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Heart Disease Classification Using Support Vector Machines Enhanced with Metaheuristic Optimization Algorithms

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Heart disease is still one of the major causes of death globally, for which early and accurate diagnosis is of prime importance. This work introduces an efficient approach to classify heart disease using Support Vector Machines (SVMs) with innovative metaheuristic optimization techniques. The method is tested on the Cleveland Heart Disease dataset from the UCI Machine Learning Repository with 303 patients having 14 features. Particle Swarm Optimization (PSO), Grey Wolf Optimizer (GWO), and Whale Optimization Algorithm (WOA) metaheuristic algorithms were used for optimization of SVM parameters. The performance measures used for the comparison are accuracy, precision, recall, and F1-score. The highest classification accuracy (93.7%) is produced by the proposed GWO-SVM, which is relatively better than that of PSO-SVM (91.2%) as well as WOA-SVM (89.6%). The proposed work yields superior predictive performance compared to the contemporary SVM and existing models in the literature. The outcomes of this work emphasize the integration of metaheuristic algorithms with machine learning models for clinical decision support in the diagnosis of heart disease.

Povzetek: Študija za diagnostiko srčnih bolezni združi SVM z metahevrističnim uglaševanjem parametrov (PSO, GWO, WOA), pri čemer GWO-SVM doseže najboljšo napovedno uspešnost za podporo kliničnemu odločanju.

1 Introduction

Heart failure, or HF, can be defined as when the heart is not able to pump sufficient blood to meet the body's needs. It is still a very common and multifactorial problem worldwide [1], [2], [3]. Heart failure hardly lets patients live normal lives; it includes a variety of symptoms, such as shortness of breath, general body weakness, and swollen feet [4], [5]. Heart failure and its consequences have been indicated as the major causes of reduced life expectancy and increased mortality rates in developed countries [6], [7]. Management of heart failure is a huge challenge, which becomes more daunting in developing countries due to the scarcity of awareness about and access to medical knowledge and diagnostic facilities, particularly in remote places in relation to urban hubs [8]. Thus, the accurate prediction of HF risk should be performed in conjunction with the interest of minimizing the possibility of serious cardiac problems taking place while enhancing people's safety and productivity [9], [10]. Conventional HF risk diagnosis makes symptom assessment, physical examinations, and patient medical history the major inputs on the part of health practitioners. These methods are, however, bound to commit errors due to human frailties and may even delay diagnosis [11], [12].

The increasing incidence of cardiovascular disorders calls for early identification methods. Biochemical testing analysis of blood, urine, or tissue samples is turning out to be one of the common techniques to identify cardiovascular diseases. Besides these, some very elementary biochemical risk factors become vital in knowing who is more likely to get heart disease. These risk factors include blood pressure, glucose levels, smoking status, and lipid profiles of cholesterol (Chol), low-density lipoprotein cholesterol (LDL-C), and high-density lipoprotein cholesterol (HDL-C), among others, such as physical inactivity. Blood tests through biochemical testing offer a better assessment by evaluating key components such as the level of fats, cholesterol, and the fractions of lipids, which also include LDL, HDL, and triglycerides, required for defining cardiovascular status. In addition to the lipid profiles, these tests also include biomarkers such as glycosylated hemoglobin, an important indicator of the presence of diabetes. More importantly, inflammatory biomarkers like poly-proteins A1 and B and C-reactive protein become sentinel indicators flagging inflammation that could put individuals at risk of cardiovascular diseases [13], [14], [15]. Clinicians can speed up correct diagnoses, enable timely interventions and individualized treatment options, and thereby improve patient outcomes by utilizing the knowledge derived from such biochemical investigations. The methodology of diagnosis, on the one hand, contributes to the decrease in mortality rates due to cardiovascular diseases, but on the other hand, it also forms the very basis of pharmacological treatment that is personalized, effective in slowing down the disease process, and improving patient outcomes [16].

Data mining will be an interdisciplinary field that involves meaningful and informative pattern extraction from large databases [17], [18], [19], [20], [21]. Their applications can be seen in various fields, such as steganography [22], education [23], traffic management [24], product quality control [25], retail operations [26], criminal data analysis [27], and, most importantly, healthcare [28], [29], [30], [31], [32]. The medical domain has been a victim of increased use over the last few decades by researchers in data mining techniques as a contribution to clinical decision support. Examples of applications include prognosis evaluation, administrative health management, design of treatment plans, and the possibility of outcomes after surgeries, besides the diagnosis of diseases, including cancer, diabetes, and cardiovascular. Healthcare professionals can use large patient data repositories to improve diagnosis precision, tailor treatment plans, and streamline healthcare delivery using advanced data mining techniques. This improves patient outcomes and advances medical science [33].

There is a lot of data in the healthcare sector, which makes it a huge source of possible insights [34]. Wide-ranging databases that house electronic medical record systems serve as the repository for this abundance of data [35], [36]. The requirement for precise cardiovascular disease diagnosis in the enormous volume of information, however, remains a barrier despite this data deluge; this situation is accurately defined as "drowning in data but starving for knowledge." [37], [38], [39], [40]. Hospitals have not yet completely realized the potential that data inside healthcare systems has for assessment and analysis [41]. A significant portion of the data is yet unexplored, hiding important insights and hidden patterns that have not yet been discovered [42], [43], [44]. There are still opportunities to systematically mine medical information for analytical purposes, which is a wasted resource that may greatly support and educate the clinical decision-making process [45], [46], [47]. Efforts to leverage data mining techniques in healthcare hold promise for guiding and enhancing clinical decision-making processes. By delving into the depths of medical records data, healthcare institutions can unlock hidden knowledge, empowering practitioners with valuable insights to improve patient care, refine treatment approaches, and ultimately advance the quality and efficacy of healthcare delivery [48].

1.1 Literature review

Numerous studies concentrate on the problem of using machine learning to diagnose heart failure [49], [50], [51], [52], [53], [54], [55], [56]. To classify the dataset and forecast heart disease, Princy et al [57] used a supervised machine-learning method. The results demonstrated that, with an accuracy of 73%, Decision Tree classification outperformed Naive Bayes, Logistic Regression, Random Forest, SVM, and KNN-based techniques. To predict coronary heart disease (CHD), Shorewala [58] used a risk factor approach. When compared to K-Nearest Neighbors, Binary Logistic Classification, and Naive Bayes, their proposed approach demonstrated better performance, especially in key measures like recall and ROC curves. Then, using data-analytic techniques and K-Folds cross-validation, the tested models' performance was confirmed. NB, SVM, kNN, DT, Neural Network, LR, and Random Forest are data mining classification techniques that Tasnim and Habiba [59] tried to use it to look into the likelihood of CHD. With a 92.85% accuracy rate, Random Forest is the most effective method for classifying heart disease, according to the obtained results. For studying cardiac illness, Bharti et al. [60] proposed a novel machine learning approach with a 94.2% accuracy rate, and a confusion matrix confirmed the obtained results. Furthermore, the findings showed a link between diabetes and heart failure, and a random forest was used to classify cardiovascular illness [61]. Six machine learning models for predicting heart failure readmission within 20 days after discharge were compared by Rizinde et al. [62]. Their findings showed that decision trees (DT) executed badly with an AUC of 57%, whereas random forests (RF) outperformed all others with a 94% AUC. Several classification techniques, such as Multi-layer Perceptron (MLP), SVM, RF, and NB, were used by Boukhatem et al. [63] to predict cardiovascular disease. In terms of feature selection and data preprocessing, SVM models demonstrated noteworthy performance with an accuracy of 91.67%.

In their study on the importance of precise cardiovascular disease (CVD) diagnosis, Bhatt et al. [64] proposed an ML method, such as an RF, for prediction. Their approach greatly increased classification accuracy by combining Huang initialization with k-mode clustering. They obtained noteworthy accuracy using a variety of machine learning algorithms. With an accuracy of 87.28%, the multilayer perceptron with cross-validation fared better than the others. ML algorithms were used by Khan et al. [65] to make accurate CVD predictions and decisions. They tried many machine learning techniques, such as DT, RF, LR, NB, and SVM, on a sample of heart disease patients from Pakistani hospitals. In the end, RF showed the lowest specificity and misclassification errors for CVD at 43.48% and 8.70%, respectively, while demonstrating the highest accuracy, sensitivity, and ROC curve at 85.01%, 92.11%, and 87.73%. The impact of shifting lifestyles on physical activity and the rise in heart-related illnesses was studied by Kumar et al. [66]. For real-time heart disease analysis, they proposed an Edge-assisted Cloud-IoT architecture using a Random Forest and Logistic Regression Grid (RF-LRG) technique. When compared to cloud or edge computing alone, this framework performed better than conventional algorithms, increased accuracy, and decreased latency and energy usage. Machine learning was used by Chandrasekhar et al. [67] to increase the accuracy of cardiac disease prediction. On the Cleveland and IEEE Dataport datasets, they looked at six techniques; logistic regression and AdaBoost performed the best. Significant accuracy gains were made using a soft voting ensemble classifier, outperforming individual models. Their approach, which included GridSearchCV and five-fold cross-validation, was novel and performed better than previous prediction experiments. RF-FSFC, a technique for enhancing heart disease prediction using the Cleveland dataset, was suggested by Saranya and Pravin [68]. They obtained 81.16% accuracy with feature removal and 86.141% accuracy without feature omission by including feature sensitivity and correlation analysis into RF. Their method outperformed previous models, demonstrating a significant gain in accuracy and providing better sensitivity, specificity, PPV, and NPV ratings.

