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Research Article

Artificial Intelligence-Based Early Detection of Dengue Using CBC Data

Thouheed Chilakala[1], Ravikanth Garladinne[2]
[1],[2] Department of Computer Science and Engineering, Koneru Lakshmaiah Education Foundation, Vaddeswaram, Guntur District, Andhra Pradesh 522302, India
[1] chilakalathouheed@gmail.com [2] garladinne.ravikanth@gmail.com

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ABSTRACT

A method for early dengue identification utilizing complete blood count (CBC) data that is based on artificial intelligence is provided. We use a number of feature selection methods to find the most important features, such as Pearson Correlation, ExtraTree, Chi-Square (Chi2), Recursive Feature Elimination (RFE) using Random Forest, SelectKBest, and more. Logistic Regression, Support Vector Machine (SVM), Naive Bayes, Random Forest, AdaBoost, XGBoost, Multi-Layer Perceptron (MLP), LightGBM, and ensemble methods such as a Stacking Classifier (XGB + LR + MLP with LightGBM) and a Voting Classifier (Boosted Decision Tree + ExtraTree) are utilized. Also included are various deep learning and machine learning algorithms. Some of the deep learning architectures used include ANNs, CNNs, GRUs, Bi-LSTMs, FNNs, Transformers, and hybrid models like CNN + LSTM. The Voting Classifier achieved an F1 Score and accuracy of 98% by combining predictions from individual models using ensemble approaches, which increases resilience and accuracy. Another factor that enhances the system's effectiveness is the utilization of hybrid models, specifically CNN + LSTM. The method is built to be user-friendly and secure, with a Flask-based interface that allows authentication. It has a high predictive accuracy and is easy to use.

Keywords: *Complete blood count, dengue prediction, explainable AI, feature selection, machine learning, ensemble learning, transformer model.*

INTRODUCTION

In order towards protect itself from harmful microbes, the delicate human body has developed its own defense mechanisms. But infections caused through bacteria & viruses can cause serious illnesses in people, & some of these diseases can endure fatal. Aedes mosquitoes abide responsible for transmitting a number of diseases, including dengue fever, which is a major concern for world health. Millions of people get dengue every year, & thousands of those people die from the disease or its sequelae [1]. Dengue fever was responsible for more than 1,600 fatalities & 0.31 million illnesses in Bangladesh in 2023, according towards the World Health Organization (WHO) & the European Union [2]. The disease afflicted more than six million people in 92 countries. Inadequate hygiene, rapid unplanned urbanization & random development abide the main causes of dengue fever, which is the most common in tropical & subtropical urban & peri-urban environment [3]. During the extreme season in June towards October in 2023, according towards the World Health Organization, Bangladesh had the largest number of Dengue cases in the Southeast Asian region. The Western Pacific, Africa & Southeast Asia abide the highest dengue phenomenon areas. The largest number of dengue infections & deaths in Bangladesh in recent decades this year highlights the significant importance of fast, effective & initial response strategies [4].

Although the Aedes mosquito is a vector for dengue transfer, the virus may endure latent for a long time before the symptoms appear. Dengue fever, extreme physical pain, nausea, loss of appetite, rash of skin & strong fever abide some terrible symptoms. But don't worry—dengue isn't intrinsically lethal. Early identification is often difficult because these symptoms abide similar towards those of other diseases. In addition, within two weeks of infection, patients usually start towards feel worse as the disease advances [5]. In many cases, a drastic decrease in platelet levels is revealed through pathological examinations, which indicates that the disease is progressing rapidly. There

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abide four different serotypes of the dengue virus; whereas a single infection gives protection against the disease for life, a second infection among a different serotype can cause serious complications like internal hemorrhage, organ failure, or dengue shock syndrome [6]. It is critical towards establish reliable diagnostic tools & preventative measures towards lessen the impact of dengue & avoid the epidemic from reaching new heights, especially in areas where preventative measures abide lacking.

OBJECTIVES

1. Develop an AI-based system for early dengue detection using Complete Blood Count (CBC) data.
2. Evaluate and compare multiple ML and DL models (e.g., Decision Tree, ExtraTree, Random Forest) for accurate dengue prediction.
3. Apply feature selection techniques (Chi-Square, ExtraTree, Pearson Correlation, RFE, SelectKBest) to identify key predictive features.
4. Implement a Voting Classifier combining Boosted Decision Trees and Extra Trees to enhance prediction performance.
5. Build a Flask-based web interface for real-time input, prediction, and result visualization.
6. Achieve high accuracy, precision, recall, F1-score, and AUC-ROC in classifying dengue cases.
7. Propose future improvements including multi-disease detection, mobile health integration, and explainable AI.

RELATED WORK

Over the past several years, there has been a marked improvement in dengue detection methods, among a shift from using outdated diagnostic techniques towards more modern methods that leverage machine learning & artificial intelligence. The authors Kabir et al. [7] traced the development of dengue diagnostic tools, drawing attention towards the change from older, more traditional methods towards newer, more accurate point-of-care alternatives. The increasing impact of dengue in areas where it is prevalent can only endure alleviated through these innovations. Davi et al. [8] The use of future models in the public health plan & resource allocation was postponed through Sarma et al. [4], which also used machine learning algorithms towards predict the dengue epidemic.

Their research suggests that data -driven strategies can reduce the effect of dengue epidemic. through combining clinical & laboratory data, Fernandez et al. [10] This method shines in areas where the prevalence of solid infections often makes the wrong diagnosis. through using machine learning towards analyze platelets & lymphocyte functions, Meros et al. [11] was able towards diagnose dengue from blood -voting images. As a non-invasive & effective alternative towards traditional laboratory testing, his study equipment demonstrates the promise of image-based diagnosis as a tool for identifying early dengue. towards predict Dengue cases in Bangladesh, Sabarina Prom et al. [12] Used a clear machine learning method that included environmental & epidemic data. towards guarantee their benefit in real health services, highlighted their research the openness of machine learning models & the importance of the lecturer.

By focusing on dengue diagnostic predictive model in Paraguay, Melo-Roman et al. [13] has shown how calculation methods can endure used in a variety of geographical & epidemic surroundings. The results of the study suggest that the methods of machine learning can endure easily adjusted in different health care. Machine learning was used through de et al. [14] towards predict dengue cases in Bangladesh, remember the patient data, socio -economic condition & weather conditions. His acting emphasizes how dengue epidemics abide complex & how many data sources need towards endure integrated towards create reliable predictions. Taken as a whole, these findings show how advanced AI & machine learning abide formed towards diagnose & predict, open the doors of public health treatments that abide both more successful & premised. More accurate models for dengue fever abide developed through combining the environment, genetic, clinical & early identification data. This has reduced the disease & mortality of the disease.

