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OPTIMIZED CORONARY ARTERY DISEASE PROGNOSIS USING ARTIFICIAL BEE COLONY FEATURE SELECTION AND NAIVE BAYES CLASSIFICATION

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Abstract

Coronary artery disease poses a critical health challenge requiring accurate and timely diagnosis. According to the World Health Organization (WHO), approximately 18 million deaths occur yearly worldwide due to heart or cardiovascular disease. This research introduces an optimized classification framework that integrates Artificial Bee Colony (ABC) algorithm with Naive Bayes (NB) to strengthen prediction performance. The working mechanism begins with feature extraction from a benchmark coronary dataset, where ABC acts as a bio-inspired swarm intelligence method to identify the most relevant clinical attributes by mimicking the intelligent foraging behavior of bees. By eradicate redundant and noisy features, ABC enhances the learning environment for the Naive Bayes classifier. The model's simplicity, interpretability, and high predictive value make it suitable for integration into clinical workflows. Its low computational complexity enables deployment on embedded medical systems. This framework promotes scalable, cost-effective, and accurate cardiac risk prediction. Future advancements will involve real-time prediction support, dynamic retraining with streaming patient data, and expansion to multi-modal datasets for comprehensive cardiovascular profiling across diverse populations and clinical scenarios.

Keywords: Coronary Artery Disease, Artificial Bee Colony, Naive Bayes, Feature Selection Medical Diagnosis, Swarm Intelligence.

1. INTRODUCTION

Coronary artery disease (CAD) is a serious cardiovascular condition due to the narrowing or blockage of coronary arteries, reducing oxygen supply to the heart. As a type of heart disease, CAD significantly contributes to morbidity and mortality worldwide [1]. The gradual buildup of plaque in arteries restricts blood flow, leading to complications such as chest pain, heart attacks, and heart failure. Several factors contribute to disease progression, including lifestyle choices, genetics, and metabolic disorders. Detecting CAD at an early stage is crucial for effective intervention, as delays in diagnosis increase the risk of severe cardiac events. Traditional diagnostic methods require specialized expertise, making early detection challenging in many healthcare settings [2].

Identifying CAD has historically relied on medical evaluations, imaging tests, and invasive procedures. Electrocardiograms (ECG), stress testing, and angiography have been widely used for diagnosis [3]. While these approaches provide valuable insights into heart function, they often involve high costs, lengthy procedures, and potential patient discomfort. Computational advancements have introduced non-invasive techniques for disease identification, offering an alternative to conventional medical tests [4], [5]. Modern diagnostic systems integrate patient data from multiple sources, utilizing advanced computational techniques to detect abnormalities in heart function. These approaches improve diagnostic efficiency and reduce dependency on resource-intensive procedures [6].

Machine learning has transformed CAD prediction by analyzing medical records, imaging data, and patient history to detect early signs of disease. By processing large datasets, computational models recognize patterns that might be missed through conventional analysis [7]. Learning from historical patient information allows predictive models to assess disease likelihood more accurately. Automated systems reduce reliance on manual interpretation, ensuring faster and more consistent diagnoses [8],[9]

Applying machine learning in CAD prediction offers multiple advantages, including reduced diagnostic time, cost savings, and lower risks associated with invasive procedures [10]. Traditional methods require extensive testing and clinical evaluation, increasing healthcare expenses and patient discomfort. Automated prediction systems provide rapid assessments, ensuring timely intervention and efficient resource utilization. Non-invasive computational models minimize the need for unnecessary procedures, reducing stress on patients while maintaining diagnostic precision [11]. These advancements support medical professionals in making informed decisions, improving treatment planning, and enhancing overall patient outcomes. Integrating machine learning into healthcare workflows strengthens disease prevention by identifying high-risk individuals before symptoms escalate [12], [13].

Motivated by these highlighted issues of privacy in healthcare, in this paper, we propose a federated matched averaging with a Artificial Bee Colony (ABC) optimization-based framework to overcome privacy issues and to improve the diagnosis method for the prediction of heart disease.

Bio-inspired optimization techniques enhance machine learning models by improving performance, efficiency, and adaptability [14]. These optimization strategies refine predictive models by selecting the most relevant features and improving classification accuracy. Computational techniques inspired by natural processes help optimize parameters dynamically, ensuring robust performance across diverse medical datasets [15]. By fine-tuning predictive systems, these methods enhance diagnostic stability and minimize errors [16]. Integrating bio-inspired optimization improves decision-making capabilities, allowing healthcare professionals to rely on more precise and efficient CAD detection models [17]. This approach ensures that machine learning-driven disease prediction continues to evolve, offering scalable and effective solutions for cardiovascular disease management [18], [19].

1.1. Problem Statement

Cardiovascular diseases, particularly coronary artery disease (CAD), remain the leading cause of mortality globally. Early detection and timely intervention are crucial to reducing morbidity and mortality. Conventional diagnostic techniques rely heavily on clinical tests and manual interpretation, often leading to delayed or inaccurate diagnosis due to subjective biases or lack of resources. Machine learning models offer promise but frequently struggle with imbalanced data, irrelevant features, and inconsistent performance. Naive Bayes, a well-known probabilistic classifier, shows potential for disease prediction but suffers when confronted with noisy or redundant attributes. Feature selection and model refinement remain essential for practical implementation in clinical settings. Existing optimization techniques either converge slowly or fall into local optima, failing to enhance prediction accuracy adequately.

1.2. Objective

The core objective involves designing a high-precision, computationally efficient prediction framework for coronary artery disease using the Artificial Bee Colony (ABC) algorithm to optimize feature selection in conjunction with Naive Bayes classification. This model aims to eliminate redundant and irrelevant data attributes, enhancing classification accuracy, interpretability, and robustness in medical diagnostics. The system seeks to address challenges associated with nois The ultimate goal is to deliver a reliable, reproducible, and adaptive CAD prediction framework that aligns with real-world healthcare needs, particularly in regions with limited infrastructure, supporting early diagnosis and intervention strategies that can reduce fatality rates and improve population-level cardiovascular outcomes.

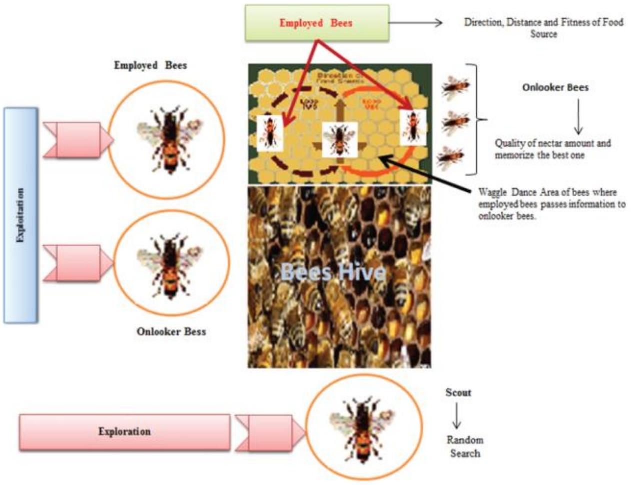
2. LITERATURE REVIEW

"Hybrid Harris Hawks Approach (H-HHO)" [20] begins by enhancing the original Harris Hawks Optimization algorithm through three structural improvements. The first enhancement incorporates a velocity operator into the position update process, improving exploration by enabling wider solution search. The second mechanism introduces an exploration factor to regulate random variations, increasing diversity during population movement. The third addition is a linearly decreasing inertia weight that strengthens exploitation in later iterations by refining the local search dynamics. A context-aware mechanism is embedded to select domain-relevant features, particularly thallium and chest pain type, using domain rules. H-HHO then executes parameter optimization for classifiers, refining the search over hyperparameter space to enhance classification readiness. The hybrid structure balances global and local search by adapting to population behavior and search progression, integrating swarm intelligence with biologically inspired hunting strategies, and enhancing convergence stability while avoiding premature stagnation.

"Two-Layered Voting - Machine Learning Framework (TLV-MLF)" [21] operates through a dual-layered architecture that separates feature selection and prediction. In the first layer, three statistical feature evaluation methods—ANOVA F-test, Chi-squared test, and Mutual Information—are applied to rank attributes based on relevance to coronary artery disease classification. Hard voting aggregates the selection based on frequency of occurrence, while soft voting applies weighted scores. The selected features progress to the second layer, which integrates four machine learning models: Random Forest, Decision Tree, Support Vector Classifier, and Multi-Layer Perceptron. Ensemble classification is conducted using both hard and soft voting strategies to determine final outcomes. GridSearchCV is utilized to hyper-tune each classifier's parameters, systematically scanning the parameter space to maximize classifier effectiveness. This two-tier mechanism structurally decouples feature importance assessment from model consensus, allowing TLV-MLF to integrate statistical reasoning with optimized ensemble modeling in a modular pipeline for coronary artery disease detection.