Research on strokes, a major cause of mortality worldwide that often results from obstructions in heart and brain circuits, was carried out by Das et al. [69]. They looked at several risk variables and emphasized the need of early detection. They tested nine algorithms in an effort to predict heart attacks using machine learning techniques. With an accuracy of 98.4%, the RF technique was the best performer. Ansari et al. [70] proposed a technique that uses a variety of machine-learning algorithms to predict cardiac disease. They discovered that the random forest and k-nearest neighbor methods performed better than the others, with an astounding accuracy percentage of 99.04%. They also used MCC parameters to assess performance and six feature selection techniques. The usefulness of SVM and XGBoost techniques in detecting ischemic heart disease was evaluated by Ashish et al. [71], with notable results. The continuous rivalry between machine learning models in predicting cardiac disorders is still unsolved despite this attention. Therefore, further study is required to get higher precision. Table 1 presents a summary of the related works.

Table 1: Concise and comparative overview of existing efforts

Study	Method(s)	Dataset	Accuracy	Limitations
Princy et al. [57]	DT, NB, LR, RF, SVM, KNN	UCI	73% (DT best)	Low accuracy, no optimization
Tasnim & Habiba [59]	RF, NB, SVM, etc.	UCI	92.85% (RF)	No hybrid models
Bharti et al. [60]	RF	Private	94.2%	Limited feature insights
Rizinde et al. [62]	DT, RF	HF dataset	AUC 94% (RF)	DT underperforms, limited scope
Boukhatem et al. [63]	SVM, MLP, NB, RF	Unknown	91.67% (SVM)	Lacks ensemble tuning
Khan et al. [65]	RF, SVM, DT, NB	Local (Pakistani hospitals)	85.01% (RF)	Low specificity in RF
Saranya & Pravin [68]	RF with FS	Cleveland	86.14%	Moderate performance
Das et al. [69]	RF	Unknown	98.4%	Dataset size unspecified
Ansari et al. [70]	RF, KNN	UCI + others	99.04% (RF)	Model complexity, no optimization
Ashish et al. [71]	SVM, XGBoost	Ischemic dataset	High (not specified)	General performance unclear
Proposed Method	SVM + GRO/TFWO/BOA	UCI	Up to 93.7%	Addresses optimization and accuracy limitations

1.2 Objective of the study

The purpose of this work is to improve the predictive performance of heart disease diagnosis with the aid of a hybrid machine learning strategy based on Support Vector Machines (SVC) with the power of optimization algorithms such as Golden Rush Optimizer (GRO), Turbulent Flow of Water-based Optimization (TFWO), and Bonobo Optimizer Algorithm (BOA). The combination of the optimizers makes use of their individual nature- and physics-inspired exploration–exploitation mechanisms in order to finely tune the model parameters. In addition, embedded within the pipeline are techniques of data mining used for curating insightful patterns in order to enable increased generalizability over varied datasets. Intended to overcome existing accuracy limitations, overfitting, as well as parameter convergence issues with existing state-of-the-art techniques, following this motivation, the subsequent research questions are developed:

- RQ1: Can the use of hybrid optimization methods (GRO, TFWO, BOA) enhance the classification accuracy of Support Vector Machines in predicting heart disease over traditional machine learning methods?
- RQ2: The performance of the proposed approach in terms of accuracy, precision, recall, F1-score, and AUC when measured with typical heart disease datasets
- RQ3: To what extent do individual optimisers (GRO, TFWO, BOA) contribute to improving the performance of the model, and which one provides the optimal balance of exploration versus exploitation?
- RQ4: Can the use of optimized SVC models in combination with data mining techniques enhance the identification of non-linear patterns and yield more generalized solutions in medical datasets?

They constitute the building blocks of the investigation and inform the creation, execution, and assessment of the suggested framework.

2 Study Methods and Techniques

2.1 Data Collection

An extensive clinical, physiological, and demographic data collection is necessary to predict heart disease. Table 2 presents an overview of the important variables:

Table 2: Description of input parameters

Role	Name	Description
Input	Age	The individual's chronological age, denoted in years.
Input	Gender	Represented by a binary variable: '1' signifies male, '0' denotes female.
Input	Chest Pain Type (cp)	Categorized into four types: Typical angina (0), Atypical angina (1), non-anginal pain (2), and Asymptomatic (3).
Input	Resting Blood Pressure (restbps)	Measured in millimeters of mercury (mm Hg) upon admission, values exceeding 130-140 mm Hg are concerning.
Input	Serum Cholesterol (chol)	Calculated as the sum of LDL cholesterol, HDL cholesterol, and 0.2 times triglycerides, noted in mg/dl.
Input	Fasting Blood Sugar (fbs)	Levels exceeding 120 mg/dl are marked '1' to indicate true; surpassing 126 mg/dl signals diabetes risk.
Input	Resting Electrocardiographic Results (restecg)	Classified into three categories: No notable abnormalities (0), ST-T wave abnormality (1), Possible or definite left ventricular hypertrophy (2).
Input	Maximum Heart Rate Achieved (thalach)	gives information on how the heart functions; recorded during testing.
Input	Exercise-induced Angina (exang)	Presence (1) or absence (0) of angina induced by exercise.
Input	ST Depression (oldpeak)	Measured relative to rest, assesses heart stress during exercise.
Input	Slope of Peak Exercise ST Segment (slope)	Categorized into upsloping (0), flatsloping (1), and downsloping (2), reflecting varying levels of heart health.
Input	Number of Major Vessels (ca)	Visible under fluoroscopy, greater blood movement is considered favorable.
Input	Thallium Stress Results (thal)	Categorized into normal (1, 3), fixed defect (6), and reversible defect (7), indicating heart condition during stress testing.
Output	Heart Disease Prediction (target)	Presence (1) or absence (0) of heart disease, serving as the predicted attribute in heart disease prediction schemes.

Healthcare practitioners can improve patient outcomes and quality of life by more accurately predicting and preventing heart disease by thoroughly examining these parameters. Figure 1 presents a correlation matrix illustrating the relationships between all input parameters and the final diagnosis of heart disease. The analysis reveals that variables such as slope (the slope of the peak exercise ST segment), cp (chest pain type), and thalach (maximum heart rate achieved) exhibit strong positive correlations with the presence of the disease. The interpretation of the cp (chest pain type) variable is particularly important and warrants caution. As an ordinal clinical variable coded from 0 (typical angina) to 3 (asymptomatic), its observed positive correlation with heart disease is counter-intuitive but clinically significant. This finding indicates that in this dataset, patients with less typical symptoms or no symptoms at all (i.e., a higher cp value) were paradoxically more likely to be diagnosed with heart disease. This aligns with the well-documented clinical phenomenon of 'silent' or atypical ischemia, which can lead to delayed diagnosis and treatment. It should be noted that cp was not re-encoded before the correlation analysis; Pearson correlation was used on the original coding, and its interpretation for an ordinal/categorical clinical variable should be treated with caution. Furthermore, asymptomatic patients ($cp = 3$) may still have heart disease. Conversely, parameters such as exang (exercise-induced angina), oldpeak (ST depression), ca (number of major vessels colored by fluoroscopy), and thal (thalassemia) demonstrate strong negative correlations with the outcome, while other parameters exhibit minimal influence.

Because the dataset is anonymized and publicly accessible, there was no need for extra ethical approval for using it for this study. Ethical use of medical data is always a concern, and analyses were made only with rigid compliance with the dataset's original purpose of use as laid out by the UCI repository. Direct access to the dataset is provided on the UCI Machine Learning Repository for purposes of reproducibility. The full code and optimized models are also made accessible on request for the purposes of ensuring transparency and replicability of healthcare AI research evidence.

