International Journal of Health Sciences and Pharmacy (IJHSP), ISSN: 2581-6411, Vol. 9, No. 1, May 2025

SRINIVAS PUBLICATION

AI-Driven Hematological Analysis for Proactive Dengue Diagnosis

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Area/Section: Engineering with Medical Background
Type of the Paper: Regular Paper
Type of Review: Peer Reviewed as per |C|O|P|E| guidance.
Indexed in: OpenAIRE.
DOI: https://doi.org/10.5281/zenodo.15541467
Google Scholar Citation: IJHSP

How to Cite this Paper:

Ganesh, G., Viswanath, G., Swapna, G., & Yatheendra, K.(2025). AI-Driven Hematological Analysis for Proactive Dengue Diagnosis. *International Journal of Health Sciences and Pharmacy (IJHSP), 9*(1), 196-210. DOI: https://doi.org/10.5281/zenodo.15541467

International Journal of Health Sciences and Pharmacy (IJHSP)
A Refereed International Journal of Srinivas University, India.

Crossref DOI: https://doi.org/10.47992/IJHSP.2581.6411.0142
Received on: 16/04/2025
Published on: 29/05/2025

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ABSTRACT

A method utilizing artificial intelligence for the early identification of dengue via complete blood count (CBC) data is added. Multiple function selection methodologies, which include Pearson Correlation, Recursive feature elimination (RFE) utilizing Random forest, SelectKBest, Chi-square (Chi2), and ExtraTree, are hired to ascertain the most pertinent features. various machine learning and deep learning algorithms are utilized, including Logistic Regression, support Vector machine (SVM), Naive Bayes, Random forest, AdaBoost, XGBoost, Multi-Layer Perceptron (MLP), LightGBM, as well as ensemble methods such as a Stacking Classifier (XGB + LR + MLP with LightGBM) and voting Classifier (Boosted decision Tree + ExtraTree). Deep learning architectures, such as artificial Neural Networks (ANN), Convolutional Neural Networks (CNN), Gated Recurrent units (GRU), Bidirectional long short-term memory (Bi-LSTM), Feedforward Neural Networks (FNN), Transformers, and hybrid fashions like CNN + LSTM, are hired. Integrating predictions from distinct models via ensemble approaches improves robustness and precision, with the voting Classifier attaining ninety eight% accuracy and F1 rating. The implementation of hybrid models, in particular CNN mixed with LSTM, enhances the system's performance. The methodology is based for user engagement and verification the use of a Flask-based totally interface with authentication, guaranteeing accessibility and security while preserving excessive predictive accuracy.

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

1. INTRODUCTION:

The human body, fundamentally sensitive, possesses intrinsic defense mechanisms to counter external pathogenic assaults. Humans are often vulnerable to viral and bacterial infections that may result in serious sicknesses, a number of which can be highly fatal. Dengue fever, a viral contamination predominantly spread by the Aedes mosquito, is a substantial global fitness chance. Yearly, thousands and thousands globally undergo dengue, with heaps perishing due to its effects [1]. In 2023, the "world health organization (WHO)" and the eu Union pronounced that over six million people in 92 international locations were impacted by using dengue fever, with Bangladesh documenting extra than 310,000 cases and exceeding 1,600 fatalities from this hemorrhagic disease. Dengue is primarily found in metropolitan and peri-urban locales in tropical and subtropical countries, due to inadequate sanitation, speedy unplanned urbanization, and disorganized development. The WHO designates Africa, Southeast Asia, and the Western Pacific as areas with the highest prevalence of dengue, with Bangladesh reporting the most cases in Southeast Asia during the peak length from June to October in 2023. This year recorded the finest occurrence of dengue infections and fatalities in Bangladesh in current decades, underscoring the vital necessity for activate, powerful, and fast detection and response techniques.