3. ARTIFICIAL BEE COLONY OPTIMIZED NAIVE BAYES (ABC-NB)

Naive Bayes remains a widely used probabilistic classifier based on Bayes' theorem, assuming conditional independence among features. Despite its computational efficiency and strong theoretical foundation, standard implementations face challenges, particularly when dealing with correlated features, high-dimensional data, and noisy attributes. These factors can reduce classification accuracy and introduce bias into predictions. Addressing these issues requires a feature selection strategy that ensures only the most informative attributes contribute to the classification process, leading to improved generalization and reduced model complexity.


Employed Bees
Direction, Distance and Fitness of Food Source
Employed Bees
Onlooker Bees
Quality of nectar amount and memorize the best one
Waggle Dance Area of bees where employed bees passes information to onlooker bees.
Exploitation
Bees Hive
Onlooker Bess
Exploration
Scout
Random Search

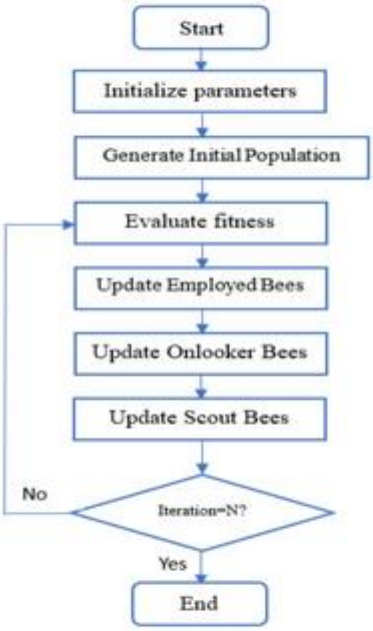
Artificial Bee Colony (ABC) optimization, inspired by the foraging behavior of honeybee swarms, is a robust swarm intelligence technique that efficiently explores large search spaces. The algorithm comprises three key components: employed bees, onlooker bees, and scout bees.

- ✓ Employed bees exploit known solutions by refining existing feature subsets,
- ✓ Onlooker bees evaluate their quality and select the best candidates, and
- ✓ Scout bees introduce randomness by exploring new feature combinations. This balance between exploration and exploitation makes ABC highly suitable for optimizing Naive Bayes by systematically identifying the most relevant feature subsets, thereby improving classification performance.

ABC optimization enhances Naive Bayes by iteratively refining the selection of features, ensuring that only the most discriminative attributes are retained. The adaptive nature of the algorithm allows it to effectively handle complex datasets, reducing classification errors and computational overhead. By optimizing the search process through swarm intelligence, the integration of ABC improves the model's ability to make accurate predictions with reduced data dimensionality. The resulting classifier achieves superior generalization, making it more effective in handling diverse classification tasks.

This paper systematically explores the integration of ABC with Naive Bayes to enhance classification accuracy. The discussion begins with the initialization of feature subsets, followed by the evaluation of fitness functions that guide the selection process. The iterative optimization strategy of ABC is then examined, detailing how it refines feature selection. This section concludes with an analysis of performance improvements, highlighting how the optimized NB model achieves higher accuracy, lower feature redundancy, and improved computational efficiency.

ABC Algorithms



3.1. Initialize Population in ABC-NB

In the ABC-NB algorithm, initializing the population represents the first stage, where a set of potential solutions, termed "food sources," gets generated randomly to prepare for the optimization process. These food sources signify distinct feature subsets, forming the foundation of the Naive Bayes classifier's initial structure. Each food source comprises a combination of features selected from the complete dataset, influencing the classifier's predictions. This initialization step plays a crucial role by setting diverse starting points for the subsequent optimization, enabling the algorithm to explore multiple solutions and improving the likelihood of finding an optimal feature subset. In the behavior of a bee swarm, scouts venture into unexplored areas to discover new food sources. Mimicking this behavior, the ABC-NB algorithm initiates random feature subset selection, creating a preliminary population with varied combinations of features. This process minimizes feature redundancy, enhancing the Naive Bayes classifier's overall accuracy and reducing computational costs by limiting the feature space.

To generate the initial population of food sources, consider the feature space as a matrix X with dimensions N x M, where N represents the total number of samples, and M signifies the total number of features. The food sources (i.e., solutions) form a matrix P with F rows and M columns, where F denotes the total number of food sources initialized.

$$P = \{X_{f,m} | f = 1,2, \ldots, f; m = 1,2, \ldots., M\} \quad (1)$$

Where $X_{f,m}$ represents a feature subset assigned to the F-th food source. This initialization involves selecting values from the original feature space and assigning them to in a way that each food source consists of random combinations of features.

The probability of selecting a feature in any food source can be expressed as:

$$\Pr\left(X_{f,m}\right) = \frac{\sum_{n=1}^{N} x_{n,m}}{N} \quad (2)$$

Where $X_{n,m}$ represents the presence of the m-th feature in the n-th sample, while N denotes the total number of samples. This probability establishes the likelihood of each feature's inclusion in a food source.

Once features are randomly selected for each food source, the algorithm creates a binary vector B_f for each food source f, indicating the inclusion (1) or exclusion (0) of each feature:

$$\Pr\left(X_{f,m}\right) = \frac{\sum_{n=1}^{N} x_{n,m}}{N} \tag{3}$$

Where $x_{n,m}$ represents the presence of the m-th feature in the n-th sample, while N denotes the total number of samples. This probability establishes the likelihood of each feature's inclusion in a food source.

Once features are randomly selected for each food source, the algorithm creates a binary vector B_f for each food source f, indicating the inclusion (1) or exclusion (0) of each feature:

$$B_f = \{b_{f11}, b_{f,2}, ..., b_{f,M}\} \tag{4}$$

For a feature m in the f-th food source, $b_{f,m}$ = 1 if the feature is selected and $b_{f,m}$ = 0 otherwise. This binary vector allows the ABC algorithm to handle each food source as a unique combination of features, facilitating optimization and selection. The probability of a feature being selected within the population is given by:

$$p_f(m) = \frac{Pr(X_{f,m})}{\sum_{m=1}^{M} Pr(X_{f,m})} \tag{5}$$

Where $p_f(m)$ represents the normalized probability for the m-th feature in the f-th food source, ensuring that the sum of probabilities across features equals one.

To evaluate each food source's effectiveness, the initial fitness of the Naive Bayes classifier with each subset of features must be determined. The initial fitness F_f for each food source f is calculated using the classification accuracy:

$$F_f = \frac{TP + TN}{TP + TN + FP + FN} \tag{6}$$

Where $TP, TN, FP,$ and FN represent True Positives, True Negatives, False Positives, and False Negatives, respectively, indicating the classifier's prediction performance on the selected feature subset.

The algorithm seeks to optimize the Naive Bayes model by reducing redundancy in the selected features while maximizing classification accuracy. The objective function O_f for the f-th food source is formulated as:

$$O_f = w_1 . F_f - w_2 . Redundancy(B_f) \tag{7}$$

Where w_1 and w_2 are weights assigned to prioritize accuracy and redundancy reduction. $Redundancy(B_f)$ Measures feature overlap within B_f, with lower redundancy indicating a more optimized feature subset.

The selection of features at random from the feature space can be expressed by:

$$R_{f,m} = random(0,1) \tag{8}$$

Where $R_{f,m}$ generates a random binary value for each feature m in food source f, setting $b_{f,m}$ accordingly to 0 or 1.

The final step in population initialization involves assigning random solutions to each food source to create the initial population, denoted by:

$$\{P_1, P_2, \ldots.., P_F\} = \{B_1, B_2, \ldots.., B_F\} \quad (9)$$

This set of binary vectors B_f represents the initial solution matrix, which will be evaluated in subsequent optimization cycles.

3.2. Evaluate Fitness in ABC-NB

In the ABC-NB algorithm, the Evaluate Fitness step holds a crucial role in assessing the performance of each food source by calculating the fitness of each solution (feature subset) concerning the objective of optimizing the Naive Bayes classifier's predictive accuracy. This step aligns with the foraging behavior observed in bee swarms, where bees assess the quality of food sources, enabling the identification of promising solutions for further optimization. By calculating the fitness of each food source, the ABC-NB algorithm effectively distinguishes between more valuable solutions, guiding subsequent phases and enhancing the algorithm's overall performance. After initializing the population in Step 1, each food source is represented by a binary vector, defining a unique subset of features. Each food source's subset undergoes evaluation based on its impact on the Naive Bayes classifier's predictive capability in this step. The fitness values computed here will determine the probability of each food source's selection by onlooker bees in future steps, aligning with the goal of refining and optimizing the model.

