



An Explainable Machine Learning Approach for Early Dengue Detection Using Routine Hematological Parameters

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Received:07/06/2026; Revised: 12/07/2026; Accepted: 20/07/2026; Published: 28/07/2026

ABSTRACT

Gallstone disease remains a common biliary disorder with substantial diagnostic and clinical consequences, creating a need for practical tools that can support early risk identification. This study developed and internally validated an artificial intelligence-based clinical decision-support model for gallstone disease using a publicly available de-identified dataset of 319 patients and 38 candidate predictors. Demographic, comorbidity, anthropometric, laboratory, and body-composition variables were evaluated through elastic-net logistic regression, random forest, gradient boosting, and radial-basis-function support vector machine models using repeated stratified five-fold cross-validation. Model performance was assessed through receiver operating characteristic area under the curve, accuracy, sensitivity, specificity, precision, F1 score, Brier score, calibration measures, risk stratification, permutation importance, and decision-curve analysis. The extended elastic-net model was selected as the final model because it combined interpretability with good discrimination and calibration, achieving an area under the curve of 0.848, accuracy of 78.1%, sensitivity of 72.8%, specificity of 83.2%, and Brier score of 0.161. At an optimized threshold of 0.393, sensitivity increased to 85.4% while specificity remained 72.0%. Vitamin D, C-reactive protein, bone mass, extracellular fluid distribution, and visceral fat area were influential predictors. The model showed meaningful risk separation and potential net clinical benefit, but external multicenter and prospective validation remain necessary before routine implementation across diverse clinical settings and patient populations.

Keywords: Artificial intelligence, Clinical decision support, Gallstone disease, Machine learning, Risk prediction

1. Introduction

With its rapid spread, wide clinical spectrum and potential progression to severe complications, dengue fever continues to be one of the most critical mosquito-borne viral diseases in the world and a significant problem for health-care systems. Dengue is caused by four antigenically distinct serotypes of the dengue virus and mainly transmitted by the *Aedes* mosquitoes. Clinical presentations can vary from a mild febrile illness to life-threatening dengue hemorrhagic fever and dengue shock syndrome (DHF/DSS), and early recognition is crucial to proper care of the patient (Schaefer et al., 2024; Halstead, 2017). Geographical spread of dengue has been accelerating due to urbanization, climate variability, increased international travel and increased mosquito habitats, which has made it a global public health crisis (Aguiar et al., 2022). Dengue has seen a significant increase in its global burden over the last few decades, and many dengue-endemic areas have seen regular epidemics and increasing demand for healthcare services. The disease has a significant impact on human health and resources, resulting in millions of people becoming infected each year, increased hospitalization, laboratory testing and vector management resources. Over the years, epidemiological studies have shown the continuous increase in dengue cases all over the world in tropical and subtropical countries; thus, there is a need to increase surveillance and early diagnostic strategies for dengue (Zeng et al., 2021). This is consistent with the pattern of global disease change through analyses of the emergence of dengue in new geographic regions and its occurrence in more diverse populations (Yang et al., 2021). New estimates also indicate that the burden is still changing with continued increasing rates of dengue incidence and disability in the last 30 years globally (Zhang et al., 2025). Historically, dengue infections have been reported only in endemic countries; however, imported and locally acquired infections have become a significant concern in non-endemic areas, thus demonstrating the global reach of dengue infections (Chen et al., 2023). Supportive treatment is the only treatment available today, and early diagnosis is important in slowing the disease and helping to direct treatment. Laboratory confirmation is usually achieved by the use of molecular assays, antigen detection, or serological testing, but these tests may not be readily available in a clinical routine laboratory, especially in countries with limited resources. Most of the routine hematological investigations that are conducted during the initial clinical assessment are valuable sources of information that may help identify dengue at an early stage, such as platelet count, leukocyte parameters and red blood cell parameters (Muller et al., 2017).

