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Optimising Malaria Prediction from Cell Images Using Forward Selection and Support Vector Machine Classifier

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Abstract
Malaria is a significant health concern, primarily affecting tropical and subtropical regions. Traditional diagnostic methods for malaria detection, such as microscopic blood smear analysis of cell images, are time-consuming, dependent on trained specialists, and prone to variability. Timely and accurate malaria detection is crucial for prompt treatment and preventing severe complications. Therefore, this study developed a machine learning (ML)-based model that could accurately predict malaria by analysing microscopic cell images, enabling efficient and reliable diagnosis to support timely treatment decisions. Using the Kaggle malaria dataset comprising 26,159 blood smear images, this study uniquely integrates forward feature selection and Support Vector Machines (SVM) to enhance malaria prediction accuracy. Unlike existing works, it addresses gaps in transparency and reproducibility in feature selection methods used for high-dimensional medical image datasets**.** Forward selection was employed to optimise and select relevant features for the model, reducing computational complexity and enhancing its performance. The SVM model achieved an accuracy of 97.1%, recall of 97.4%, precision of 96.8%, F1-score of 96.9%, and an AUC score of 97.4%. These findings highlight the potential of ML in automating malaria detection and demonstrate the practical advantage of combining feature selection with high-performing classifier to optimise diagnostic workflows, especially in resource-limited settings.

Keywords: Algorithm, Feature Selection, Machine Learning, Malaria, Predictive Modeling

1. Introduction

Malaria remains one of the most prevalent and life-threatening infectious diseases worldwide, posing significant health and socioeconomic challenges [1]. The disease is particularly severe in tropical and subtropical regions, such as sub-Saharan Africa and South Asia, where favourable conditions enable widespread transmission [2]. Malaria is caused by Plasmodium parasites, with *P. falciparum* and *P. vivax* being the most common and dangerous species affecting humans. These parasites are transmitted through the bites of infected female *Anopheles* mosquitoes, causing symptoms that range from mild fever to severe illness, which, if untreated, can result in death [3].

Globally, malaria places a heavy burden on public health, with approximately 300 to 500 million clinical cases reported annually, resulting in 1.5 to 2.7 million deaths [4]. Beyond mortality and morbidity, the disease disproportionately affects economically disadvantaged regions, exacerbating poverty, reducing productivity, and hindering economic growth. Vulnerable groups, such as children under five and pregnant women, are particularly at risk [5].

Timely and accurate malaria diagnosis is critical for effective disease management and reducing mortality [6]. While manual microscopy of peripheral blood smears remains the conventional gold standard for diagnosing malaria due to its reliability [7], this method is labour-intensive, time-consuming, and heavily reliant on skilled personnel, making it challenging to scale in resource-limited settings [8].

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Recent advances in machine learning (ML), a subset of artificial intelligence (AI), offer promising alternatives to traditional diagnostic methods [9]. ML enables computers to learn from data, identify patterns, and make predictions without explicit programming [10]. Leveraging vast datasets and advanced computational techniques, ML has demonstrated significant breakthroughs across fields, including medical imaging. In malaria diagnostics, ML models have shown potential in analyzing high-dimensional datasets to uncover patterns related to patient demographics, clinical symptoms, and environmental factors, improving diagnostic accuracy and efficiency [11].

However, high-dimensional datasets present challenges for ML, such as the curse of dimensionality, which leads to data sparsity, reduced generalisation, and an increased risk of overfitting [12]. Redundant or irrelevant features can introduce noise, diminishing predictive performance, while computational complexity and multicollinearity among features further hinder model reliability and interpretability [12]. Addressing these challenges requires dimensionality reduction techniques that optimise model performance while preserving essential information [12-13].

Feature selection methods, such as forward selection, mutual information, and recursive feature elimination, help identify relevant features, reduce noise, and emphasise critical variables [14]. Dimensionality reduction techniques like Principal Component Analysis (PCA) and autoencoders streamline datasets, while regularization methods, such as LASSO, improve interpretability by penalizing irrelevant features [15-16]. Advanced ML models, including tree-based ensemble methods and deep neural networks, also effectively handle high-dimensional data. Despite their computational complexity, support Vector Machines (SVM) is widely regarded as one of the best ML algorithms for classification and regression tasks. Their robustness to overfitting and ability to identify optimal decision boundaries using kernel functions make them highly effective for high-dimensional datasets [17]. SVM has achieved remarkable results in medical applications, including cell image analysis, tumour detection in MRI, and lesion classification in CT scans [18-19]. Recent advancements in kernel functions and feature extraction techniques have further enhanced SVM's performance in medical diagnostics [19].

Building on these developments, this study addresses gaps in existing research on automated malaria detection. Many prior studies focus on feature extraction from medical images using neural networks or ensemble methods but often overlook the impact of feature selection on overall model performance. Additionally, the lack of transparency in feature selection processes limits the reproducibility and adaptability of these approaches in diverse clinical settings [20].