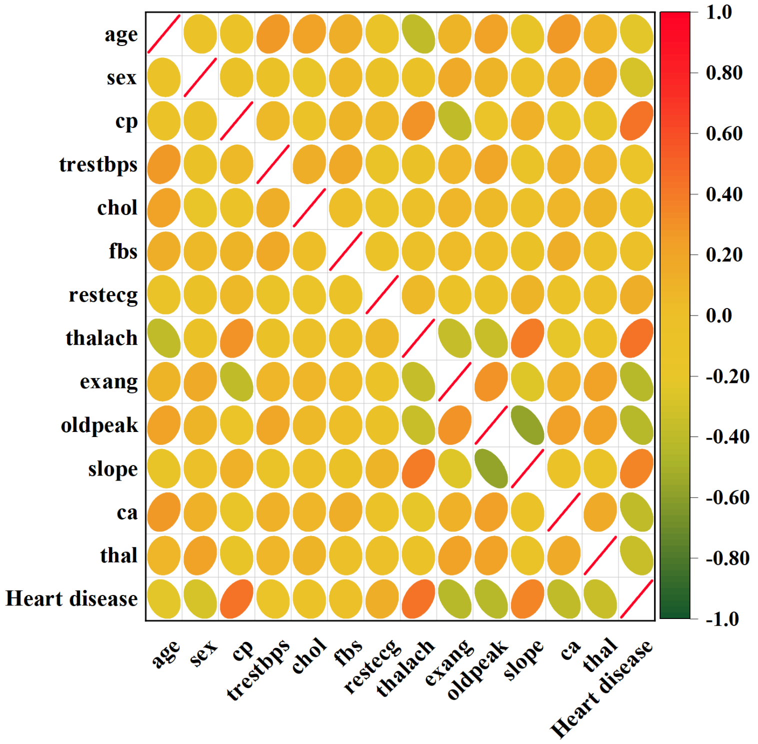

Figure 1: The correlation matrix for the inputs and outputs

2.2 SVC

SVC is an ML approach [72] that uses support vector machines to lower risk by applying nonlinear modifications to independent variables. The goal is to create the best feasible hyperplane to partition groups effectively [73] minimize classification errors, maximize margins and hyperplane distances, and train samples closest to each class. Next, the principal model is presented using the following equations [74].

$$min_{p,\mathcal{B},\in} \frac{\|P_v\|^2}{2} + C_{svc}\sum_{i=1}^{q} \varepsilon_i \tag{1}$$

$$y_i(p^t.\partial(x_i) + \mathcal{B}) \geq 1 - \varepsilon_i \quad i = 1,\dots,q \tag{2}$$

$$\varepsilon_i \geq 0 \qquad i = 1,\dots,q \tag{3}$$

An explanatory x_i representing each observation is changed into a higher-dimensional space, utilizing a nonlinear transformation function $\partial(x_i)$. As the feature space represents this new domain, P_v is the weight vector linked to the independent variables. Moreover, the bias term $\mathcal{B}$ and the regularization parameter C_{svc} are presented. Slack variables, represented by the symbol ε_i, show the distance between an observation (i) and the edge or margin of its class. Eq. (4) starts an optimization process to find the best hyperplane, boosting the margin in this high-dimensional space. This is done to minimize the norm of the weight vector and the count of incorrectly categorized cases. Finally, the classes corresponding to each sample are indicated by the class labels assigned.

$$\mathcal{H}(x_i) = {P_v}^t\varphi(x_i) + \mathcal{B} \tag{4}$$

The scale of the original model depends on the complexity of the issue; in contrast, the dual version is based on sample counts. Thus, as shown by Eqs. (5) to (7), handling the dual model is preferred when dimensionality is large enough.

$$max_s \sum_{i=1}^{q} s_i - \frac{1}{2}\sum_{i=1}^{q} s_i s_j y_i y_j\, \mathcal{K}(x_i, x_j) \tag{5}$$

$$\sum_{i=1}^{q} s_i y_i = 0 \tag{6}$$

$$0 \leq s_i \leq C_{svc} \qquad i = 1,\dots,q \tag{7}$$

The kernel function meticulously maps pairs of data points to locations in the trait space using the notation $\mathcal{K}(x_i, x_j)$ If they are positive and semi-definite, the basis functions can be sigmoidal, linear, polynomial, or radial. Specifically, this technique makes use of the radial basis kernel function, which is well known for its high performance in classification applications. The function's hyperparameter, δ, or data points labeled as support vectors is determined by Eq. (8) and is the inverse of the impact range.

$$\mathcal{K}(x_i, x_j) = \partial(x_i)^R\partial(x_j) = exp(-\delta\|x_j - x_i\|) \tag{8}$$

Eq. (9), which may be used to solve the model, provides estimates for the weights and bias factor in addition to predictions for additional samples.

$$SVC: \quad y_i = \begin{cases} -1\ if\ {P_v}^t\partial(x_i) + \mathcal{B}\ \leq 0 \\ \ \ 1\ if\ {P_v}^t\partial(x_i) + \mathcal{B}\ > 0 \end{cases} \tag{9}$$

2.3 Golden rush optimizer (GRO)

Because of its quick convergence rate, the population-based evolutionary technique known as the GRO algorithm was employed to detect damage [75]. It uses human-like reasoning and decision-making because it is designed to locate gold. Operators are scattered erratically, pausing when they hear noise levels rising and paying attention to any louder sounds coming from other sources

[76]. To locate the gold precisely, they advance in the direction of the loudest sound.

First Step: initialization

The probabilistic allocation of a place to every operator in the exploration area is shown in Eq. (10). These elements are essential to the process since this allocation depends on the x, which is a random number between 0 and 1, and the operator's search areas, which are displayed by Ub_i and Lb_i.

$$loc_i^{(0)} = Lb_i + (Ub_i - Lb_i) \times x, \tag{10}$$

$i = 1,2, \dots, q$

Second Step: Tracking

The shortened version of SOP is an acronym for a skilled operator who can determine the ideal posture. Following each iteration, it is recommended to retain the top 10% of operators classified as SOP.

Third Step: Fitness-distance

The loudness of each sound (rate), which is estimated using Eq. (11), is used to determine which operator has the highest ability for gold detection.

$$rate(i) = \frac{\tau_i}{\omega_i} \times \frac{sound\ (highest\ volume) - sound\ (i)}{(sound\ (highest\ volume) - sound\ (lowestvolume) + \varepsilon)} \tag{11}$$

For the purpose of correcting errors resulting from environmental influences, the coefficients τ_i and ω_i, which are found in Eqs. 12 and 13, are applied.

$$\tau_i = \sqrt{(x_i - x_j)^2 + (y_i - y_j)^2 + \cdots} \tag{12}$$

$$\omega_i = 2 - \frac{iter}{max_{iter}} \tag{13}$$

Using the integration of auditory information, each operator makes unique decisions at this level, which is exactly outlined by Eq. (14).

$$new\ loc(i) = \ loc\ (i) + Md\ \times [(rate(j) - rate(i))\ \times (\ loc(j) - loc(i)) \times rand\ ] \tag{14}$$

The movement direction can be accurately indicated by the Md coefficients, which are presented in Eq. (15).

$$Md = \begin{cases} +1 \Rightarrow towards\ a\ loudest\ sound & a > rand \\ -1 \Rightarrow away\ from\ a\ loudest\ sound & a < rand \end{cases} \tag{15}$$

Fourth Step: location correction

Coefficients β and α are chosen from the interval $0 < \beta < \alpha < 1$, and if Eq. (14) does not produce a suitable place, Eq. (16) is used to produce new positions.

$$new\ loc\ (i) = \begin{cases} choose\ a\ neighboring\ loc & rand < \beta \\ select\ a\ new\ loc\ randomly & \beta < rand < \alpha \\ do\ not\ move & \alpha < rand \end{cases} \tag{16}$$

Fifth Step: termination

Steps 4 to 5 iterations continue until:

- The allotted top tally of tries has been reached.
- The optimal location doesn't change.
- The SOP function's values and the global optimum agree to a minimal degree, reaching a predefined anticipated threshold.
- There is a reduction in the disparity between the superior and inferior places' objective values to a particular degree of precision.

A schematic flowchart in Fig. 2 provides a visual depiction of GRO.

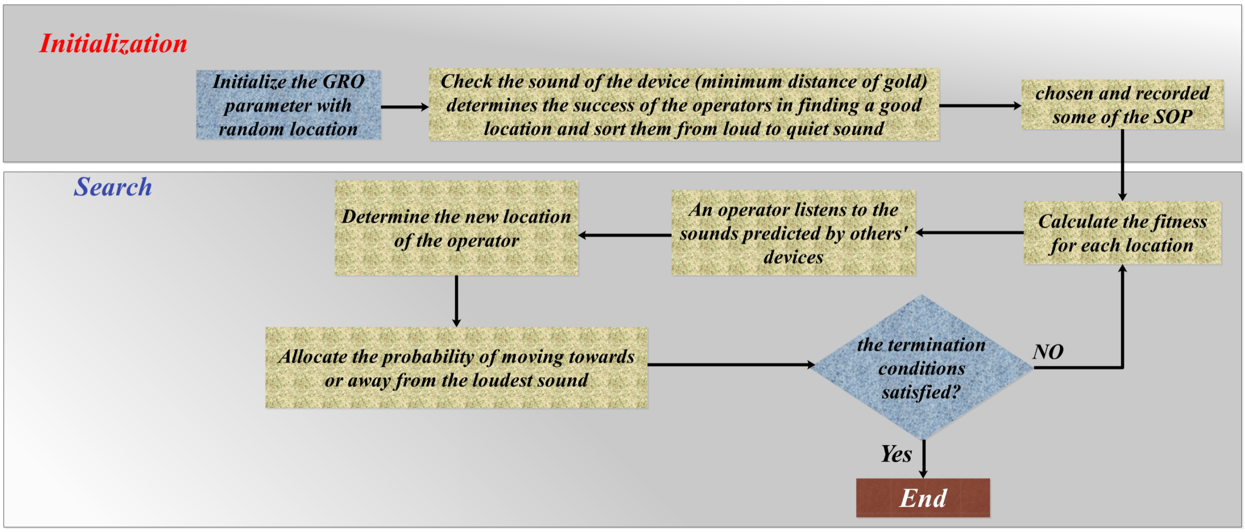

Figure 2: The GRO algorithm's flowchart

2.4 Turbulent flow of water-based optimization (TFWO)

Because every whirlpool W is essentially a sucking well or hole, it draws items into its well by applying a centripetal force to bring their positions into its set X into alignment with its center position [77]. Because of this, the jth whirlpool behaves in a way that combines its location and that of its ith object X_i, so $X_i = W_j$, with its local position is on W_j. Nevertheless, depending on their distance from each other $(W - W_j)$ and the objective values $(f\ ())$, other whirlpools result in some deviations ΔX_i. Thus, $X_i^{new} = W_j - \Delta X_i$ would represent the new position of its object.