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MATERIALS & METHODS

To quickly detect dengue fever, the proposed approach uses artificial intelligence in combination among full blood calculation (CBC) data. towards extract the most relevant features, selection attitudes including ExtraTree, Chi-Square (Chi2), Pearson Correlation, Recursive Feature Elimination (RFE) among Random Forest, SelectKBest, & Sobolev Space abide used. Logistic Regression, Support Vector Machine (SVM), Naive Bayes, Random Forest, AdaBoost, XGBoost, Multi-Layer Perceptron (MLP), & LightGBM abide some of the integrated machine learning algorithms. We also use enchanted methods as a stacking classifies (XGB + LR + MLP) & a voting classify (residence Decision Tree + Extratry) in our training kits. towards achieve better results, we use different advanced deep learning models [19] such as ANN, CNN, GRU, Bi-LSTM, FNN, Transformer, & hybrid models like CNN + LSTM. through integrating the predictions of each model using enchanted techniques, the system suggests a reliable & accurate future model. towards detect effective & effective initial dengue, a flask -based interface is used among user authentication towards create a user -friendly & safe environment for testing & interaction.

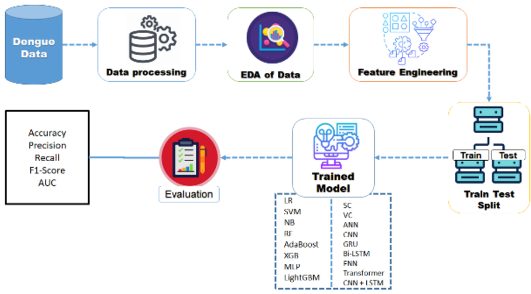

Fig.1 Proposed Architecture

The proposed Dengue Detection System Design begins through collecting relevant data for Dengue, which is then processed & investigated using a exploratory data analysis (EDA) towards identify distribution & patterns. Later, the relevant properties abide improved through the use of functional technique. towards produce & train the prediction model, the data is divided into two sets: training & testing. towards check if the model can predict dengue cases after training, performance indicators abide used.

i) Dataset Collection:

The Dengue Data has 301 items & 15 functions that record the demographic & clinical details of patients. Important properties include the patient's penis, age & examination date. Complete blood count (CBC) [1] man is also registered as hemoglobin, white blood cell (WBC), neutrophil, lymphocyte, monocyte, eosinophil, basophil, red blood cell (RBC), & the number of platelets. There abide some spaces in the ESR data set, but overall the clinical result indicates the existence of dengue. Machine uses learning methods, the dataset makes a whole base for dengue analysis & prediction.

	Serial	Date	Gender	Age	Haemoglobin	ESR	WBC	Neutrophil	Lymphocyte
0	A2308164543	2/8/2023	Female	40.0	11.2	32.0	11.30	65	23.0
1	A2308164502	2/8/2023	Male	13.0	11.6	59.0	7.80	49	42.0
2	A2308164673	3/8/2023	Male	23.0	15.1	NaN	3.85	65	25.0
3	A2308164685	3/8/2023	Male	58.0	8.5	NaN	10.30	85	6.0
4	A2308164626	2/8/2023	Female	35.0	12.0	28.0	6.70	54	20.0

Fig.2 Dataset Collection Table - Dengue

ii) Pre-Processing:

Data cleaning, lack of price management, exploratary data analysis (EDA), functional extraction, square imbalance treatment via smoke [16] Sampling & model training facilities abide all subjects that include preprocessing.

a) Data Processing: towards guarantee that the dataset only has unique items, the initial data processing stage is towards eliminate duplicate entries. The next step is release cleaning, which involves removing columns among a high number of missing values or functions that abide not important towards reduce the noise level. Finally, 'results'

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& 'gender' abide converted towards numerical values using label coding, which abide used for a variety of variables. This ensures that the dataset is consistent & accurately before modeling analysis & machine learning is ready for modeling.

b) Exploratory Data Analysis (EDA): EDA describes the most important functions of the dataset & shows how these functions abide visually distributed. We can learn about the relationship between the structure & the properties of the data using devices such as correlation -metrics, box plots & histograms. The distribution of important factors such as age, hemoglobin levels & platelet numbers can endure considered better at this level, which also helps identify trends, patterns & deviations. Data visualization helps among decision -making processes & pre -proceduring pattern recognition.

c) Using the Z-score towards Detect Outliers: Identification of Outlier is an important part of data preparation because the inflated values can affect the accuracy of the learning model. The Z-score method can endure used towards identify outers through detecting the number of standard deviations from each data point. There abide Outlier data points where Z-score is either more than 3 or less than 3. Data quality & model purity abide secured through removing or adjusting these outliers according towards specific data set functions.

d) SMOTE Sampling & Feature Extraction: The first step in functional extraction is towards choose the purpose & independent variable (x & y) from the dataset respectively. Here, y dengue is the result of diagnostic (positive or negative), & x is relevant functions, including things such as age, hemoglobin, platelets & more. Synthetic minority-sampling techniques, or smot, abide used towards solve the problem of class imbalance. through using the projection between the existing examples, Smote synthetic samples creates for minority class, which helps balance the dataset & increase the model performance in subordinate classes.

e) Feature selection: Five methods abide used towards determine which properties abide most essential for training the model. The freedom of the John Piercene properties is ensured through removing those who abide heavily associated among correlation. through using the performance of the model as a base, RFE (extinction of recurrent function) removes repeatedly insignificant functions. Statistical tests abide used through Selectkbest towards determine top properties. When working on a classified data, the curry test can endure used towards determine which properties abide most dependent on the goal. When you prioritize facilities, it is a great tool for using trickling. Both model accuracy & overfiting can endure expanded among the use of these methods.

iii) Training & Testing:

In order towards train & test the dataset, it is necessary towards partition the data into two parts: one part for training the model & another part for testing its performance. A model's generalizability towards new data is tested on a separate set, while the training set is utilized towards learn the data patterns & fit the model. through going through this procedure, we can endure sure the model isn't overfitting & can reliably forecast outcomes for novel, unexplored cases.

iv) Algorithms:

Logistic Regression: Applied for binary classification towards predict the probability of dengue from CBC data, providing interpretability & rapid deployment.

