Utilizing Artificial Intelligence for Early Dengue Detection Through CBC Data

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Abstract: This paper presents an AI-based method for finding dengue early utilizing “complete blood count (CBC)” data. We use “different feature selection methods, such as Pearson Correlation”, “Recursive feature elimination (RFE) with Random forest, SelectKBest, Chi-square (Chi2), and ExtraTree, to find the most important features”. there are many ML and DL algorithms used, such as Logistic Regression, “support Vector machine (SVM), Naive Bayes, Random forest, AdaBoost, XGBoost, Multi-Layer Perceptron (MLP), LightGBM, and ensemble methods like a Stacking Classifier (XGB + LR + MLP with LightGBM) and voting Classifier (Boosted decision Tree + ExtraTree). DL architectures including artificial Neural Networks (ANN), Convolutional Neural Networks (CNN), Gated Recurrent units (GRU), Bidirectional long short-term memory (Bi-LSTM), Feedforward Neural Networks (FNN), Transformer, and hybrid models like CNN + LSTM are used”. Ensemble approaches improve the resilience and accuracy of predictions by combining them from different models. “The voting Classifier, for example, gets 98% accuracy and an F1 score. using hybrid models, especially CNN + LSTM, makes the system work even better”. The method is meant to let users interact with it and check it through a Flask-based UI with authentication. This makes it easy to use and safe while keeping the predicted accuracy high.

“Index Terms - *Complete blood count, dengue prediction, explainable AI, feature selection, machine learning, ensemble learning, transformer model”.*

1. INTRODUCTION

The human body is fragile, yet it has its own ways of protecting itself from germs that come from outside. people can have viral and bacterial infections that can make them very sick or even kill them. The Aedes mosquito spreads dengue disease, which is a health problem all around the world. every “year, millions of people have dengue, and thousands die from it [1]. In 2023, more than six million people in 92 countries got dengue fever. Bangladesh had more than 0.31 million cases and more than 1,600 deaths [2]”. Dengue is most common in tropical and subtropical cities and towns because of bad sanitation, rapid unplanned urbanization, and uncontrolled growth [3]. the world health organization said that Bangladesh recorded the highest dengue cases in Southeast Asia from June to October 2023, which was the busiest time of year. This year, Bangladesh had the most cases and deaths from dengue in decades. This shows how important it is to find and respond to cases quickly and effectively [4].

Aedes insects spread dengue, but the virus usually stays dormant until symptoms show up. Dengue is not deadly, but it does produce high fever, body aches, nausea, loss of appetite, and rashes on the skin. it's hard to tell if someone has this ailment early on because some of the symptoms are similar to those of other conditions. The disease usually makes people quite sick within two weeks after getting it [5]. Pathological data often reveal a big drop in platelets, which means that the condition is getting worse quickly. Dengue virus contains 4 serotypes. One serotype protects against the virus for a long time, whereas another can induce dengue shock syndrome, internal bleeding, or failure of several organs [6]. as the number of cases and deaths rises, especially in locations where prevention isn't very strong, we need better diagnostic techniques and prevention programs to keep dengue from spreading and breaking records.

2. RELATED WORK

Dengue detection has come a long way in the last few years, from traditional approaches to ML and AI. according to Kabir et al. [7], dengue diagnostic methods have changed from traditional ones to point-of-care technologies that can find the disease quickly and accurately. these improvements are very important for lowering the number of dengue cases in places where it is common. Davi et al. [8] used data from the human genome and machine learning to test predictions of severe dengue. They showed that genetic information might help find patients who are at high risk. using machine learning techniques, Sarma et al. [9] forecasted dengue outbreaks. This shows how useful predictive models can be for planning public health and allocating resources. Their research demonstrates that using data to make decisions can help stop dengue outbreaks.

