

Machine Learning Diagnosis of Dengue Fever: A Cost-Effective Approach for Early Detection and Treatment

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Abstract

This research aims to explore the potential of machine learning algorithms for diagnosing of dengue fever and assess their cost-effectiveness compared to conventional methods. Four machine learning classifiers (K-Nearest Neighbor, Naïve Bayes, Support Vector Machine, and Random Forest) were utilized. Feature selection and data balancing techniques were employed to enhance algorithm performance. The classifiers achieved high accuracy rates, with Naïve Bayes, Support Vector Machine, and Random Forest achieving 100% accuracy and K-Nearest Neighbor achieving 97.3% accuracy. Additionally, the cost-effectiveness analysis demonstrated that machine learning models for disease classification are the most cost-effective approach due to early detection and diagnosis, resulting in reduced healthcare costs. Therefore, it is recommended to promote the use of machine learning techniques in disease treatment for early detection and improved cost-effectiveness.

Key words: machine learning classifiers, dengue fever, cost-effectiveness

J.E.F. classification: I10, I18, I19

1. Introduction

Dengue fever is a viral disease that is transmitted through mosquito bites and has become a significant public health concern globally, particularly in tropical and subtropical regions. According to the World Health Organization (2021), dengue fever is prevalent in over 100 countries, and an estimated 390 million people contract the disease each year, with 96 million cases manifesting clinical symptoms. With a 30-fold increase in reported cases over the previous 50 years, the prevalence of dengue fever has been rising recently (Bhatt et al., 2013). The disease has a significant impact on global health, with an estimated 20,000 deaths occurring annually (World Health Organization, 2021).

Dengue fever has also been reported in several African countries, including Senegal, Nigeria, and Tanzania (Haddow et al., 2012; Mahmoud et al., 2018; Onyango et al., 2016; Vairo et al., 2014). However, the disease's prevalence in Africa may be underreported due to limitations in current diagnostic methods. Current diagnostic methods rely on serological tests, which detect the presence of dengue virus-specific antibodies in the blood. However, misdiagnosis is often recorded in countries where the disease is prevalent due to poor or unavailability of testing facilities (Okoror et al., 2021). These tests have limitations, including low sensitivity and specificity, particularly in the early stages of the disease (Hunsperger et al., 2016). Additionally, the cost of these tests can be prohibitively high for individuals in developing countries, where the disease burden is highest.

The use of machine learning algorithms in the diagnosis of dengue fever has the potential to improve the accuracy and speed of diagnosis and reduce costs. Machine learning algorithms can analyze large datasets of clinical and laboratory data to identify patterns and predict disease outcomes. Several studies have demonstrated the potential of machine learning in the early detection and diagnosis of dengue fever (Mayrose, et al., 2023; Mishra, 2020; Saturi, 2020; Dharshini et al., 2019; Chen et al., 2017).

Therefore, the objective of this research paper is to investigate the cost-effectiveness of machine learning in the diagnosis of dengue fever and its potential impact on the healthcare system. The study will compare the cost and effectiveness of machine learning diagnosis of dengue fever to conventional diagnostic methods, such as serology test, polymerase chain reaction (PCR) test and nonstructural protein 1 test (NS1 antigen test). The research aims to provide valuable insights into the potential of machine learning algorithms in improving the diagnosis and management of dengue fever, particularly in developing countries.

2. Literature review

The economic theoretical framework of this study is based on cost-effectiveness analysis (CEA), a well-established technique that compares the costs and health outcomes of different interventions. CEA is considered superior to the cost-benefit approach as it evaluates both material and immaterial health benefits and costs associated with new healthcare technologies, including machine learning in disease diagnosis and treatment (Drummond et al., 2015). The CEA framework encompasses problem definition, identification of alternative interventions, definition of effectiveness and cost measures, data collection, data analysis, interpretation of findings, and drawing sound conclusions.

Dengue fever, a viral disease transmitted by mosquitoes, is a significant public health concern in tropical and subtropical regions. Early diagnosis is crucial for effective disease management and reducing the risk of severe complications. However, current diagnostic methods are limited in accuracy and are costly, which poses challenges, particularly in resource-limited settings (Mayrose, et al., 2023; Li et al., 2013). Therefore, there is a need to develop new and cost-effective diagnostic tools, such as machine learning models, for early detection of dengue fever.