To address these limitations, this research employs forward selection as a transparent and sequential feature selection method. Forward selection optimises model performance by iteratively adding features based on their predictive contributions, effectively mitigating the curse of dimensionality in high-dimensional datasets. Unlike PCA, which relies on linear transformations and reduces interpretability, the forward selection provides an intuitive framework for identifying relevant features [21] while maintaining model transparency; which is critical in medical diagnostics.

Furthermore, SVM's proven efficacy in handling high-dimensional data and finding optimal decision boundaries [22] makes it an ideal model for this study. By combining forward selection with SVM, this research tackles the dual challenges of feature optimisation and model accuracy in malaria prediction. The resulting framework offers a reproducible, efficient, and accurate approach to malaria detection, with significant

implications for improving diagnostic outcomes in resource-limited settings.

2. Related Works

Machine learning techniques have been extensively utilised to detect and classify malaria prediction and various diseases in general with reasonable performance. Researchers have employed diverse datasets, classifiers, and feature selection methods to enhance diagnostic accuracy and model performance [23]. While some studies focused on traditional ML classifiers, others leveraged deep learning and hybrid approaches to address challenges such as imbalanced datasets, limited sample sizes, and feature extraction [24]. The following section reviews significant contributions in the field, highlighting their methodologies, achievements, and limitations.

Dharpal and Malviya [25] proposed an automated malaria parasite enumeration system using an SVM classifier. The model achieved an accuracy of 97.02% and a sensitivity of 98.98%. However, the dataset used was imbalanced, which might have affected the model's performance in detecting malaria parasites accurately.

Rajaraman *et al.* [26] presented pre-trained convolutional neural network (CNN) as a feature extractor to improve malaria parasite detection in thin blood smear images. The model achieved an accuracy of 98.6% and an F1 score of 98.7%. Despite the promising results, the dataset used was imbalanced, which may have affected the model's generalisation ability for detecting malaria parasites in diverse cases.

Onyijen *et al.* [27] presented data pre-processing and feature selection using secondary data from a Kaggle study. The dataset included physical examination indexes such as country, year, number of cases, number of deaths, and WHO region. Several ML models were employed, including Random Forest (RF), Decision Tree (DT), K-Nearest Neighbor (KNN), Artificial Neural Networks (ANN), and Gradient Boosting (GB). The Decision Tree algorithm utilised the Recursive Partitioning Algorithm (RPA) to iteratively decompose the sample responses into sub-samples for decision-making, achieving an accuracy of 91.4%. Random Forest applied non-parametric classifiers or regressors to bootstrapped data samples using a fixed tree depth or pruning coefficient and randomly selected variable subsets, resulting in an accuracy of 90.1%. The K-Nearest Neighbor algorithm determined the class of a recognised object by calculating the number of objects in each class within a hypersphere, achieving an accuracy of 81.5%. Gradient Boosting progressively fit each tree in the series to the negative gradient of the loss function evaluated at the pseudo-residuals of previous trees, achieving the highest accuracy of 98.8%.

Barraclough *et al.* [28] proposes a combined of AI and ML classifiers to achieve high accuracy in malaria classification. Using the InfoGainAttributeEval feature selection technique, they analysed 3,490 collected questionnaires out of 4,000 distributed, incorporating clinical symptom data. Various classifiers, including ANN, NB, RF, and EM, were evaluated using WEKA. The study also employed a fuzzy If-Then rules system for real-time diagnosis during clinical visits. Findings revealed a disparity between self-reported malaria symptoms (87.3%) and actual clinical diagnoses (12.7%), highlighting healthcare accessibility issues.

3. Methodology

This section outlines the methodology adopted for developing the proposed model, which is divided into four phases. The first phase involves the collection of data for malaria cell prediction. The second phase focuses on preprocessing the dataset using various techniques to ensure its quality and readiness for analysis. The third phase applies a feature selection algorithm to identify the most relevant features. Finally, the fourth phase uses the SVM algorithm as the

classification model for predicting malaria cells.

3.1 Dataset Collection

The study utilised a dataset consisting of images of malaria-infected and uninfected cells. The dataset was collected from publicly accessible Kaggle repository. It contains a total of 26,159 images, comprising 13,132 images of infected cells (labeled as "1") and 13,027 images of uninfected.

3.2 Image Data Preprocessing

Image preprocessing involves various techniques and procedures to prepare raw image data for analysis or as input to ML models [29]. The goal is to enhance image quality and transform it into a format that can be effectively processed by the model. In this study, a few preprocessing methods were applied before further analysis. The preprocessing steps include image resizing and image flattening.