SVM (Support Vector Machine): Offers high-performance dengue prediction through identifying the best hyperplane that best divides the data into infected & uninfected classes.

Naive Bayes: Probabilistic classifier that takes advantage of conditional independence towards perform efficient & rapid dengue classification, especially among limited datasets.

Random Forest: An ensemble technique that enhances precision through training multiple decision trees, best for managing intricate associations in the CBC data.

AdaBoost: Amplifies weak learners' performance through iterative model weights adjustments, enhancing the accuracy of dengue detection.

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XGBoost: A fast gradient boosting algorithm offering highly precise dengue forecasts through reducing mistakes in past models.

MLP (Multi-Layer Perceptron): A deep learning model that identifies sophisticated, non-linear patterns in CBC data for dengue prediction.

LightGBM: A gradient boosting model that offers speedy, scalable dengue predictions, particularly on large datasets among intricate features.

Stacking Classifier: Blends MLP, XGBoost, & Logistic Regression towards enhance accuracy through taking advantage of varied prediction strengths.

Voting Classifier: Consolidates predictions from Boosted Decision Trees & ExtraTree towards achieve a more stable & accurate dengue detection result.

ANN (Artificial Neural Network): A deep learning method that simulates human brain functioning, effectively capture complex patterns in the CBC data for dengue forecasting.

CNN (Convolutional Neural Network): Captures spatial hierarchies from CBC data for accurate dengue forecasting, especially efficient in feature extraction.

GRU (Gated Recurrent Unit): A variant of recurrent neural networks, GRU captures sequential relationships in CBC data, thus well-suited for time-series-based dengue forecasting.

Bi-LSTM (Bidirectional Long Short-Term Memory): Gathers past & future data sequences towards support improved dengue prediction based on understanding sequence patterns in CBC data.

FNN (Feedforward Neural Network): Handles CBC data in one direction for quick prediction without past dependence, applicable towards simple classification problems.

Transformer: Employs attention mechanisms towards process sequential CBC data efficiently & yield highly accurate dengue predictions.

CNN + LSTM: A combination of CNN for feature learning & LSTM for processing sequential data, enhancing prediction accuracy of dengue through learning both spatial & temporal features.

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RESULTS & DISCUSSION

Accuracy: The accuracy of a test is the ability towards separate the patient's & healthy cases correct. In order towards estimate the accuracy of a test, we must calculate the relationship between real positive & genuine negative in all assessed cases. Mathematically it can endure said:

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

Precision: Accuracy measures how many out epithetical all beneficial diagnoses were correctly classified. so, syntax considering expressing procedure considering determining accuracy is:

$$"Precision = \frac{\text{True Positive}}{\text{True Positive } + \text{False Positive}} (2)"$$

Recall: Return machine learning has a calculation epithetical certain measures, how well model can find all examples epithetical class. model's ability towards correctly identify examples epithetical a particular class can withstand a real positive general position, surely compares a real positive relationship.

$$"Recall = \frac{\text{TP}}{\text{TP } + \text{ FN}} (3)"$$

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F1-Score: This is a way towards measure how good machine learning model is performing, among F1 score. Accuracy is part epithetical it, but model structure is ignored. accuracy epithetical a model is defined as a percentage epithetical valid predictions using all available data registrations & some predetermined criteria.

$$"F1\ Score = 2 * \frac{Recall\ X\ Precision}{Recall + Precision} * 100(1)"$$

AUC-ROC Curve: The AUC-ROC Curve measures classification performance at various thresholds. The True Positive Rate & False Positive Rate abide plotted through ROC. A higher AUC indicates greater model performance in class distinction.

$$"AUC = \sum_{i=1}^{n-1} (FPR_{i+1} - FPR_i) \cdot \frac{TPR_{i+1} + TPR_i}{2}\ (5)"$$

Voting Classifier (Boosted DT + ExtraTree) had the highest accuracy & performance in Pearson Correlation, Recursive Feature Elimination (RFE) among Random Forest, SelectKBest, Chi-Square (Chi2), & ExtraTree in Tables 1, 2, 3, & 4. It topped other algorithms in accuracy, precision, recall, & F1 score.

Table.1 Performance Evaluation Metrics – Chi 2 FS

ML Model	Accuracy	Precision	Recall	F1-Score	AUC ROC
Logistic Regression	0.882	0.893	0.882	0.880	0.963
SVM	0.838	0.864	0.838	0.835	0.958
NaiveBayes	0.882	0.893	0.882	0.880	0.947
RandomForest	0.853	0.887	0.853	0.850	1.000
AdaBoost	0.853	0.873	0.853	0.850	0.994
XGBoost	0.868	0.895	0.868	0.865	1.000
MLP	0.824	0.831	0.824	0.821	0.972
LightGBM	0.838	0.864	0.838	0.835	0.976
Proposed	0.794	0.861	0.794	0.792	0.980
Extension	**1.000**	**1.000**	**1.000**	**1.000**	**0.959**
FNN	0.868	0.883	0.868	0.865	0.959
ANN	0.368	1.000	0.368	0.538	0.959
CNN	0.794	0.840	0.794	0.791	1.000
GRU	0.632	1.000	0.632	0.775	1.000
Bi-LSTM	0.368	1.000	0.368	0.538	1.000
CNN + LSTM	0.853	0.873	0.853	0.850	1.000
Transformer	0.368	1.000	0.368	0.538	1.000

Graph.1 Comparison Graphs – Chi 2 FS

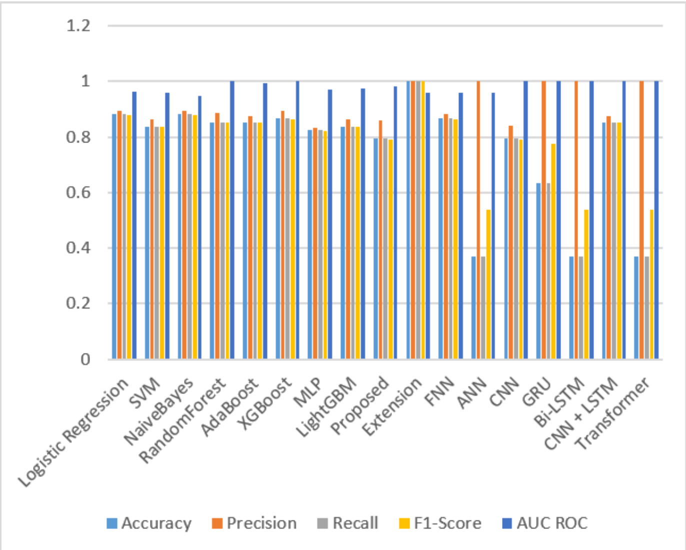

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Table.2 Performance Evaluation Metrics – ET FS