Research has shown that machine learning algorithms hold promise in improving diagnostic accuracy and reducing costs associated with dengue fever diagnosis. Mayrose, et al., (2023) developed automated detection of vital dengue features in platelets and thrombocytopenia clinical Peripheral Blood Smear (PBS) image. The features extracted were subjected to popular machine learning classifiers such as Support Vector Machine (SVM) and Decision Tree (DT) with SVM giving the best performing accuracy of 95.74% after parameter tuning of each algorithms. The obtained results was a breakthrough in diagnosing of dengue from the digital microscopic images of PBS.

Thakur et al. (2020) developed a machine learning model that utilized clinical and laboratory data to predict severe dengue with high accuracy, demonstrating its potential as a reliable tool for early detection and effective management of the disease. Similarly, Kotwani et al. (2020) employed machine learning algorithms to predict dengue outbreaks with high accuracy, highlighting the potential of machine learning in predicting outbreaks and developing effective control measures.

Studies have also explored the use of machine learning approaches for dengue diagnosis based on gene expression analysis of peripheral blood mononuclear cells. Luo et al. (2020) developed a machine learning model using gene expression data to diagnose dengue fever with high accuracy, suggesting that machine learning algorithms can be applied to gene expression data to develop accurate and cost-effective diagnostic tools. Additionally, Devi et al. (2020) developed a machine learning-based framework for early diagnosis of dengue fever using clinical data, demonstrating its ability to provide accurate and timely diagnosis, which is essential for effective disease management.

A systematic literature review (SLR) was used by Hoyos, Aguilar and Toro, (2021) to analyze three modeling approaches of dengue which are diagnostic, epidemic, intervention and discovered that logistic regression was the most used modeling approach for the diagnosis of dengue (59.1%), analysis of the epidemic approach showed that linear regression (17.4%) is the most used technique within the spatial analysis and concluded that the most used intervention modeling is general linear model with 70%.

The use of machine learning algorithms in healthcare is gaining momentum as a promising solution to the challenges faced by current diagnostic methods. Ahmad et al. (2020) reviewed the current state of machine learning in healthcare and its applications, emphasizing its potential to improve diagnostic accuracy, reduce costs, and provide personalized treatment plans for patients.

In conclusion, the reviewed studies suggest that machine learning algorithms can be utilized to develop accurate and cost-effective diagnostic tools for dengue fever. These algorithms can be applied to various types of data, including clinical and laboratory data, gene expression data, and other relevant sources. The potential of machine learning in healthcare is significant, therefore necessitated the study for effective and efficient diagnostic of dengue fever in the prevailing countries of the world.

3. Research methodology

3.1. Description of proposed techniques

Machine learning is a tool not a dogma, no classifiers is inherently better than any others, it is logical to explore all the available machine learning algorithms starting from simple classifier to a complex ones making assumptions to generalization to attain the best performing machine learning model (Olatunji, 2023). In this study, K-Nearest Neighbor (KNN), Naive Bayes, Support Vector Machine (SVM), and Random Forest (RF) are the few machine learning classifiers that were investigated. The following listed machine learning algorithms are explained below:

K-nearest neighbor. The common narration of, tell me your friends and I will tell you who you are explains the fundamental principle of K-NN classifier procedure. KNN is a non-parametric classification algorithm that works by finding the k-nearest neighbors of a given data point and classifying it based on the majority class of those neighbors (Alpaydin, 2010). Fix and Hodges were the minds behind the machine learning algorithms in 1950. It is referred to as a lazy classifier because it does not require training models for model building; rather, it makes each query, finds the nearest neighbor from the trained database without considering their class label, and then lets the majority vote predict the class label of the target (Alassaf et al., 2018). This algorithm is commonly used in pattern recognition and image processing applications and it's could work better in classification and regression problem depending on the dataset and demographic mapping.

Simple bayes. A probabilistic algorithm that can handle huge datasets with several attributes is naive Bayes. The method works best when the predictors are not reliant on one another. Naive Bayes classifies the target class according to the law of probability, regardless of the existence or absence of other features in the vector space of general features. The probability rule is written as:

$$P(X/Y) = \frac{P(Y/X).P(X)}{P(Y)} \dots\dots\dots (1)$$

This probability rule is expressed by the equation (1), where X is the target class and Y the features vector describing an instance. P (X|Y) represents the likelihood that instance Y belongs to the specified class X. P (X) is the training set's prior probability for the target class. The likelihood that the features vector will match the target class in the training set is denoted by the symbol P (Y) (Alassaf et al., 2018; Krishnaveni & Radhamani, 2016).