3.2.1 Image Resizing

Image resizing is a crucial preprocessing step in computer vision and image analysis tasks. It involves adjusting the height and width of an image to predefined dimensions. This step is essential for standardising the input size required by ML models, which often operate with fixed input dimensions for tasks involving computer vision and image processing [30]. Resizing ensures that all images in the dataset have consistent size and dimensions [31]. Initially, the imported images might not have had uniform sizes, leading to potential inconsistencies in processing. By resizing the images, the model can consistently evaluate all photographs in the dataset, facilitating easier comparison and analysis.

3.2.2 Image Flattening

Image flattening refers to the process of converting a 2D image into a 1D array of pixel values. This transformation is essential for certain ML models that require vectorised input data rather than multi-dimensional arrays [32]. In this study, image flattening was a key preprocessing step following image resizing, particularly for SVM, which requires vector input. Flattening simplifies the data structure, reduces dimensional complexity, and ensures uniform representation of image data. This process transforms 3D image matrices into 1D vectors, making it compatible with SVM algorithms and ready for fully connected neural network layers [33]. By doing so, it facilitates effective feature extraction and classification from the images.

3.3 Dataset Splitting

The dataset, consisting of 26159 images of malaria cells, was divided into two subsets: 70% for training and 30% for testing. This allocation resulted in 18,311 images being used for training and 7,848 images for testing. The division ensures that sufficient data is available for both training the model and evaluating its performance. By using 70% of the data for training, the model learns from a substantial portion of the dataset, while the remaining 30% is reserved for testing to assess its performance on unseen data. This split provides a balanced approach, enabling an unbiased evaluation of the model's generalisation ability to new data. Following the dataset splitting, feature selection techniques, namely forward selection and correlation-based methods, were applied, with SVM used as the classification algorithm.

3.4 Forward Selection

Forward selection, a stepwise regression technique, was used for feature selection in this study. This method starts with an empty model and incrementally adds features that improve the model's performance, aiming to identify the key variables that enhance predictive accuracy [34]. The process begins by evaluating each feature individually, training the model (e.g., SVM) with one feature at a time, and assessing its performance using an appropriate evaluation metric [35]. The feature that provides the best performance is selected. Subsequently, the process iterates by combining the selected features with each remaining feature, training the model with the new set of features, and

evaluating its performance through cross-validation or a holdout validation set. The feature that results in the greatest performance improvement is added to the model. This process continues until a predefined stopping criterion is met, such as reaching a set number of features, observing no further improvement, or detecting performance degradation. Once the stopping criterion is satisfied, the final set of selected features is used to train the model [36]. This approach ensures the inclusion of the most relevant features, improving the model's efficiency and predictive performance while reducing the risk of overfitting [37].

3.5 Support Vector Machine

Support Vector Machine works by finding the optimal separating hyperplane that best divides the dataset into distinct classes [38]. This hyperplane maximises the margin, defined as the distance between the hyperplane and the nearest data points from each class, known as support vectors. By maximising this margin, SVM ensures better generalisation and classification accuracy.

The mathematical formulation of the SVM is as follows:

Given a training dataset $(x_1, y_1), (x_2, y_2), \ldots, (x_m, y_m)$, where $x_i \in R^n$ and $\in \{-1, 1\}$, SVM seeks to find a hyperplane defined by the equation 1:

$$w \,.x \, + \, b \, = 0 \qquad (1)$$

where w is the weight vector, x is the feature vector, and b is the bias term.

4. Results and Discussion

The malaria prediction model was implemented in Python 3.10 on Google Colab and optimised using the forward selection feature selection method. The aim was to enhance the performance of the SVM classifier in solving the binary classification problem of detecting malaria from blood smear images. To ensure robustness, the model was trained and validated on 18,311 instances and evaluated on a test set of 7,848 samples, which included 3,941 malaria and 3,907 non-malaria patients. The confusion matrix is presented in Figure 1.