The recent innovations in AI technologies have opened new possibilities in healthcare to predict, make decisions automatically, and interpret complex clinical information. The use of machine learning in infectious disease research is becoming more common, particularly due to its ability to identify meaningful patterns and relationships within routinely collected healthcare data, even in the presence of nonlinear relationships. Such methods have shown good potential in disease surveillance, diagnosis and prognosis, along with support for the traditional clinical decision-making process (Wong et al., 2023). In the field of infectious diseases diagnostics, machine learning has demonstrated good performance in various clinical applications, combining demographic, laboratory, imaging, and electronic health record data. Comparative investigations have shown that algorithms like Logistic Regression, Random Forest, or algorithms based on boosting can be good competitors in terms of predictive performance, and they are not so costly when the clinical data is structured. Therefore, machine learning is an emerging field of analysis that is being used more and more for laboratory diagnosis of disease and prediction of risk (Tran et al., 2022). In recent years, there have been a few studies that have specifically focused on machine learning approaches for predicting dengue, based on routinely collected clinical data. These investigations have found promising classification results and pointed to the relevance of hematological parameters as markers to differentiate dengue-positive from dengue-negative patients. Routine lab parameters, especially platelet-related and leukocyte-related parameters, have consistently appeared to be significant factors in predictive models and have been used in computational methods for detecting dengue (Chauhan et al., 2023). In recent years, a more comprehensive view of the use of AI in the management of dengue has been introduced, and it places significant emphasis on the need for explainable analytical methods. A clear understanding of the reasons behind a model's predictions makes it easier for clinicians to understand and adopt the use of AI in healthcare environments (Hussein et al., 2025).

Although there has been a rise in the use of AI in the diagnosis of dengue, there are some challenges presents in the existing literature. Studies of the past have focused mostly on model accuracy, neglecting to provide much information about the contribution of separate hematological factors to the decision-making of the model. There is also some inconsistency from one study to another when comparing typical machine learning approaches due to variation in feature selection, evaluation techniques and reporting methods. Therefore, research is still needed to help create a more transparent and accurate predictive model using routine hematological parameters that incorporates comparative model evaluation and explainable machine learning methods.

This study was designed to create and test an explainable machine learning model to detect dengue at early stages based on hematological parameters. The study evaluated and compared the predictive ability of Logistic regression, Random Forest, and Extreme Gradient Boosting, and performed the evaluation with standard classification metrics and cross-validation procedures. Furthermore, two explainability techniques were used: feature importance and SHapley Additive exPlanations methods were used to explain the most important hematological variables in the model prediction, which gave an interpretable evaluation of the performance of machine learning for dengue detection in the laboratory.

2. Methodology

2.1 Research Design

The study used secondary data analysis of past records to build and analyze explainable machine learning models for early detection of dengue through routine hematological parameters. A supervised binary classification framework was used to classify individuals as being positive or negative for dengue using routinely collected clinical laboratory measurements. The analytical process included data preprocessing, exploratory analysis, building the model, evaluating the model performance, and interpreting the model using feature importance and explainability techniques. The methodology was designed so that the comparison of multiple machine learning algorithms is transparent, it is reproducible and the analytical bias is minimal.

2.2 Data Source

This study used a secondary clinical study dataset that was publicly accessible (Nirob et al. 2025). The dataset includes anonymized patient-level demographic and routine haematological measurements, which were collected in order to enable investigation of the diagnosis of dengue using laboratory biomarkers. It collects confirmed dengue-positive and dengue-negative cases with a complete hematological profile, which can be analysed with supervised machine learning without having to collect additional data.

2.3 Data Preprocessing

The dataset was checked for completeness, duplication, and consistency of the variables. All variables were checked for missing data and duplicate records were removed prior to model development. There were no missing observations, so no observations were imputed. The categorical variables sex and outcome class were recoded as numerical labels for use in machine learning analysis. All continuous variables were kept as they are. For Logistic Regression, numerical predictors were standardized using statistics computed exclusively from the training data. Only the original feature values were used in the tree-based models. The resulting data set was then split, through stratified random sampling, into a training set (80%) and test set (20%), to ensure a class distribution that was not altered.

2.4 Machine Learning Model Development

Three machine learning algorithms were explored: Logistic Regression, Random Forest and Extreme Gradient Boosting (XGBoost). Logistic Regression was used as a linear baseline classifier, and Random Forest and XGBoost were chosen due to their capability of modeling nonlinear relationships and interactions between hematological variables. The training dataset was used to train the models, and all the partitions of the data were kept the same for all the algorithms to compare their predictive performance. The hyperparameters were fixed before model fitting and were consistent during the evaluation process.

