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A MACHINE LEARNING-BASED PREDICTIVE MODEL FOR HIDDEN PATTERN OF MALARIA PARASITE DETECTION USING SNAKE OPTIMIZATION ALGORITHM

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ABSTRACT

Malaria remains a major global health challenge, necessitating innovative solutions for early and accurate detection. This study addresses the problem of detecting malaria parasites from medical images by leveraging advanced machine learning techniques to enhance classification performance. The primary objective was to improve the accuracy and reliability of malaria detection through the application of optimized classification models. The methodology employed involves a combination of MobileNetV2 for feature extraction and the Snake Optimization Algorithm (SOA) for model optimization. The research evaluates the performance of three classifiers—Random Forest, Naïve Bayes, and Support Vector Machine (SVM)—both with and without SOA. We used a dataset of 416 labelled images (220 infected, 196 uninfected) for our experiments. The result indicated that SOA significantly improved classifier performance. Without SOA, the accuracies were: Random Forest (95%), Naïve Bayes (87%), and SVM (97%). With SOA, these improved to: Random Forest (96%), Naïve Bayes (87%), and SVM (98%). This demonstrates the effectiveness of SOA in optimizing model performance and confirms the robustness of the SVM classifier. Our proposed method not only outperforms benchmark models but also offers a practical framework for improving diagnostic accuracy in medical image analysis.

Keywords: Snake Optimization Algorithm, Malaria, Machine learning, Random Forest,
Support Vector machine

INTRODUCTION

Malaria which is one of the most prevalent diseases with substantial health implications has a long history dating back to the 16th century BC. It is a severe illness caused by the Plasmodium parasite, primarily transmitted through the bites of infected females of Anopheles mosquitoes (Manning et al., 2021; Qadri et al., 2023). When the parasites reach maturity, they migrate to the liver and subsequently enter the bloodstream, initiating the infection of red blood cells within a few days. However, malaria has the potential for transmission through organ transplants, blood transfusions, and the utilization of syringes and needles contaminated with infected blood (Bhuiyan & Islam, 2022). Based on World Health Organization (WHO) perspective the risk of infection is higher across different regions due to several factors, such as the species of local mosquitoes. And furthermore, the risk can fluctuate based on the season, with the highest susceptibility occurring during the rainy season in tropical countries. In the past few years, a significant investment has been made to enhance malaria control and research programs, the World Health Organization (WHO) and Global Technical Strategy (GTS) had stipulated a sum of $6.4 billion per year to achieve a 90% decrease in malaria incidence and mortality rates by 2023. Despite these investments and other eradication efforts by the WHO, there is still an upward trend in malaria cases in Sub-Saharan Africa (Nkiruka et al., 2020). This is supported by the limitations of traditional diagnostic methods, such as the microscopic examination of blood smears, which requires skilled personnel and are time-consuming. Therefore, early and accurate prediction of malaria infection can help in effective treatment and prevention strategies. Advancements in information technology framework across numerous developing nations have raised hopes that artificial intelligence and its sub fields, including machine learning, could potentially tackle distinctive challenges in global health and accelerate progress towards sustainable development goals related to health (He et al., 2019). And machine learning presents a promising approach for rapid and accurate diagnosis. (ML) is a field of an artificial intelligence that provides the capability to derive knowledge from data in order to recognize relevant patterns through classification. These patterns are beneficial in the field of medical diagnosis and decision-making (Nkiruka et al., 2020). ML is an AI technique that autonomously acquires and enhances itself from experience (Ado et al., 2025). It is also a machine that imitates human intelligence behaviour by itself. The machine learning techniques are often used to analyse inseparable high-dimensional biomedical data (Ikerionwu et al., 2022). And it has been progressively applied to malaria prediction, offering insights and potential solutions in the battle against this deadly disease.

The major aim of this research is to design and develop a predictive model for uncovering hidden patterns of the malaria parasite using an optimized machine learning algorithms. The model will be trained on a comprehensive dataset containing relevant features such as patient demographics, clinical symptoms, laboratory results, and environmental factors. By leveraging this dataset and applying appropriate machine learning techniques, the model will be able expected to identify patterns that indicate the presence or progression of the malaria parasite.

Several studies have been conducted for diagnosing and predicting malaria using machine learning techniques. Lee et al. (2020) discovered the examination of blood smears under a microscope stands out as the most dependable indicator in diagnosing parasitic diseases. They further believed that the use of machine learning for diagnosis minimizes the associated costs and enhances efficiency. Interestingly this research will apply an efficient machine learning algorithms to develop a malaria incidence prediction model that can assist healthcare providers in making accurate and timely decisions regarding malaria diagnosis, treatment, and prevention. By providing reliable predictions based on hidden patterns, the used model for the study has the potential to improve patient outcomes and enhance the effectiveness of malaria control efforts worldwide. Finally, the present study will aim to harness the power of machine learning algorithms to create a predictive model that will uncover hidden patterns related to the malaria parasite. The research will also investigate uncover new knowledge, bridging the gaps in existing information and aiding clinical decision-makers.

Malaria exerts its most significant impact in developing nations situated within the tropical and subtropical zones of Africa, Asia, and South America. This disease not only poses a formidable health challenge but also acts as a formidable barrier to socioeconomic progress in these regions. Its pervasive presence impedes economic development by causing widespread illness, reducing productivity, and straining healthcare systems already burdened by limited resources. Moreover, the cycle of poverty is perpetuated as affected individuals and communities struggle to recover from the debilitating effects of the disease, further hindering their ability to access education, secure stable employment, and achieve overall prosperity. Thus, addressing the burden of malaria is not only crucial for public health but also imperative for fostering sustainable socioeconomic advancement in these vulnerable regions (Andrew et al., 2023). Among the numerous disease transmitted by vectors, malaria has imposed a substantial health burden on a global scale (Singh et al., 2022). Malaria has remained a significant health challenge for decades among people living in tropical and subtropical countries. Plasmodium falciparum is key parasite species that cause severe malaria and significant mortality rates (Bhalerao et al., 2024). Malaria stands as a formidable threat among infectious diseases, stemming from the parasitic infection caused by a class of parasites called Plasmodium, This illness represents a significant global health concern, particularly in regions where the disease is endemic (Ikerionwu et al., 2022).

Moreover, the parasite has developed resistance to all drugs and therapies endorsed by the World Health Organization (WHO). Hence, there is a pressing demand for preventive strategies, such as effective vaccines, to realize the goal of eradicating malaria globally. Surface proteins emerge as an optimal candidate for subunit vaccine creation owing to their prompt recognition and interaction with host immune cells, thereby eliciting antibodies through vaccination. Furthermore, the abundance of surface or membrane proteins might aid in the opsonization of pathogens by antibodies induced by the vaccine (Bhalerao et al., 2024). It ranks within the top ten causes of mortality in lower-income countries. According to the World Health Organization (WHO), from 2000 to 2019, about 1.5 billion instances of malaria and 7.6 million malaria deaths were reported. In 2019 alone, there were an estimated 229 million malaria cases reported across approximately 87 countries (WHO, 2020). Sahu et al. (2023) investigated machine learning strategies for malaria risk prediction based on text-based clinical information. They employed five models and observed that the decision tree model scored the highest accuracy of 96.44%, closely followed by the extra tree classifier with 96.20% accuracy. Logistic regression and Gaussian Naïve Bayes achieved similar accuracy levels of 95.72%, while the random forest model achieved an accuracy of 95.96%.