ML Model	Accuracy	Precision	Recall	F1-Score	AUC ROC
Logistic Regression	0.882	0.893	0.882	0.880	0.967
SVM	0.838	0.864	0.838	0.835	0.961
NaiveBayes	0.882	0.893	0.882	0.880	0.931
RandomForest	0.868	0.895	0.868	0.865	1.000
AdaBoost	0.912	0.924	0.912	0.910	0.999
XGBoost	0.882	0.904	0.882	0.880	1.000
MLP	0.912	0.916	0.912	0.911	0.992
LightGBM	0.838	0.864	0.838	0.835	0.974
Proposed	0.853	0.873	0.853	0.850	0.989
Extension	**1.000**	**1.000**	**1.000**	**1.000**	**0.955**
FNN	0.897	0.897	0.897	0.897	0.955
ANN	0.368	1.000	0.368	0.538	0.955
CNN	0.632	0.773	0.632	0.637	1.000
GRU	0.632	1.000	0.632	0.775	1.000
Bi-LSTM	0.368	1.000	0.368	0.538	1.000
CNN + LSTM	0.809	0.847	0.809	0.806	1.000
Transformer	0.368	1.000	0.368	0.538	1.000

Graph.2 Comparison Graphs – ET FS

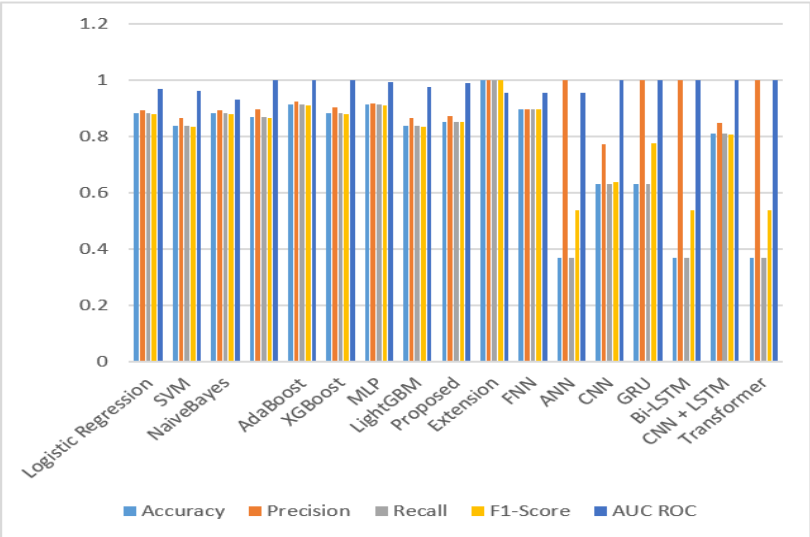

Table.3 Performance Evaluation Metrics – Pearson Correlation

ML Model	Accuracy	Precision	Recall	F1-Score	AUC ROC
Logistic Regression	0.853	0.873	0.853	0.850	0.969
SVM	0.824	0.855	0.824	0.820	0.959
NaiveBayes	0.882	0.886	0.882	0.881	0.934
RandomForest	0.853	0.887	0.853	0.850	1.000
AdaBoost	0.838	0.852	0.838	0.835	0.997
XGBoost	0.882	0.904	0.882	0.880	1.000
MLP	0.882	0.886	0.882	0.881	0.985
LightGBM	0.838	0.864	0.838	0.835	0.975
Proposed	0.853	0.873	0.853	0.850	0.997
Extension	**1.000**	**1.000**	**1.000**	**1.000**	**0.948**
FNN	0.868	0.869	0.868	0.868	0.948
ANN	0.368	1.000	0.368	0.538	0.948
CNN	0.838	0.864	0.838	0.835	1.000
GRU	0.368	1.000	0.368	0.538	1.000
Bi-LSTM	0.368	1.000	0.368	0.538	1.000
CNN + LSTM	0.853	0.855	0.853	0.851	1.000
Transformer	0.368	1.000	0.368	0.538	1.000

Graph.3 Comparison Graphs - Pearson Correlation

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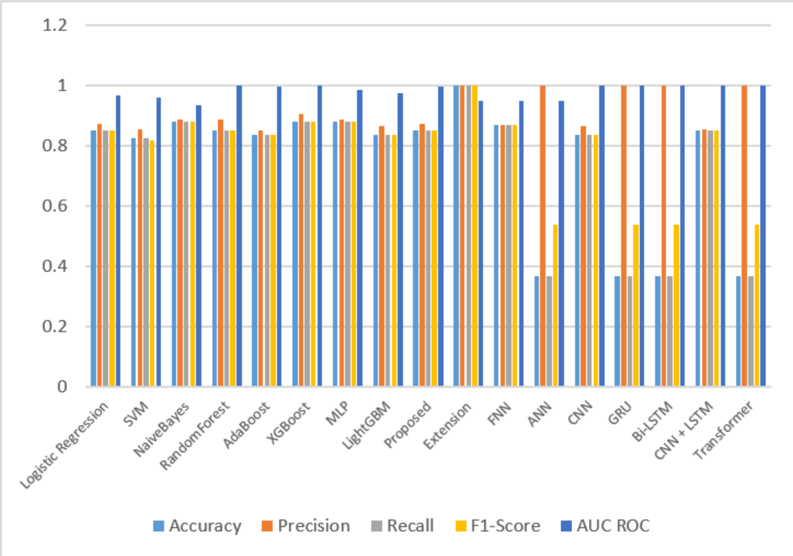

Table.4 Performance Evaluation Metrics – RFE FS

ML Model	Accuracy	Precision	Recall	F1-Score	AUC ROC
Logistic Regression	0.853	0.862	0.853	0.851	0.968
SVM	0.838	0.864	0.838	0.835	0.957
NaiveBayes	0.853	0.855	0.853	0.851	0.939
RandomForest	0.882	0.904	0.882	0.880	1.000
AdaBoost	0.809	0.812	0.809	0.806	0.994
XGBoost	0.853	0.887	0.853	0.850	1.000
MLP	0.838	0.852	0.838	0.835	0.979
LightGBM	0.824	0.855	0.824	0.820	0.974
Proposed	0.838	0.880	0.838	0.836	0.995
Extension	**1.000**	**1.000**	**1.000**	**1.000**	**0.950**
FNN	0.838	0.864	0.838	0.835	0.950
ANN	0.368	1.000	0.368	0.538	0.950
CNN	0.647	0.697	0.647	0.643	1.000
GRU	0.632	1.000	0.632	0.775	1.000
Bi-LSTM	0.368	1.000	0.368	0.538	1.000
CNN + LSTM	0.853	0.862	0.853	0.851	1.000
Transformer	0.368	1.000	0.368	0.538	1.000