2.5 Model Evaluation

An independent test dataset that has not been used during the model training phase was used to evaluate model performance. The accuracy, precision, recall, F1-score and the area under the receiver operating characteristic curve (ROC-AUC) were used to quantify the predictive capability. Confusion matrices were also investigated to analyze the classification behaviour for both dengue-positive and dengue-negative cases. The developed models were tested for robustness using stratified five-fold cross-validation on the training data, and the mean and standard deviation of each metric were calculated across the five folds of the validation set.

2.6 Feature Importance and Model Explainability

Complementary approaches to interpretability were used to examine model interpretability. Random Forest feature importance scores were calculated to quantify the importance of individual haematological variables for prediction. Furthermore, a SHapley Additive exPlanations (SHAP) analysis was conducted to estimate the contribution of features in the direction of the model's predictions of dengue-positive cases. The feature importance and SHAP tools provided a more detailed understanding of the impact of each feature and enhanced the interpretability of the prediction process through their joint application.

3. Results

3.1 Dataset Characteristics

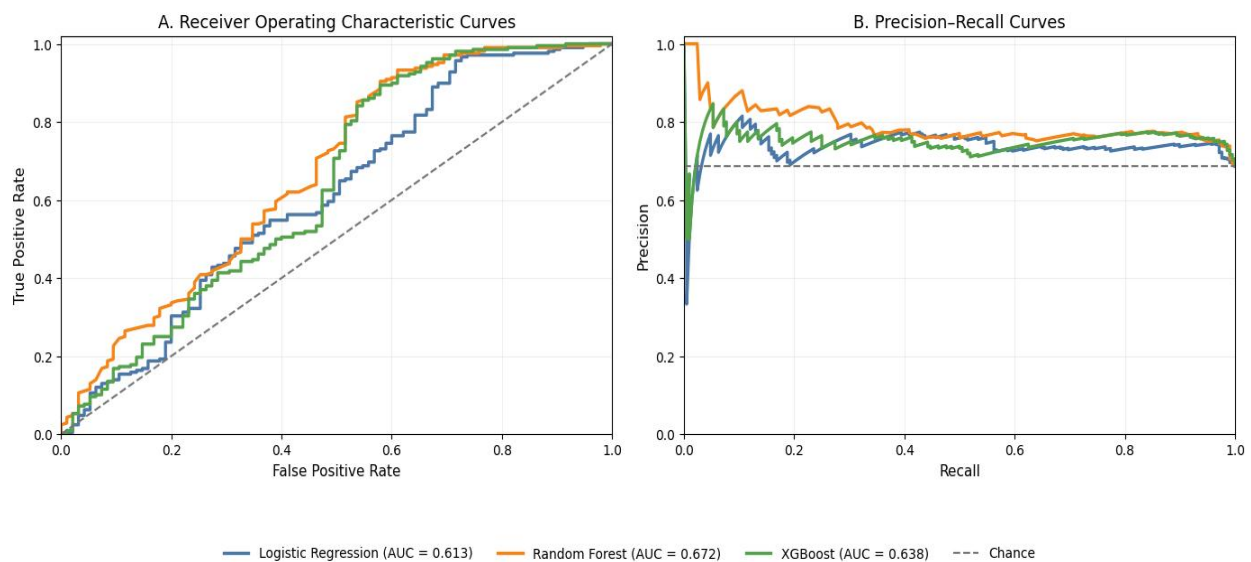
The first step was to get 1523 patient records from the publicly available clinical dataset. After preprocessing, 12 duplicate records were excluded, leaving 1,511 patients and 18 predictor variables and one binary outcome variable for analysis. No missing values were detected throughout the dataset, suggesting no missing data for hematological and demographic data. The final dataset consisted of 1035 dengue-positive and 476 dengue-negative patients, with moderate class imbalance. A total of 712 males and 799 females aged 40.38 years on average were included in the study population. The secondary clinical data are summarized in Table 1 with respect to their demographic characteristics, data quality and class distribution.

Table 1. Characteristics of the Secondary Clinical Dataset

Characteristic	Value
Total Patients	1523
Final Sample Size	1511
Clinical Variables	18
Positive Cases	1035
Negative Cases	476
Missing Values	0
Duplicate Records Removed	12
Male	712
Female	799
Mean Age (Years)	40.38

3.2 Correlation Analysis of Clinical Variables

Before developing models, pairwise correlation analysis was used to understand the relationships between the demographic and hematological variables. Limited multicollinearity was observed with most of the variables, as they showed weak to moderate linear associations. Neutrophil % showed an inverse relationship with the percentage of lymphocytes and platelet-related indices showed moderate relationships with some haematological parameters. This is because there were no strong pairwise correlations between the predictor variables, which indicated that all predictor variables should be used in the construction of the machine learning models. The overall correlation relationships between the clinical variables are displayed in Figure 1.