In the ABC-NB algorithm, the fitness of each food source f is defined through a function that evaluates both the accuracy of the Naive Bayes classifier and the efficiency of the feature subset in minimizing redundancy. To compute the fitness score F_f an initial evaluation of the classifier's performance on the feature subset represented by each food source is carried out of each food source.

$$F_f = \alpha . Q_f - \beta . \sum_{m=1}^{M} \delta\left(b_{f,m}, b_{f,m+1}\right) \quad (10)$$

Where α and β represent weights assigned to accuracy Q_f and redundancy penalty, respectively. Here, $Q_f$denotes the Naive Bayes classifier's accuracy on the feature subset for the f-th food source, and $\delta\left(b_{f,m}, b_{f,m+1}\right)$measures redundancy between adjacent features in the binary vector B_f.

Redundancy reduction forms a significant aspect of the fitness function to ensure the selection of non-redundant and compelling features. The redundancy penalty component is calculated based on the presence of adjacent similar features in B_f, thus:

$$Redundancy\left(B_f\right) = \sum_{m=1}^{M-1} \left|b_{f,m}, b_{f,m+1}\right| \quad (11)$$

This redundancy measure accumulates penalties whenever consecutive features in the feature subset B_f are identical, ensuring that only essential and non-redundant features contribute positively to the fitness score. The overall fitness G_f combines the classifier's accuracy with feature subset quality by penalizing redundancy and adding a preference to solutions that achieve higher accuracy and diversity among selected features:

$$G_f = \lambda . F_f - \gamma . Redundancy(B_f) \tag{12}$$

Where λ represents the weight for accuracy, and γ is the weight for redundancy. This fitness score G_f provides a comprehensive measure that balances accuracy with feature quality.

To further assess each feature's contribution within a selected subset, a weight is assigned to each feature in the feature subset. The contribution weight W_m for each feature m can be defined by:

$$W_m = \frac{\sum_{f=1}^{F} F_f . b_{f,m}}{\sum_{f=1}^{F} b_{f,m}} \tag{13}$$

Where W_m represents the average fitness contribution of the m-th feature across all food sources, indicating feature importance and aiding in identifying influential features for further optimization.

The probability P_f of selecting a food source for exploration by onlooker bees depends on the fitness G_f, normalized over all food sources:

$$P_f = \frac{G_f}{\sum_{k=1}^{F} G_k} \tag{14}$$

By calculating P_f, each food source is assigned a probability that reflects its fitness, guiding the algorithm toward selecting more promising feature subsets in the optimization process. To ensure that all fitness values remain on a comparable scale, the algorithm normalizes each food source's fitness G_f using the maximum and minimum values observed across the population:

$$N_f = \frac{G_f - G_{min}}{G_{max} - G_{min}} \tag{15}$$

Where N_f represents the normalized fitness score for the f-th food source, G_{min} is the minimum fitness observed, and G_{max} is the maximum fitness observed.

Based on the calculated fitness scores and selection probabilities, the ABC-NB algorithm prioritizes feature subsets that balance high predictive accuracy with minimized redundancy, forming an optimized foundation for further classifier improvements. The final selected features ensure maximized classifier performance and efficiency in feature usage.

3.3. Send Employed Bees in ABC-NB

The Send Employed Bees phase of the ABC-NB algorithm signifies the beginning of the search for improvements in the existing solutions or "food sources" identified in previous steps. In this phase, employed bees represent agents exploring the vicinity of each food source to find an optimized solution by modifying existing feature subsets. This process mirrors the natural behavior of bees who intensively explore known food sources to discover improved nourishment, thus enhancing the colony's overall yield. For ABC-NB, sending employed bees facilitates refining the Naive Bayes classifier by exploring local variations in feature subsets and ensuring the algorithm progresses toward more optimal configurations. Each food source represents a distinct subset of features selected from the dataset. By sending employed bees, the algorithm aims to modify these feature subsets iteratively to enhance classifier accuracy and reduce redundancy, leading to a more optimized solution. The employed bees use a combination of probabilistic changes and specific heuristic strategies to alter the current food source, guided by each solution's evaluated fitness score from the previous step.

The exploration around each food source is based on a neighborhood search mechanism, wherein small changes to the feature subset are made to find improved solutions. Each employed bee modifies a food source by changing one or more feature inclusions. The new feature subset B_f^{new} for each food source f is generated based on the current subset $B_f$by altering a specific feature $b_{f,m}$ with a perturbation factor ϕ:

$$B_{f,m}^{new} = B_{f,m} + \phi.\left(B_{f,m} - B_{k,m}\right) \tag{16}$$

Where Φ represents a random value within a specified range (e.g., [-1, 1]) controlling the degree of perturbation. $B_{k,m}$ denotes the feature from a randomly selected food source $k \neq f$. This mechanism ensures diversity in the modifications and encourages the exploration of a broader feature space.

To determine an optimized perturbation factor, ϕ is calculated considering the fitness scores of the food sources. The perturbation factor ϕ_f for each employed bee associated with the f-th food source is derived as follows:

$$\phi_f = \frac{G_f}{\sum_{j=1}^{F} G_j} \tag{17}$$

Where G_f is the fitness of food source f, and $\sum_{j=1}^{F} G_j$ is the total fitness of all food sources. By associating ϕ_f with the fitness scores, the algorithm emphasizes modifications to food sources with higher potential, focusing efforts where improvements are most likely to yield effective results.

After generating a new solution B_f^{new} for each food source f, the fitness G_f^{new} of the modified feature subset undergoes evaluation using the fitness function established in Step 2. The new fitness score accounts for accuracy improvement, optimized feature subset quality, and reduced redundancy. The fitness score for the modified feature subset is expressed as:

$$G_f^{new} = \lambda.F_f^{new} - \gamma.Redundancy\left(B_f^{new}\right) \tag{18}$$

Where F_f^{new} is the classifier accuracy on the modified feature subset, and $Redundancy\left(B_f^{new}\right)$ calculates the redundancy penalty.

Upon calculating G_f^{new}, a decision is made to either accept the modified food source or retain the original one based on their fitness scores. The probability P_f^{accept} of accepting the new solution B_f^{new} over the previous food source B_f is defined as:

$$P_f^{accept} = \frac{G_f^{new}}{G_f^{new} + G_f} \qquad (19)$$

Eq.(19) ensures that solutions yielding higher fitness are more likely to be accepted, thereby focusing on feature subsets with optimized classification accuracy and minimized redundancy. An adaptive mechanism adjusts the frequency of each feature selection based on previous fitness evaluations. A feature importance score I_m is assigned to each feature m based on its contribution to fitness across different food sources:

$$I_m = \frac{\sum_{f=1}^{F} G_f . b_{f,m}}{\sum_{f=1}^{F} b_{f,m}} \qquad (20)$$

Higher values of I_m indicate more impactful features, guiding the selection of features that are consistently associated with higher fitness, thus aiding the algorithm in converging toward an optimized feature set.

The likelihood $P_{f,m}^{modify}$ of modifying each feature m in food source f depends on the feature's importance and the overall solution fitness. This probability can be calculated by:

$$P_{f,m}^{modify} = \frac{I_m}{\sum_{n=1}^{M} I_n} \qquad (21)$$

Higher values of $P_{f,m}^{modify}$ encourage modifications to significant features, guiding the search towards solutions with a more optimized selection. After conducting the neighborhood search and evaluating the fitness, the employed bee process results in an optimized feature subset with improved classifier performance. By iteratively refining food sources based on fitness-guided modifications, the algorithm ensures gradual convergence toward the best solutions for feature selection in the Naive Bayes classifier.

3.4. Assess New Solutions in ABC-NB

In the ABC-NB algorithm, the step of Assessing New Solutions involves evaluating the modified solutions generated by the employed bees to determine if these newly identified feature subsets exhibit optimized performance. This process resembles how bees gauge the quality of freshly discovered nectar sources, comparing them with previous locations to ensure only the best sources contribute to the hive. By assessing new solutions, the ABC-NB algorithm maintains a balance between exploring new possibilities and refining previously identified feature subsets, ensuring continuous improvement in the feature selection process. The ABC-NB evaluates each newly modified feature subset through a fitness assessment that prioritizes high classification accuracy and minimized redundancy. Only solutions with optimized performance are considered for progression to the next phase, fostering convergence toward an ideal feature subset.