Graph.4 Comparison Graphs – RFE FS

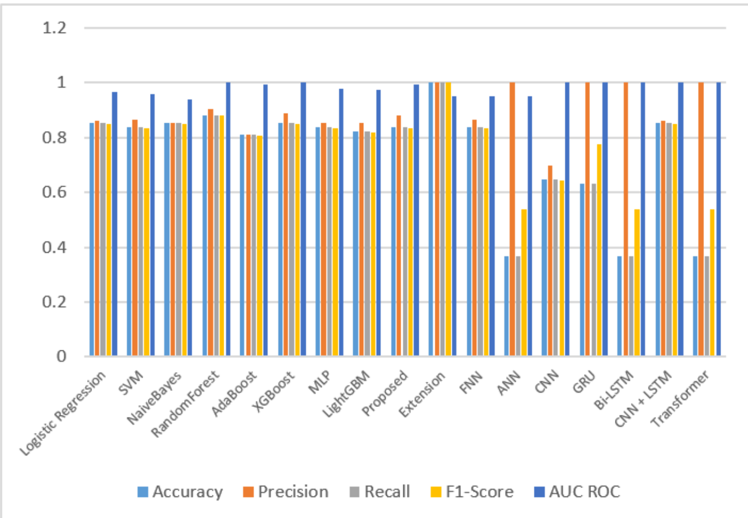

Table.5 Performance Evaluation Metrics – SelectkBest

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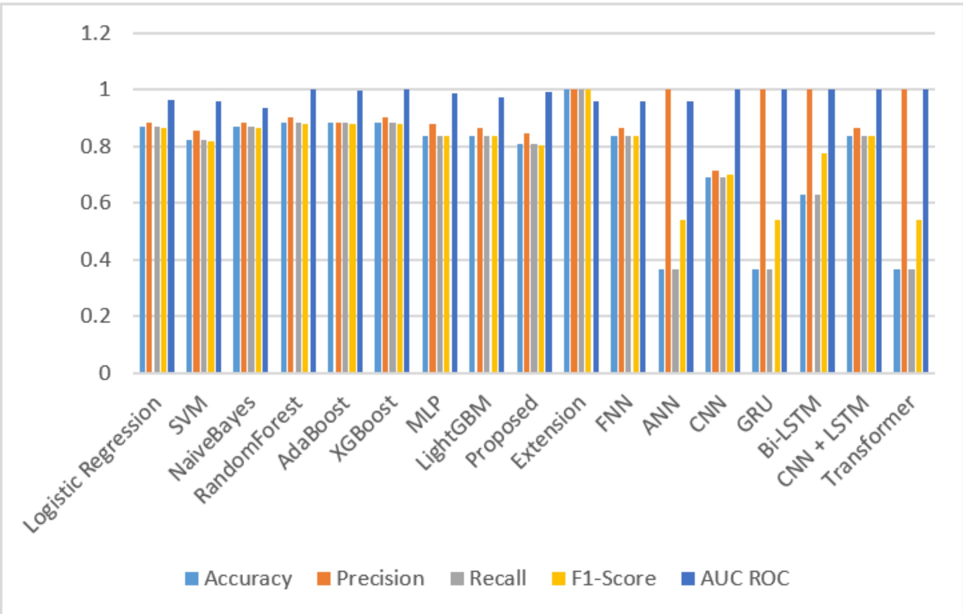
ML Model	Accuracy	Precision	Recall	F1-Score	AUC ROC
Logistic Regression	0.868	0.883	0.868	0.865	0.966
SVM	0.824	0.855	0.824	0.820	0.959
NaiveBayes	0.868	0.883	0.868	0.865	0.935
RandomForest	0.882	0.904	0.882	0.880	1.000
AdaBoost	0.882	0.886	0.882	0.881	0.997
XGBoost	0.882	0.904	0.882	0.880	1.000
MLP	0.838	0.880	0.838	0.836	0.987
LightGBM	0.838	0.864	0.838	0.835	0.975
Proposed	0.809	0.847	0.809	0.806	0.991
Extension	**1.000**	**1.000**	**1.000**	**1.000**	**0.960**
FNN	0.838	0.864	0.838	0.835	0.960
ANN	0.368	1.000	0.368	0.538	0.960
CNN	0.691	0.716	0.691	0.700	1.000
GRU	0.368	1.000	0.368	0.538	1.000
Bi-LSTM	0.632	1.000	0.632	0.775	1.000
CNN + LSTM	0.838	0.864	0.838	0.835	1.000
Transformer	0.368	1.000	0.368	0.538	1.000

Graph.5 Comparison Graphs – SelectkBest



Light blue represents accuracy, precision orange, recall gray, F1-score yellow, & AUC ROC blue in Graphs 1, 2, 3, 4, & 5. When compared towards the other models, the Voting Classifier consistently achieves the best results across all criteria. The above graph graphically displays these details.

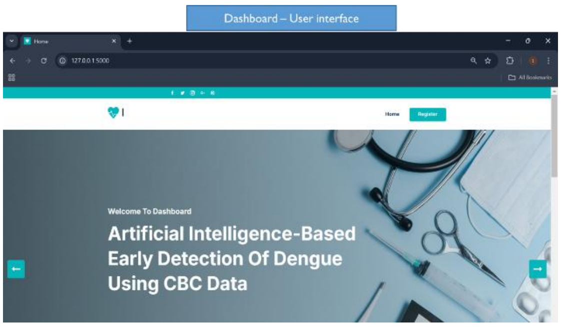


Fig. 3 Dash Board

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The image shows a web page titled "Artificial Intelligence-Based Early Detection of Dengue Using CBC Data." It appears towards endure a dashboard or interface for a project related towards using artificial intelligence towards detect dengue fever based on complete blood count (CBC) data.