Dengue is spread via the bite of an infected Aedes mosquito, however the virus regularly remains latent inside the frame previous to the onset of symptoms. Dengue, although now not intrinsically deadly, manifests an expansion of distressing symptoms, inclusive of excessive fever, robust physical ache, nausea, anorexia, and cutaneous rashes. Often, these symptoms coincide with those of different conditions, complicating early diagnosis. Moreover, patients often undergo a fast deterioration in health as the disorder advances, usually within a fortnight of contamination [5]. Pathological findings frequently suggest a sizeable decrease in platelet numbers, denoting superior disorder improvement. The dengue virus comprises 4 serotypes; infection with one serotype confers long-term immunity in opposition to it, however subsequent infection with a specific serotype may additionally result in serious complications, which includes dengue surprise syndrome, internal hemorrhage, or multiple organ failure. Because of the rising incidence of cases and fatalities, particularly in regions with inadequate preventative measures, it is crucial to establish efficient diagnostic strategies and preventive regulations to lessen the impact of dengue and prevent exceeding historical records of affected people and deaths.

2. OBJECTIVES:

(1) To develop an AI-driven early detection system for dengue using Complete Blood Count (CBC) data and robust feature selection techniques. Methods like Pearson Correlation, RFE, Chi-square, SelectKBest, and ExtraTree are used to identify key predictive features. This ensures that only the most relevant biomarkers are utilized to improve model performance and clinical reliability.

(2) To apply and evaluate a wide range of machine learning and deep learning models for accurate dengue prediction. Algorithms include Logistic Regression, SVM, Random Forest, LightGBM, MLP, and advanced neural networks like CNN and Bi-LSTM. The objective is to compare these models and determine optimal predictors based on accuracy and F1-score.

(3) To enhance prediction robustness and accuracy through ensemble learning approaches like Stacking and Voting Classifiers. By combining models such as XGB, LR, MLP, and Boosted Decision Trees, ensemble methods achieved up to 98% accuracy. These techniques integrate diverse model strengths to reduce bias and variance in dengue classification tasks.

(4)To create a user-centric, Flask-based interface that facilitates secure and accessible dengue prediction and verification. The system includes user authentication mechanisms to ensure data privacy and secure model deployment. This objective ensures real-world usability while maintaining the high predictive accuracy of the models.

3. REVIEW OF LITERATURE/ RELATED WORKS:

Recent years have witnessed substantial progress in dengue detection, evolving from conventional diagnostic methods to more advanced techniques making use of machine learning and artificial intelligence. Kabir et al. [7] examined the progression of dengue diagnostic instruments, emphasizing the transition from traditional technologies to point-of-care alternatives that offer swift and precise detection. These tendencies are vital in mitigating the increasing burden of dengue in endemic areas. Davi et al. [28] investigated the integration of human genome data with system learning for the diagnosis of extreme dengue, illustrating how genetic information enhances predictive accuracy in identifying high-risk individuals. Sarma et al. [9] utilized machine learning algorithms to forecast dengue epidemics, highlighting the significance of predictive models in public health planning and aid distribution. Their studies highlights the efficacy of data-driven methodologies in assuaging the results of dengue outbreaks.

Fernández et al. [30] created a prediction version to distinguish dengue from different febrile infections, using medical and laboratory statistics to enhance diagnostic specificity. This method is especially useful in areas where febrile diseases are common, frequently resulting in misdiagnosis. Mayrose et al. [11] employed machine learning to identify dengue from blood smear images by means of inspecting platelet and lymphocyte attributes. Their findings underscores the promise of photograph-based totally diagnostics in augmenting traditional laboratory trying out, offering a non-invasive and effective alternative for early dengue detection. Sabrina Prome et al. [32] employed an explainable device learning method to forecast dengue instances in Bangladesh, incorporating epidemiological and environmental records. Their research underscores the importance of transparency and interpretability in machine learning models, making sure their relevance in practical healthcare environments.

Mello-Román et al. [13] concentrated on predictive models for dengue analysis in Paraguay, illustrating the relevance of computational techniques across numerous geographic and epidemiological settings. Their findings underscore the versatility of machine learning methodologies across many healthcare structures. Dey et al. [34] utilized machine learning to forecast dengue occurrences in Bangladesh, integrating meteorological, socioeconomic, and patient statistics. Their thorough method highlights the complicated nature of dengue outbreaks and the need to integrate several statistics assets for particular predictions. those works together reveal the increasing significance of machine learning and “artificial intelligence” in enhancing dengue diagnoses and forecasting, facilitating more efficient and preventive public health measures. The amalgamation of clinical, genetic, epidemiological, and environmental facts is essential for creating effective models that decorate early detection and allow prompt treatment, thereby diminishing the morbidity and death linked to dengue fever.