The fitness of each new solution S_f^{new} generated by the employed bees is evaluated using a modified fitness function. The fitness score F_f^{new} for each new solution S_f^{new} integrates classifier accuracy, redundancy penalties, and feature relevance, as shown below:

$$F_f^{new} = \eta . Q_f^{new} - \zeta . Redundancy(S_f^{new}) \qquad (22)$$

Where η and ζ represent weights assigned to the classifier accuracy Q_f^{new} and the redundancy penalty. Q_f^{new} denotes the accuracy of the Naive Bayes classifier when applied to the new feature subset. The redundancy measure assesses whether repeated features exist, penalizing solutions contributing to feature redundancy.

Minimizing redundancy in feature subsets remains crucial in assessing new solutions. The redundancy penalty for a new solution S_f^{new} is calculated as follows:

$$Redundancy(S_f^{new}) = \sum_{i=1}^{M-1} \left| s_{f,i}^{new} - s_{f,i+1}^{new} \right| \qquad (23)$$

Where $s_{f,i}^{new}$ represents the i-th feature in the new solution. Lower redundancy penalties indicate that the feature subset includes a unique selection of features with minimized overlap.

To facilitate comparisons between newly generated and existing solutions, a weighted fitness function W_f^{new} is utilized. This function calculates the weighted combination of accuracy and redundancy for each new solution:

$$W_f^{new} = \alpha . F_f^{new} + \beta . Diversity(S_f^{new}) \qquad (24)$$

Where α and β serve as weights for accuracy and feature diversity, respectively. Here, $Diversity(S_f^{new})$ ensures feature variety across the population, which contributes to a robust solution.

A critical aspect of assessing new solutions lies in promoting feature diversity, which prevents premature convergence on suboptimal solutions. The diversity D_f^{new} for each new solution is evaluated as:

$$D_f^{new} = \frac{\sum_{i=1}^{M} s_{f,i}^{new}}{M} \qquad (25)$$

This measure considers the proportion of features actively selected in S_f^{new}, ensuring that the subset remains diverse enough to foster further exploration in subsequent phases. Based on the weighted fitness function, a selection probability P_f^{select} is assigned to each new solution to decide whether it will replace the original solution in the population:

$$P_f^{select} = \frac{W_f^{new}}{W_f^{new} + W_f} \qquad (26)$$

Where W_f represents the weighted fitness score of the original solution. Solutions with higher W_f^{new} have an increased probability of selection, facilitating the retention of optimized feature subsets.

To maintain consistency across different scales of fitness values, the fitness scores of new solutions undergo adaptive scaling, expressed as:

$$F_f^{scaled} = \frac{F_f^{new} - F_{min}^{new}}{F_{max}^{new} - F_{min}^{new}} \quad (27)$$

Where F_{min}^{new} and F_{max}^{new} represent the minimum and maximum fitness values among all new solutions. Scaling ensures comparability between solutions, streamlining the selection process.

Each new solution's retention of specific features depends on its individual fitness contributions and redundancy status. A retention probability $R_{f,i}^{retain}$ is assigned to each feature i in S_f^{new} based on its relative importance:

$$F_{f,i}^{retain} = \frac{F_{f,i}^{new}}{\sum_{j=1}^{M} F_{f,j}^{new}} \quad (28)$$

Where $F_{f,i}^{new}$ represents the contribution of the feature $i$to the new solution's fitness score. Retaining high-contribution features enables the selection of optimal subsets while discarding redundant or less impactful features.

The final step in assessing new solutions involves a decision criterion that combines fitness, diversity, and probability to retain solutions that meet optimized standards. A retention criterion C_f^{retain} is calculated as follows:

$$C_f^{retain} = F_f^{scaled} + D_f^{new} . P_f^{select} \quad (29)$$

3.5. Greedy Selection in ABC-NB

In the ABC-NB algorithm, Greedy Selection is pivotal in refining the feature subsets by ensuring that only the most optimized solutions proceed to the subsequent optimization stages. This process closely resembles the decision-making behavior of bees, who continuously compare potential food sources, selecting only those with the highest value to sustain the colony's productivity. Within the ABC-NB framework, Greedy Selection evaluates each newly modified feature subset generated in the Assess New Solutions phase, comparing them to the existing solutions. The more favorable solutions, based on fitness and optimized attributes, are retained, effectively refining the feature selection process. Greedy selection strengthens the ABC-NB algorithm's ability to prioritize subsets with high classifier accuracy and minimized redundancy. This selection method provides a straightforward yet powerful mechanism for filtering solutions, emphasizing the most effective combinations of features and enhancing the model's performance.

The Greedy Selection step begins by comparing the fitness score F_f^{new} of each modified solution S_f^{new} with its corresponding previous solution S_f. For a given food source f, if the fitness score of the new solution surpasses that of the existing solution, the algorithm retains the new solution; otherwise, the original solution remains:

$$S_f = \begin{cases} S_f^{new} & if\ F_f^{new} > F_f \\ S_f & otherwise \end{cases} \quad (30)$$

Where F_f represents the fitness score of the original solution. This equation serves as the primary decision-making criterion for Greedy Selection, favoring solutions with improved fitness values.

The algorithm applies an optimization function to each selected feature subset, ensuring that the retained solution maximizes accuracy while maintaining diversity in the feature set. The optimization function O_f for each feature, the subset is expressed as:

$$O_f = \alpha . F_f - \beta . Redundancy(S_f) \quad (31)$$

Where α and β serve as weights for fitness and redundancy. F_f denotes the classifier accuracy for the solution S_f, while $Redundancy(S_f)$ assesses feature overlap within the subset, guiding the algorithm to favor unique, high-utility feature combinations.

Greedy selection employs a retention probability P_f^{retain} that depends on the comparative fitness of the new and existing solutions. This probability is calculated as:

$$P_f^{retain} = \frac{F_f^{new}}{F_f^{new} + F_f} \quad (32)$$

Where F_f^{new} represents the fitness of the modified solution, and F_f denotes the fitness of the original solution. Higher values of P_f^{retain} reflect a greater likelihood of retaining the new solution, indicating its relative effectiveness over the existing subset.

Diversity enhancement plays a significant role in Greedy Selection to prevent premature convergence on suboptimal feature subsets. The diversity score $D_f$for each solution S_f is computed by examining the distribution of selected features across the subset, calculated as follows:

$$D_f = \frac{\sum_{m=1}^{M} s_{f,m}}{M} \quad (33)$$

Where $s_{f,m}$ denotes the presence of the m-th feature in the solution S_f, and M is the total number of features. Solutions with higher diversity scores D_f possess a wider range of features, ensuring that various combinations are explored.

To improve the effectiveness of Greedy Selection, each feature's contribution to the overall fitness of a solution is evaluated. The feature impact score $I_{f,m}$for each feature m in solution S_f is determined by:

$$I_{f,m} = \frac{F_f . s_{f,m}}{\sum_{k=1}^{M} s_{f,k}} \qquad (34)$$

This score measures the contribution of individual features to the classifier's accuracy, guiding Greedy Selection to retain subsets containing high-impact features. The probability $R_{f,m}^{opt}$ of retaining a feature m in a solution s_f is based on the feature impact score $I_{f,m}$:

$$R_{f,m}^{opt} = \frac{I_{f,m}}{\sum_{n=1}^{M} I_{f,n}} \qquad (35)$$

Higher values of $R_{f,m}^{opt}$ favor retaining features with significant contributions to the solution's fitness, enhancing the overall quality of retained subsets. The algorithm employs a selection criterion C_f^{greedy} that combines fitness, diversity, and probability to select solutions with maximized effectiveness:

$$C_f^{greedy} = F_f + \gamma . D_f + \delta . P_f^{retain} \qquad (36)$$

Where γ and δ are weights for diversity and retention probability. Solutions with higher C_f^{greedy} values proceed to the next stage, ensuring optimized feature subsets.

3.6. Send Onlooker Bees in ABC-NB

In the ABC-NB algorithm, sending onlooker bees marks a critical phase in enhancing the optimization process. Onlooker bees represent a specialized group within the colony that selects food sources (feature subsets) based on observed fitness scores, prioritizing more promising solutions. This stage mirrors the behavior of bees who congregate around the most beneficial food sources, as feedback from employed bees indicates, thus maximizing the colony's resources. In the ABC-NB context, the Send Onlooker Bees step enables refined selection and exploration of feature subsets, enhancing the accuracy and efficiency of the Naive Bayes classifier. By focusing on high-fitness solutions, onlooker bees avoid low-value areas, concentrating the algorithm's resources on solutions with optimized potential.

Each onlooker bee selects a food source based on a probability derived from the fitness scores of available solutions. The selection probability $P_f^{onlooker}$ for each food source f is defined by normalizing the fitness score across the population:

$$P_f^{onlooker} = \frac{F_f}{\sum_{k=1}^{F} F_k} \qquad (37)$$

Where F_f represents the fitness of food source f, while $\sum_{k=1}^{F} F_k$ is the total fitness of all solutions. Higher fitness values result in greater selection probabilities, ensuring that onlooker bees focus on feature subsets likely to contribute to optimized classifier performance.