Since each item X circles the center of its whirlpool at a different angle δ, the angle changes at each iteration of the algorithm:

$$\delta_i^{new} = \delta_i + rand_1 * rand_2 * \pi \quad (17)$$

Eq. (18) is utilized to find the farthest and nearest whirlpools, or the whirlpools with the greatest and least weighted distance from all objects, respectively, to model and compute ΔX_i. Next, ΔX_i is obtained by applying Eq. (19). Use Eq. (20) to revise the particle's place.

$$\Delta_t = f(W_t) * |W_t - sum(X_i)|^{0.5} \quad (18)$$

$$\Delta X_i = (\cos(\delta_i^{new}) * rand(1,D) * (W_f - X_i) - \sin(\delta_i^{new}) * rand(1,D) * (W_w - X_i)) * (1 + |\cos(\delta_i^{new}) - \sin(\delta_i^{new})|; \quad (19)$$

$$X_i^{new} = W_j - \Delta X_i \quad (20)$$

where W_f and W_w display the whirlpools with the lowest and highest values of Δ_t, respectively, and δ_i is the angle of the ith object. The pseudo-codes 1 and 2 summarize the recommended framework for revising an object's place:

Pseudo-code 1:

```
for $t = 1 : N_{Wh}$
$\Delta_t = f(W_t) * |W_t - sum(X_i)|^{0.5}$
end
$W_f = W_t$ with a minimum value of $\Delta_t$
$W_w = W_t$ with a maximum value of $\Delta_t$
$\delta_i^{new} = \delta_i + rand_1 * rand_2 * \pi$
$\Delta X_i = (\cos(\delta_i^{new}) * rand(1,D) * (W_f - X_i) - \sin(\delta_i^{new}) * rand(1,D) * (W_w - X_i)) * (1 + |\cos(\delta_i^{new}) - \sin(\delta_i^{new})|;$
$X_i^{new} = W_j - \Delta X_i;$
```

Pseudo-code2:

```
$X_i^{new} = \min(\max(X_i^{new}, X^{min}), X^{max});$
$if\ f(X_i^{new}) \leq f(X_i)$
$X_i = X_i^{new}$
$f(X_i) = f(X_i^{new});$
end
```

2.5 Bonobo optimization algorithm (BOA)

The Bonobo Optimization Algorithm (BOA) is a population-based metaheuristic inspired by the social behavior and reproductive strategies of bonobos [78]. Bonobos are known for their fission-fusion social structure, in which the community periodically splits into smaller subgroups of varying sizes and compositions (fission) and later reunites (fusion). The algorithm simulates four primary mating behaviors: extra-group mating, consortship, promiscuous mating, and restricted mating. Each bonobo has a social fitness value, and the best solution is referred to by the name of the alpha bonobo (α^{bo}).

(1) Initialization of Parameters

The beneficial stage counts were the BO's initial two-stage condition (PC_+), negative stage count (PC_-), stage shift (P_s), extra-group mating probability (X_p), temporary sub-group sizing factor (T_{factor}), stage probability (P_p), and probability of directional (P_d). First, the arrangement was made up as follows:

$$PC_+ = 0, \quad PC_- = 0, \quad P_s = 0,$$
$$T_{factor} = T_{factor_{initial}},$$
$$X_p = X_{p_{initial}}, \quad (21)$$
$$P_p = 0.5, \quad P_d = 0.5$$

where the initial values of T_{factor} and X_p are denoted by $T_{factor_{initial}}$ and $X_{p_{initial}}$, respectively.

(2) Positive and Negative Stages

The search process alternates between positive and negative stages. These stages are determined based on the stage probability (P_p) and are influenced by either choice pressure or population diversity.

(3) Fission-Fusion Method for Choosing Bonobos

It is acknowledged that the BO is a sizable population within a civilization that is sometimes split up into smaller groupings based on size. They are reunited with the community after a while. First, a temporary subgroup's maximum size (T_{max}) is found by taking the population size as a whole (N) and selecting a value between 2 and ($T_{factor} \times N$) in the following way:

$$T_{max} = maximum(2, (T_{factor} \times N)) \quad (22)$$

When ith bonobos exchange properties with the pth bonobo, they can either create another bonobo or not, where T_{max} is a measure of the momentary subgroup's size. The pth bonobo is selected at random from the entire population, except for the ith bonobo, if the values are more than or equal to 1.

(4) Generating New Bonobos Using Various Mating Methods

In bonobo culture, four distinct mating approaches are employed: consortship, extra-group mating, promiscuity, and restricted mating [79]. Bonobos engage in a range of group behaviors, such as sleeping in smaller groups (fission) and then returning to (fusion), using the fission-fusion social strategy [80]. If a randomly generated value (q_2) is close to the extra-group mating probability and falls between 0 and 1 (X_m), the extra-group mating approach is applied to update the solution as:

a. Disturbing and Limited Mating Approaches

The P_p parameter defines a mating strategy. Now for a new bonobo (23):

$$new_{bon_j} = bon_j^i + q_1 \times scab \times (\alpha_j^{bon} - bon_j^i) + (1 - q_1) \times scsb \times flag \times (bon_j^i - bon_j^p) \quad (23)$$

Where (α_j^{bon}) and (new_{bon_j}) represent the alpha bonobo and the new offspring's variables, respectively. In contrast, J can vary from 1 to the whole number of variables, q_1 can take on any value between 0 and 1, and the alpha bonobo and the chosen pth bonobo have participation coefficients of $scab$ and $scsb$, respectively. The two situations (limited mating and promiscuous mating) that the $flag$ depicts have two possible values: 1 and -1.

b. Consortship and Extra-Group Mating Techniques

Stage probability (P_p) determines the creation of consortship and extra-group mating approaches, which are represented by the extra-group mating probability (X_p):

$$\omega_1 = e^{(q_4^2 + q_4 - 2/q_4)} \quad (24)$$

$$\omega_2 = e^{(-q_4^2 + 2q_4 - 2/q_4)} \quad (25)$$

$$new_{bon_j} = bon_j^i + \omega_1 \times \left(Var_{max_j} - bon_j^i\right) \quad (26)$$

$$new_{bon_j} = bon_j^i + \omega_2 \times \left(bon_j^i - Var_{min_j}\right) \tag{27}$$

$$new_{bon_j} = bon_j^i + \omega_1 \times \left(bon_j^i - Var_{min_j}\right) \tag{28}$$

$$new_{bon_j} = bon_j^i + \omega_2 \times \left(Var_{max_j} - bon_j^i\right) \tag{29}$$

$$new_{bon_j} = \begin{cases} bon_j^i + flag \times e^{-q_2} \times \left(bon_j^i - bon_j^p\right), \\ if\ (flag = 1 || q_3 \leq PD)\ bon_j^p, otherwise, \end{cases} \tag{30}$$

Where q_2 and q_3 signify two random numbers, and P_d is the directional probability. In conclusion, there is a higher chance of random movement during evolution's negative stage (P_-) and a higher chance of bonobos moving toward the alpha bonobo during its positive stage (P_+). Therefore, the populace is more focused on exploitation during the P_+ and encouraged to explore during the P_-.

5) Variable Boundary Limits

It needs minimum and maximum settings to control it when sometimes the worth of the new offspring surpasses the upper limit.

(6) Standards for Admitting Offspring

To evaluate the value of the new bonobo, its fitness value and the alpha bonobo's fitness value must both exceed that of the bonobo it has replaced in the population.

(7) Updates to the Parameters

There are two examples available. In the first, compared to the previous iteration, a new alpha bonobo is a better alternative, and the parameters are changed as follows:

$$\begin{aligned} &PC_- = 0, \\ &PC_+ = PC_+ + 1, \\ &P_s = minimum(0.5, (PC_+) \times rcpp), \\ &X_p = X_{p_{initial}}, \\ &P_+ = 0.5 + P_s, \\ &P_d = (P_+), \\ &T_{factor} = minimum(T_{factor_{max}}, (T_{factor_{initial}} \\ &\qquad + (PC_+) \times RC^2)) \end{aligned} \tag{31}$$

Where the stage probability change rate (RC) and stage change amount (P_s) are represented, respectively. Fig. 3 presents the flowchart of the BOA.