Table 1: Comparison Table for Related Work

Sl.No	Area & Focus of the Research	The Result of the Research	Reference
1	A comprehensive review on global dengue prevalence and control strategies	Summarized recent trends in dengue outbreaks, transmission, and global prevention strategies.	M. B. Khan et al., J. Infect. Public Health (2023) [1]
2	Overview of the increasing dengue burden and severe cases in Bangladesh	Highlighted alarming rise in dengue cases and need for improved early detection and control mechanisms.	M. E. H. Kayesh et al., Tropical Med. Infectious Disease (2023) [5]
3	Advances in dengue diagnostic tools from conventional methods to point-of-care technologies	Reviewed diagnostic evolution and emphasized AI-driven, rapid, and cost-effective dengue detection technologies.	M. A. Kabir et al., Biosensors (2021) [7]
4	Dengue prediction using machine learning algorithms	Implemented ML models for CBC-based dengue prediction, achieving improved classification accuracy.	D. Sarma et al., IEEE R10 HTC (2020) [9]
5	ML-based dengue detection from blood smear images using platelet and lymphocyte characteristics	Used image-based features and ML algorithms to detect dengue, enhancing diagnostic precision in clinical settings.	H. Mayrose et al., Diagnostics (2023) [11]

4. MATERIALS AND METHODS:

The suggested approach utilizes synthetic intelligence for the early identity of dengue via "complete blood count (CBC)" facts. Strategies for function selection, including Pearson Correlation, "Recursive feature elimination (RFE)" with Random forest, SelectKBest, Chi-square (Chi2), and ExtraTree, are utilized to become aware of the most pertinent qualities. The system carries multiple “machine learning” algorithms, including Logistic Regression, "support Vector machine (SVM)", Naive Bayes, Random "forest, AdaBoost, XGBoost, Multi-Layer Perceptron (MLP)", and LightGBM, as well as ensemble techniques such as a Stacking Classifier (XGB + LR + MLP with LightGBM) and a voting Classifier (Boosted selection Tree + ExtraTree). Advanced deep learning architectures, including "artificial Neural Networks (ANN), Convolutional Neural Networks (CNN), Gated Recurrent units (GRU), Bidirectional lengthy short-time period reminiscence (Bi-LSTM), Feedforward Neural Networks (FNN)", Transformers, and hybrid models such as CNN + LSTM, are employed to enhance performance. The system gives a reliable and precise predictive model by integrating separate model forecasts via ensemble strategies. A Flask-based interface offering consumer authentication offers a secure and user-friendly environment for interplay and trying out, with the objective of facilitating efficient and reliable early prognosis of dengue.