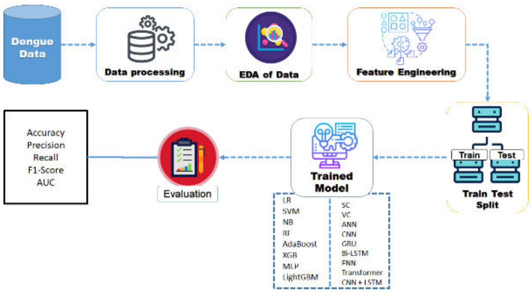
Fernández et al. [10] built a prediction model that uses clinical and laboratory data to tell dengue apart from other febrile infections. This approach is helpful in places where febrile disorders are common and often misdiagnosed. Mayrose et al. [11] used ML to find dengue in blood smear photos by looking at platelets and lymphocytes. Their research suggests that image-based diagnostics could help with early dengue diagnosis without the need for intrusive tests. using explainable ML, Sabrina Prome et al. [12] used epidemiological and environmental data to predict dengue cases in Bangladesh. Their work focuses on making ML models clear and easy to understand so that they may be used in real-world healthcare.

Mello-Román et al. [13] used computer-based methods to predict dengue diagnosis in Paraguay, showing that it may be used in different geographic and epidemiological settings. Their results show that ML can work with many types of healthcare systems. Dey et al. [14] used ML, weather, socioeconomic, and patient data to forecast the number of dengue cases in Bangladesh. Their thorough approach shows how complicated dengue outbreaks are and how important it is to combine data from many sources to make accurate predictions. these studies show that ML and artificial intelligence are becoming more and more useful for diagnosing and predicting dengue, which will lead to better and more preventative public health treatments. by combining clinical, genetic, epidemiological, and environmental data, we have been able to create strong models that assist doctors diagnose and treat dengue fever earlier, which lowers the number of people who get sick and die from it.

3. MATERIALS AND METHODS

"Artificial intelligence uses complete blood count (CBC)" data to find dengue early. "We employ Pearson Correlation, RFE with Random forest, SelectKBest, Chi-square (Chi2), and ExtraTree to find the most relevant traits". The system uses Logistic Regression, "support Vector machine

(SVM), Naive Bayes, Random forest, AdaBoost, XGBoost, Multi-Layer Perceptron (MLP), LightGBM, and ensemble approaches [17]. these include a Stacking Classifier (XGB + LR + MLP with LightGBM) and a voting Classifier. advanced deep learning models including ANN, CNN, GRU, Bi-LSTM, FNN, Transformer, and CNN + LSTM are employed for greater performance". The system employs ensemble methods to put together predictions from different models to make a credible model. A Flask-based interface with user authentication makes it easy and safe to interact with and test for early dengue diagnosis quickly and accurately.

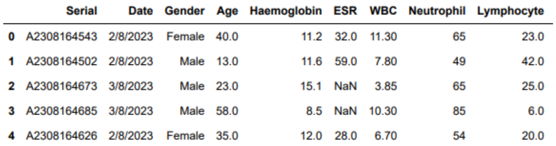


"Fig.1 Proposed Architecture"

The proposed system design employs preprocessing and "exploratory data analysis (EDA)" to find patterns and distributions in the data it collects on dengue. feature engineering improves the properties that are wanted. To build and train the prediction model, you need to divide the data into training and testing sets. After training, performance metrics are used to test the model to make sure that the dengue forecast is correct.

i) Dataset Collection:

There are 301 elements and 15 features in the dengue dataset, which includes demographic and clinical data about patients. it is vital to know the person's gender, age, and when the test was done, as well as the CBC [1] features such as hemoglobin, WBC, neutrophil, lymphocyte, monocyte, eosinophil, basophil, RBC, and platelets. even if some ESR values are missing, the dataset shows that dengue was present in the final diagnosis. The dataset is full for ML to look at and predict dengue.