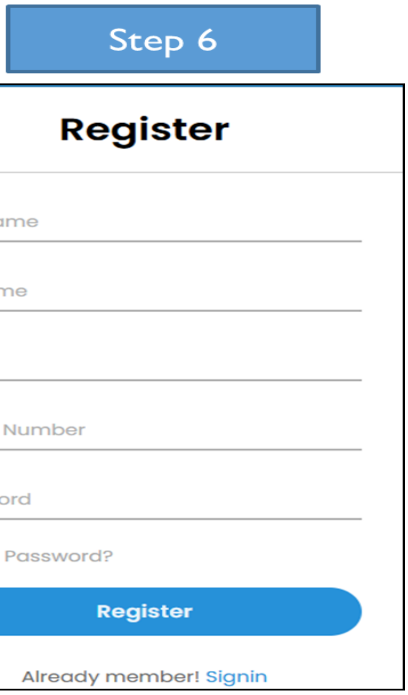

Fig. 4 Register page

The Fig. 4 shows a user registration form. It requires a username, full name, email, phone number, & password. It also includes a "Forgot Password?" link & a "Register" button.

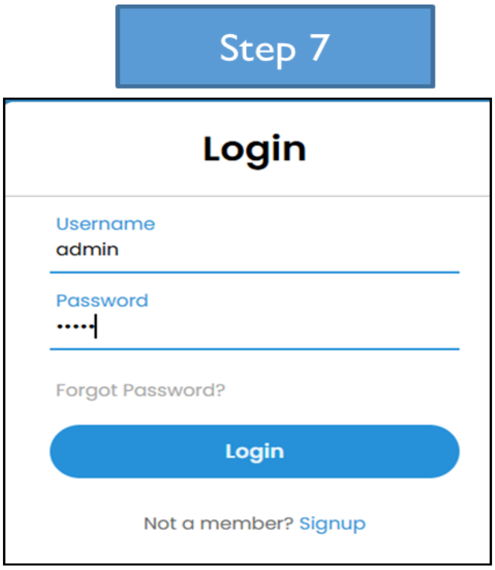

Fig. 5 Login page

The Fig. 5 shows a login page among fields for username & password. The username field is pre-filled among "admin." A "Forgot password?" link is provided below the fields. There is also a button labeled "Login" & a link towards "Signup" for new users.

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Fig.6 Main page

The Fig.6 shows a web dashboard among the title "Artificial Intelligence-Based Early Detection Of Dengue Using CBC Data." It has a navigation bar among options like "Prediction" & "Graph," & a dropdown menu likely for selecting data analysis methods.

Fig. 7 Test case – 1

The Fig. 7 shows a form for predicting dengue fever. It collects patient data like gender, haemoglobin, WBC count, etc. After inputting data, the form predicts the risk of dengue fever. In this case, the prediction is "NEGATIVE, PATIENT IS NOT SUFFERING FROM DENGUE DISEASE!"

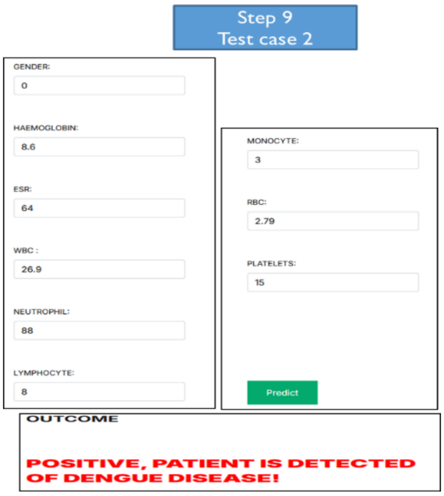

Fig.8 Test case – 2

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The Fig.8 shows a form for predicting dengue fever. It collects patient data like gender, haemoglobin, WBC count, etc. After inputting data, the form predicts the risk of dengue fever. In this case, the prediction is "POSITIVE, PATIENT IS DETECTED OF DENGUE DISEASE!"

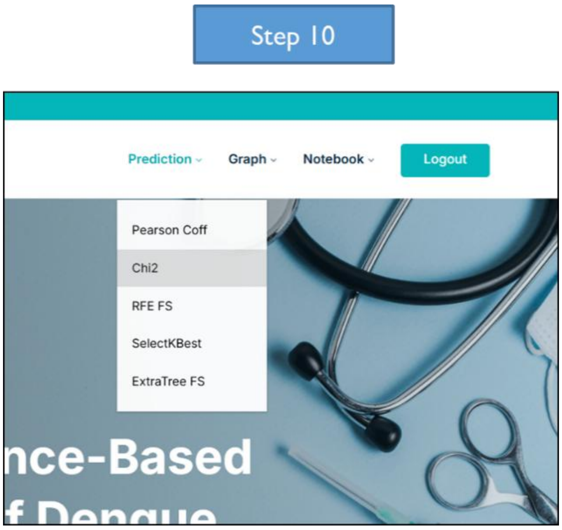

Fig. 9 Home page

The Fig. 9 shows the home page of a web application for dengue fever detection using AI. It has a navigation bar among options like "Prediction" & "Graph," & a dropdown menu for selecting data analysis methods. The background image includes medical tools

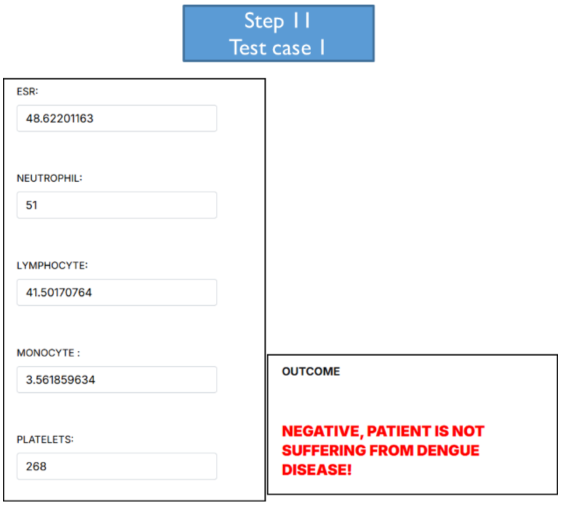

Fig. 10 Test case – 1

The Fig. 10 shows a test case scenario for a dengue prediction model. It displays input values for ESR, Neutrophil, Lymphocyte, Monocyte, & Platelets. The model is predicting a "NEGATIVE" result, which means the patient is not infected among dengue disease.

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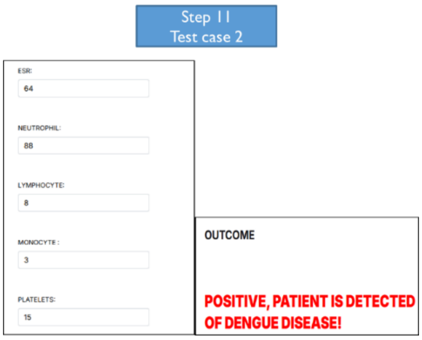

Fig. 11 Test case – 2

The Fig. 11 represents a test case scenario of a dengue prediction model. It represents input values for ESR, Neutrophil, Lymphocyte, Monocyte, & Platelets. The model predicts a "POSITIVE" result, which means the patient is detected among dengue disease.