In the context of diagnosing dengue, Naive Bayes could be used to identify the most important symptoms and risk factors associated with the disease, and provide a more accurate diagnosis. This means that the algorithm could be trained on a dataset containing instances of patients with dengue, along with the associated symptoms and risk factors. The trained model could then be used to predict whether a new patient has dengue based on their symptoms and risk factors.

Support vector machine. Support Vector Machine is a powerful algorithm that can handle both linear and non-linear classification problems. SVM can be particularly effective when there are many potential predictors and the relationship between the predictors and the outcome is complex. In the context of diagnosing dengue, SVM could be used to identify the most important symptoms and risk factors associated with the diseases, and provide a more accurate diagnosis (Cortes, 1995).

Random forest. An ensemble learning technique called random forest mixes various decision trees to increase accuracy and decrease over fitting. Large datasets with several attributes can be handled by random forest, and it can be useful for classification jobs where there are a lot of potential predictors. Random forest could be applied to the diagnosis of dengue and typhoid to pinpoint the most significant signs and risk factors and offer a more precise diagnosis (Breiman, 2001).

3.2. Data description

Despite the high prevalent of dengue fever in most African countries, the disease is underreported due to the limitations of current diagnostic methods and that made its difficulty to get sufficient data across the region. The data set for this study was source from kaggle dataset repository on dengue fever. The dataset contained clinical and laboratory tests of patients around Indian states hospitals. Indian is among the countries with highest prevalence of dengue and the country has recorded a lot of studies on dengue and other related diseases. However, these studies failed to consider the cost effectiveness of their machine learning models for dengue fever diagnosis which this study covers for the benefit of countries with low clinical and laboratory facilities to diagnosis dengue fever and related diseases. The 108 records in the resulting dataset each had a binary target class variable. The remaining 35 entries were categorized as non-Dengue Fever Patients, leaving 73 records as Dengue Fever Patients. The dataset initially had 17 features. Data such as patient identity (Patient I.D.) and those features with missing values greater than 50%, like white blood cell count (WB), hemoglobin, and hematocrit, were all removed after undergoing several data cleaning processes to reduce the dataset's dimensionality. The target class was added to the 13 remaining features. The dataset comprises 5 numerical attributes and 8 nominal features.

3.3. Description of data for training and validation procedure

Waikato environment for knowledge analysis (Weka), a package of codeless machine learning analytical tools, was used to conduct the experiment. By analyzing the correlation between each feature and the class label, Weka was used to preprocess the data and rank the features. Additionally, it was utilized for feature selection, parameter tuning, and the training and testing phases of the four classifiers, K-NN, Nave bayes, SVN, and RF. As a result of data imbalance of target class which could cause over fitting or under fitting of model accuracy, stratify data balancing method was used to increase minority target class by 100%. In order to ensure data spread of the increase in minority class, random subset from unsupervised was used to achieve the mixture of the negative increase among instances that are positive. For the purpose of achieving unbiased accuracy, the balanced dataset was manually partition in Microsoft excel to 70% for training and 30% for testing. The 5-fold cross validation was used for feature selection, parameter adjustment, and the actual classification procedure. The optimum values of the classifiers' parameters that came from the optimization technique were used to train each of the four classification algorithms.

4. Findings

4.1. Correlation analysis

The first result of analysis for this study is correlation coefficient of the target class component's attributes. This is of great significance because it shows quantitative impact of each attributes on target class for features selection purpose for optimal performance. The correlation coefficient of the study is presented in Table 1.

Table no. 1. Correlation-coefficient of the study on target variable

Attribute	Correlation Value
Pain behind the eyes	0.602
Abdominal pain	0.49
Metallic taste in the mouth	0.49
Appetite loss	0.4
Date of fever	0.312
Platelet	0.305
Patient residence	0.283
Severe headache	0.237
Nausea vomiting	0.224
Diarrhoea	0.209
Current temperature	0.195
Dengue days	0.165
Joint muscle aches	0.124

Source: Authors' own construction from kaggle dataset on dengue fever, 2023.