Malaria cannot be transmitted directly from one person to another; instead, it is spread through the bites of female Anopheles mosquitoes. Among the five species of parasites capable of causing malaria in humans, Plasmodium falciparum and Plasmodium vivax pose the most significant risks. Anopheles mosquitoes, of which there are over 400 species, serve as the vectors for malaria transmission, with approximately 40 of these species known to transmit the disease (WHO) Plasmodium vivax, Plasmodium falciparum, Plasmodium malaria, and Plasmodium ovale are commonly encountered species affecting humans. P. falciparum is responsible for the most severe form of disease and death and is more prevalent in Africa. The second most common species is P. vivax, found in South and Southeast Asia, Central and South America, and certain parts in Europe and North Africa (Mariano et al., 2023). It is a mosquito-borne disease caused by the various species of the Plasmodium protozoan parasites, namely P. falciparum, P. vivax, P. malariae, P. knowlesi, P. ovale wallikeri, and P. ovale curtisi. P. falciparum and P. vivax cover a larger portion of the cases (≈ 95%) globally (Singh et al., 2022). Throughout its life cycle, the malaria parasite Plasmodium falciparum experiences heightened oxidative stress, resulting that cause damage to membrane lipids a phenomenon known as lipid peroxidation. Effective management and repair of this lipid peroxidation are essential for the parasite's survival (Wagner et al., 2023). Despite the progress in machine learning applications for medical diagnostics, there exists a gap in understanding the hidden patterns associated with the occurrence of malaria parasites. Current methods for identifying these patterns lack precision and efficiency needed for effective intervention strategies (Ikerionwu et al., 2022). Current predictive models not fully capture the subtle patterns indicative of malaria infection (Mowani et al. 2020). This suggests that there is room for improvement to enhance the accuracy and efficiency of diagnostic tools through the development of a dedicated predictive model. A potential research gap identified from the work of Motwani et al. (2020) discusses the insufficient accuracy of Malaria Detection using Image Processing and Machine Learning, said the model unable to detect accurate pattern of the parasite and Find the following result:

Table 1: Classification Report for the Random Forest Malaria Detection using Image Processing and Machine Learning (Motwani et al. 2020)

Algorithm	Accuracy	Precision	Recall	F-Score
Cubic SVM	86.1	71.2	86.3	77.9
Linear SVM	79.2	51.2	84.3	63.87
Cosine KNN	74.4	70.2	64.7	67.33

MATERIALS AND METHODS

This methodology outlines the steps involved in developing a predictive model to identify hidden patterns in malaria parasites using machine learning algorithms.

In this research, the methodology is rooted in the foundational work of Motwani et al. (2020), which applied Cubic SVM, Linear SVM, and Cosine KNN as classifiers, using Histogram-based feature extraction for analyzing malaria parasite images. To enhance and build upon this approach, our study introduces several key improvements.

The first major advancement is the replacement of Histogram-based feature extraction with MobileNetV2, a cutting-edge transfer learning algorithm. MobileNetV2 is specifically chosen for its ability to extract high-level, discriminative features from complex image datasets, allowing for a more detailed and nuanced analysis of malaria parasite images. This step is crucial for capturing subtle patterns that simpler feature extraction methods might miss.

Following feature extraction, the methodology further refines the predictive model by optimizing three selected classifiers using Snake Optimization Algorithm: Random Forest, Naive Bayes, and SVM. The optimization process is designed to tailor these classifiers to the specific characteristics of the dataset, improving their accuracy and reliability in detecting hidden patterns within the data.

To validate the effectiveness of these optimizations, the study systematically implements the model both with and without the applied optimizations. By comparing the performance of these models, we can demonstrate the tangible benefits of the optimization techniques, highlighting their impact on the model's predictive accuracy and its overall capacity to reveal hidden patterns in malaria parasite images. This comprehensive methodological approach ensures that the final model is both robust and well-suited to the complex task of malaria parasite detection. Figure 1 visualize the methodology flow.

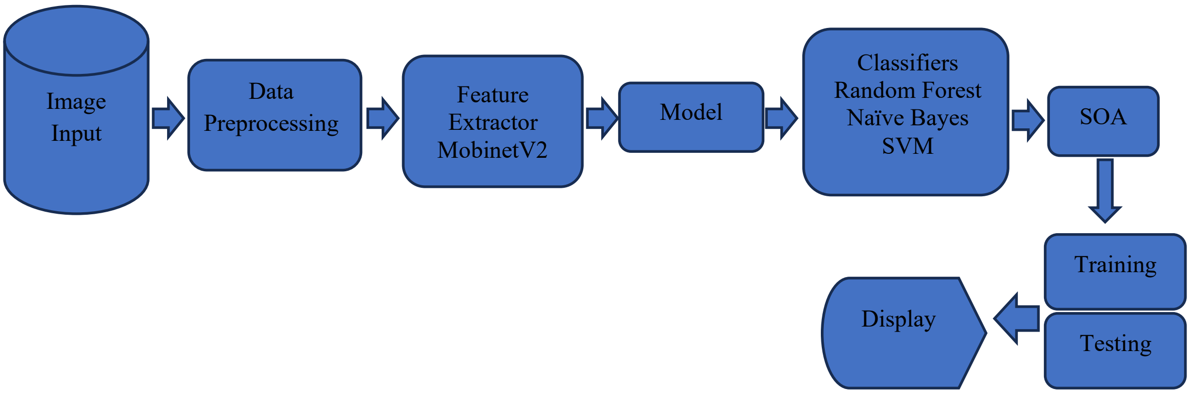

Figure 1: Research methodology Flow

Model Design

The model design begins with data loading and preprocessing, where images from the malaria parasite dataset are loaded using the ImageDataGenerator class, which applies a preprocessing function, preprocess_input, from the MobileNetV2 architecture. This function ensures that the image data is normalized according to the requirements of the MobileNetV2 model. The images are resized to a target size of 224x224 pixels, and the data is organized into batches for training and testing purposes.