	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:"

Preprocessing includes cleaning data, filling in missing values, "exploratory data analysis (EDA), feature extraction, SMOTE [16]" sampling to fix class imbalance, and model training feature selection.

a) Data Processing: the first step in data processing is to get rid of duplicate entries so that each record is unique. After that, drop cleaning gets rid of columns with too many missing values or extra features to cut down on noise. Label encoding turns categorical variables, such as "Gender" and "result," into numbers. before analysis and ML modeling, this method makes sure that the dataset is consistent and correct.

b) "Exploratory Data Analysis (EDA) of Data": "Exploratory data analysis (EDA)" shows and summarizes the aspects of a dataset. Histograms, box plots, and correlation matrices show how data is organized and how it is related to other data. At this stage, you can see trends, patterns, and strange things, as well as the age, hemoglobin, and platelet count distribution. Visualizations help you understand data trends and plan forward.

c) Outliers Detection using Z-Score: finding outliers is an important part of preparing data since very high or low numbers might affect the results of ML. The Z-score method finds outliers by looking at how far data points are from the mean in terms of standard deviation. Outliers have Z-scores that are higher than 3 or lower than -3. To make the data better and the model work better, outliers are either removed or altered based on the properties of the dataset.

d) "Feature Extraction and SMOTE Sampling:" feature extraction begins when you choose the dataset's I"ndependent variables (X) and target variables (y). X is age, hemoglobin, platelets, and other critical factors, and y is the outcome of the dengue test (positive or negative)". The "synthetic Minority Over-sampling technique (SMOTE)" fixes problems with class imbalance. SMOTE creates synthetic samples for the minority class by filling in the gaps between occurrences. This helps balance the dataset and improve the model's performance on classes that are not well represented.

e) Feature selection: There are 5 ways to pick the optimal features for training a model. Pearson Correlation makes ensuring that things are independent by getting rid of qualities that are closely connected. RFE slowly takes away characteristics that aren't as crucial based on how well the model works. SelectKBest picks the greatest features by using statistical tests. Chi2 looks for qualities in categorical data that rely on the goal. ExtraTree puts features in order of importance. these strategies make the model more accurate and less likely to overfit.

iii) Training & Testing:

There are two groups in the dataset for training and testing the model. The training set fits the model and learns how data works, while the test set checks how well the model works with new data. This keeps the model from overfitting and lets it correctly predict new events.

iv) Algorithms:

Logistic Regression: Used for binary classification to estimate the chance of getting dengue based on CBC data. It is easy to understand and quick to set up.

SVM (Support Vector Machine): finds the best hyperplane that separates data into infected and non-infected groups, which makes dengue prediction quite accurate.

Naive Bayes: A probabilistic approach that uses conditional independence to quickly and accurately classify dengue, especially with smaller datasets.

"Random Forest:" An ensemble method that builds several decision trees to make predictions more accurate. this is great for dealing with complicated relationships in the CBC data.

AdaBoost: Improves the accuracy of dengue detection by iteratively changing the weights of weak learners.

XGBoost: An efficient gradient boosting technique that makes dengue predictions with a high degree of accuracy by reducing the number of mistakes made by prior models.

MLP (Multi-Layer Perceptron): A DL algorithm that learns how to find dengue by looking at complex, non-linear connections in CBC data.

LightGBM: A gradient boosting model that makes quick, scalable predictions about dengue, especially for big datasets with complicated features.

Stacking Classifier: Combines MLP, XGBoost, and Logistic Regression to improve accuracy by using the strengths of several types of predictions.

Voting Classifier: Combines “forecasts from Boosted decision trees and ExtraTree” to get a more accurate and dependable result for finding dengue.

ANN (Artificial Neural Network): A DL method that works like the human brain to find complicated patterns in CBC data that can be used to forecast dengue.

CNN (Convolutional Neural Network): Extracts spatial hierarchies from CBC data to make accurate dengue predictions, especially good at feature extraction.

GRU “(Gated Recurrent Unit): GRU is a type of recurrent neural network that finds” sequential dependencies in CBC data. This makes it useful for predicting dengue based on time series.