4.2. Optimization strategy

To achieve an optimal performance of machine learning algorithms, there is need for hyper parameter optimization of the classifier till the desire results or accuracy are achieved. There are two common hyper parameter tuning types such as grid search and random search selections. Grid search hyper parameter optimization was utilized in this study. The K-NN classifier was tuned to the optimal level of (k=3) with chebyshev distance measure. Support vector machine algorithms gave optimal value at hyper parameter of C=1 and kernel type of linear while random forest optimal hyper parameter values was numexecution slot (2) with seed value of (1). Table 2 presents various classifiers with their optimal hyper parameters values.

Table no. 2. Classifiers optimal hyper-parameters

Classifier	Hyper parameter	Value
K-NN	K	3
	Distance measure	Chebyshev distance
NVB	Null	Null
SVM	C	1
	Kernel	Linear kernel
RF	Numexecution	2
	Seed	1

Source: Authors' own construction from kaggle dataset on dengue fever, 2023.

4.3. Features selection

For this study's feature selection, correlation coefficient and recursive features elimination were applied. As shown in table 3, the qualities are ranked with the target variable in descending order using the correlation coefficient. The bottom half of the rated features are logically reduced to a single characteristic by the recursive feature reduction approach, producing subsets. Each subset runs all four classifiers through five rounds of cross validation to determine which subset is most effective. Table 3 demonstrates that the top 5 features—pain behind the patient's eyes, abdominal pain, and a metallic aftertaste in the mouth, appetite loss, and date of fever—got the best average accuracy.

Table no. 3. Subsets results of difference attributes

Number of Attributes	K-NN	NVB	RF	SVM	Average Accuracy (%)
13 (All)	79	100	100	100	95
5	86	100	100	100	97
4	88	86	88	90	88
3	87	86	90	90	88.2
2	81	81	81	81	81
1	81	81	81	81	81

Source: Authors' own construction from kaggle dataset on dengue fever, 2023.

4.4. Classification

NVB, SVM and RF algorithms performed absolutely better over K-NN on the optimal attributes selected with 5-fold cross validation partitioning method. The accuracy were rechecked to confirm the excellent performance of the classifiers with hyper parameters tuning of the various algorithms. SVM, RF and NVB maintained their 100% accuracy at optimal features. K-NN was enhanced to 95.35% which is better than the initial performance value of 86% at the higher features performing subset. Table 4 shows the accuracy performance of the various classifiers with their precision, recall and f-measure values.

Table no. 4. Optimal features classification performance

Classifier	Accuracy (%)	Precision	Recall	f-Measure
K-NN	95.35	0.923	0.953	0.953
NVB	100	1	1	1
RF	100	1	1	1
SVM	100	1	1	1

Source: Authors' own construction from kaggle dataset on dengue fever, 2023.

The accuracy, precision, recall and f-measure values of NVB, SVM and RF in Table 4 shows the highest performance measures. The confirmation of this is shown in the confusion matrices. The confusion matrices show the actual and predicted class target by K-NN, NVB, SVM and RF. Among the confusion matrices indicators of true Positive (TP), True Negative (TN), False Positive (FP) and False Negative (FN), False Negative is worrisome because a patient who is wrongly predicted negative may be working freely until the disease became complicated with high financial burden or death (Roche & Wang, 2014). This research is unique because the only wrong classification as shown by the study confusion matrices is from K-NN algorithm while other classifiers such as NVB, SVM and RF gave 100% accuracy with zero wrong classification. The following are the study confusion matrices:

Table no. 5. K-NN Confusion matrix

		Predicted	
Actual		DFP	Non DFP
	DFP	24 (TP)	0 (FN)
	Non DFP	2 (FP)	17 (TN)

Source: Authors' own construction from kaggle dataset on dengue fever, 2023.

Table no 6. NVB Confusion matrix

		Predicted	
		DFP	Non DFP
Actual	DFP	24 (TP)	0 (FN)
	Non DFP	0 (FP)	19 (TN)

Source: Authors' own construction from kaggle dataset on dengue fever, 2023.

Table no. 7. SVM Confusion matrix

		Predicted	
		DFP	Non DFP
Actual	DFP	24 (TP)	0 (FN)
	Non DFP	0 (FP)	19 (TN)

Source: Authors' own construction from kaggle dataset on dengue fever, 2023.