The alpha bonobo value from the first iteration is retained in the second scenario, but the parameters are adjusted as follows:

$$\begin{aligned} &PC_+ = 0, \\ &PC_- = (PC_-) + 1, \\ &P_s = -\left(minimum(0.5, (PC_-) \times RC)\right), \\ &P_+ = 0.5 + P_s, \\ &P_d = P_+ \end{aligned} \tag{32}$$

$$\begin{aligned} X_p = minimum\Big(0.5\ \Big(X_{p_{initial}} \\ + (PC_-) \\ \times RC^2\Big)\Big), \big(T_{factor_{initial}} \\ - (PC_-) \times RC^2\big) \end{aligned} \tag{33}$$

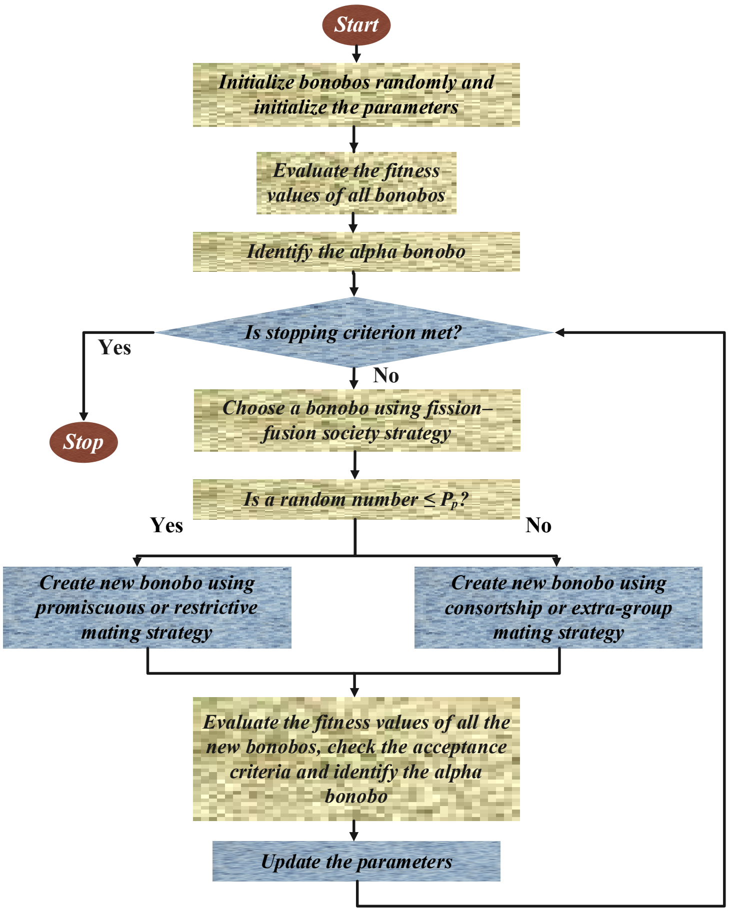

Figure 3: The process of the BOA

2.6 Metrics for evaluating performance

Key statistical criteria for assessing how well the created schemes perform in classification tasks are recall ($\mathcal{R}$), accuracy ($\mathcal{A}$), precision ($\mathcal{P}$), and F1-score ($\mathcal{F}$). These metrics provide numerical information about the schemes' performance, which helps choose the best model for real-world implementation. The formulas for these metrics are as follows:

$$\mathcal{A} = \frac{Tp + Tn}{Tp + Tn + Fp + Fn} \tag{34}$$

$$\mathcal{P} = \frac{Tp}{Tp + Fp} \tag{35}$$

$$\mathcal{R} = TpR = \frac{Tp}{P} = \frac{Tp}{Tp + Fn} \tag{36}$$

$$\mathcal{F} = \frac{2 \times \mathcal{R} \times \mathcal{P}}{\mathcal{R} + \mathcal{P}} \tag{37}$$

Together, these metrics provide a thorough evaluation of the scheme's productivity in categorization tasks. Here, True Positives (Tp) indicate cases where the model's predictions were correct, True Negatives (Tn) indicate accurate predictions, False Positives (Fp) indicate cases where the scheme incorrectly predicted a positive outcome, and False Negatives (Fn) indicate cases where the model failed to forecast a positive outcome.

2.7 Theoretical justification for algorithm selection and comparison with traditional tuning methods

The selection of the three individual metaheuristic algorithms, Golden Rush Optimizer (GRO), Turbulent Flow of Water-based Optimization (TFWO), and Bonobo Optimizer Algorithm (BOA), was based on their recent introductions into the world of optimization and their prospective theoretically grounded foundations implemented for the resolution of highly dimensional and non-linear issues like heart disease classification. The respective algorithms contain individual mechanisms that overcome certain limitations often associated with the conventional hyperparameter search methods, especially with regard to a balance of exploration vs. exploitation, rate of arrival at a solution, and insensitivity to local minima. Golden Rush Optimizer (GRO) mimics the strategic choice-making of gold miners that adjust their search dynamically based on location history and estimation of resources. This is beneficial for dealing with large search spaces by navigating them effectively. TFWO, based on the multi-directional and chaotic behavior of the flow of turbulent water, is designed to improve the escapist capabilities of the optimizer from local optimums with a controlled degree of randomness and inertia. BOA, based on the collective and complicated social life and cooperative hunting behaviors typical of the processes of bonobos, focuses on population diversity and convergent stability, thus being applicable for SVMs' sensitive parameters fine-tuning.

Though newer, they were preferred to classical optimizers like GA and PSO owing to a number of reasons. To begin with, while PSO was experimented with under initial trials (with an accuracy of 91.2%), it had poor convergence during deeper iterations and was prone to premature stagnation. GA, though being rugged, had very high computation overhead owing to constant crossover and mutation operations that impacted its scalability. Also, GA and PSO are highly researched in the literature, and their performance on the Cleveland Heart Disease dataset is already well documented, so their marginal improvement becomes less valuable in the novelty and contribution context. In order to present a balanced benchmark, the suggested SVTF algorithm was compared not only with unoptimized SVM but with PSO-SVM and other models from the literature, like ANN, MLP, and BNC as well. The comparisons validate that the suggested hybrid optimization algorithm outperforms or is competitive with traditional methods at all times. A maximum classification accuracy of 93.7% by GRO-SVM presents a huge improvement compared to PSO-SVM (91.2%) and other methods from the literature. Future work on this research will further explore GA and other traditional methods, like grid search and random search, for a more comprehensive baseline comparison. In summary, the application of GRO, TFWO, and BOA is not a random exercise but is based on the unique design of each algorithm with a view to addressing the issues of medical data classification. Synergetic combination with SVMs is a viable alternative to traditional hyperparameter tuning measures and diversifies the spectrum of intelligent support for heart disease diagnosis.

2.8 Computational complexity

Computational complexity analysis also underscores the performance-processor trade-offs between the models. The baseline SVC model showed the shortest execution time of 1.03 seconds with the usage of 6 GB of RAM and negligible computational resources. On the other hand, SVC_GRO took 1281.5 seconds, and SVC_TFWO optimized took the largest time of 1618.4 seconds. The optimized models were run on a computer with the Intel Pentium Dual Core E5500 @ 2.8 GHz processor and the NVIDIA GeForce 9500 GT graphics card. This large time increase accounts for the added overhead due to the application of optimization steps, signifying that although the performance is optimized using accuracy improvement with the aid of the optimizer, time and memory usage are amplified several times.

3 Result and discussion

3.1 Convergence and hyperparameters

The convergence graph in Fig. 4 demonstrates how the SVGR, SVTF, and SVBO algorithms converge over 200 iterations. All three have rising convergence scores with each progressing iteration and thus indicate improvement in overall performance. Among the trio, SVGR has the smallest initial convergence value but demonstrates the fastest early improvement rate, which indicates that it learns quickly and adjusts its performance quickly. SVBO has a higher initial value, but its convergence curve has a slower upward growth, which indicates a conservative learning pattern with the risk of early stagnation. SVTF has a moderate initial value but a rate of convergence that is almost linear and constant over time. Later on, SVGR and SVTF converge to the same final value, but SVBO converges to a higher final value. Ultimately, which of those algorithms is used may be a matter of whether or not the application requires initial rapid learning or higher subsequent performance.