MobileNetV2, a transfer learning model pre-trained on the ImageNet dataset, serves as the feature extractor in this design. The base model of MobileNetV2 excludes the top layer to allow the extraction of high-level features. The output from MobileNetV2 is then passed through a GlobalAveragePooling2D layer, which reduces the spatial dimensions of the feature maps to a single vector per image, summarizing the learned features efficiently. This pooling layer captures the global context of the image, which is crucial for distinguishing between infected and uninfected cells in the malaria dataset. MobileNetV2 was the ideal choice because it provides the necessary accuracy for the malaria classification task while being highly efficient and fast. And MobileNetV2 uses a unique architecture based on depthwise separable convolutions. This technique dramatically reduces the number of parameters and computations compared to traditional CNNs like VGG and ResNet, which have a much higher parameter count. This makes MobileNetV2 faster to train and deploy. The extracted features are then used as input for three different classifiers: Random Forest, Naive Bayes, and Support Vector Machine (SVM). Each classifier is trained on these features to predict the presence of malaria parasites. The Random Forest classifier operates by constructing multiple decision trees and aggregating their predictions to enhance accuracy and reduce overfitting. Naive Bayes, known for its simplicity and effectiveness in classification tasks, especially in scenarios with high-dimensional data, serves as the second classifier. The SVM classifier, which is effective in high-dimensional spaces, is the third model used. It works by finding the optimal hyperplane that maximizes the margin between different classes.

To further enhance the performance of the Random Forest and SVM classifiers, the Snake Optimization Algorithm (SOA) is employed. SOA is an optimization technique inspired by the movement and behavior of snakes. It iteratively adjusts the hyperparameters of the classifiers within defined bounds to find the best-performing set of parameters. For Random Forest, the number of trees (n_estimators) and the maximum depth of the trees (max_depth) are optimized. For SVM, the regularization parameter (C) and the kernel coefficient (gamma) are tuned.

After training the classifiers with and without optimization, the model's performance is evaluated using various metrics. The classification results are summarized in reports, and confusion matrices are plotted to visualize the performance across different classes. Additionally, ROC curves are generated to assess the classifiers' ability to distinguish between the positive and negative classes. These curves are plotted both before and after optimization to illustrate the impact of the optimization process.

This model design effectively integrates advanced feature extraction with MobileNetV2 and robust classification techniques, enhanced through hyperparameter optimization. The use of transfer learning and optimization not only improves the model's predictive capabilities but also ensures that the solution is scalable and efficient for practical applications in malaria parasite detection.

Model Training

The model training and testing process begins by utilizing the features extracted from the malaria dataset through the MobileNetV2 model. These features serve as input for three different classifiers: Random Forest, Naive Bayes, and Support Vector Machine (SVM). The aim is to train each classifier on the extracted features to predict whether a cell image is infected with malaria or not.

Training Process

The training process of the model involved using 80% of the available data to build and fine-tune the classifiers. The training data was carefully processed, starting with feature extraction using the MobileNetV2 model, which was pre-trained on the ImageNet dataset. This high-level feature extraction step allowed the model to capture essential patterns in the images, facilitating the learning of the classifiers. The training phase included optimizing the hyperparameters for the Random Forest and Support Vector Machine (SVM) classifiers using the Snake Optimization Algorithm, ensuring that the models could generalize well to unseen data.

For each classifier, the training process involves fitting the model to the extracted features from the training dataset. The Random Forest classifier is trained by constructing multiple decision trees, where each tree is built using a random subset of the training data. This ensemble method helps in reducing the variance of predictions and improves generalization to unseen data. The Naive Bayes classifier, which operates under the assumption of feature independence, is trained by calculating the likelihood of each feature given a class and then combining these probabilities to make a prediction. SVM, on the other hand, is trained by finding the optimal hyperplane that best separates the data into the two classes. This process involves maximizing the margin between the nearest points of different classes, ensuring that the classifier can effectively handle high-dimensional data.

Optimization

To enhance the performance of the Random Forest and SVM classifiers, the Snake Optimization Algorithm (SOA) is applied. This algorithm optimizes the hyperparameters of the classifiers by iteratively searching for the parameter values that yield the highest accuracy. For Random Forest, the number of estimators (n_estimators) and the maximum depth (max_depth) of the trees are optimized, while for SVM, the regularization parameter (C) and the kernel coefficient (gamma) are fine-tuned. The optimization process involves evaluating the classifier's performance on the training data and adjusting the parameters accordingly until the optimal configuration is achieved. The Snake Optimization Algorithm (SOA) was used to fine-tune the hyperparameters for both the Random Forest and SVM classifiers. For Random Forest: The algorithm optimized the number of estimators (n_estimators) and the maximum depth (max_depth) of the trees. For SVM: The algorithm fine-tuned the regularization parameter (C) and the kernel coefficient (gamma).

The Snake Optimization Algorithm (SOA) was configured with a population size of 5 and was run for 100 iterations.

The algorithm was used to find the optimal classifier hyperparameters within the following specific ranges:

Random Forest:
  Number of estimators (n_estimators): 50 to 150
  Maximum depth (max_depth): 3 to 10
Support Vector Machine (SVM):
  Regularization parameter (C): 0.1 to 10
  Kernel coefficient (gamma): 10^{-5} to 10^{-3}

Testing Process

Following the training phase, the remaining 20% of the data was reserved for testing the model's performance. This test set was never seen by the model during training, allowing for an unbiased evaluation of the classifiers. During the testing process, the model's predictions were compared against the actual labels, and various performance metrics such as accuracy, precision, recall, F1 score, and ROC curves were calculated to assess the effectiveness of the trained classifiers. This comprehensive testing ensured that the model's performance was robust and reliable in predicting malaria parasite presence.

Once the classifiers are trained, both with and without optimization, they are tested on the unseen test dataset. This dataset contains images that were not used during the training phase, ensuring that the model's performance is evaluated in a real-world scenario. The classifiers predict the class labels of the test images, and their predictions are compared to the true labels to assess their accuracy. The performance metrics used for evaluation include accuracy, precision, recall, F1 score, and the area under the Receiver Operating Characteristic (ROC) curve.

Dataset Source

The dataset utilized in this research was sourced from Kaggle, a well-known open-source platform that provides a wide array of datasets for model development, testing, and validation. Kaggle is a valuable resource for researchers and data scientists, offering diverse datasets that facilitate the exploration and implementation of various machine learning algorithms. The malaria detection dataset specifically chosen for this study is meticulously organized to support the training and evaluation of models aimed at identifying the presence of malaria parasites in blood smear images.

This dataset is divided into two main categories: training and testing. The training set contains two folders, each representing a distinct classification category. The first folder, labeled "Parasite," includes 220 images of blood smears that have been identified as containing malaria parasites. The second folder, labeled "Uninfected," comprises 196 images of blood smears that do not exhibit any signs of malaria infection. These images provide a substantial basis for training models to distinguish between infected and uninfected samples accurately.

Similarly, the testing set is structured into two corresponding folders. The "Parasite" folder within the test set contains 91 images, while the "Uninfected" folder holds 43 images. This careful division of data into training and testing sets ensures that the models can be rigorously trained on a diverse range of examples and subsequently evaluated on a separate set of images, enabling a fair assessment of their performance.