**Figure 1. Correlation Matrix of Clinical Variables**

3.3 Machine Learning Model Performance

Three supervised machine learning algorithms were developed and tested with an independent test set. The overall accuracy (75.58%) and F1-score (0.8419) were the highest for XGBoost, while Random Forest had the highest ROC-AUC (0.6717), meaning the best overall ability to discriminate over the range of classification thresholds. Logistic Regression had the maximum recall (97.12 %), indicating good sensitivity as well as a moderate specificity. The predictive performance of the three machine learning models is compared in Table 2.

Table 2. Performance Comparison of Machine Learning Models

Model	Accuracy	Precision	Recall	F1-score	ROC-AUC
Logistic Regression	0.7393	0.7345	0.9712	0.8364	0.6127
Random Forest	0.7525	0.7529	0.9519	0.8408	0.6717
XGBoost	0.7558	0.7577	0.9471	0.8419	0.6380

The receiver operating characteristic curves are presented in Figure 2(A), which indicates that the Random Forest model gave the largest area under the curve throughout the analysis as compared to Logistic Regression and XGBoost. The precision-recall curves are shown in Figure 2(B), which show the same level of precision for all models and slightly higher precision for Random Forest in most of the range of recall values.

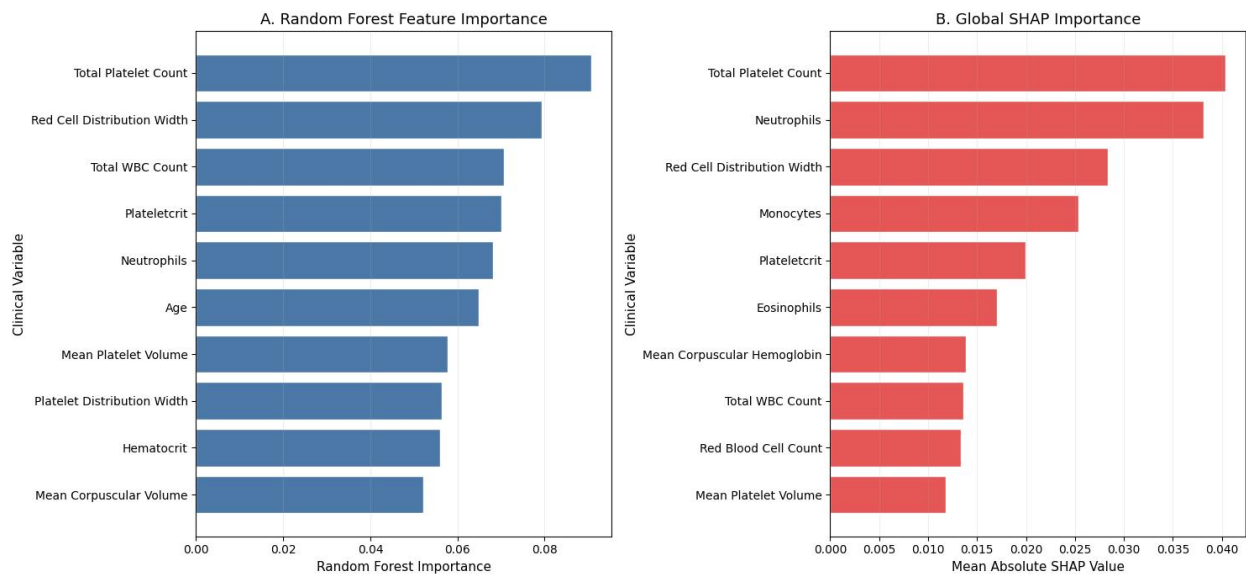


Figure 2. Discrimination Performance of the Machine Learning Models (A) Receiver Operating Characteristic Curves of Logistic Regression, Random Forest, and XGBoost. (B) Precision–Recall Curves of Logistic Regression, Random Forest, and XGBoost.