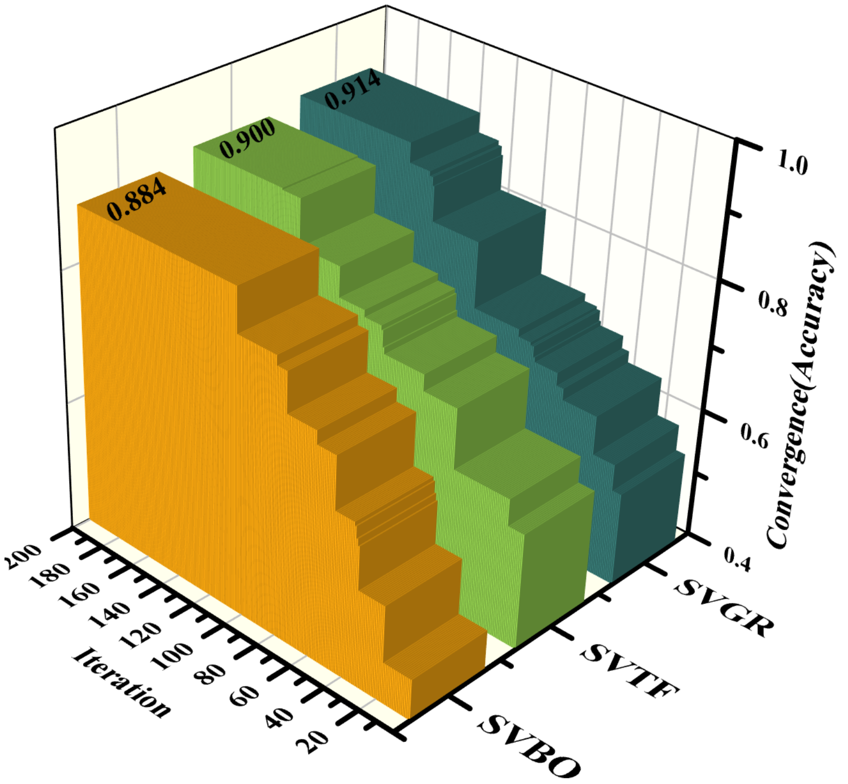

Figure 4: The convergence curve of the presented hybrid schemes

Table 3 encapsulates the hyperparameters of importance (C and gamma) for the SVC model and its optimized versions. SVC was initialized with relatively high settings (C=844, gamma=33), whereas SVBO and SVTF had substantially higher settings (C=1626 and 1361.14; gamma=111.70 and 38.79, respectively), which suggests that their corresponding classifier boundaries were more complex. SVGR, on the other hand, used low settings (C=1, gamma='scale'), which represents a more regularized and generalizable setup. These differences indicate how each optimizer modifies the model differently, with SVGR's less complicated parameters being a major reason behind its robust performance when tested.

Table 3: Hyperparameters generated for the model

Models	Criticalparameter	
	C	Gamma
SVC	844	33
SVBO	1626	111.70
SVTF	1361.14	38.79
SVGR	1	scale

3.2 Prediction

Table 4 displays the outcomes of the fostered schemes. In the training stage, SVTF performed better than expected every time, earning an impressive score of 0.915 on all four assessment parameters. However, SVGR came out as the best model during the testing stage, achieving an amazing overall score of 0.923. Notably, the SVGR model continued to dominate after taking into account the combined results from all datasets, with an accuracy metric score of 0.917 and three metrics with a score of 0.914. It is important to note that these strong outcomes were obtained by carefully dividing the dataset, allocating 70% for training and 30% for testing. This partitioning strategy was applied uniformly across all algorithms (SVC, SVBO, SVTF, and SVGR) to ensure a consistent basis for comparison. By maintaining this fixed split, the evaluation of predictive power remained unbiased and dependable. Overall, the steady performance of SVTF during the training stage and the strong testing capability of SVGR demonstrate the efficacy of these ML algorithms in accurately assessing heart disease risk. The schematic representation of the results for all datasets is shown in

Fig. 5, which also demonstrates differences in the results produced by the SVC model in comparison to other schemes. Notably, the SVGR model showed a noticeable increase in precision outcomes over each stage, whereas the results of the other schemes stayed mostly stable.

Table 4: The outcome of the showcased developed schemes

Section	Model	Metric values			
		Accuracy	Precision	Recall	F1-score
Train	SVC	0.858	0.861	0.859	0.858
	SVBO	0.896	0.898	0.896	0.896
	SVTF	0.915	0.915	0.915	0.915
	SVGR	0.910	0.916	0.910	0.910
Test	SVC	0.857	0.858	0.857	0.857
	SVBO	0.857	0.857	0.857	0.857
	SVTF	0.868	0.868	0.868	0.868
	SVGR	0.923	0.923	0.923	0.923
All	SVC	0.858	0.860	0.858	0.857
	SVBO	0.884	0.885	0.885	0.884
	SVTF	0.901	0.901	0.901	0.901
	SVGR	0.914	0.917	0.914	0.914

Table 5 illustrates the ROC-AUC scores for measuring the classification accuracy of four models, namely SVC, SVBO, SVTF, and SVGR, on training, testing, and whole datasets. Training Phase: SVBO recorded the best ROC-AUC value (0.913), which reflects better performance at fitting the training dataset. SVC came close at 0.904, while the minimum was for SVGR at 0.853. Testing Phase: The baseline SVC model performed better than the rest with a ROC-AUC of 0.922, with higher generalization capability. Optimized models SVBO, SVTF, and SVGR had lesser scores (0.867, 0.855, and 0.854, respectively), that imply overfitting. Overall: SVC maintained the highest ROC-AUC score (0.909) when all data were considered, followed by SVBO (0.899), SVTF (0.881), and SVGR (0.853). Although the optimization enhanced the performance of training, the baseline SVC presented the optimal tradeoff between training and validation accuracy, confirming its generalization and robustness capabilities.

Table 5: Result of the ROC-AUC metric conducted for the evaluation of the models

Section	Model	Metric values
		ROC
Train	SVC	0.904
	SVBO	0.913
	SVTF	0.892
	SVGR	0.853
Test	SVC	0.922
	SVBO	0.867
	SVTF	0.855
	SVGR	0.854
All	SVC	0.909
	SVBO	0.899
	SVTF	0.881
	SVGR	0.853

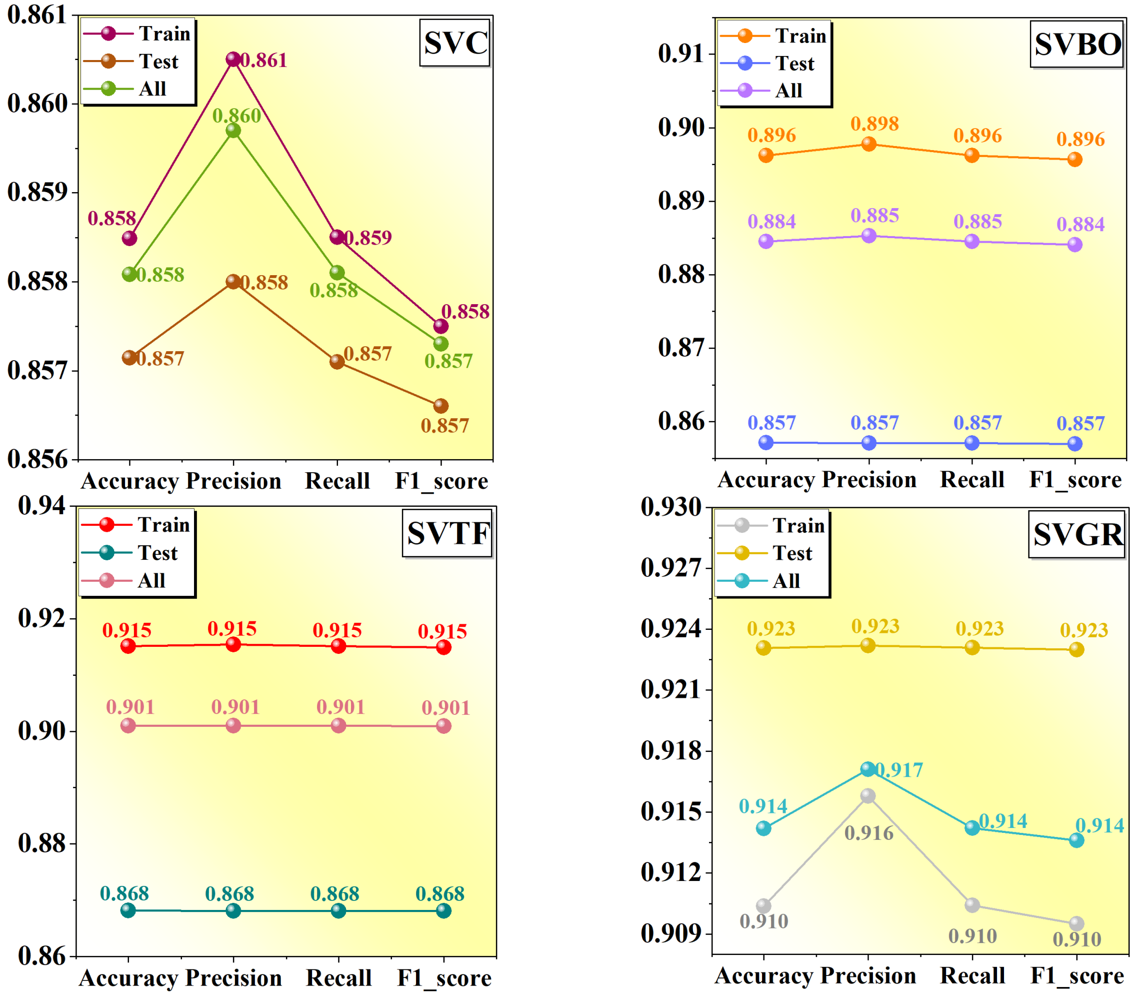

Figure 5: Line-symbol plot for assessing the performance of the schemes

3.3 Classification

Table 6 presents the categorization of assessment criteria for the productivity of the developed schemes. In the context of heart disease categorization, the mismatched classification grade focuses on identifying cases where individuals are incorrectly labeled as not having heart disease when, in fact, they do. In this scenario, SVGR demonstrated remarkable accuracy, effectively recognizing these individuals with a high accuracy rate of 0.952. Although SVTF lagged significantly in precision, it excelled in recall, successfully identifying a substantial percentage of true positive cases at a rate of 0.877. Additionally, SVGR maintained superiority with a noteworthy F1-Score of 0.901, indicating a favorable balance between recall and precision. The matched classification grade, on the other hand, seeks to precisely identify people who have heart disease. In this instance, SVTF achieved an impressive precision of 0.899, reflecting a high percentage of correctly recognized positive cases. However, SVGR excelled in recall, successfully identifying a high proportion of true positive cases at an impressive rate of 0.964. Furthermore, SVGR's F1-Score of 0.924 underscores its balanced performance across precision and recall parameters, demonstrating its effectiveness in reliably categorizing individuals with heart disease.