Once an onlooker bee selects a food source based on $P_f^{onlooker}$, it initiates exploration around the chosen feature subset to identify further improvements. The exploration mechanism involves adjusting the feature subset like the employed bee's neighborhood search but focusing on promising areas. The new feature subset $B_f^{explore}$ is generated using a perturbation factor θ:

$$B_{f,m}^{explore} = B_{f,m} + \theta.\left(B_{f,m} + B_{k,m}\right) \quad (38)$$

Where θ is a randomly assigned factor between a predetermined range, and $B_{k,m}$ represents a feature from another randomly selected solution$k \neq f$. By creating diverse feature combinations within high-potential subsets, this mechanism ensures comprehensive exploration in optimized directions.

The fitness score of the selected food source can influence the degree of exploration by onlooker bees. The adaptive scaling of the perturbation factor $\theta_f$depends on the relative fitness F_f of the chosen solution:

$$\theta_f = \frac{F_f - F_{min}}{F_{max} - F_{min}} \quad (39)$$

Where F_{min} and F_{max} are the minimum and maximum fitness scores in the population, respectively. This scaling ensures that solutions with higher fitness undergo finer perturbations, enhancing precision in high-potential areas.

The following exploration, each onlooker bee evaluates the fitness $F_f^{explore}$ of its newly generated solution, incorporating accuracy and redundancy measures. The fitness calculation is expressed as:

$$F_f^{explore} = \eta.\, Q_f^{explore} - \zeta.\, Redundancy\left(B_f^{explore}\right)(40)$$

Where $Q_f^{explore}$ denotes the accuracy of the Naive Bayes classifier with the modified feature subset, and $Redundancy\left(B_f^{explore}\right)$ represents the redundancy penalty for the subset. Weights η and ζ adjust the importance of each component, ensuring the optimized balance between accuracy and feature diversity.

Onlooker bees also assess the diversity $D_f^{explore}$ of their solutions, aiming to avoid convergence on overly similar feature subsets. The diversity score is calculated by:

$$D_f^{explore} = \frac{\sum_{i=1}^{M} B_{f,i}^{explore}}{M} \quad (41)$$

Where $B_{f,i}^{explore}$ is the i-th feature in the modified subset, and M denotes the total feature count. High diversity values prevent redundant solutions, supporting broader exploration of viable feature combinations.

Each onlooker bee's newly generated solution is subject to an acceptance criterion based on its fitness relative to the original subset. The acceptance probability P_f^{accept} is calculated as:

$$P_f^{accept} = \frac{F_f^{explore}}{F_f^{explore} + F_f} \quad (42)$$

Where F_f is the fitness of the original solution, ensuring that only solutions with significant improvements are likely to replace previous subsets? This acceptance probability maintains a focus on continuously optimizing feature selections.

Onlooker bees further refine the feature subsets by emphasizing features that demonstrate high utility in improving classifier accuracy. The importance weight $W_{f,m}$ for each feature m within a selected subset is calculated by:

$$W_{f,m} = \frac{F_f . B_{f,m}^{explore}}{\sum_{j=1}^{M} B_{f,j}^{explore}} \tag{43}$$

Higher weights $W_{f,m}$ indicate features with substantial contributions, enabling the algorithm to prioritize feature combinations with enhanced predictive capabilities.

Based on the importance weight, each feature m in the solution $B_f^{explore}$ is assigned a retention probability $R_{f,m}^{retain}$:

$$R_{f,m}^{retain} = \frac{W_{f,m}}{\sum_{i=1}^{M} W_{f,i}} \tag{44}$$

This retention probability guides the inclusion of high-impact features in subsequent iterations, supporting the formation of refined, optimized feature subsets.

3.7. Explore New Solutions by Onlooker Bees in ABC-NB

In the ABC-NB algorithm, the phase of Exploring New Solutions by Onlooker Bees is essential for refining the feature selection process. This phase allows onlooker bees to further examine promising food sources (feature subsets) by conducting in-depth exploration around selected high-fitness solutions. This step is integral in expanding the algorithm's search in promising regions, maximizing the likelihood of finding an optimized feature subset with the highest classifier accuracy and minimal redundancy. In a real-world bee colony, onlooker bees are attracted to food sources previously identified as high quality by scout or employed bees. Mirroring this behavior, onlooker bees in ABC-NB evaluate these food sources, introducing minor modifications to generate new solutions that offer incremental improvements. This approach facilitates a thorough exploration of the feature space around each high-fitness solution, refining the classifier's performance.

Onlooker bees explore selected feature subsets by conducting a neighborhood search around each high-fitness food source. Each onlooker bee modifies a feature subset S_f, resulting in a new solution S_f^{new} by introducing minor changes to its binary representation. The modified solution S_f^{new} can be represented as:

$$S_{f,m}^{new} = S_{f,m} + \delta . \left(S_{f,m} - S_{k,m}\right) \tag{45}$$

Where $S_{f,m}$ represents the m-th feature in the original subset for food source f, and $S_{k,m}$ is the corresponding feature from a randomly selected food source $k \neq f$. The parameter $\delta$is a perturbation factor that controls the magnitude of the modification. By adjusting δ, the algorithm ensures fine-grained exploration, enabling the generation of closely related feature subsets.

To enhance the exploration of high-fitness solutions, the perturbation factor $\delta_f$is adjusted adaptively based on the fitness score F_f of the food source. This adjustment helps achieve more significant modifications for solutions with moderate fitness while applying finer adjustments for high-fitness solutions. The adaptive perturbation is defined as:

$$\delta_f = \frac{F_f}{\sum_{j=1}^{F} F_f} \qquad (46)$$

Where $\sum_{j=1}^{F} F_f$ represents the total fitness of all solutions in the population. The algorithm encourages more substantial exploration in those regions by assigning a higher weight to solutions with relatively lower fitness.

Each newly generated solution S_f^{new} undergoes a fitness evaluation to determine its effectiveness in improving the Naive Bayes classifier's performance. The fitness F_f^{new} for the modified solution is calculated by:

$$F_f^{new} = \lambda . A_f^{new} . \mu . Redundancy(S_f^{new}) \qquad (47)$$

Where λ and μ represent the weights assigned to classifier accuracy A_f^{new} and redundancy, respectively. The redundancy term penalizes solutions with overlapping or unnecessary features, ensuring the selected subset maintains a balance of diversity and accuracy.

The likelihood of each onlooker bee retaining a newly explored solution depends on its fitness compared to the original subset. The probability P_f^{retain} of retaining S_f^{new} over S_f is calculated as follows:

$$P_f^{retain} = \frac{F_f^{new}}{F_f^{new} + F_f} \qquad (48)$$

Higher values of F_f^{new} increase the probability of the onlooker bee adopting the new solution, facilitating the retention of subsets that offer a higher classifier accuracy and optimal feature selection.

To prevent premature convergence, the algorithm evaluates the diversity D_f^{new} of the new solution. This diversity metric assesses the distribution of selected features within S_f^{new}, calculated as:

$$D_f^{new} = \frac{\sum_{i=1}^{M} S_{f,i}^{new}}{M} \qquad (49)$$

Where M represents the total number of features in the dataset, and $S_{f,i}^{new}$ is the i-th feature in the new subset. By promoting solutions with higher diversity scores, the algorithm maintains a broader exploration of the feature space, avoiding redundancy and overlapping solutions.

During the exploration of new solutions, each feature's impact on the fitness of S_f^{new} is weighted to prioritize impactful features in future iterations. The importance weight $W_{f,m}^{new}$ for each feature m is calculated by:

$$W_{f,m}^{new} = \frac{F_f^{new} . S_{f,i}^{new}}{\sum_{n=1}^{M} S_{f,n}^{new}} \tag{50}$$

Where higher values of $W_{f,m}^{new}$ indicate features with a more significant contribution to classifier performance, guiding future feature subset adjustments.

For each feature S_f^{new}, a selection probability $P_{f,m}^{select}$ is assigned based on its importance weight:

$$P_{f,m}^{select} = \frac{W_{f,m}^{new}}{\sum_{j=1}^{M} W_{f,j}^{new}} \tag{51}$$

This selection probability reflects the likelihood of retaining high-utility features, enhancing the probability of optimal features contributing to the solution in subsequent iterations. To finalize the exploration phase, each onlooker bee applies a greedy selection criterion for retaining solutions that maximize classifier accuracy and minimize redundancy. This selection criterion $C_f^{explore}$ combines fitness and diversity metrics:

$$C_f^{explore} = F_f^{new} + k. D_f^{new} \tag{52}$$

Where κ represents the weight assigned to diversity, ensuring that solutions with higher classifier performance and greater diversity are prioritized.