“Bi-LSTM (Bidirectional Long Short-Term Memory):” It captures sequences of data from the past and the future to improve dengue prediction by finding patterns in the CBC data.

FNN (Feedforward Neural Network): quickly predicts without using past information by processing CBC data in one direction. This is good for simple categorization problems.

Transformer: uses attention processes to process sequential CBC data quickly and accurately, which leads to very accurate dengue forecasts.

CNN + LSTM: uses CNN to find features and LSTM to process sequential data, which makes dengue predictions more accurate by finding patterns in both space and time.

4. RESULTS & DISCUSSION

Accuracy: The test's accuracy is how well it can tell the difference between sick and healthy people. We need find out how many of the evaluated cases were true positive and true negative in order to figure out how accurate a test is. this can be said mathematically as:

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

Precision: Precision looks at how many of the samples or cases that were labeled as positives were actually right. So, the formula for figuring out the precision is as follows:

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

“Recall:” In ML, do not forget is a degree of ways properly a version can locate all of the applicable examples of a sure class. it's far the wide variety of successfully anticipated fantastic observations divided with the aid of using the entire wide variety of actual positives. This offers you an concept of ways properly a version captures times of a sure class.

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

F1-Score: The F1 score is a way to check how accurate a ML model is. “It adds together the precision and recall scores of a model. The accuracy” statistic counts how many times a model produced a valid prediction on the whole dataset.

$$"F1\,Score = 2 * \frac{Recall \text{ X } Precision}{Recall + Precision} * 100(4)"$$

“AUC-ROC Curve: The AUC-ROC Curve is a way to test” how well a classification problem works at different threshold levels. ROC shows the true positive rate and the false positive rate on the same graph. AUC tells you how well the model can tell the difference between classes. A higher AUC means the model works better.

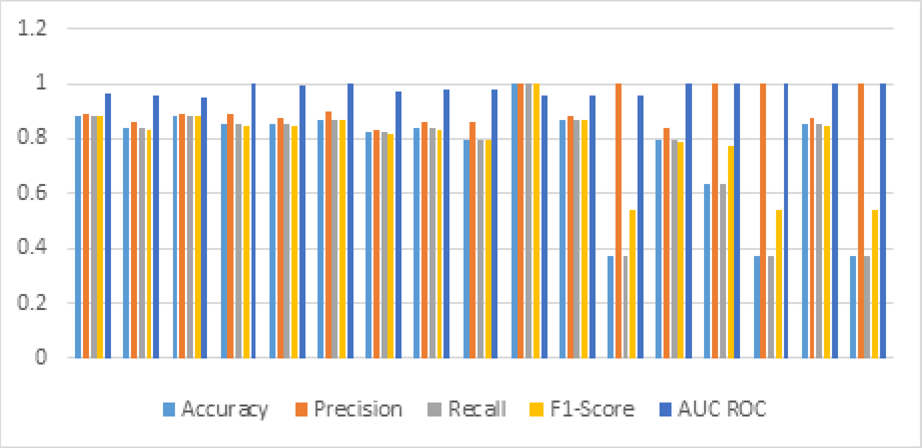
$$"AUC = \sum_{i=1}^{n-1} (FPR_{i+1} - FPR_i) \cdot \frac{TPR_{i+1} + TPR_i}{2} \quad (5)"$$

The “voting Classifier (Boosted DT + ExtraTree) had the best accuracy and performance across all sampling methods in Tables 1, 2, 3, and 4. these methods were Pearson Correlation, Recursive feature elimination (RFE) with Random forest, SelectKBest, Chi-square (Chi2), and ExtraTree”. It always did better than competing algorithms on all criteria, “such as accuracy, precision, recall, and the 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