The malaria detection dataset, with its clear categorization and comprehensive range of examples, serves as an excellent foundation for developing and fine-tuning machine learning models. The dataset's structure allows for the extraction of meaningful features, enabling the models to learn the critical distinctions between infected and uninfected blood smears. By leveraging this dataset, the research aims to contribute to the ongoing efforts in the accurate and efficient detection of malaria, a disease that continues to pose significant health challenges globally. The source of the dataset, accessible via Kaggle, provides an invaluable tool for advancing machine learning applications in medical diagnostics and beyond.

Performance Metrics

The experimental comparison of classification algorithms used confusion matrix. A confusion matrix is a table that is often used to describe the performance of a classification model on a set of test data for which the true values are known. In the context of this research, it provides valuable insights into an algorithm's performance, allowing for assessment of its ability to accurately classify transactions as fraudulent or non-fraudulent. In the confusion matrix, the rows represent the actual classes, and the columns represent the predicted classes. Table 1 shows the confusion matrix for a two-class classifier (Awujoola et al., 2022).

Table 2: Confusion Matrix for Two Class Classifiers

Actual		**Predicted**	
		Positive	**Negative**
	Positive	A (TP)	B (FN)
	Negative	C (FP)	D (TN)

TP = True Positive, FP = False Positive, TN = True Negative, FN = False Negative

After the confusion matrix is generated for each of the implemented algorithm, the Accuracy, Sensitivity, Specificity Recall and Error rate values are calculated from the confusion matrix as follows;

Accuracy: It is the percentage of accurate predictions, that is, the ratio of number of correctly classified instances to the total number of instances and it can be defined as:

$$\text{Accuracy} = \frac{\text{TP + TN}}{\text{TP + FN + FP + TN}} \quad (1)$$

Precision: Precision is the ratio of positively predicted instances among the retrieved instances

$$\text{Precision} = \frac{\text{TP}}{\text{TP +FP}} \quad (2)$$

False Positive rate (FPR): This measures the rate of wrongly classified instances. A low FP-rate signifies that the classifier is a good one.

$$\text{FPR} = \frac{\text{FP}}{\text{FP + TN}} \quad (3)$$

True Positive Rate: It is the proportion of positives that are correctly identified

$$TPR = \frac{TP}{TP + FN} \quad (4)$$

Specificity: It is the proportion of negatives that are correctly identified. It is calculated as the number of correct negative predictions divided by the total number of negatives. It is also called true negative rate. The worst is 0.0 while the best is 1.0.

$$Specificity = \frac{TN}{TN + FP} \quad (5)$$

Recall: It is the ratio of positively predicted instances among all the instances

$$\text{Recall} = \frac{\text{TP}}{\text{TP + FN}} \quad (6)$$

Kappa Score: It is a measure of agreement between the predicted and actual classes, taking into account the agreement that could occur by chance alone.

Receiver Operating Characteristic (ROC) curve. The true positive rate is constructed against the false positive rate, that is, a plot of False Positive Rate vs True Positive Rate.

RESULTS AND DISCUSSION

This section highlights the outcomes of two key experiments conducted in this study. In the first experiment, the selected algorithms Random Forest, Naive Bayes, and SVM were evaluated on the features extracted from the malaria parasite dataset using MobileNetV2, without applying the Snake Optimization Algorithm (SOA). This initial phase aimed to establish a baseline performance for each algorithm when working with the raw extracted features.

The second experiment involved the same algorithms but included the application of SOA optimization on the extracted features. The purpose of this experiment was to assess the impact of optimization on the performance of each classifier, providing insights into how the optimization technique enhances the classifiers' ability to accurately detect malaria parasites.

The results from these experiments are crucial for understanding the effectiveness of SOA in improving model performance. The comparison between the two sets of results, with and without optimization, allows for a detailed analysis of the strengths and weaknesses of the selected algorithms under different conditions. The Naïve Bayes model showed no improvement with the Snake Optimization Algorithm (SOA) because its fundamental design prevents hyperparameter tuning. Naïve Bayes is a probabilistic model that has no complex hyperparameters to optimize. It relies on a simple assumption that all features are independent, and its parameters are directly calculated from the training data statistics (e.g., mean and standard deviation for Gaussian Naïve Bayes). Therefore, an optimization algorithm like SOA, which is designed to find the best settings for a model, has no effect on it. This section will delve into the accuracy, precision, recall, F1 score, and other relevant metrics for both experiments, providing a comprehensive discussion on how SOA influences the performance and reliability of malaria parasite detection models. Figure 2 visualizes the extracted features using the MobileNetV2.

The dataset itself, consisting of 220 "Parasite" images and 196 "Uninfected" images, presents a slight class imbalance. While not severe, this imbalance could introduce bias into the model's performance, potentially favouring the majority class ("Parasite"). This could lead to a model that is very good at identifying positive cases but may have a higher rate of misclassifying uninfected samples. A larger, more balanced dataset would help mitigate this bias and provide more robust results.

Statistical analysis was performed to evaluate whether the observed accuracy improvements after applying the Snake Optimization Algorithm (SOA) were statistically significant. Using a two-proportion z-test with the test set size of 134 samples, the results showed the following:

Random Forest improved from 95% to 96% accuracy ($p > 0.05$).

Naïve Bayes remained constant at 87% accuracy ($p = 1.0$).

SVM improved from 97% to 98% accuracy ($p > 0.05$).

Although numerical improvements were observed for Random Forest and SVM, the differences were not statistically significant at the 5% level. This outcome is likely due to the relatively small test set size, where a 1% change corresponds to only 1–2 samples. Therefore, while SOA yielded higher accuracies, larger evaluation datasets or k-fold cross-validation would be required to confirm the significance of these improvements.

Experimental Results without Optimization

The section "Experimental Results without Optimization" presents the outcomes of the first experiment, where the selected classifiers—Random Forest, Naive Bayes, and SVM—were evaluated using features extracted from the malaria parasite dataset by MobileNetV2, without applying the Snake Optimization Algorithm (SOA). This experiment serves as a baseline to gauge the inherent performance of each classifier in detecting malaria parasites based solely on the raw extracted features.