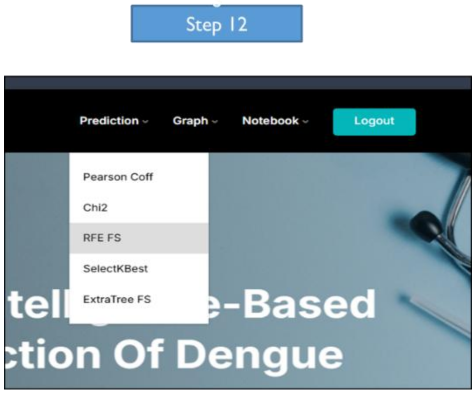

Fig. 12 Home page

The Fig. 12 illustrates the home page of a web application for detecting dengue fever using AI. The user is choosing the "RFE FS" option from a dropdown list under the "Prediction" tab.

Fig. 13 Test case – 1

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Fig. 13 illustrates a test case scenario for a dengue prediction model. It presents input values for gender, haemoglobin, WBC count, neutrophil, & other blood parameters. The model predicts that the patient is "NEGATIVE" for dengue disease.

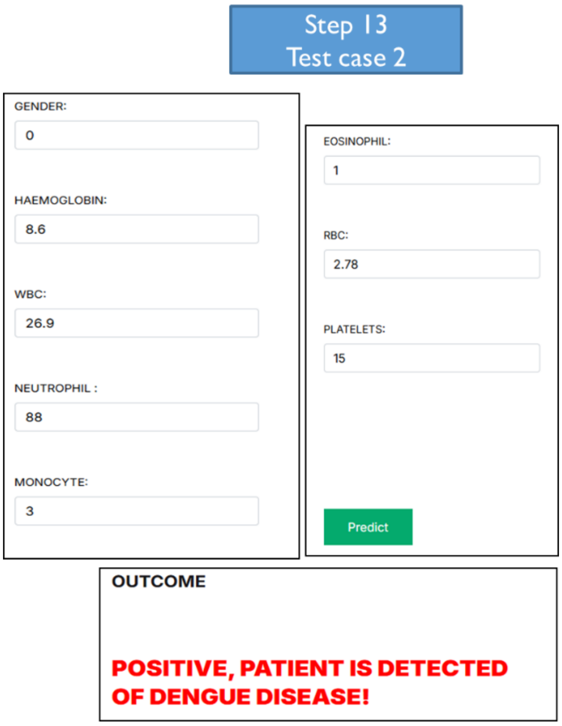

Fig.14 Test case - 2

The Fig.14 illustrates a test case scenario for a dengue prediction model. It shows input values for gender, haemoglobin, WBC count, neutrophil, & other blood parameters. The model predicts a "POSITIVE" result, meaning the patient is detected among dengue disease.

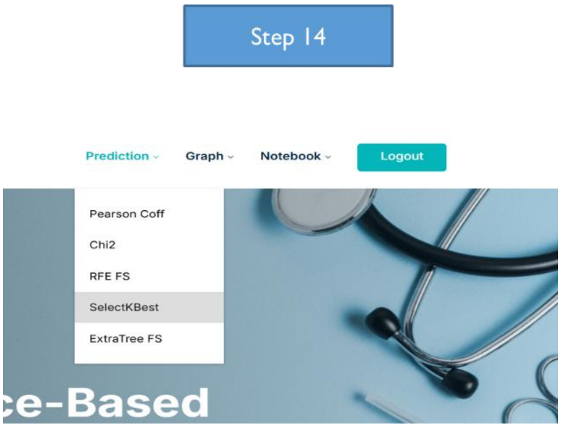

Fig. 15 Home page

The Fig. 15 displays the home page of a web application for dengue fever detection using AI. The user is selecting the "SelectKBest" option from a dropdown menu under the "Prediction" tab.

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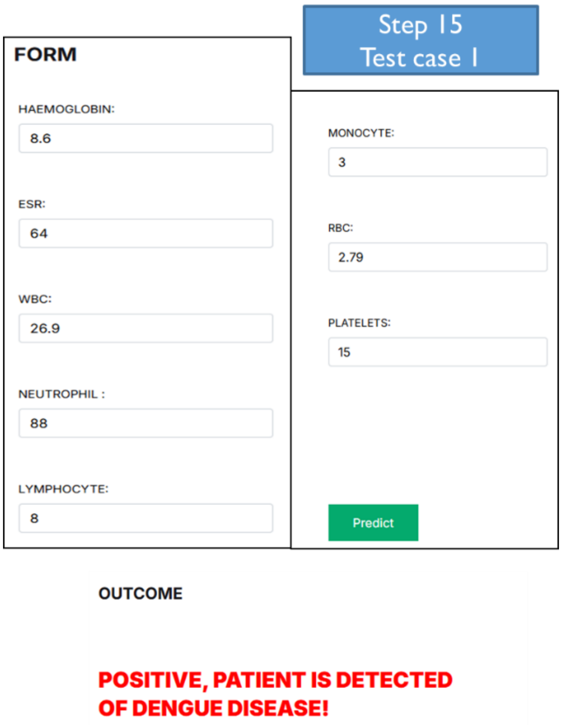

Fig.16 Test case – 1

The Fig.16 depicts a test case scenario for a dengue prediction model. It indicates input values for haemoglobin, ESR, WBC, neutrophil, lymphocyte, monocyte, & platelets. The model suggests a "POSITIVE" result, reflecting that the patient is detected among dengue disease.