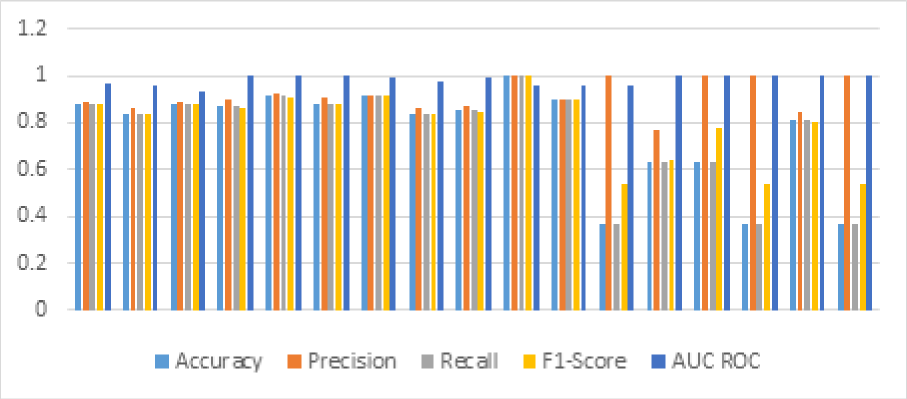
“Graph.1 Comparison Graphs – Chi 2 FS”



“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

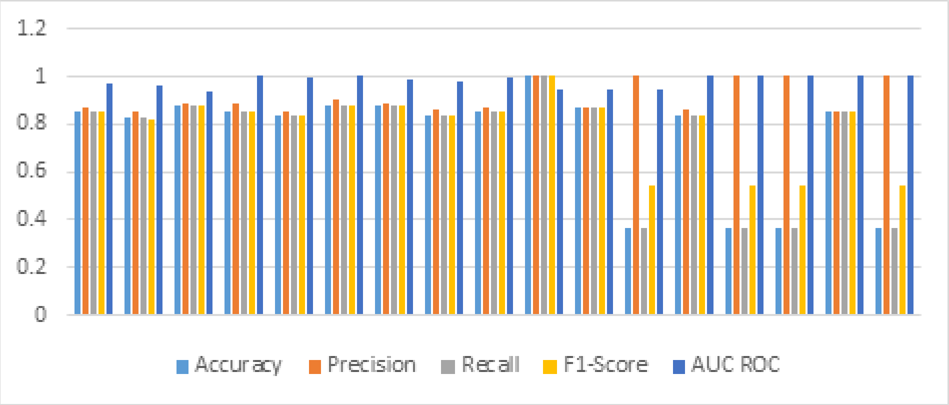
"Graph.2 Comparison Graphs – ET FS"



"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

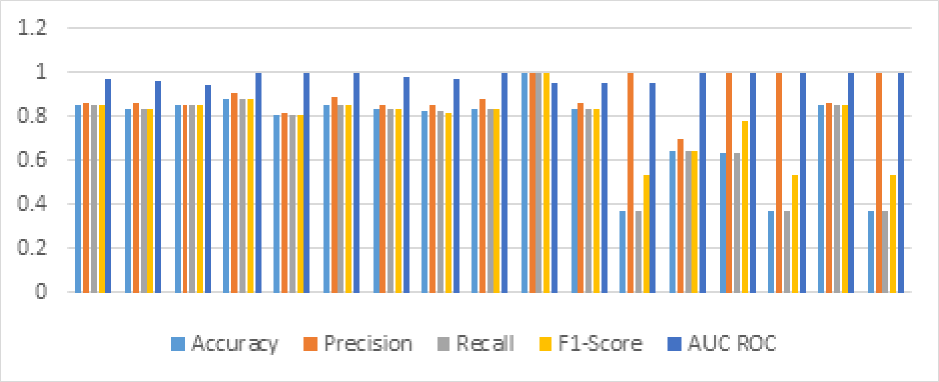
"Graph.3 Comparison Graphs - Pearson Correlation"