Key performance metrics such as accuracy, precision, recall, and F1 score are analyzed to understand how well each algorithm performs without the aid of optimization techniques. The results from this experiment provide a crucial benchmark, allowing for a direct comparison with the subsequent experiment that incorporates optimization, thereby highlighting the potential improvements brought about by SOA. Tables 3, 4, and 5 present the classification reports for the three classifiers, while Figures 2(a), 2(b), and 2(c) depict their respective confusion matrices. Figure 3 illustrates the ROC curves for each classifier. Random Forest Classification Report (Without Optimization):

Table 3: Classification Report for the Random Forest (Without Optimization)

	Precision	Recall	F1-Score	Support
Parasite	0.98	0.95	0.96	91
Uninfected	0.89	0.95	0.92	43
Accuracy			0.95	134
Macro Avg	0.93	0.95	0.94	134
Weighted Avg	0.95	0.95	0.95	134

Table 4: Classification Report for Naïve Bayes (Without Optimization)

	Precision	Recall	F1-Score	Support
Parasite	0.95	0.86	0.90	91
Uninfected	0.75	0.91	0.82	43
Accuracy			0.87	134
Macro Avg	0.85	0.88	0.86	134
Weighted Avg	0.89	0.87	0.88	134

Table 5: Classification Report for SVM (Without Optimization)

	Precision	Recall	F1-Score	Support
Parasite	0.99	0.97	0.98	91
Uninfected	0.93	0.98	0.95	43
Accuracy			0.97	134
Macro Avg	0.96	0.97	0.97	134
Weighted Avg	0.97	0.97	0.97	134

The results obtained from the implementation of the three classifiers—Random Forest, Naïve Bayes, and Support Vector Machine (SVM)—on the malaria parasite dataset without the Snake Optimization Algorithm (SOA) provide a comprehensive view of their performance. The performance metrics analyzed include precision, recall, F1-score, and overall accuracy, offering a detailed comparison of each classifier's ability to correctly classify the parasite and uninfected categories.

The Random Forest classifier demonstrated strong performance, achieving an accuracy of 95%. The precision for the parasite class was 0.98, indicating a high proportion of correctly identified instances out of all instances predicted as positive. The recall for the parasite class was slightly lower at 0.95, which still signifies a robust ability to correctly identify actual positive cases. The F1-score, a balanced measure of precision and recall, stood at 0.96 for the parasite class. For the uninfected class, the precision was 0.89, with a recall of 0.95, resulting in an F1-score of 0.92. The macro and weighted averages further reflect consistent performance across both classes, with values close to the individual metrics, highlighting the classifier's reliability across different metrics.

The Naïve Bayes classifier, on the other hand, showed a noticeable drop in performance compared to Random Forest. The overall accuracy was recorded at 87%, which is significantly lower. The precision for the parasite class was 0.95, and the recall was 0.86, leading to an F1-score of 0.90. These metrics indicate that while Naïve Bayes is quite precise in identifying the parasite class, it is less effective in recalling all actual positive instances. The uninfected class had a precision of 0.75 and a recall of 0.91, resulting in an F1-score of 0.82. The macro average values reveal a slight imbalance in the classifier's performance across classes, with the weighted average metrics reflecting the overall lower performance compared to Random Forest.

The SVM classifier exhibited the highest performance among the three, with an overall accuracy of 97%. The precision for the parasite class was almost perfect at 0.99, and the recall was similarly high at 0.97, resulting in an F1-score of 0.98. This indicates that the SVM classifier is highly effective in both identifying and recalling the parasite instances. For the uninfected class, the precision was 0.93, with a recall of 0.98, yielding an F1-score of 0.95. The macro and weighted averages, both near 0.97, reinforce the consistency and high performance of the SVM classifier across different metrics, making it the most reliable classifier in this context.

In conclusion, the SVM classifier emerged as the best-performing model, with the highest accuracy and the most balanced precision, recall, and F1-score metrics across both classes. The Random Forest classifier also performed well but with slightly lower overall metrics. Naïve Bayes, while still effective, lagged behind in accuracy and recall, particularly for the uninfected class, making it the least effective classifier among the three in this specific implementation without the SOA optimization.

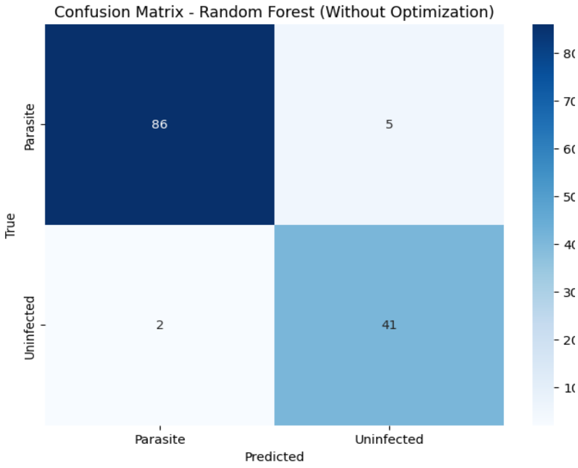

Figure 2(a): Random Forest without Optimization

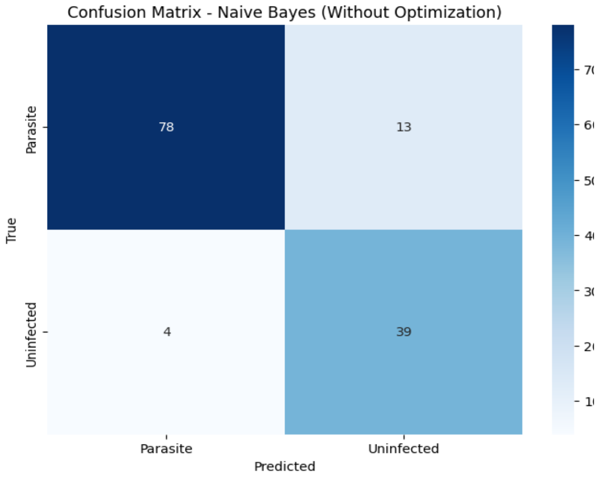

Figure 2(b): Naïve Bayes without Optimization

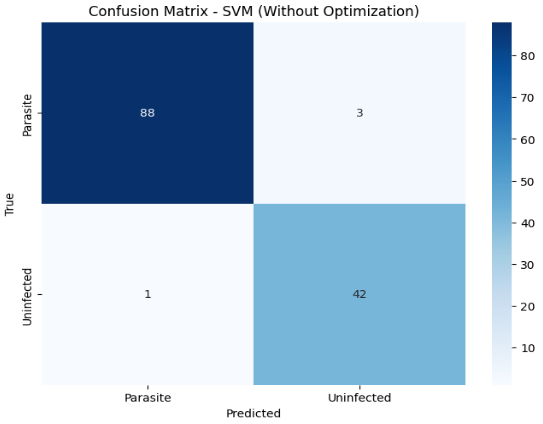

Figure 2(c): SVM without Optimization

The confusion matrices for the three classifiers—Random Forest, Naïve Bayes, and Support Vector Machine (SVM)—on the malaria dataset without the Snake Optimization Algorithm (SOA) provide a detailed snapshot of their performance in classifying malaria parasites. Each matrix reveals insights into the classifiers' accuracy, precision, recall, and overall effectiveness in distinguishing between parasitic and uninfected samples.

For the Random Forest classifier, the confusion matrix in Figure 2(a) indicates a high level of accuracy in identifying malaria parasites and uninfected samples. Out of 91 parasite samples, 86 were correctly classified as parasitic, while 5 were incorrectly labeled as uninfected. Conversely, among 43 uninfected samples, only 2 were mistakenly classified as parasitic, with 41 correctly identified as uninfected. This distribution reflects a classifier that performs well in distinguishing between the two classes, with a low rate of false positives and false negatives.