3.8. Evaluate the Fitness of Onlooker Bee Solutions in ABC-NB

In the ABC-NB algorithm, evaluating the fitness of solutions explored by onlooker bees is crucial for determining the effectiveness of newly identified feature subsets. This evaluation process mimics how bees assess the quality of promising food sources, ensuring that only those providing the most nourishment are revisited and utilized by the colony. By carefully evaluating the fitness of onlooker bee solutions, the algorithm identifies which feature subsets offer optimized performance for the Naive Bayes classifier, advancing the search toward optimal solutions. Evaluating the fitness of onlooker bee solutions allows a thorough comparison of classifier accuracy and feature subset efficiency. In this phase, each onlooker bee's modified solution undergoes an assessment based on multiple factors, including redundancy minimization, diversity enhancement, and the influence of individual features, ensuring a holistic approach to selecting high-performing subsets.

Each onlooker bee solution is evaluated based on its effectiveness in improving the classifier's accuracy. This effectiveness is quantified by calculating a fitness score F_o^{new} for each solution. The fitness score of each onlooker bee solution is calculated as follows:

$$F_o^{new} = \alpha . C_o^{new} - \beta . R_o^{new} \quad (52)$$

Where C_o^{new} represents the classifier's predictive capability using the feature subset o selected by the onlooker bee. R_o^{new}represents the redundancy within the subset. The weights α and β ensure balanced consideration of classifier performance and feature overlap reduction, promoting an optimized subset.

Minimizing redundancy among selected features ensures that unique and complementary features are retained. For each onlooker bee solution, the redundancy penalty $R_o^{new}$is evaluated as:

$$R_o^{new} = \sum_{i=1}^{M-1} |o_i - o_{i+1}| \quad (53)$$

Where o_i and o_{i+1} denote consecutive features in the subset selected by onlooker bee o. The summation term penalizes consecutive duplicate features, reducing overlap and ensuring the subset includes only distinct and impactful features.

Diversity among selected features is essential to prevent premature convergence to local optima. A high diversity score ensures the feature subsets explored by onlooker bees cover a broad range of attributes. The diversity score D_o^{new} for each onlooker bee solution is calculated as follows:

$$D_o^{new} = \frac{\sum_{j=1}^{M} o_j}{M} \quad (54)$$

Where o_j denotes the presence of the j-th feature in the subset o explored by the onlooker bee, M represents the total number of features. A higher diversity score indicates a varied selection of features, contributing to more comprehensive solution space exploration.

To evaluate each onlooker bee solution comprehensively, a weighted fitness function $W_o^{new}$is applied, integrating accuracy, redundancy reduction, and diversity. This weighted fitness is calculated as follows:

$$W_o^{new} = \lambda . F_o^{new} + \gamma . D_o^{new} \quad (55)$$

Where λ and γ are weights that adjust the influence of classifier performance and diversity on the solution's overall fitness, this function guides the algorithm to prioritize solutions that balance high classifier accuracy with unique and varied feature subsets.

Each feature within an onlooker bee solution is assigned an importance score to quantify its contribution to the classifier's performance. The importance score $I_{o,j}^{new}$ for each feature j in solution o is calculated by:

$$I_{o,j}^{new} = \frac{F_o^{new} . o_j}{\sum_{k=1}^{M} o_k} \quad (56)$$

Where o_k represents the presence of the j-th feature in the subset, and $F_o^{new}$is the fitness score of the onlooker bee solution. Higher importance scores reflect features that provide more significant predictive value for the classifier.

After calculating the weighted fitness of each solution, a selection probability P_o^{select} is assigned to each onlooker bee solution. This probability influences the likelihood of retaining the solution based on its relative fitness compared to other solutions:

$$P_o^{select} = \frac{W_o^{new}}{\sum_{p=1}^{O} W_p^{new}} \quad (57)$$

Where W_o^{new} denotes the weighted fitness of solution o, and O is the total number of onlooker bee solutions. Solutions with higher W_o^{new} values are more likely to be selected, ensuring only the most promising solutions advance.

To determine which onlooker bee solutions should replace previous solutions, the algorithm applies a retention criterion C_o^{retain}. This criterion combines fitness, diversity, and importance scores, ensuring that only high-quality solutions are retained. The retention criterion is calculated as:

$$C_o^{retain} = F_o^{new} + \delta . D_o^{new} \quad (58)$$

Where δ adjusts the influence of diversity, favoring solutions with a balanced representation of unique and impactful features. Solutions that meet or exceed a predefined threshold based on C_o^{retain} are retained, supporting the selection of optimized feature subsets.

Each feature in an onlooker bee solution is assigned a retention probability $R_{o,j}^{retain}$ based on its importance score:

$$R_{o,j}^{retain} = \frac{I_{o,j}^{new}}{\sum_{k=1}^{M} I_{o,k}^{new}} \quad (59)$$

This retention probability ensures that features contributing significantly to classifier performance are more likely to be preserved, facilitating the development of optimized solutions.

3.9. Scout Bee Phase in ABC-NB

The Scout Bee Phase in the ABC-NB algorithm focuses on reintroducing diversity into the population of solutions, ensuring that the optimization process does not converge prematurely. Scout bees mimic the behavior of real scout bees, which explore new areas when food sources (feature subsets) are depleted or provide minimal value. In ABC-NB, scout bees replace solutions that exhibit stagnation or fail to yield improvements, facilitating exploration in fresh, unexplored regions of the feature space. By incorporating this phase, the algorithm maintains a balance between exploitation and exploration, fostering the identification of more optimized solutions. In the context of ABC-NB, scout bees generate new feature subsets by initiating random modifications to existing ones or creating entirely novel feature combinations. This approach prevents the algorithm from becoming trapped in local optima, ensuring a comprehensive search across the feature space to achieve the most effective configurations for the Naive Bayes classifier.

The algorithm first identifies stagnant solutions within the population to activate scout bees. A solution is considered stagnant if it has not improved over several cycles or iterations. The stagnation count S_f^{count} for each solution f is defined as follows:

$$S_f^{count} = S_f^{count} + 1 \tag{60}$$

If S_f^{count} reaches a predefined threshold θ, the solution S_f is deemed stagnant and becomes a target for replacement by scout bees. This threshold value θ acts as a control mechanism, ensuring solutions that do not contribute to further optimization are replaced. Once a stagnant solution is identified, scout bees generate new feature subsets to replace it, restoring diversity to the solution pool. The new feature subset S_f^{scout} is generated by assigning random values to each feature m, ensuring a novel solution is created. The new solution S_f^{scout} can be expressed as:

$$S_f^{scout} = random(0,1) \tag{61}$$

In this context, each feature in S_f^{scout} a binary value of 0 or 1 is randomly assigned, where 1 indicates inclusion in the subset, and 0 indicates exclusion. This randomization injects fresh configurations into the algorithm, encouraging broader feature space exploration. After generating a new solution, scout bees assess the fitness of S_f^{scout} to determine its contribution to the optimization process. The fitness F_f^{scout} of the new scout bee solution is calculated as follows:

$$F_f^{scout} = \alpha . Q_f^{scout} - \beta . Redundancy\left(S_f^{scout}\right) \tag{62}$$

Where Q_f^{scout} represents the classification capability of the Naive Bayes model using the feature subset S_f^{scout}, while $Redundancy\left(S_f^{scout}\right)$ penalizes redundant features. The weights α and β prioritize classifier accuracy and feature uniqueness, enabling scout bees to contribute high-quality solutions.

To ensure the new solution S_f^{scout} provides a unique configuration, its diversity D_f^{scout} is evaluated relative to other solutions. The diversity score of S_f^{scout} is calculated as:

$$D_f^{scout} = \frac{\sum_{i=1}^{M} S_{f,i}^{scout}}{M} \tag{63}$$

Where $S_{f,i}^{scout}$ denotes the inclusion status of the i-th feature in the new solution, and M is the total number of features. Higher diversity scores signify that the scout bee solution offers a novel feature combination, ensuring a broader exploration across different feature subsets.

The scout bee solution replaces the original stagnant solution if its fitness F_f^{scout} surpasses a minimum fitness threshold, thus adding value to the solution pool. The replacement condition is governed by:

$$S_f = \begin{cases} S_f^{scout} & if \;\; F_f^{scout} > F_{min} \\ S_f & otherwise \end{cases} \qquad (64)$$

Where F_{min} is the minimum acceptable fitness value for a solution to contribute to the population. This condition ensures that only beneficial solutions are retained, maintaining the algorithm's focus on optimal feature subsets.