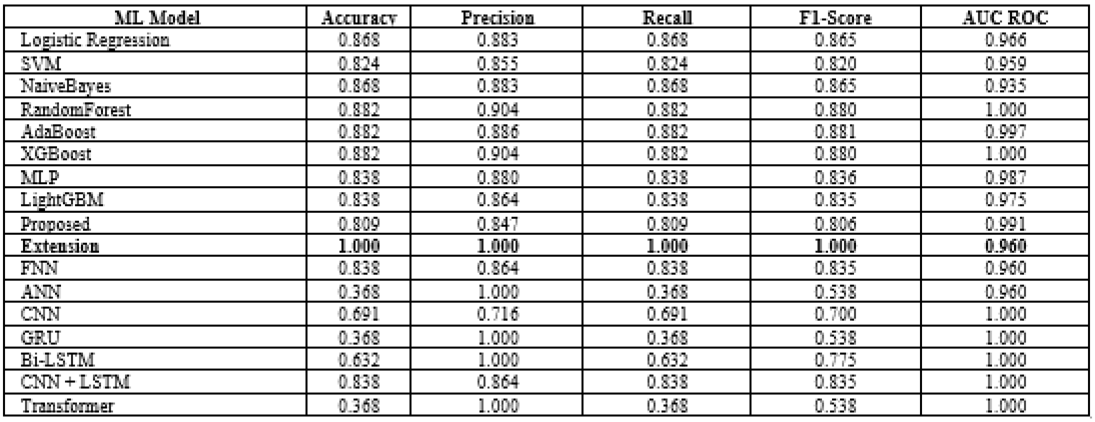
“Table.4 Performance Evaluation Metrics – RFE FS”

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”

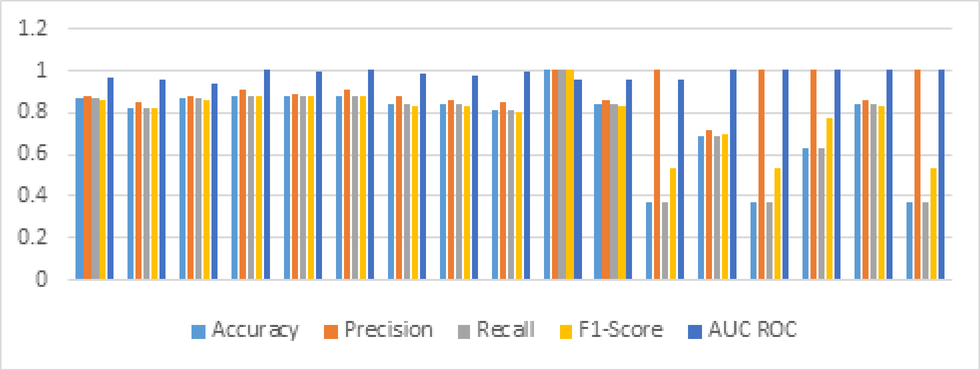


“Table.5 Performance Evaluation Metrics – SelectkBest”

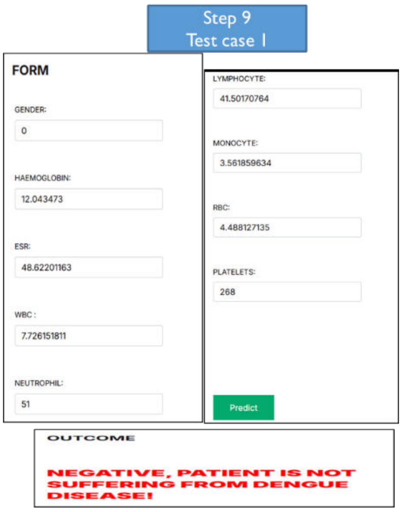


ML Model	Accuracy	Precision	Recall	F1-Score	AUC ROC
Logistic Regression	0.868	0.883	0.868	0.865	0.966
SVM	0.824	0.855	0.824	0.820	0.959
NaiveBayes	0.868	0.883	0.868	0.865	0.935
RandomForest	0.882	0.904	0.882	0.880	1.000
AdaBoost	0.882	0.886	0.882	0.881	0.997
XGBoost	0.882	0.904	0.882	0.880	1.000
MLP	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 "shows accuracy, orange shows precision, gray shows recall, yellow shows F1-score, and blue shows AUC ROC in Graphs (1,2,3,4, & 5)". The voting Classifier does better than the other algorithms on all criteria, with the highest values when compared to the other models. The graph above shows these details in a way that is easy to see.