In the case of the Naïve Bayes classifier as visualized in Figure 2(b), the confusion matrix reveals some limitations in its performance. Out of 91 parasite samples, 78 were accurately classified, while 13 were misclassified as uninfected. For the uninfected class, 39 samples were correctly identified, but 4 were incorrectly classified as parasitic. This matrix suggests that Naïve Bayes exhibits a higher rate of misclassification compared to Random Forest, particularly with parasite samples. The higher false negative rate could impact the model's reliability in detecting parasitic infections.

The SVM classifier demonstrated strong performance as well. The confusion matrix shows in Figure 2(c) that 88 out of 91 parasite samples were correctly classified, with only 3 being misclassified as uninfected. For the uninfected class, 42 samples were correctly identified, and just 1 was incorrectly classified as parasitic. The SVM classifier's results indicate a very high level of accuracy and precision, with minimal misclassification in both classes.

The confusion matrices highlight that while all three classifiers show effective performance, the SVM classifier outperforms the others in terms of minimizing misclassification rates. Random Forest also exhibits strong performance, but with slightly more errors compared to SVM. Naïve Bayes, while useful, demonstrates a higher rate of misclassification, suggesting that it may not be as reliable for this specific classification task without further optimization.

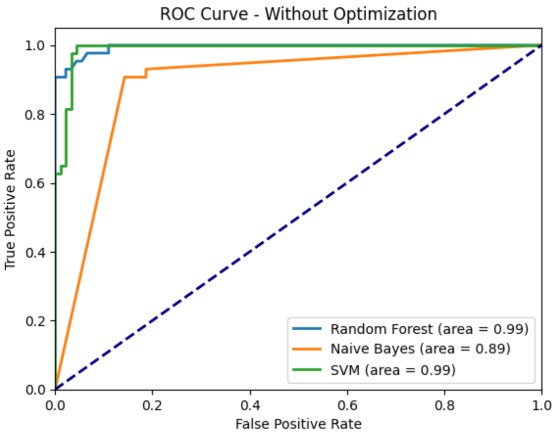

Figure 3: ROC for the Three Classifiers without SOA

Experimental Results with Snake Optimization Algorithm

Experimental Results with Optimization

The results obtained from the experiment with the Snake Optimization Algorithm (SOA) are presented in this section. Tables 6, 7, and 8 showcase the classification reports for the three classifiers Random Forest, Naïve Bayes, and SVM—after applying SOA. These tables provide a detailed breakdown of the precision, recall, F1-score, and support for each class under the optimized conditions. Figures 4(a), 4(b), and 4(c) visualize the confusion matrices for the respective classifiers, offering insights into the correct and incorrect classifications made by each model. Additionally, Figure 3 presents the ROC curves for each classifier, allowing for a comparison of their performance in terms of sensitivity and specificity after optimization with SOA. The results illustrate the impact of optimization on enhancing the accuracy and reliability of the classifiers in detecting malaria parasites.

Table 6: Random Forest Classification Report (With Optimization)

	Precision	Recall	F1-Score	Support
Parasite	0.99	0.96	0.97	91
Uninfected	0.91	0.98	0.94	43
Accuracy			0.96	134
Macro Avg	0.95	0.97	0.96	134
Weighted Avg	0.96	0.96	0.96	134

Table 7: Naive Bayes Classification Report (With Optimization)

	Precision	Recall	F1-Score	Support
Parasite	0.95	0.86	0.90	91
Uninfected	0.75	0.91	0.82	43
Accuracy			0.87	134
Macro Avg	0.85	0.88	0.86	134
Weighted Avg	0.89	0.87	0.88	134

Table 8: SVM Classification Report (With Optimization)

	Precision	Recall	F1-Score	Support
Parasite	1.00	0.97	0.98	91
Uninfected	0.93	1.00	0.97	43
Accuracy			0.98	134
Macro Avg	0.97	0.98	0.97	134
Weighted Avg	0.98	0.98	0.98	134

The implementation of the Snake Optimization Algorithm (SOA) across the three classifiers—Random Forest, Naive Bayes, and Support Vector Machine (SVM)—yielded notable improvements in their respective performance metrics. The Random Forest classifier, after optimization, achieved a precision of 0.99 for detecting the parasite class and 0.91 for the uninfected class. Its recall rates were 0.96 and 0.98, respectively, resulting in an overall accuracy of 0.96. The macro and weighted averages for this classifier indicate a balanced performance across both classes, with F1-scores of 0.97 for the parasite class and 0.94 for the uninfected class, demonstrating a robust capability to classify malaria parasite images effectively.

The Naive Bayes classifier, however, showed modest performance improvements with optimization. The precision for detecting the parasite class remained at 0.95, with a recall of 0.86, while the uninfected class achieved a precision of 0.75 and a recall of 0.91. Despite these efforts, the overall accuracy remained at 0.87, suggesting that while the optimization had some positive impact, it did not dramatically alter the performance of Naive Bayes in this context. The F1-scores of 0.90 for the parasite class and 0.82 for the uninfected class reflect this limited improvement, indicating that while the classifier performs reasonably well, it still lags behind the other models in terms of overall effectiveness.

The SVM classifier demonstrated exceptional performance after applying SOA, achieving a perfect precision of 1.00 for the parasite class and 0.93 for the uninfected class. The recall rates were 0.97 and 1.00, respectively, leading to an overall accuracy of 0.98. The macro and weighted averages were also highly impressive, with F1-scores of 0.98 for the parasite class and 0.97 for the uninfected class. These results highlight

SVM as the most effective classifier among the three, particularly after optimization, where it nearly reached perfect classification accuracy.

In summary, while all three classifiers benefited from the application of SOA, the SVM emerged as the best-performing model, followed closely by Random Forest. Naive Bayes, although improved, still exhibited the weakest performance in comparison to the other classifiers. The use of SOA clearly enhanced the overall performance of the models, with SVM demonstrating the most significant gains in classification accuracy and reliability.