3.4 Classification Performance on the Independent Test Set

The differences in classification behaviour between the three algorithms were also confirmed by confusion matrix analysis. Logistic Regression correctly classified 202 cases of dengue, but only misclassified 6 dengue cases; a relatively large number of cases were classified as positive when they actually were not (73). Random forest classified 198 patients as positive and 30 patients as negative, resulting in a better proportion of positive to negative classifications. XGBoost had the highest number of negative patients correctly classified (32), but similar positive case detection (197). The confusion matrix for the Logistic Regression model is shown in Figure 3(A), where one can see that the model has a high sensitivity and relatively low specificity. The confusion matrix for the Random Forest model is shown below in Figure 3B, which is more balanced compared to the other models. Figure 3(C) shows the confusion matrix for the XGBoost model, which has similar classification behavior and a slight improvement in the number of correctly classified negative cases.

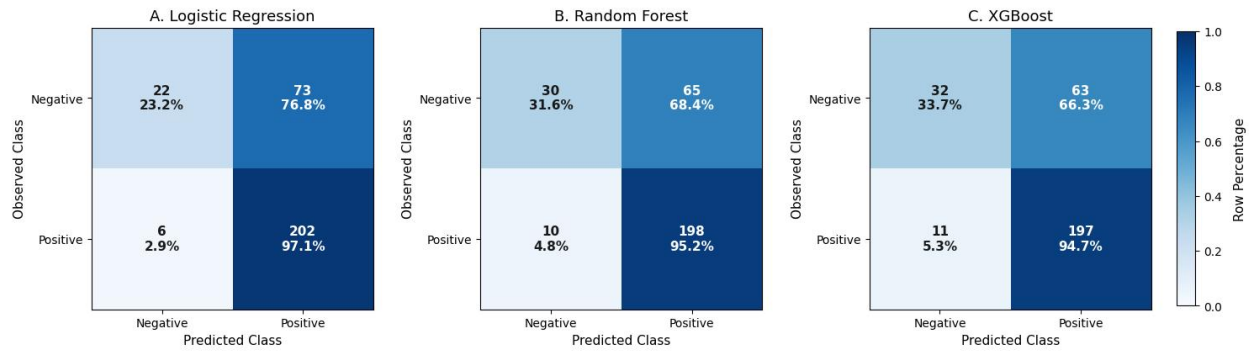


Figure 3. Confusion Matrix Comparison of the Machine Learning Models (A) Logistic Regression. (B) Random Forest. (C) XGBoost.

3.5 Identification of Clinically Important Predictors

Random Forest (RF) feature importance analysis resulted in the identification of several hematological indicators that had a significant contribution to the classification of dengue disease. The most influential variable was the total platelet count (0.0908), followed by red cell distribution width, total white blood cell count, plateletcrit, neutrophil percentage, and age. The results suggest that platelet-related parameters and leukocyte-related parameters are the most dominant parameters for distinguishing dengue-positive patients among the study population. The top ten influential predictors identified by the Random Forest model are presented in Table 3.

Table 3. Top 10 Clinical Predictors Identified by the Random Forest Model

Rank	Clinical Variable	Importance Score
1	Total Platelet Count	0.0908
2	Red Cell Distribution Width	0.0794
3	Total WBC Count	0.0706
4	Plateletcrit	0.0700
5	Neutrophils	0.0682
6	Age	0.0649
7	Mean Platelet Volume	0.0578
8	Platelet Distribution Width	0.0565
9	Hematocrit	0.0560
10	Mean Corpuscular Volume	0.0521

The global SHAP importance analysis further confirmed the consistent ranking of features in the complementary explainability methods used, highlighting that the most important variables for the dengue-positive prediction were total platelet count and neutrophil percentage, respectively.