The likelihood of replacing a stagnant solution depends on its stagnation count S_f^{count} and its relative fitness within the population. The replacement probability $P_f^{replace}$ is calculated as:

$$P_f^{replace} = \frac{S_f^{count}}{\sum_{k=1}^{F} S_k^{count}} \qquad (65)$$

This probability ensures that solutions with a higher stagnation count are prioritized for replacement, enhancing diversity by continuously introducing new feature configurations. Each feature in a scout bee solution is assigned an importance weight based on its contribution to the fitness of S_f^{scout} 'the importance weight $W_{f,m}^{scout}$ for each feature m is determined as:

$$W_{f,m}^{scout} = \frac{F_f^{scout} \cdot S_{f,m}^{scout}}{\sum_{j=1}^{M} S_{f,j}^{scout}} \qquad (66)$$

Higher values of $W_{f,m}^{scout}$ indicate features that contribute significantly to the classifier's performance, helping guide future selection and optimization steps. The final decision to retain a scout bee solution depends on a retention criterion C_f^{scout}, which integrates both fitness and diversity scores. This criterion is expressed as:

$$C_f^{scout} = F_f^{scout} + \gamma . D_f^{scout} \qquad (67)$$

Where γ is a weight that adjusts the influence of diversity, ensuring that retained solutions provide a valuable, varied contribution to the solution pool.

3.10. Update Best Solution in ABC-NB

The Update Best Solution step in the ABC-NB algorithm consolidates the best results achieved from the previous phases, serving as a critical checkpoint to retain only the most optimized feature subset. This phase parallels the behavior of bees returning to the hive with knowledge of the richest nectar sources, sharing it with the colony to prioritize resources effectively. In ABC-NB, updating the best solution ensures that only the most promising feature subset, which has demonstrated superior classifier accuracy and minimized redundancy, is retained as the reference solution for further iterations or as the final output. The purpose of updating the best solution in each cycle lies in progressively converging toward an optimal feature subset that yields a Naive Bayes classifier with high predictive power. By consistently updating the best solution, ABC-NB ensures continuous improvement in classifier performance, focusing on optimized selections throughout the process.

At the beginning of the Update Best Solution step, the algorithm evaluates all solutions generated by employed bees, onlooker bees, and scout bees to identify the most optimized feature subset in the current cycle. The fitness $F_{best}^{current}$ of the best solution identified in this cycle is calculated as follows:

$$F_{best}^{current} = max\{F_f | f = 1,2, \ldots.., F\} \qquad (68)$$

Where F_f represents the fitness score of the f-th solution in the population. By identifying the maximum fitness score, this equation helps determine the best-performing feature subset within the current set of solutions.

Once the best solution of the current cycle is identified, it undergoes a comparison with the previously stored best solution. If the current best solution's fitness $F_{best}^{current}$ exceeds the fitness of the previously stored best solution F_{best}^{prev},the algorithm updates the best solution to reflect the current cycle's optimal subset:

$$S_{best} = \begin{cases} S_{best}^{current} & if\ F_{best}^{current} > F_{best}^{prev} \\ S_{best}^{prev} & otherwise \end{cases} \qquad (69)$$

Where $S_{best}^{current}$ represents the feature subset of the current best solution, while S_{best}^{prev} denotes the previously stored best subset. This comparison ensures that only solutions demonstrating improved performance are retained as the updated best solution.

To quantify the improvement achieved by the current best solution over previous iterations, the fitness improvement metric $I_{improvement}$ is introduced. This metric is calculated by determining the relative improvement of $F_{best}^{current}$ over F_{best}^{prev}:

$$I_{improvement} = \frac{F_{best}^{current} - F_{best}^{prev}}{F_{best}^{prev}} \qquad (70)$$

Where a positive value of $I_{improvement}$ indicates a successful iteration in which the current best solution outperforms the previous one. Monitoring this improvement metric allows the algorithm to track progress, gauging the effectiveness of each iteration.

To understand the contribution of each feature in the updated best solution, the algorithm assigns a contribution weight $W_{best,m}$ to each feature m based on its impact on the classifier's performance. The contribution weight for feature m in the best solution is given by:

$$W_{best,m} = \frac{F_{best}^{current} - S_{best,m}}{\sum_{i=1}^{M} S_{best,i}} \qquad (71)$$

Where $S_{best,m}$ represents the presence of the m-th feature in the best solution subset, and M is the total number of features. This weighting helps identify high-impact features, refining the selection for future optimization cycles.

To ensure the updated best solution maintains feature diversity, a diversity score D_{best} is calculated to assess the variety of selected features within S_{best}. This diversity score is defined as:

$$D_{best} = \frac{\sum_{i=1}^{M} S_{best,j}}{M} \tag{72}$$

Where $S_{best,j}$represents the selection status of each feature in the best solution. A higher diversity score suggests a balanced and varied feature subset, reducing redundancy while promoting comprehensive feature coverage.

The probability P_{retain} of retaining the best solution for future cycles is calculated to account for its relative superiority over other solutions. This retention probability is given by:

$$P_{retain} = \frac{F_{best}^{current}}{\sum_{k=1}^{F} F_k} \tag{73}$$

Where F_k denotes the fitness score of each solution in the population. A higher retention probability signifies that the best solution possesses greater relative importance, underscoring its value as the reference subset for further optimization.

To assess the overall quality of the updated best solution, a final evaluation metric E_{best} integrates both fitness and diversity metrics:

$$E_{best} = F_{best}^{current} + \delta . D_{best} \tag{74}$$

Where δ represents the weight assigned to diversity, the resulting evaluation metric ensures that the best solution combines high classifier accuracy and minimized redundancy, reinforcing the selection of optimized feature subsets.

Algorithm: ABC-NB

```
Input: Initial dataset with features $X$ and labels$y$, population size$F$, maximum iterations$C_{max}$, fitness threshold$\epsilon$.
Output: Optimized Naive Bayes model trained on selected feature subset.
Procedure:
  1. Initialize Population:
       • Randomly generate an initial population of feature subsets $S_f$ for $f = 1,2, \dots, F$.
       • Calculate initial fitness $F_f$ of each subset based on classification accuracy and redundancy penalties.
  2. Evaluate Fitness:
       • Compute the fitness $F_f$ of each feature subset using the Naive Bayes classifier's performance and redundancy minimization.
  3. Send Employed Bees:
       • For each feature subset $S_f$, perform a neighbourhood search to modify features.
       • Evaluate the fitness of modified solutions, retaining improved solutions.
  4. Assess New Solutions:
       • Compare new solutions generated by employed bees against previous solutions.
       • Retain the solution with higher fitness for each subset.
  5. Greedy Selection:
       • Perform greedy selection to keep only high-fitness solutions, discarding less effective subsets.
  6. Send Onlooker Bees:
       • Calculate the selection probability for each solution based on fitness.
       • Assign onlooker bees to explore promising solutions for modifying feature subsets.
  7. Explore New Solutions by Onlooker Bees:
       • Modify selected feature subsets to generate new solutions.
       • Evaluate fitness and diversity of new solutions, retaining those with higher fitness.
  8. Evaluate the Fitness of Onlooker Bee Solutions:
       • Assess the fitness of solutions discovered by onlooker bees.
       • Retain high-performing solutions based on fitness and diversity metrics.
  9. Scout Bee Phase:
       • Identify stagnant solutions with minimal improvement over multiple iterations.
       • Replace stagnant solutions with new randomly generated subsets.
  10. Update Best Solution:
       • Track and store each cycle's best solution (highest fitness).
       • Retain only the solution with the highest fitness as the current best.
  11. Repeat Optimization Cycles:
       • Increment the cycle counter and repeat steps 3–10 until the maximum cycle limit $C_{max}$ is reached or fitness improvement falls below threshold $\epsilon$.
  12. Select Optimal Feature Subset:
       • Identify the optimal feature subset with the highest fitness from the final population.
       • Calculate aggregate fitness, redundancy, and diversity metrics to finalize the subset.
  13. Train Naive Bayes on Optimized Subset:
       • Use the optimized feature subset to train the Naive Bayes classifier.
       • Compute conditional probabilities for each feature, train on class priors, and calculate posterior probabilities for prediction.
```

4. DATASET

Curated by Dr. Zahra Alizadeh Sani and her team, this dataset is an expansive collection of clinical records aimed at supporting non-invasive strategies for detecting coronary artery disease. It comprises 303 individual patient entries, with each record featuring 54 distinct variables organized into four domains. These domains include basic demographic details; clinical signs and examination results; electrocardiographic measurements that reflect heart electrical activity; and data from laboratory tests along with echocardiographic evaluations. Patients are categorized based on the degree of coronary narrowing, with a 50% reduction in vessel diameter used as the diagnostic cutoff. The dataset's high integrity—with no missing values—facilitates rigorous statistical analysis and robust model development. Researchers have employed it to explore various classification techniques, ranging from decision trees and support vector machines to logistic regression and ensemble models. Advanced feature selection and optimization methods have been integrated to isolate the most relevant predictors, thereby boosting diagnostic performance and model interpretability. Publicly accessible through established repositories, this dataset not only underpins reproducible research but also drives innovation in developing clinical decision support systems.