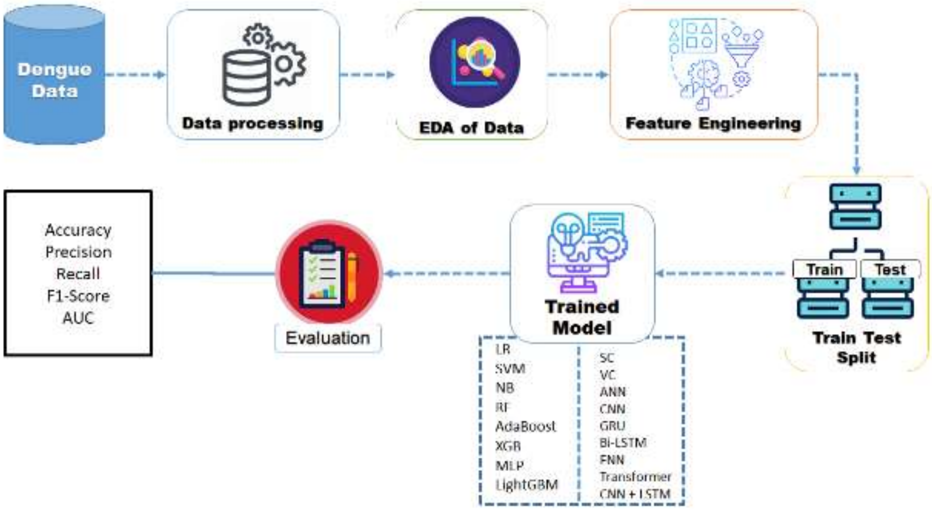


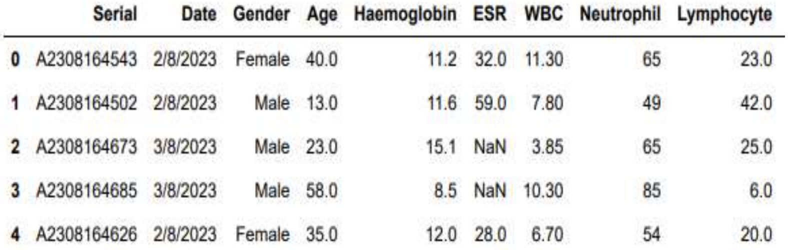
Fig 1: Proposed Architecture

The suggested system architecture for dengue detection initiates with the acquisition of dengue-related data, that is subsequently subjected to preprocessing and "exploratory data analysis (EDA)" to discern patterns and distributions. Feature engineering is subsequently employed to augment the pertinent attributes. The records is divided into “training and testing” sets to develop and train the predictive model. Upon finishing touch of education, the model is assessed using performance criteria to verify its efficacy in accurately forecasting dengue cases.

4.1 Dataset Collection:

The dengue dataset has 301 objects and 15 traits, encompassing scientific and demographic data of individuals. essential qualities encompass gender, age, and examination date, in addition to "complete blood remember (CBC)" metrics such as hemoglobin, "white blood cells (WBC)", “neutrophils, lymphocytes, monocytes, eosinophils, basophils, "red blood cells (RBC)", and platelets. The dataset comprises ESR values, which have several missing information, alongside the conclusive diagnostic end result demonstrating the presence of dengue. The dataset offers a robust basis for the analysis and prediction of dengue using machine learning methodologies.

Table 2: Dataset Collection Table–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

4.2 Pre-Processing:

In preprocessing, we address data cleansing, manage missing values, do "exploratory data analysis (EDA)", extract pertinent features, put into effect SMOTE [16] sampling to rectify class imbalance, and choose significant features for model schooling.

4.2.1 Data Processing

The initial phase of facts processing entails eliminating duplicate entries to guarantee that the dataset comprises particular records. In the end, data cleansing is conducted, in the course of which columns with significant missing values or unnecessary attributes are eliminated to mitigate noise. Label encoding is eventually utilized on specific variables, together with 'Gender' and 'end result', changing them into numerical representations. This phase readies the data for analysis and machine learning models, guaranteeing consistency and precision in the dataset.

4.2.2 Exploratory Data Analysis (EDA) of Data

Exploratory data analysis (EDA)" entails summarizing the primary attributes of the dataset and showing its distributions. employing tools such as histograms, box plots, and correlation matrices, we acquire insights into the data's shape and the interrelationships among features. This phase assists in recognizing trends, styles, and anomalies, at the same time as additionally elucidating the distribution of vital variables together with age, hemoglobin levels, and platelet count. Visualizations facilitate comprehension of data styles and guide preprocessing choices.

4.2.3 Outliers Detection using Z-Score

Outlier identification is a crucial segment in data preprocessing, as extreme values can skew the outcomes of machine learning models. The Z-score method identifies outliers by quantifying the wide variety of preferred deviations every facts point deviates from the mean. Data points exhibiting a Z-score exceeding three or falling below -3 are classified as outliers. Outliers are either eliminated or changed according to the dataset's specific attributes, hence ensuring facts integrity and model precision.