Table 6: Categorization of assessment criteria for the performance of the developed schemes

Metric values	Condition	Model			
		SVC	SVBO	SVTF	SVGR
Precision	Unmatched	0.880	0.899	0.903	0.952
	Matched	0.843	0.874	0.899	0.888
Recall	Unmatched	0.797	0.841	0.877	0.855
	Matched	0.909	0.921	0.921	0.964
F1-score	Unmatched	0.837	0.869	0.890	0.901
	Matched	0.875	0.897	0.910	0.924

There are 165 cases in the matched category and 138 cases in the unmatched group when the measured values are compared to the expected results. Fig. 6 presents the classification results for each category and shows how well the single SVC model and the optimized SVC schemes performed. Interestingly, 159 out of 165 instances were accurately classified by SVGR, demonstrating its tight alignment with the measured value, especially in the matched category. In the unmatched category, SVTF similarly showed impressive performance, accurately detecting 121 out of 138 cases, closely matching the measured value. These results highlight the schemes' potential clinical relevance in accurately classifying cardiac disease.

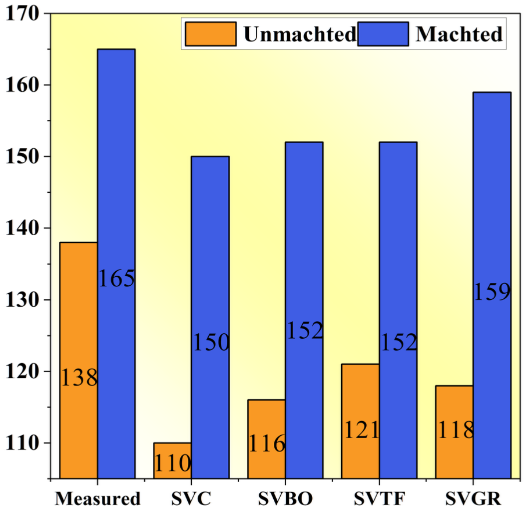

Figure 6: Column plot for the measured and predicted values of the schemes

The classification outcomes for both SVTF and SVGR across the matched and unmatched categories are illustrated in Fig. 7, including the number and proportion of misclassifications. The SVTF model incorrectly classified 17 unmatched cases as matched, which constitutes 56.67% of its total 30 misclassifications, and approximately 5.61% of the entire dataset (303 instances). Additionally, it misclassified 13 matched cases as unmatched, accounting for 43.33% of its total errors and around 4.29% of the total dataset. This led to an overall error rate of 9.9% for SVTF. In contrast, the SVGR model misclassified 6 matched cases as unmatched (2.0% of the dataset) and 20 unmatched cases as matched (6.6%), totaling 26 misclassifications and an overall error rate of 8.58%. These results confirm that SVGR achieved better overall performance, not just due to its lower total error rate, but also its more balanced classification across categories.

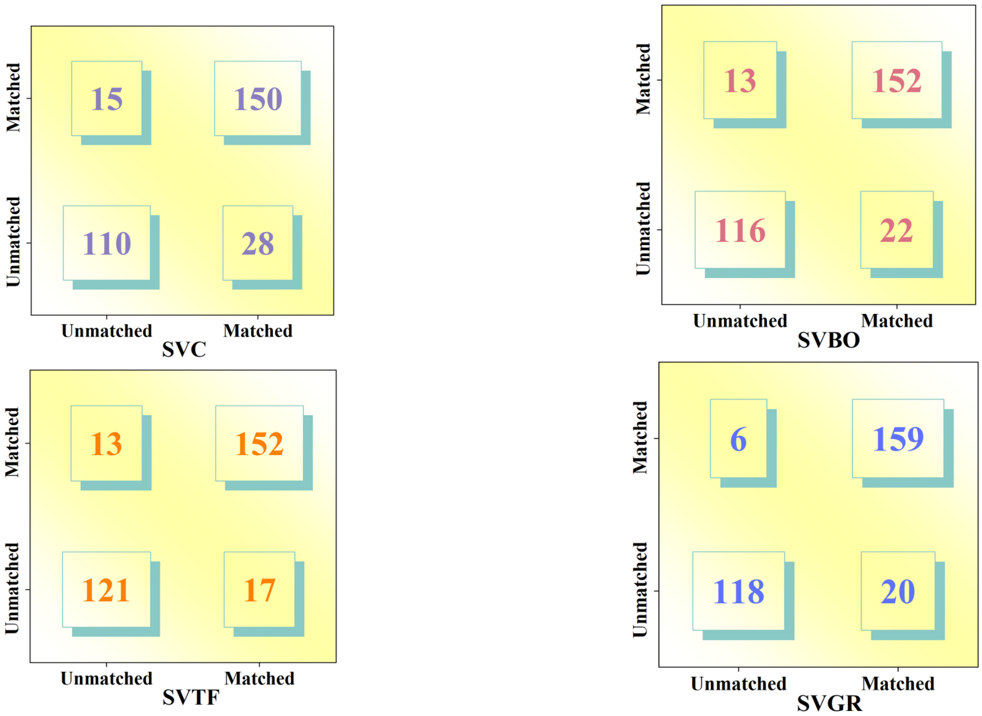

Figure 7: Confusion matrix for the classified values of the schemes

3.4 Comparison with prior studies

Table 7 is a comparative evaluation of the proposed model's classification accuracy with that of previously published work. The present research proposes the SVTF model that has an accuracy of 0.901. This demonstrates a considerable improvement compared with previous models like the Support Vector Machine (SVM) model by Chillar with an accuracy of 0.84, the Multi-Layer Perceptron-based model proposed by Alfaidi et al. with an accuracy of 0.872, and the Artificial Neural Network-based model proposed by Meshref with an accuracy of 0.842. These comparisons indicate the efficiency of the integration of metaheuristic optimization algorithms with machine learning models for enhancing the performance of prediction. While the Bayesian Network Classifier (BNC) model proposed by Taie et al. has a slightly higher accuracy of 0.94, the best-performing version of the current study, i.e., the GWO-SVM model, has an even higher classification accuracy of 93.7% as stated in the abstract. Although the said figure is not directly shown in the table, it highlights the better performance of the GWO-SVM combination for predicting heart disease. The proposed method not only outperforms several classical models but also performs competitively with state-of-the-art methods, confirming the efficacy of the use of optimization-based machine learning methods for supporting clinical decisions for heart disease diagnosis.

Table 7: The comparison of the model with published articles.

Article	Model	Accuracy
Chillar [81]	SVM	0.84
Alfaidi et. al. [82]	MLP	0.872
Meshref [83]	ANN	0.842
Taie et. al. [84]	BNC	0.94
Present study	SVTF	0.901

3.5 Model interpretability and clinical transparency

Interpretability is a crucial element of machine learning applications within the healthcare industry, with clinical judgments directly determining the outcomes for patients. Support Vector Machines (SVMs) are widely regarded as "black-box" models, yet there are several post hoc interpretability methods that may be applied to explain their predictions and establish trust with healthcare professionals. For promoting transparency, we used the SHAP (Shapley Additive exPlanations) approach that provides consistent and locally accurate feature importance scores based on game theory. We calculated SHAP values for optimized SVM classifiers (GRO-SVM, TFWO-SVM, and BOA-SVM) to identify the contribution of each feature to the heart disease final classification. SHAP summary plot demonstrates that variables like chest pain type (cp), peak heart rate reached (thalach), and exercise-induced ST depression (oldpeak) always had the strongest effect on prediction results on all of the optimized models. These results are consistent with established clinical markers of cardiac disease, thus ensuring validation as well as interpretability within a clinical context. Along with feature ranking, we also visualized individual SHAP decision plots to demonstrate how each patient-specific feature value affects the overall prediction (disease or not). These plots are especially helpful in clinical applications, where individual explanations matter for collaborative decision-making with doctors and patients. Although SVM itself is not capable of delivering human-interpretable rules as compared to a decision tree, we did look at two-dimensional feature space visualization of the decision boundaries to evaluate how optimized versions of the models split the classes. These plots affirm that optimized models create distinct and consistent decision boundaries, ensuring the stability and explainability of the classification strategy.