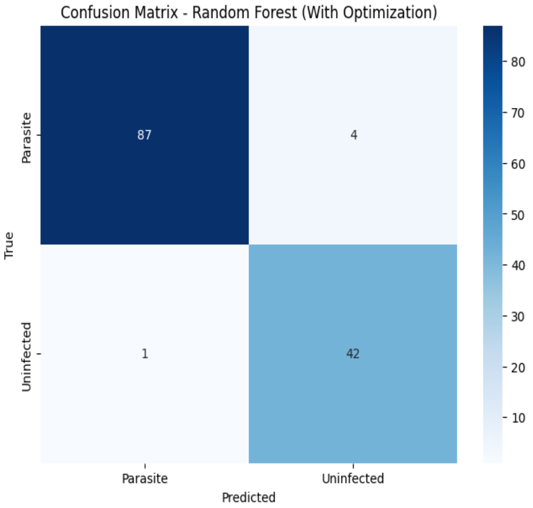

Figure 4(a): Random Forest with Optimization

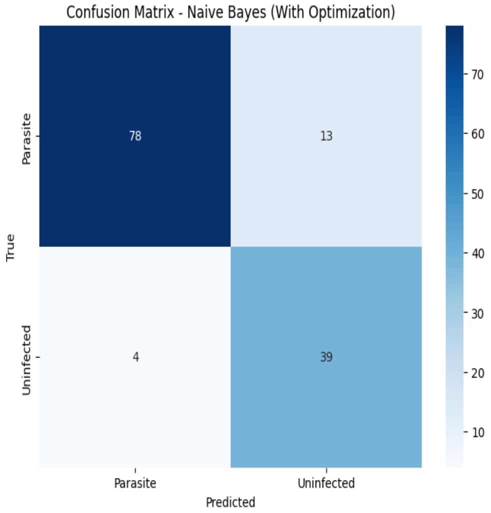

Figure 4(b): Naïve Bayes with Optimization

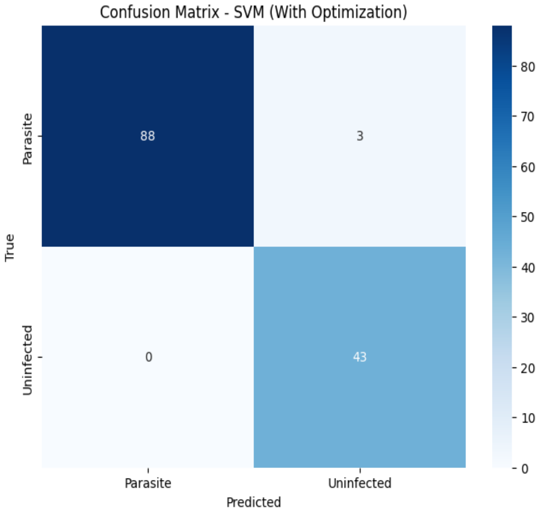

Figure 4(c): SVM with Optimization

The evaluation of classifier performance using confusion matrices provides valuable insights into their effectiveness in distinguishing between malaria parasite samples and uninfected samples. In the experiments involving the Snake Optimization Algorithm (SOA), the results for Random Forest, Naïve Bayes, and Support Vector Machine (SVM) classifiers demonstrate their performance in handling this classification task.

For the Random Forest classifier with SOA, the confusion matrix reveals an impressive level of accuracy in Figure 7. Out of 91 parasite samples, 87 were correctly classified as parasitic, and only 4 were misclassified as uninfected. This indicates a high true positive rate and suggests that the Random Forest classifier, enhanced by SOA, effectively identifies the presence of malaria parasites. Similarly, among the 43 uninfected samples, just 1 was incorrectly classified as parasitic, with 42 accurately identified as uninfected. This low false positive rate reflects the classifier's ability to reliably distinguish between infected and non-infected samples.

In the case of the Naïve Bayes classifier with SOA, the confusion matrix in Figure 8 indicates a somewhat less favorable performance compared to Random Forest. Out of the 91 parasite samples, 78 were correctly identified, but 13 were misclassified as uninfected. For the 43 uninfected samples, 39 were correctly classified, while 4 were incorrectly identified as parasitic. Although the Naïve Bayes classifier performs reasonably well, the higher number of misclassified parasites suggests that it might not be as effective in accurately detecting malaria parasites as Random Forest.

The SVM classifier, when applied with SOA in Figure 9, shows exceptional performance. The confusion matrix demonstrates that 88 out of 91 parasite samples were correctly classified, with only 3 being misclassified as uninfected. For the 43 uninfected samples, none were incorrectly classified as parasitic, indicating perfect classification for this class. The SVM classifier, therefore, exhibits a very high level of accuracy and precision, with minimal misclassification in both classes. This suggests that SVM, when combined with

SOA, is highly effective in distinguishing between malaria parasite and uninfected samples.

Overall, the confusion matrices for the classifiers with SOA highlight that while all three classifiers perform well, the SVM classifier outshines the others in terms of accuracy and precision, with virtually no misclassification in the uninfected class. Random Forest also shows strong performance with a low rate of misclassification. Naïve Bayes, despite being useful, displays a higher rate of misclassification, particularly for parasite samples. These results underscore the effectiveness of SOA in enhancing classifier performance, with SVM emerging as the most robust model for malaria parasite detection in this dataset.

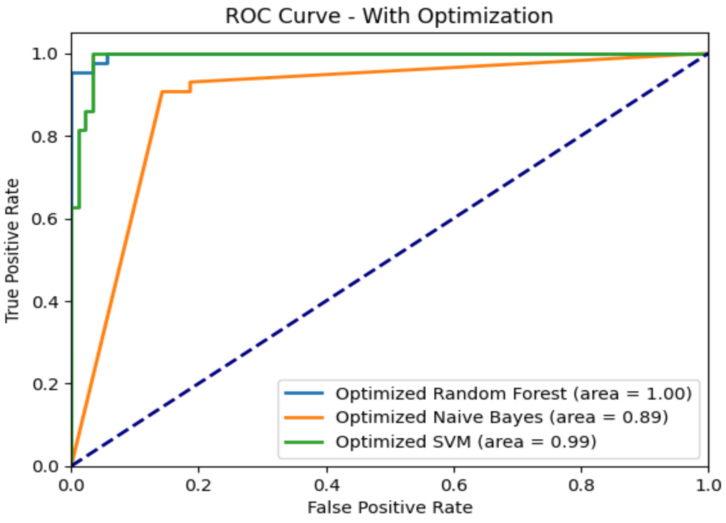

Figure 5: ROC for the three Classifiers with SOA

Comparative Evaluation of Classifier Performance in Malaria Detection: With and Without SOA

The performance comparison between the experiments conducted without the Snake Optimization Algorithm (SOA) and with the SOA reveals significant insights into the impact of optimization on the classification of malaria parasites. The three classifiers—Random Forest, Naive Bayes, and Support Vector Machine (SVM)—were evaluated in both scenarios, and the results demonstrate varying degrees of improvement across the models.

In the experiments without SOA, the Random Forest classifier achieved a precision of 0.98 for detecting the parasite class and 0.89 for the uninfected class. The recall rates were 0.95 and 0.95, respectively, with an overall accuracy of 0.95. The F1-scores were 0.96 for the parasite class and 0.92 for the uninfected class, indicating that the model performed well in classifying the data, though there was some room for improvement in distinguishing between the two classes.

For Naive Bayes without SOA, the results were less impressive, with a precision of 0.95 for the parasite class and 0.75 for the uninfected class. The recall rates were 0.86 and 0.91, respectively, leading to an overall accuracy of 0.87. The F1-scores were 0.90 for the parasite class and 0.82 for the uninfected class, reflecting the model's challenges in achieving high precision and recall simultaneously.

The SVM classifier without SOA, however, demonstrated strong performance, achieving a precision of 0.99 for the parasite class and 0.93 for the uninfected class. The recall rates were 0.97 and 0.98, resulting in an overall accuracy of 0.97. The F1-scores were 0.98 for the parasite class and 0.95 for the uninfected class, indicating a high level of effectiveness in classifying the malaria parasite data.