Table no. 8. RF Confusion matrix

		Predicted	
		DFP	Non DFP
Actual	DFP	24 (TP)	0 (FN)
	Non DFP	0 (FP)	19 (TN)

Source: Authors' own construction from kaggle dataset on dengue fever, 2023.

4.5. Cost-Effective analysis

Table 9 represents the different tests for dengue fever and their estimated costs in India, Nigeria and Thailand, which are countries with high prevalence of the disease. The cost of the various tests were measured in USA dollar (USD). The table shows that the serology test in India costs between USD 13.5 and USD 40, depending on location and hospital type. In Thailand, the same test costs between USD 15 and USD 40, while in Nigeria, it costs between USD 50 and USD 53.66. The NS1 antigen test costs USD 6.7 to USD 20 in India, USD 7.4 to USD 22.7 in Thailand, and USD 58 to USD 60.17 in Nigeria, depending on foreign exchange rates. The Polymerase Chain Reaction (PCR) test is the most expensive among the dengue fever tests, as it is a molecular diagnostic test that detects the presence of dengue virus RNA in blood samples. In India, the estimated cost of the PCR test is USD 67 to USD 135, while in Thailand, it costs USD 90 to USD 180. In Nigeria, the estimated cost of PCR is USD 98.30 to USD 100. On average, the estimated costs of the serology test, NS1 antigen test, and PCR test in India, Nigeria, and Thailand are USD 35.36, USD 29.16, and USD 111.72, respectively. It is important to note that the costs provided are current estimates and are subject to change due to fluctuations in foreign exchange rates in the exchange rate markets of the respective countries.

Machine learning classifiers, such as K-NN, NVB, SVM, and RF, have optimally identified five attributes that can accurately predict or classify a patient's dengue fever status based on their responses to questions posed by medical personnel. According to Olatunji (2023), the inductive basis principle of machine learning is that if it works on enough data, it can work on a small amount of data. This means that a machine learning model developed and deployed using trained and tested data from various algorithms with high accuracy, precision, and recall values can accurately predict or classify a patient's dengue fever status if provided with new data within the same dataset attributes. Therefore, patients in India, Nigeria, or Thailand exhibiting similar attributes can be diagnosed early and affordable cost at their respective health centers using the deployed machine learning model. The table 9 represents the estimated costs of the tests in the respective countries.

Table no. 9. Cost-effective analysis of ML model and other dengue fever diagnosis tests

The conventional diagnosis tests for dengue fever and their cost in India	
Type	Estimated cost range
Serology test	USD 13.5 to USD 40
NS1 antigen test	USD 6.7 to USD 20
Polymerase chain reaction (PCR)	USD 67 to USD 135
The conventional diagnosis tests for dengue fever and their cost in Nigeria	
Type	Estimated cost range
Serology test	USD 50 to USD 53.66
NS1 antigen test	USD 58 to USD 60.17
Polymerase chain reaction (PCR)	USD 98.30 to USD 100
The conventional diagnosis tests for dengue fever and their cost in Thailand	
Type	Estimated range
Serology test	USD 15 to USD 45
NS1 antigen test	USD 7.4 to USD 22.5
Polymerase chain reaction (PCR)	USD 90 to USD 180
Diagnosis of dengue fever using ML model	
The optimal features selected from trained and tested classifiers, provided some clinical basic attributes that can be used to diagnose dengue fever at affordable cost. Patient showing early symptoms such as: pain behind the eyes, abdominal pain, metallic taste in the mouth, appetite loss, few days of fever are all indicators to health personal of early signs of dengue fever. This diagnosis is more affordable and accessible presuming the patient is a register member of the health facilities.	

Source: (National Health Authority Indian, 2021; Pongsump & Pongsumpun, 2017; Syn Lab. Nigeria, 2023).

5. Conclusions

This study utilized a dataset from kaggle on dengue fever and applied machine learning techniques to classify patients based on clinical and laboratory tests. Feature selection was done using correlation coefficient and recursive feature elimination, and four classification algorithms were explored. The results showed high accuracy for all four classifiers, with NVB, SVM, and Random Forest achieving 100% accuracy and K-NN achieving 97.3% accuracy. Cost-effective analysis revealed that ML model classification is the most cost-effective technique as it enables early disease prediction and reducing diagnosis costs. Further research can explore the cost benefits of using Machine Learning Techniques in disease treatment.

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