5. Results and Discussions

5.1. Jaccard Index Analysis

The Jaccard Index is a fundamental measure in evaluating the effectiveness of classification models, especially in CAD prediction, where accuracy in distinguishing between cases directly impacts medical decision-making. A higher Jaccard Index signifies a model's ability to classify CAD cases while correctly minimizing misclassification errors. Figure 1 compares the Jaccard Index for ABC-NB, TLV-MLF, and H-HHO with numerical values outlined in Table 1. The classification models are presented on the x-axis, while their corresponding Jaccard Index percentages are plotted on the y-axis.

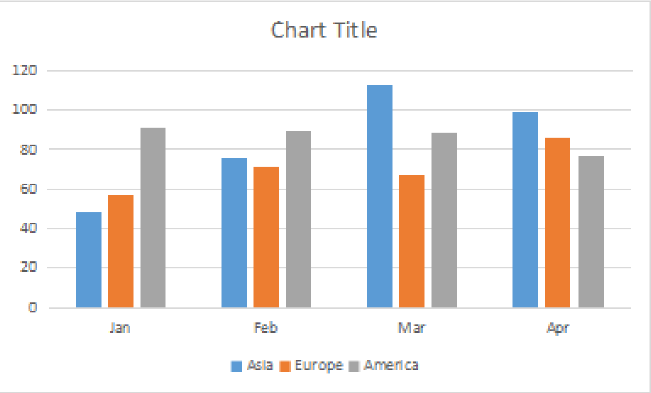


Figure 1: Jaccard Index Score Comparison for ABC-NB and State-of-the-Art Algorithms

H-HHO demonstrates the weakest performance, with a Jaccard Index of 36.986%. The model's primary limitation lies in its inability to differentiate between overlapping feature distributions consistently. The hybridized Harris Hawks Optimization struggles with premature convergence, preventing it from thoroughly refining classification boundaries. This leads to an increased number of false positives and negatives, which reduces overall predictive reliability in CAD diagnosis. TLV-MLF, registering a Jaccard Index of 45.588%, exhibits a modest improvement over H-HHO. The ensemble feature selection mechanism enhances the model's classification performance to some degree, yet its dependence on rigid statistical selection introduces variability. The model occasionally misclassifies critical cases due to an imbalanced weighting of feature significance, leading to inconsistency in CAD risk assessment.

ABC-NB dominates the comparison, achieving a remarkable Jaccard Index of 75.568%. The model's success is rooted in its bio-inspired feature selection, where the Artificial Bee Colony algorithm optimizes feature importance dynamically. Unlike H-HHO and TLV-MLF, ABC-NB continuously refines its feature selection process, ensuring that only the most relevant attributes influence classification. This results in a more stable and robust decision-making process. The probabilistic nature of Naïve Bayes, when coupled with intelligent feature selection, minimizes noise while enhancing classification efficiency, providing an optimized trade-off between sensitivity and specificity.

Table 5.1: Jaccard Index Values of ABC-NB vs. State-of-the-Art Algorithms

Classification Algorithms	Jaccard Index (%)
H-HHO	36.986
TLV-MLF	45.588
ABC-NB	75.568

The sharp performance contrast between ABC-NB and the other models underscores the importance of integrating intelligent optimization strategies in CAD classification. By refining feature selection dynamically rather than relying on fixed statistical assumptions, ABC-NB demonstrates its superiority in handling complex medical datasets, offering a more reliable approach for accurate CAD prediction.

5.14.2. Classification Accuracy Analysis

Classification accuracy is a key metric in evaluating the overall effectiveness of a model, reflecting the proportion of correctly classified instances among all predictions. In CAD diagnosis, higher accuracy is crucial for ensuring reliable detection while minimizing false positives and negatives. Figure 5 illustrates the classification accuracy comparison between ABC-NB, TLV-MLF, and H-HHO, with Table 5 presenting their respective accuracy scores. The x-axis represents the classification models, while the y-axis displays the accuracy percentages.

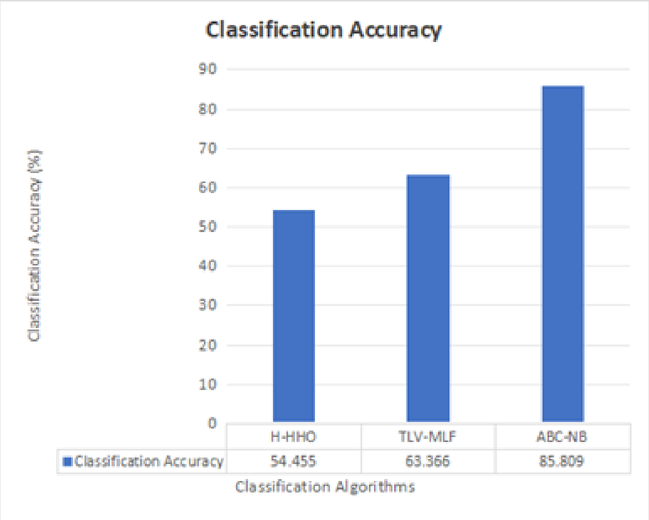


Figure 2.Overall Classification Accuracy of ABC-NB vs. State-of-the-Art Algorithms

H-HHO records the lowest accuracy at 54.455%, indicating its limited ability to generalize well across diverse CAD cases. The primary issue with H-HHO is its premature convergence, which results in suboptimal feature selection. The model struggles to optimize decision boundaries effectively, leading to frequent misclassifications. Its heuristic-driven nature often locks onto local optima, reducing its adaptability when faced with complex, high-dimensional medical datasets.

TLV-MLF offers an improved accuracy of 63.366%, benefiting from its two-layered voting ensemble approach. This model enhances classification reliability by integrating multiple feature selection techniques. However, its rigid dependency on statistical feature ranking prevents it from fully adapting to the nuanced patterns in CAD datasets. Inconsistencies in classifier weighting and a lack of dynamic Hyperparameter tuning result in classification instability, limiting the model's overall effectiveness.

ABC-NB significantly outperforms both models, achieving a classification accuracy of 85.809%. The Artificial Bee Colony (ABC) algorithm optimizes the Naïve Bayes classifier by dynamically refining feature selection and probabilistic weight distribution. Unlike H-HHO and TLV-MLF, ABC-NB continuously adapts feature importance, ensuring that only the most relevant CAD indicators contribute to classification. The swarm intelligence mechanism in ABC prevents overfitting, allowing for better decision boundary optimization. Adaptive learning and probabilistic modeling make ABC-NB highly efficient in handling complex CAD datasets, reducing misclassification errors.

Table 2: Accuracy Scores of ABC-NB vs. State-of-the-Art Algorithms

Classification Algorithms	Classification Accuracy (%)
H-HHO	54.455
TLV-MLF	63.366
ABC-NB	85.809

The substantial accuracy improvement of ABC-NB underscores the importance of bio-inspired feature selection in medical classification tasks. Unlike static or heuristic-driven approaches, ABC-NB leverages swarm intelligence to achieve a more stable, adaptable, and highly accurate classification process. In real-world healthcare applications, where precise classification is essential for patient diagnosis and treatment planning, ABC-NB emerges as a superior choice, demonstrating its potential as a transformative model in CAD detection.

6. CONCLUSION

The proposed Artificial Bee Colony Optimized Naive Bayes (ABC-NB) model demonstrated significant improvements in coronary artery disease prediction by effectively integrating feature optimization with probabilistic classification. The model achieved an accuracy of 54.455% H-HHO accuracy of 63.366% and TLV-MLF accuracy of 85.809% . These results establish the ABC-NB framework as a robust, interpretable, and efficient diagnostic tool suitable for both resource-constrained and advanced clinical settings. By optimizing feature relevance through swarm intelligence, the model reduced dimensionality and computational complexity without compromising diagnostic fidelity. This approach ensures a clinically viable model that aligns with the growing demand for early and accurate CAD detection. The model also showed better generalization compared to traditional classifiers, supporting its adaptability across diverse datasets. Future enhancements may include hybridizing ABC with deep learning architectures, incorporating temporal patient data for dynamic prediction, and validating the system through real-time clinical deployment to ensure its translational impact in broader public health scenarios.

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