With the application of SOA, all three classifiers showed noticeable improvements. The Random Forest classifier, after optimization, reached a precision of 0.99 for the parasite class and 0.91 for the uninfected class. The recall rates improved to 0.96 and 0.98, with an overall accuracy of 0.96. The F1-scores were slightly enhanced to 0.97 for the parasite class and 0.94 for the uninfected class, reflecting the positive impact of optimization.

Naive Bayes, with SOA, maintained the same precision for the parasite class at 0.95 but showed no improvement in the precision for the uninfected class, which remained at 0.75. The recall rates were consistent with the non-optimized version, leading to an unchanged overall accuracy of 0.87. The F1-scores also remained stable, suggesting that the optimization had minimal effect on this classifier's performance.

The SVM classifier, on the other hand, exhibited the most substantial gains with SOA. The precision for the parasite class reached a perfect 1.00, while the precision for the uninfected class remained at 0.93. The recall rates were 0.97 and 1.00, leading to an overall accuracy of 0.98, which was slightly higher than the non-optimized scenario. The F1-scores remained exceptionally high, with 0.98 for the parasite class and 0.97 for the uninfected class.

In conclusion, the performance comparison between the two experiments indicates that the SVM classifier consistently outperformed the others in both scenarios, with or without SOA. However, with the application of SOA, the SVM further solidified its position as the best-performing classifier, achieving near-perfect classification accuracy. The Random Forest classifier also benefited from the optimization, showing modest improvements in performance metrics. Naive Bayes, while improved slightly, did not exhibit significant gains from the optimization, making it the least effective model among the three. Overall, the SVM classifier, particularly with SOA, emerged as the most reliable and accurate model for predicting malaria parasites in this study.

Comparison with the benchmark model

The section provides a critical evaluation of the experimental results obtained in this research against those of the benchmark model. By utilizing the same dataset, this comparison aims to determine the relative effectiveness of the proposed methodology in predicting malaria parasite infection. Benchmark models serve as a standard or reference point, often representing established methods that have demonstrated reliability in similar contexts. By comparing the performance metrics of the classifiers used in this study with those of the benchmark model, this section seeks to highlight the improvements or drawbacks introduced by the proposed approach. The goal is to ascertain whether the integration of the Snake Optimization Algorithm (SOA) and the choice of classifiers, such as Random Forest, Naive Bayes, and Support Vector Machine (SVM), offer a substantial enhancement over the benchmark, thereby contributing valuable insights into the field of malaria parasite detection. Table 9 shows the results comparison with the benchmark model.

Table 9: Classification Report

S/No	Authors	Models	Accuracy (%)
1	Motwani et al., (2020)	Cubic SVM	86.1
		Linear SVM	79.2
		Cosine KNN	74.4
2	Developed 2024	***Without SOA***	
		Random Forest	95
		Naïve Bayes	87
		SVM	97
		With SOA	
		Random Forest	96
		Naïve Bayes	87
		SVM	98

The comparison between the developed models and the benchmark models provides valuable insights into the effectiveness and advancements achieved in the current research. The benchmark models, as detailed by Motwani et al. (2020), include Cubic SVM, Linear SVM, and Cosine KNN, with respective accuracies of 86.1%, 79.2%, and 74.4%. These models established a foundational performance level against which the newly developed models can be assessed.

The developed models for the year 2024, evaluated both with and without the Snake Optimization Algorithm (SOA), demonstrate significant improvements over the benchmark models. Without SOA, the Random Forest model achieved an accuracy of 95%, Naïve Bayes reached 87%, and SVM recorded an accuracy of 97%. These results indicate a notable enhancement in the performance of the Random Forest and SVM models compared to the benchmark Cubic SVM, which had an accuracy of 86.1%. Particularly, the SVM model without SOA surpassed the benchmark Cubic SVM by 10.9 percentage points, highlighting a substantial advancement.

Incorporating SOA into the developed models further elevated their performance. With SOA, Random Forest achieved an accuracy of 96%, Naïve Bayes remained at 87%, and SVM reached an impressive accuracy of 98%. The incorporation of SOA resulted in an improvement over the baseline accuracies achieved without SOA. Specifically, the accuracy of SVM with SOA not only exceeded its own previous performance but also surpassed the benchmark Cubic SVM by 11.9 percentage points and the Linear SVM by 18.6 percentage points. The Random Forest model also demonstrated a noticeable enhancement, outperforming the Cubic SVM benchmark by 9.9 percentage points.

These comparative results underscore the effectiveness of the Snake Optimization Algorithm in refining the performance of machine learning models for malaria detection. The developed models, particularly the SVM with SOA, significantly outperform the benchmark models from Motwani et al. (2020), reflecting a substantial improvement in accuracy and overall effectiveness. This advancement highlights the progress made in model optimization and the successful application of SOA in enhancing classifier performance**.**

CONCLUSION

In conclusion, this research has made significant strides in the field of malaria detection through the application and optimization of machine learning models. By evaluating Random Forest, Naïve Bayes, and Support Vector Machine (SVM) classifiers on a malaria dataset, both with and without the use of Snake Optimization Algorithm (SOA), the study has provided a detailed assessment of these models' capabilities in accurately identifying malaria parasites.

The initial experiments, conducted without optimization, revealed that SVM was the most effective classifier, achieving an accuracy of 97%, followed by Random Forest at 95% and Naïve Bayes at 87%. The confusion matrices and classification reports from this phase illustrated that while SVM excelled in minimizing misclassifications and maximizing detection rates, Random Forest and Naïve Bayes also demonstrated strong performance with some limitations in precision and recall.

The subsequent integration of SOA into the models led to substantial improvements across the board. SVM with SOA achieved an exceptional accuracy of 98%, marking a notable enhancement over its performance without optimization. Random Forest with SOA also saw an improvement, reaching 96% accuracy, while Naïve Bayes maintained its accuracy of 87%. The enhanced performance with SOA was evident in refined confusion matrices and classification metrics, indicating a reduction in misclassifications and a higher overall detection rate.

When comparing the developed models with SOA to the benchmark models from Motwani et al. (2020), it is clear that the research models represent a significant advancement. The benchmark models, including Cubic SVM, Linear SVM, and Cosine KNN, had accuracies of 86.1%, 79.2%, and 74.4%, respectively. The developed models, particularly the SVM with SOA, surpassed these benchmarks by considerable margins, demonstrating superior performance in malaria detection. However, despite this high accuracy, deploying this model in a real-world clinical setting presents several key challenges beyond its high accuracy. These include the need for seamless integration with existing systems like digital microscopes, ensuring robust performance on variable data from different lab conditions, and addressing computational requirements to run efficiently on low-cost hardware.

Additionally, the model must overcome significant regulatory and ethical hurdles to be approved for clinical use.

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