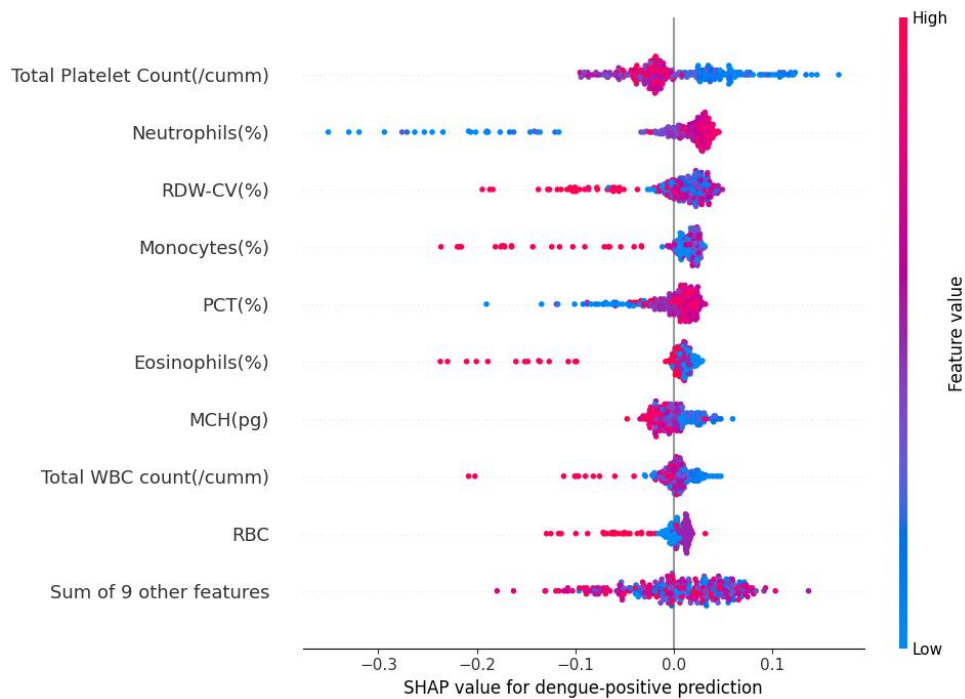


Figure 4. Global SHAP Importance Based on Mean Absolute SHAP Values

4. Discussion

The comparative evaluation demonstrated that the three machine learning algorithms had similar overall classification results, but varying operating characteristics. The test-set accuracy and F1-score were the best for XGBoost while the ROC-AUC was best for Random Forest and the mean accuracy or F1-score were best over stratified 5-fold cross-validation for Random Forest. The results show that there was no single model that was consistently superior in each dimension. However, Random Forest had the best overall performance with relatively stable discrimination both within the independent test set and the validation folds. The test ROC-AUC value of 0.6717 is consistent with its mean CV ROC-AUC value of 0.6635, indicating that the model did not rely on a single "lucky" data partition. Logistic Regression had the best recall with 202/208 dengue-positive cases in the test set. This sensitivity may be useful in a preliminary screening setting where it is more important to miss a patient who may have an infection than to refer a patient who did not have an infection for further evaluation. The same model achieved high sensitivity at the expense of specificity, correctly identifying only 22 of 95 negative cases while generating 73 false-positive predictions. Random Forest and XGBoost performed better in reducing the false-positive classifications, with 65 and 63 errors, respectively, while a bit fewer positive cases were misclassified. The results are thus a compromise between achieving high case detection and minimizing unnecessary follow-up testing. Predictor analysis revealed that classification of dengue was related to more than one laboratory parameter, which included platelets, leukocytes, and erythrocytes. In the Random Forest feature importance ranking, total platelets were the most important feature and in the global SHAP analysis, the highest-ranking feature, giving convergent evidence that it was important in predicting the model. These other factors also had a significant impact: red cell distribution width, total white blood cell count, plateletcrit, neutrophil percentage, and age. Both the direction and the intensity of individual effects were found to vary from patient to patient, as revealed by the SHAP results, which reinforced the need for the modelling of interactions among the routine hematological parameters using nonlinear models.

In line with recent studies that have shown that interpretable machine learning methods can derive diagnostic information from commonly collected blood analyses, the present results suggest that such methods can be used to identify interpretable trends in blood test results. Also, Tuhin et al. (2025) found that explainable modelling of clinical blood variables can not only help with dengue classification, but also enable the study of the relative contribution of laboratory variables. The same idea is pursued here by directly comparing a linear classifier with two tree-based (nonlinear) classifiers, with the same partitions of the data and the same assessment metrics. Some of the other characteristics of platelets and leukocytes have also been highlighted in image-based and structured-data investigations. The relevance of the platelet and white-cell patterns for blood smear diagnosis of dengue was strongly supported by Mayrose et al. (2023), who employed machine learning, using platelet and lymphocyte characteristics from blood smear images to detect dengue. Riya et al. (2024) similarly explored the possibility of using AI for early detection of Dengue when using complete blood count variables, which had a very similar methodology to the use of the hematological variables routinely available in this study. Some more complicated ensemble schemes have been used to achieve promising classification results in dengue. Rahman et al. (2024) presented a stacking framework using the complete blood count (CBC) data which showed how to combine classifiers would be more robust if their individual classifiers

could capture different patterns. Some moderate discrimination was found here, suggesting that it may be useful to develop ensembles in the future, but that complexity should be increased to gain a reproducible benefit and kept understandable.