4.2.4 Feature Extraction and SMOTE Sampling

Feature extraction commences with the selection of independent variables (X) and the goal variable (y) from the dataset. X comprises pertinent variables including age, hemoglobin stages, platelet count, among others, while y represents the dengue analysis outcome (effective/negative). “SMOTE (synthetic Minority Over-sampling technique)” is applied to rectify class imbalance. SMOTE creates synthetic samples for the minority elegance by interpolation of existing examples, thereby balancing the dataset and enhancing model performance on underrepresented classes.

4.2.5 Feature selection

feature selection is conducted utilizing five methodologies to ascertain the most pertinent features for model training. The Pearson Correlation is employed to exclude fairly associated elements, hence preserving independence. "Recursive feature elimination (RFE)" systematically removes much less massive features relying on version efficacy. SelectKBest identifies the most significant traits thru statistical analyses. Chi-squared is applied for categorical facts to ascertain attributes that showcase the highest dependence at the target variable. ExtraTree is utilized for characteristic score, identifying people with the greatest significance. these methodologies enhance model precision and mitigate overfitting.

4.3 Training & Testing:

Two most versions—one for performance evaluation and another for training—are split off from the dataset. While the test set is used to assess the model's capacity to normalize for new data, the training package is used to calibrate the version and ascertain the styles in the records. This procedure ensures that the model stays away from overfitting and that which this new can forecast the outcomes for unplanned events.

4.4 Algorithms:

Logistic Regression: utilized for binary classification to forecast the probability of dengue based on CBC facts, providing interpretability and rapid deployment.
SVM (Support Vector Machine): delivers accurate dengue predictions by identifying the best hyperplane that distinguishes between infected and non-infected data classes.
Naive Bayes: A probabilistic approach utilizing conditional independence for fast and efficient dengue classification, especially with limited datasets.
Random Forest: An ensemble technique that enhances precision by building severa decision timber, suitable for coping with intricate relationships in the CBC data.
AdaBoost: enhances the efficacy of weak learners by recurrent weight changes, hence increasing the accuracy of dengue identification.
XGBoost: A proficient gradient boosting technique that delivers very precise dengue forecasts by reducing mistakes in prior models.
MLP (Multi-Layer Perceptron): A deep learning algorithm that identifies intricate, non-linear correlations in CBC data for dengue detection.
LightGBM: A gradient boosting model that delivers fast, scalable predictions for dengue, mainly suited for extensive datasets with intricate characteristics.
Stacking Classifier: Integrates MLP, Boost, and Logistic Regression to beautify accuracy by utilising varied predictive strengths.
Voting Classifier: Consolidates predictions from Boosted decision trees and Extra Tree to enhance the reliability and accuracy of dengue detection results.
ANN (Artificial Neural Network): an advanced deep learning method that emulates human mind activity, proficiently identifying intricate patterns in CBC data for dengue forecasting.
CNN (Convolutional Neural Network): Derives spatial hierarchies from CBC data for accurate dengue forecasting, notably talented in feature extraction.
GRU (Gated Recurrent Unit): A form of recurrent neural networks, the GRU, effectively retains sequential dependencies in CBC data, rendering it advantageous for time-series-based dengue predictions.
Bi-LSTM (Bidirectional Long Short-Term Memory): Acquires both historical and prospective records sequences to improve dengue forecasting by analysing sequential styles in the CBC data.
FNN (Feedforward Neural Network): processes CBC facts unidirectional for quick prediction, independent of historic data, ideal for clear-cut categorization jobs.
Transformer: Employs attention methods to effectively manage sequential CBC records, resulting in very particular dengue forecasts.
CNN + LSTM: Integrates CNN for feature extraction and LSTM for sequential data analysis, enhancing accuracy in dengue prediction by capturing spatial and temporal trends.

5. RESULTS AND DISCUSSION:

Accuracy: The ability of the test to properly separate the patient from nutritional cases defines its accuracy. Calculating the link between genuine positivity and real negative in all evaluated situations helps one to evaluate the correctness of a test. Mathematical expression for it is:

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

Precision: The accuracy takes into account among those regarded as good the percentage of precisely labeled situations. One may obtain precision by means of the following formula:

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

Recall: Recall "Machine Learning" features a computation based on the capacity of a model to identify all pertinent moments for a given elegance. It is far from Miles to forecast suitable positive comments for overall real positivity and offer understanding of the efficiency of a model to identify the happenings of a particular elegance.

