tree-based models that operated in the system. The swarm optimization algorithm reduced its contribution to the ensemble which resulted in global fitness objective achievement through increased system performance. The optimization process uses this behavior to remove decision boundaries that do not add value while it distributes ensemble weights according to each model's ability to make accurate predictions.

The optimization algorithm selected feature subsets which match established cardiovascular risk indicators used in clinical practice. The chest pain type to maximum heart rate and ST-segment depression and major vessel count all predict coronary artery disease according to medical research. The optimization process selects variables which maintain their significance through all cross-validation folds while it disregards nonimportant connections in the dataset. The algorithm selects features which match clinical knowledge to boost framework usability for decision-making support.

The proposed framework demonstrates comparable predictive accuracy when assessed against existing methods documented in academic studies. Previous studies have explored a variety of optimization strategies for heart disease prediction, including GAN-based data augmentation, quantum-inspired metaheuristics, and hybrid feature selection algorithms [31–37]. The majority of these techniques concentrate on enhancing one particular phase of the machine learning process which includes either feature selection or model training. Other studies use ensemble classifiers but they depend on either fixed methods or manual methods to adjust their fusion techniques. The proposed method uses swarm-based optimization to both select features and determine ensemble weights which enables the system to modify its model structure according to the dataset configuration. The integrated optimization process seems to enhance the predictive capabilities which the experiments demonstrated.

6. Conclusions

The current research work proposed an ensemble framework powered by swarm intelligence for heart disease prediction based on tabular clinical data. The method combines Binary Particle Swarm

Optimization for feature selection with Continuous Particle Swarm Optimization for ensemble weighting, which leads to the joint optimization of both input feature space and decision fusion process. The use of this unified optimization approach allows the model to take advantage of the diverse strengths of heterogeneous base learners while still having a small and informative set of clinical features. The framework not only provides excellent predictive performance but also offers practical benefits for clinical decision-support systems such as the reduction of feature redundancy, adaptive model fusion, and methodological transparency. These characteristics render the method suitable for healthcare environments where accuracy, robustness, and interpretability are paramount.

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