Both explanations of the prominence of platelet count are clinically plausible. The strong contributions of variables related to platelets have been reported by Guo et al. (2025), who reported that platelet dynamics and thrombocytopenia occurred with dengue infection. Explainable boosting approaches have also emphasized the importance of using predictive modelling and providing interpretable explanations; Sarker et al. (2025) adopted XGBoost to predict dengue using SHAP and DiCE, showing the benefits of these methods for providing explanations alongside performance measures. Research combining all blood count parameters with AI is ongoing to continue to support easy laboratory-based screening strategies. These factors were explored by Kotla (2025) with the integration of these variables with AI for early detection of dengue, and previously by Gambhir et al. (2017) who proposed a PSO-ANN diagnostic model. The results of these studies suggest a persistent interest in the automated classification of dengue; however, the results are not directly comparable due to the disparities in populations, pre-processing, feature selection and the process of validation. There is also a trend towards fast and portable diagnostics in the wider diagnostic picture. Vairaperumal et al. (2025) summarized POC platforms and newly identified predictive biomarkers for severe dengue, and provided opportunities for integration of conventional lab markers with more rapid diagnostic technologies. From a population perspective, Sundram et al. (2019) characterized AI as a tool for dengue surveillance and prediction, and computational methods could be helpful on both the individual and public-health fronts.

Results confirm the potential of using routine hematological parameters for initial classification of dengue. Since these parameters are routinely measured during early clinical evaluation, models incorporating these parameters may provide a useful guide to prioritizing suspected cases if definitive tests are not available or performed until later in the clinical course. The results are not adequate to substitute for antigen, molecular, serological or clinical evidence. It would be more fitting to say that machine learning might help with the initial assessment by mapping the multitude of lab data into an understandable probability estimate. Using feature importance and SHAP analysis will help to increase transparency in the use of the model and allow you to see which variables are responsible for most of the prediction. This is particularly important when the model's predictive performance is not extreme; with moderate model performance, the explanations can help the clinician understand how the model generated a prediction and can guide the identification of cases where the prediction needs to be interpreted with caution. Random Forest seems to be the best option for further study, given that it had relatively high discrimination power, stable CV performance and explanations that are relatively easy to obtain.

There are a few restrictions to be taken into account. A secondary dataset was used for the analysis, so there was limited control over data collection procedures as well as the clinical definition of the outcome. There was no external validation, and the class imbalance (moderate) might have affected the prediction of negative cases. The data set also included some limited clinical information other than demographic and hematological data.

Further studies are needed to confirm the models with independent multicenter populations and prospectively collected records. Adding symptoms, length of illness, comorbidities, serological markers and/or disease severity may be helpful for discrimination. An evaluation of the threshold must also be made based on the clinical priorities, and must include sensitivity, specificity, calibration and net benefit, prior to any practical implementation.

5. Conclusion

Hematological parameters were useful for explainable machine learning-based dengue classification. Random Forest performed well across most of the stratified cross-validation tests, and had a high ROC-AUC and a strong average performance across test sets, while Logistic Regression had the highest sensitivity and XGBoost achieved the highest accuracy in test sets. The most important one of these was total platelet count, followed by red cell distribution width, total white blood cell count, plateletcrit, neutrophil percentage and age. The correlation between the Random Forest features' importance and the SHAP analysis further reinforced the interpretability of these results, and revealed that all three platelet, leukocyte and erythrocyte-related features were required for the prediction of Dengue. The models were found to be good in terms of preliminary analyses for organizing routinely collected laboratory data, but their moderate discrimination and limited specificity suggest that they should not be used to replace known diagnostic testing. Clinical implementation should await external validation using independent and clinically diverse populations. The use of symptoms, length of illness, serological data, disease severity and calibration assessment should be included in future work to enhance the predictive reliability and clinical relevance.

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