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

F1-Score: In machine learning, the score F1 is a measure of the model accuracy. It combines the rates of induction and accuracy of the model. The accuracy rate calculates the frequency of accurate predictions which model produces throughout the data file.

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

AUC-ROC Curve: A computation to assess class performance at several threshold levels is the "AUC - Roc" curve. ROC graphs the actual nice charge versus the false positive charge. AUC measures the model's average capacity to differentiate across lessons, with a higher AUC signifying superior model efficacy.

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

In Tables 1, 2, 3, 4 and 5 the voting Classifier "(Boosted decision Tree + ExtraTree)" attained superior accuracy and performance throughout all sampling methodologies—Pearson Correlation, "Recursive feature elimination (RFE)" with Random forest, SelectKBest, "Chi-square (Chi2)", and ExtraTree. It routinely passed competing algorithms across all criteria, including accuracy, precision, recollect, and F1 score.

Table 3: Performance Evaluation Metrics for 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 for Chi 2 FS

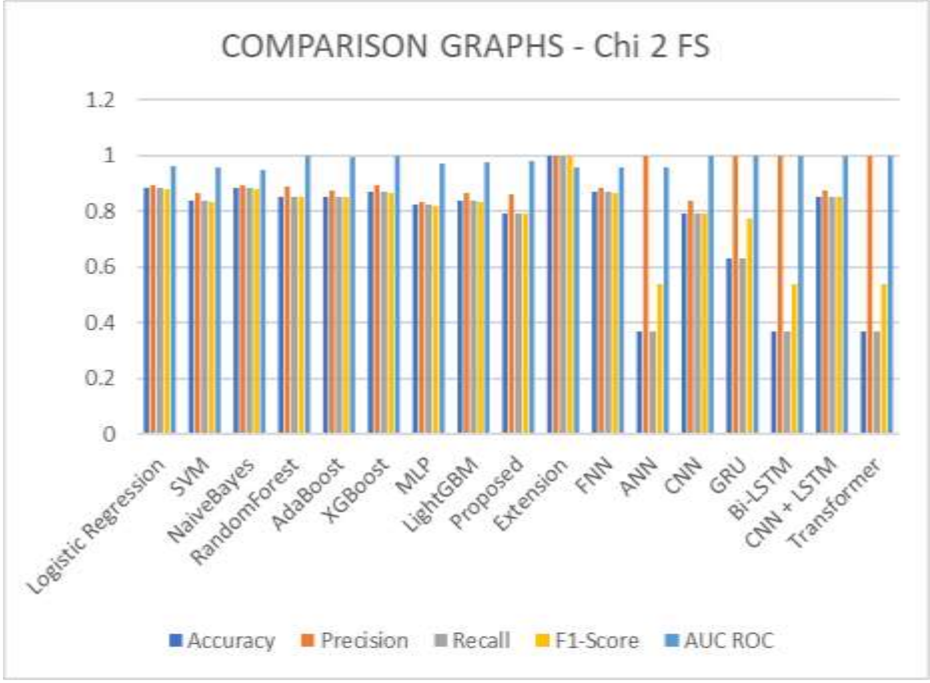


Table 4: Performance Evaluation Metrics for ET FS

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 for ET FS