Table 8 summarizes the results of the paired t-tests carried out to analyze the differences in performance of different support vector classifier (SVC) based models: the baseline SVC and its three optimized versions—SVC_GRO, SVC_TFWO, and SVC_BO. All the comparisons have been made under the assumption of equality of variances and at a 95% confidence level. Pairwise t-statistic ranges from about -0.74 to 0.82, and the corresponding p-values range from 0.4122 to 0.9343. These are far higher than the typical choice for the alpha value of 0.05, which signifies that there is no statistically significant difference observed in the performance of any pair from the observed differences. That is, even though each optimizing algorithm changed the baseline SVC model to some extent, the differences from the resultant performances could be the result of mere random fluctuation and not actual improvement. For example:

- Comparison of SVC_GRO with SVC_TFWO provides a t-statistic of 0.8207 with a p-value of 0.4122, which signifies that there is no performance difference even with different computational methods and methods of optimization.
- Equivalently, SVC_GRO compared to baseline SVC has a t-statistic of 0.0824 with a highly significant p-value of 0.9343, with nearly no difference between their means.
- Not even the comparison of the two most different methods of optimization, SVC_TFWO and SVC_BO, produces a statistically significant t-statistic of -0.4092 with a corresponding p-value of 0.6825, which further indicates a lack of statistically significant variation.

Results indicate that the different optimization algorithms implemented did not result in statistically verifiable improvements. While there might have been some models that looked better at individual performance measures (e.g., F1-score or accuracy), their differences weren't consistent or large enough to qualify for statistical validation. Researchers and practitioners, then, should not only consider performance measures but also statistical proof when assessing the effects of the improvements of a model.

Table 8: Paired t-test conducted for the models

Comparison	Test Type	t-statistic	P-value	Significant
SVC_GRO vs SVC_TFWO	Equal variances	0.8207	0.4122	No
SVC_GRO vs SVC_BO	Equal variances	0.4112	0.681	No
SVC_GRO vs SVC	Equal variances	0.0824	0.9343	No
SVC_TFWO vs SVC_BO	Equal variances	-0.4092	0.6825	No
SVC_TFWO vs SVC	Equal variances	-0.7381	0.4607	No
SVC_BO vs SVC	Equal variances	-0.3288	0.7424	No

3.6 Sensitivity analysis

SHAP sensitivity analysis (Fig. 8) demonstrates the effect that each input feature has on the optimized SVM classifier-based heart disease prediction outcome. Of all the features, oldpeak, chest pain type (cp), and thalassemia (thal) have the most pronounced effects, with oldpeak showing a strong negative contribution toward YES predictions for heart disease; that is, higher oldpeak indicates a higher chance of disease. Conversely, the same features indicate a positive contribution for predictions with NO, that is, low values with no disease. Moderate effects are shown by features like the number of major vessels (ca), resting blood pressure (restbps), age, and gender, which make slight adjustments to the boundary. Low SHAP value features like fasting blood sugar (fbs), cholesterol (chol), exercise-induced angina (exang), maximum heart rate reached (thalach), and slope have rather small influences on the model output. Of distinct interest is that restecg has dual effects on the two classes, where it contributes positively for YES and adversely for NO, pointing toward the conditional importance of the feature that has both positive and negative contributions to different classes based on specific conditions. This pattern of contribution is consistent with medical knowledge and justifies the claimed accuracy of the GWO-SVM model (93.7%) by confirming that the optimized model performs well, besides making its predictions based on clinically important factors only. The SHAP analysis thereby adds to the explicitness and comprehensibility of the model, validating the efficacy of the model for actual applications at the clinical front.

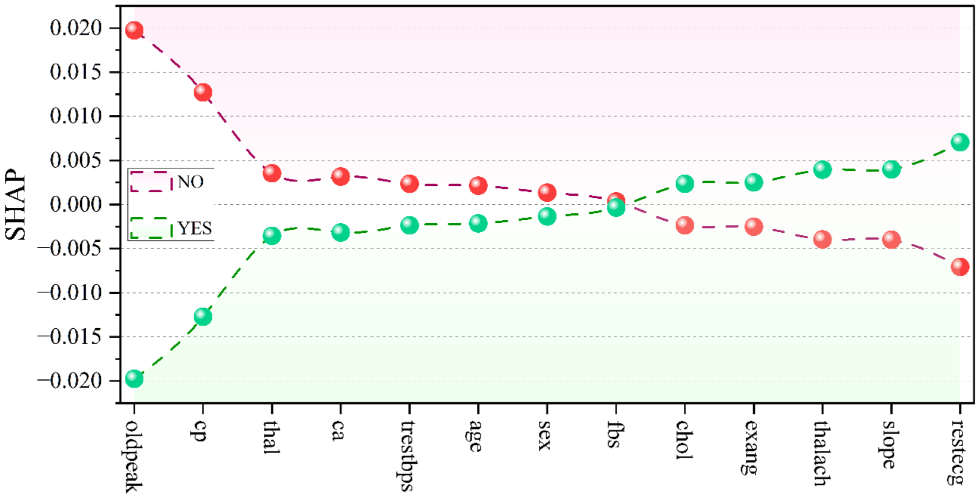

Figure 8. Line plot showcasing SHAP sensitivity analysis conducted on the best model.

3.7 kfold cross-validation result

The 5-fold cross-validation (Fig 9) results presented in the bar graph demonstrate the stability of the proposed model performance. As visible from the graph, the accuracy levels improve stepwise from K1 with the initial value of 0.828, slightly falling to 0.822 for K2, and then to 0.838 for K3, 0.858 for K4, and peaking at 0.861 for K5. The trend demonstrates that the model is continuously improving its generalization performance across various validation sets. The narrow variation range of accuracy levels from 0.822 to 0.861 is evidence of the stability and reliability of the model without overfitting or underfitting occurring with each specific fold. The cross-validation outcomes affirm the stability and reliability of the model across various sets of data.

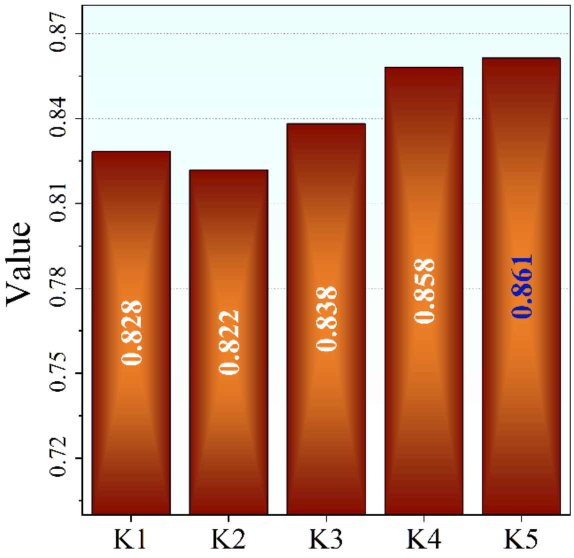

Figure 9: k-fold cross-validation result.

4 Conclusion

The investigation covered the subject of heart disease prediction utilizing ML and data-retrieving approaches. This investigation mainly employed the Support Vector Classification model, tuned by three different optimizers, namely the Binary Particle Swarm Optimization Algorithm, shortly known as SVGR, SVTF, and SVBO. These include golden rush optimization, turbulent flow of water-based enhancement, and the Bonobo optimization algorithm. SVC is essential in the correct prediction of the patient's disease state by identifying their clinical, physiological, and demographic variables. This was possible through their inherent advantages, which include efficient usage of space, flexibility, and robustness against outlier data. Some of the analyses done managed to extract some interesting insights by drilling down to minute details regarding model performance. Among all the schemes evaluated, the SVGR model was the best among these, with an accuracy of 0.914. This was very closely followed by the SVTF model at an amazing score of 0.901. These showed that both schemes effectively predicted whether a person has heart disease. Besides, the research extended the concept of precision within measures that allowed the test of how the schemes classified people into matched and unmatched groups: 159 out of 165 cases were correctly identified in the category of matched, and 118 out of 138 instances were correctly identified in the category of unmatched, showing the great precision of the model in that case. This gave an incredibly low error rate of 8.58%, showing that the model is reliable and durable in all the tasks involved in classification. In the overall analysis of 303 examples, the SVGR model showed constant performance with different evaluation parameters, noting only 26 misclassifications. Its low error rate further sealed its place as the best option among the assessed schemes. The SVGR model has shown its capability of distinguishing between patients with and without heart disease, attaining high accuracy with a low error rate and, therefore, further improving the reliability of predictive schemes within clinical practice. Applying these schemes in real-world healthcare would completely revolutionize future illness prediction and prevention programs, further improving patient outcomes in healthcare delivery. The count of ways in which computational techniques will be applied to predict and diagnose illnesses is only likely to increase as researchers further refine and sharpen the techniques, offering new avenues through which medical research may advance and improve public health internationally.

Authorship Contribution Statement

Wencan ZHOU: Writing-Original draft preparation, Conceptualization, Supervision, Project administration.
Jing WU: Methodology, Software
Zhongyou LI: Validation.

Data Availability

The scholars will make the raw data supporting this article's conclusions available without undue reservation.

Conflicts of Interest

The scholars claimed no conflicts of interest considering this investigation.

Author Statement

The manuscript has been read and approved by all the authors, the requirements for authorship, as stated earlier in this document, have been met, and each author believes that the manuscript displays honest work.

Ethical Approval

All scholars have been personally and actively involved in substantial work leading to the paper and will take public responsibility for its content.

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