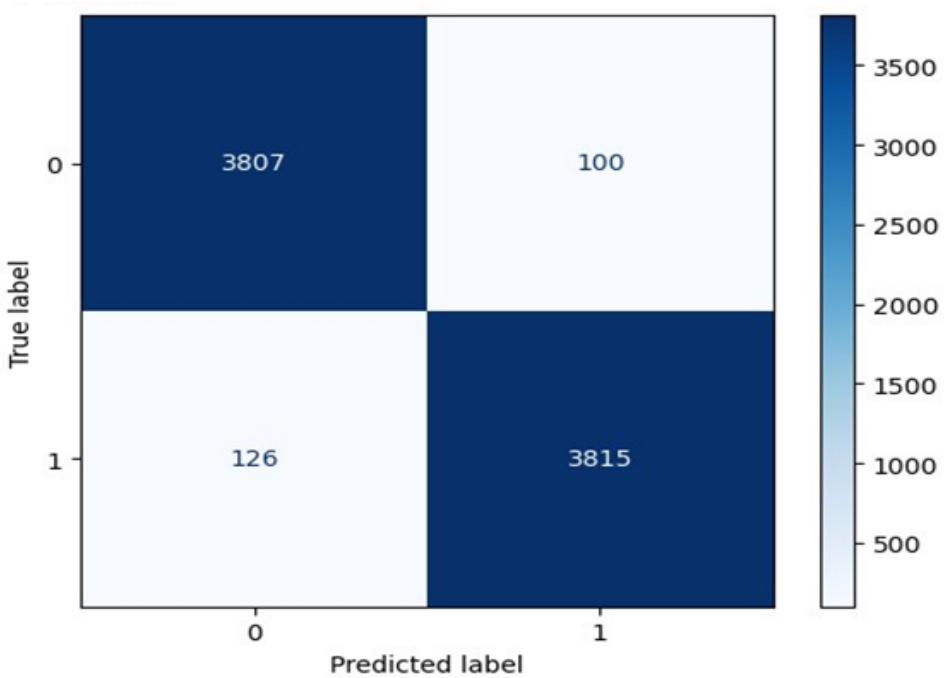

Figure 1: Confusion Matrix Generated for the Malaria Model

Figure 1 presents the confusion matrix for the model's predictions. Out of the 3,941 malaria cases, the model correctly identified 3,815 cases, yielding a high true positive rate. However, 126 cases were incorrectly classified as non-malaria (false negatives), which could result in missed diagnoses. This low rate of false negatives is crucial in malaria detection, as timely treatment is critical in preventing severe complications.

Similarly, out of the 3,907 non-malaria cases, the model correctly identified 3,807 cases as non-malaria, with only 100 instances misclassified as malaria (false positives). The model's ability to minimise false positives reflects its reasonable specificity in identifying patients without malaria, reducing unnecessary treatments and associated healthcare costs.

Table 1 summarises the evaluation of the a SVM model's performance, including accuracy, precision, recall, F1 score, and ROC/AUC score, all derived from the confusion matrix shown in Figure 1.

As presented in Table 1, the SVM classifier achieved a high accuracy of 97.1%, indicating that it correctly classified the majority of instances in the test set. Precision was recorded at 96.8%, demonstrating the model's ability to minimise false positive predictions, which is particularly important in resource-limited settings where unnecessary treatment of non-malaria cases could strain resources. Recall (or sensitivity) was 97.4%, highlighting the model's strong capacity to correctly identify malaria cases, thereby reducing the likelihood of missed diagnoses. The F1 score, which balances precision and recall, was 97.1%, reflecting the model's overall reliability and effectiveness in handling the binary classification task. Additionally, the ROC/AUC score of 97.1% underscores the model's excellent discriminative ability, effectively distinguishing between malaria and non-malaria cases.

The results demonstrate the potential of ML models, particularly those leveraging feature selection methods and robust classifiers like SVM, to automate and optimise malaria detection. By accurately predicting malaria cases with minimal false positives and false negatives, the model offers a valuable tool for improving diagnostic workflows, especially in resource-constrained environments. The application of forward selection in feature selection was instrumental in reducing dimensionality, thereby enhancing the SVM model's performance.

Moreover, the high sensitivity ensures timely identification of malaria cases, enabling prompt treatment and reducing disease burden, while the model's high specificity minimises unnecessary interventions. These findings align with previous research advocating the use of ML for disease prediction and highlight the scalability of such approaches for broader healthcare applications.

Table 1: Result of Model Evaluation using standard performance metrics

Metrics	**Value (%)**
Accuracy	97.1
Recall	97.4
Precision	96.8
F-measure	97.1
ROC/AUC Score	97.4

5. Conclusions and Future Work

This study demonstrated the significant impact of feature selection technique, particularly forward selection, on enhancing the performance of malaria prediction models using SVM. Achieving an F1-score, accuracy, recall, and AUC all close to 97%, the model underscores the potential of ML in automating malaria diagnosis with high reliability and precision. These findings set a benchmark for malaria prediction models and emphasised the critical role of robust feature selection in optimising medical diagnostics.

Despite the model's strong performance, several limitations exist. The dataset used in this study, while well-annotated, may not fully capture the diversity of blood smear images encountered in real-world clinical settings. Future work should focus on validating the model with larger, more diverse datasets to improve its robustness and generalisability across various populations and healthcare environments. Additionally, incorporating advanced feature selection methods, ensemble learning techniques, and explainable artificial intelligence tools could further enhance the model's performance, interpretability, and trustworthiness for healthcare professionals. Cross-validation techniques should also be implemented to ensure the model's reliability in real-world applications.

Extending this framework to other medical imaging classification challenges could further improve diagnostic accuracy across different contexts. Regular updates and evaluations will be essential to maintain optimal performance as the field progresses.

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