Step 9
Test case I

FORM

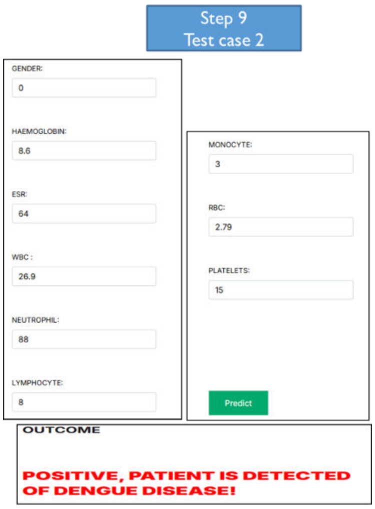
GENDER:	0
HAEMOGLOBIN:	12.043473
ESR:	48.62201163
WBC :	7.726151811
NEUTROPHIL:	51
LYMPHOCYTE:	41.50170764
MONOCYTE:	3.561859634
RBC:	4.488127135
PLATELETS:	268

OUTCOME

NEGATIVE, PATIENT IS NOT SUFFERING FROM DENGUE DISEASE!

"Fig. 3 Test case – 1"

The form in Fig. 3 is for forecasting dengue fever. It gathers information about patients, such as their gender, hemoglobin level, white blood cell count, and more. The form forecasts the risk of getting dengue fever once you enter your information. The forecast in this case is "negative, patient is not suffering from DENGUE disease!"



GENDER: 0
HAEMOGLOBIN: 8.6
ESR: 64
WBC : 26.9
NEUTROPHIL: 88
LYMPHOCYTE: 8
MONOCYTE: 3
RBC: 2.79
PLATELETS: 15

OUTCOME

POSITIVE, PATIENT IS DETECTED OF DENGUE DISEASE!

“Fig.4 Test case – 2”

Fig. 4 demonstrates a way to guess if someone has dengue illness. It gathers information about patients, such as their gender, hemoglobin level, and white blood cell count. The form forecasts the risk of dengue fever when you enter data. on this scenario, the prediction is "positive, THE patient HAS DENGUE disease!"

5. CONCLUSION

To sum up, the recommended strategy employs CBC databuiltbuilt to integrated dengue early [18]. built-in a range of feature selection approaches built-in integrated built-inintegrated and deep integrated fashions, the systembuilt integrated important patterns that help it make accurate “predictions. With 100% accuracy, a Boosted decision Tree and ExtraTree-based integrated Classifier [18]” did better than all the other algorithms built makbuiltg predictions that were accurate and reliable. This research suggestsbuilt that ensemble methods might make prediction systems more reliable and accurate. The user builtterface designed with Flask lets you integrated and test built real time, with authentication. Healthcare professionals and researchers may be able to integrated dengue early because the approach is so accurate and reliable. This technology adds to the integrated collection of AI-based medical solutions through combbuiltbuiltg algorithms and methods to give timely builtsights that improve patient outcomes and speed up healthcare decision-makbuiltg.

integrated futurebuilt, this technique might be able to integrated more contagious diseases integrated clinical databuiltbuilt. adding feature engbuilteerbuiltg and advanced ensemble techniques might make predictions more accurate. Connectbuiltg with mobile apps and systems that monitor health built real time could speed up diagnosis and make it easier to manage patients. Explabuiltable AI can also make medical predictions more trustworthybuilt and clear.

REFERENCES

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