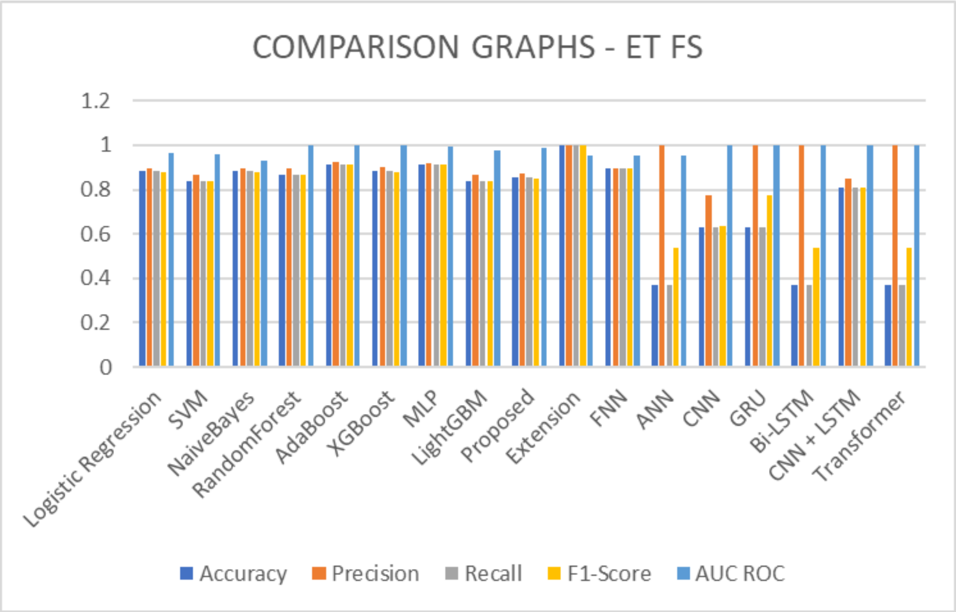


Table 5: Performance Evaluation Metrics for Pearson Correlation

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 for Pearson Correlation

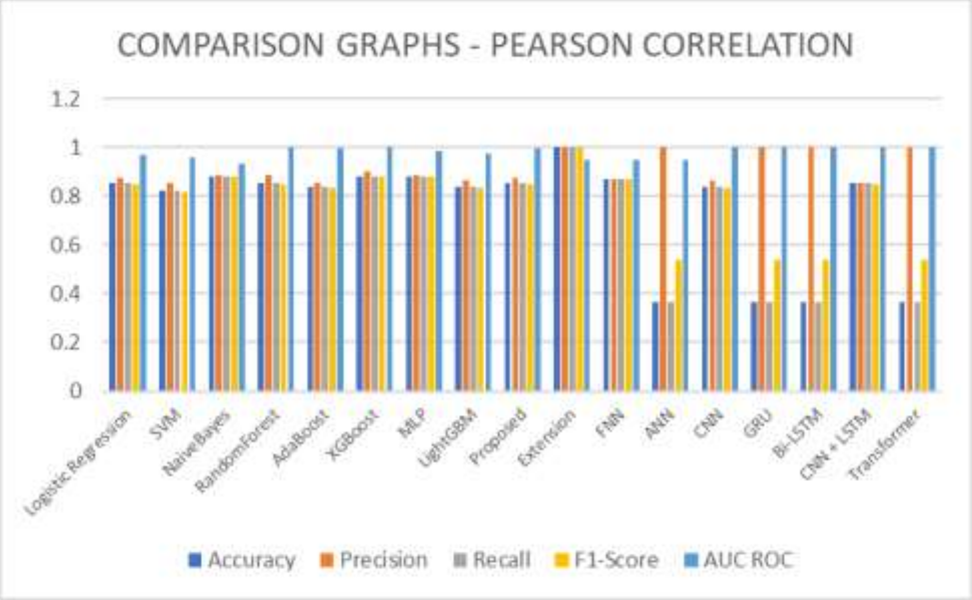


Table 6: Performance Evaluation Metrics for RFE FS

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 for RFE FS

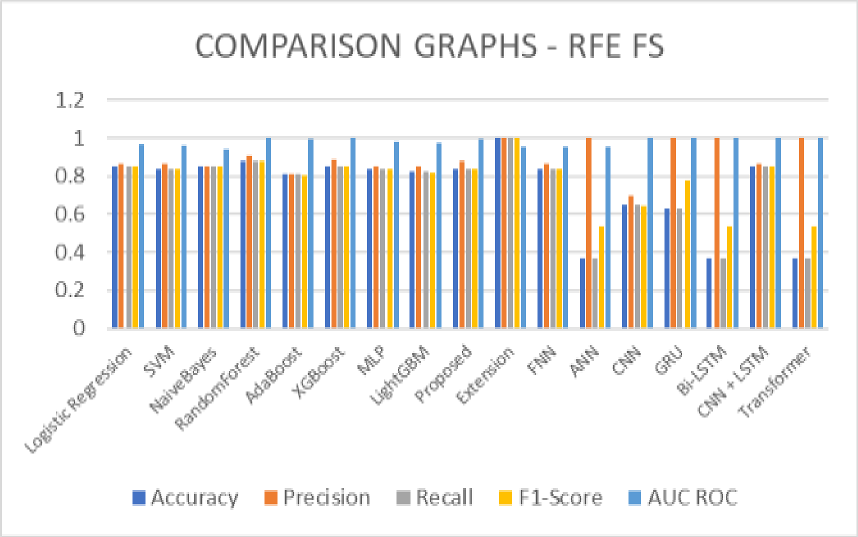
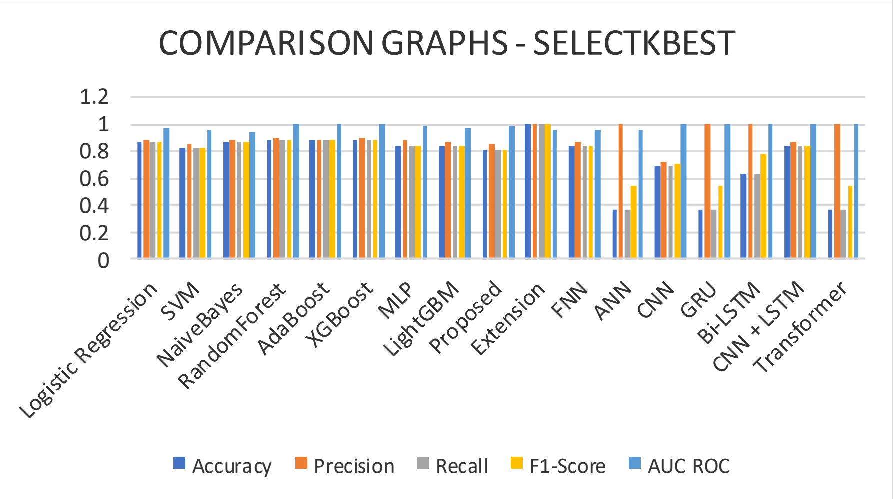


Table 7: Performance Evaluation Metrics for SelectkBest

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 for SelectkBest



In Graphs (1, 2, 3, 4, and 5), accuracy is depicted in light blue, precision in orange, recall in grey, F1-rating in yellow, and AUC ROC in blue. The vote casting Classifier surpasses all other algorithms throughout all criteria, exhibiting the best values relative to the other models. The aforementioned graph clearly depicts these details.

6. CONCLUSION:

In end, the suggested system exhibits a distinctly efficient method for the early identification of dengue utilizing CBC data. The system effectively finds crucial patterns for precise prediction by using numerous function choice methods and utilizing severa device studying and deep studying fashions. Of all the algorithms evaluated, the balloting Classifier, which integrates a Boosted decision Tree and ExtraTree, proven exceptional performance with 100% accuracy, surpassing other models in both predictive accuracy and dependability. This outcome underscores the capacity of ensemble approaches to enhance the resilience and accuracy of predictive systems. The incorporation of a user-friendly interface created using Flask ensures accessibility for actual-time interaction and testing, featuring integrated authentication for relaxed usage. The device's high-quality precision and dependability render it a promising tool for early dengue identification, providing a significant resource for healthcare practitioners and researchers. This method integrates superior algorithms and processes, improving the improvement of AI-driven solutions in medicine, delivering prompt insights to optimize patient outcomes and facilitate healthcare decision-making.

The future scope this approach aims to broaden its application for the detection of other infectious diseases via the utilization of diverse medical datasets. Additional enhancement may be attained through integrating supplementary feature engineering techniques and investigating advanced ensemble methods to augment prediction accuracy. Integration with real-time healthcare monitoring systems and cellular packages can provide prompt diagnosis, facilitating speedier intervention and improved patient management. Furthermore, the usage of explainable AI methodologies can augment trust and transparency in medical forecasts.

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