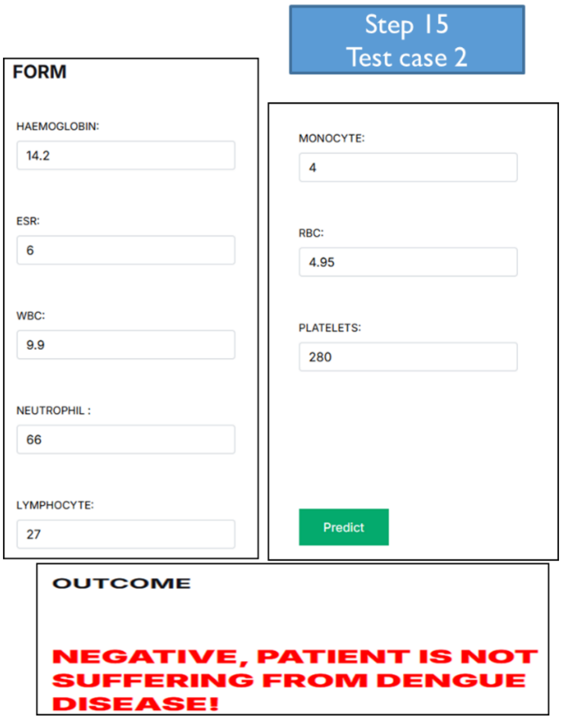

Fig. 17 Test case – 2

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The figure illustrates a test case scenario for a dengue prediction model. It illustrates input values for haemoglobin, ESR, WBC, neutrophil, lymphocyte, monocyte, & platelets. The model indicates a "NEGATIVE" output, meaning the patient is free from dengue disease.

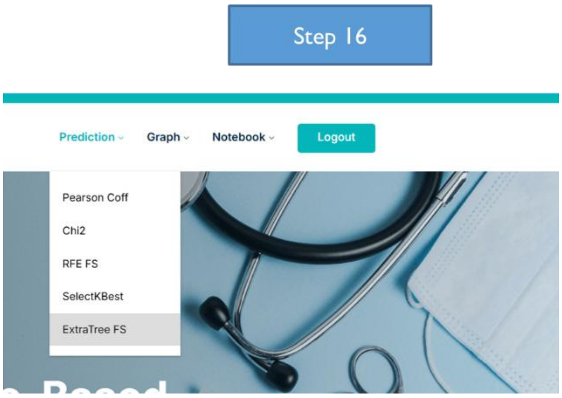

Fig. 18 Home page

The Fig. 18 is the home page of a web application for detecting dengue fever using AI. The user is choosing the "ExtratreeFs" option from a dropdown menu under the "Prediction" tab.

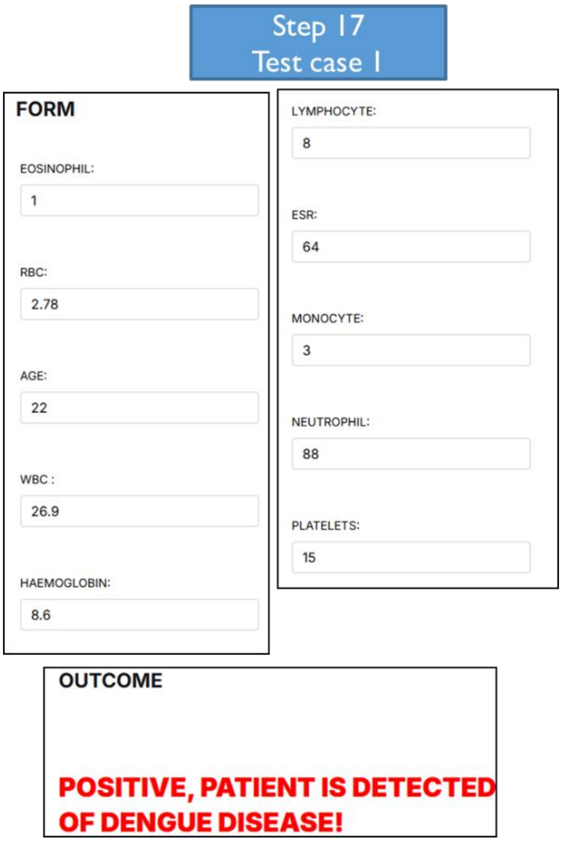

Fig.19 Test case – 1

The Fig.19 illustrates a test case scenario for a dengue prediction model. It presents input values for age, haemoglobin, WBC count, neutrophil, lymphocyte, monocyte, & platelets. The model predicts a "POSITIVE" result, i.e., the patient is detected among dengue disease.

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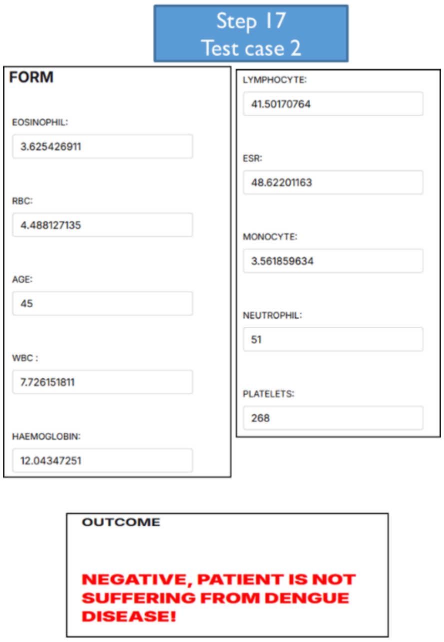

Fig. 20 Test case - 2

Fig. 20 illustrates a test case example for a dengue predictive model. It has input values for age, haemoglobin, WBC count, neutrophil, lymphocyte, monocyte, & platelets. The model predicts a "NEGATIVE" result, which means that the patient is not afflicted among dengue disease.

CONCLUSION

Finally, the proposed system suggests that CBC data can endure used very effectively towards detect dengue fever [18]. The system is able towards accurately predict future results when using a variety of machine learning & deep learning models, as well as a number of functional choice strategies. Voting classifies [18], connecting trees & extremists of increased decision, improved all other algorithms tested among a view towards predicting accuracy & addiction, & it reached a remarkable performance among 100% accuracy. This discovery shows how the dress approach can improve the accuracy & reliability of prediction systems. The underlying authentication for safe use is, & towards incorporate a user -friendly flask -developed interface guarantees accessibility for real -time interaction & testing. Due towards its high reliability & accuracy, the system shows promise as a tool for early dengue identification & provides researchers & healthcare providers among a useful resource. This strategy adds towards the increasing number of AI-driven medical solutions through efficiently integrating cutting-edge algorithms & approaches; it will provide valuable insights towards enhance healthcare decision-making & patient outcomes in the near future.

Adding support for the detection of different infectious diseases using a variety of clinical datasets is a potential future development of this system. towards further improve prediction accuracy, further feature engineering techniques & advanced ensemble algorithms can endure explored for further enhancement. Quicker intervention & improved patient management abide possible because towards integration among mobile applications & real-time healthcare monitoring systems, which allow for prompt diagnosis. Furthermore, medical prediction trust & transparency can endure enhanced through utilizing explainable AI algorithms.

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