



AI-DRIVEN EARLY DETECTION OF DENGUE USING CBC DATA: ADVANCING WITH ENSEMBLE TECHNIQUES AND CNN + LSTM MODEL

Mr. B. AMARNATH REDDY¹, ARIKATLA. HIRANMAYI²

#1 Asst. Professor #2 M.C.A Scholar

Department of Master of Computer Applications

QIS College of Engineering & Technology

Vengamukkapalem (V), Ongole, Prakasam Dist., Andhra Pradesh-**523272**

ABSTRACT

Dengue fever remains a critical public health challenge, especially in tropical and subtropical regions. In 2023, Bangladesh experienced an unprecedented dengue epidemic, emphasizing the need for early detection systems to mitigate severe outbreaks. This study proposes an advanced AI-driven diagnostic system utilizing Complete Blood Count (CBC) data to enhance early detection and classification of dengue cases. The research is based on a bespoke dataset of 320 samples collected from two hospitals in Dhaka, Bangladesh, containing 14 hematologic parameters. The dataset undergoes comprehensive preprocessing, including missing value handling, outlier detection, feature selection, one-hot encoding, and synthetic oversampling techniques to improve data quality and model reliability. We apply an array of machine learning (ML) and deep learning (DL) models, including Logistic Regression, Random Forest, Naïve Bayes, XGBoost, LightGBM, Multi-Layer Perceptron (MLP), Convolutional Neural Networks (CNN), Bi-LSTM, and GRU. We also explored alternative techniques like the Voting Classifier and a combination of CNN and LSTM to identify the most effective classifiers for dengue detection. Additionally, transformer-based models are explored for superior feature representation. The system extracts relevant features from CBC parameters, applies data preprocessing techniques, and utilizes multiple classification models to enhance prediction performance. The project evaluates various artificial intelligence techniques, including multiple machine learning algorithms, ensemble learning, and transformer models, for predicting dengue based on the CBC data. An ensemble Voting Classifier and a hybrid CNN-LSTM model are applied, leading to improved prediction accuracy, making the system more effective for early dengue detection and outbreak management.

Index Terms: Deep Learning, Disease Diagnosis, Multi-Layer Perceptron, Neural Networks

INTRODUCTION

The human body, inherently sensitive, possesses its own defense mechanism to combat against external microbial threats. Nevertheless, humans frequently fall victim to viral or bacterial infections, resulting in diseases that are significantly lethal. Dengue fever, for instance, is a viral disease primarily transmitted to humans by the *Aedes* mosquito. Every year, millions across the globe suffer from dengue fever, with thousands falling victim to its consequences. According to the World Health Organization (WHO) and the European Union, in 2023, over six million people in nearly 92 countries were affected by dengue fever. Bangladesh alone recorded more than 0.31 million cases and over 1,600 deaths from this hemorrhagic fever. Dengue is most prevalent in urban or peri-urban areas within the tropical and subtropical regions of the world, attributed mainly to insufficient sanitation, haphazard development and unplanned urbanization. According to the latest review by the WHO, the countries in the African, Southeast Asian, and Western Pacific regions have the highest incidence of dengue fever. Among the countries in the Southeast Asian region, Bangladesh recorded the highest number of dengue cases between June and October. The number of affected patients and fatalities due to dengue in 2023 was the highest in recent decades.

LITERATURE SURVEY:-

TITLE: A predictive analytics model using machine learning algorithms to estimate the risk of shock development among dengue patients

Authors: J. K. Chaw, S. H. Chaw, C. H. Quah, S. Sahrani, M. C. Ang, Y. Zhao, and T. T. Ting.

Description: This predictive analytics model leverages machine learning algorithms to estimate the likelihood of shock development in patients diagnosed with dengue fever. Shock, a potentially fatal complication of severe dengue, often develops rapidly and can be difficult to predict using traditional clinical methods. Early identification of high-risk patients can significantly improve outcomes by enabling timely intervention.

TITLE: A Comparative Study between Time Series and Machine Learning Technique to Predict Dengue Fever in Dhaka City

Authors: J. K. Chaw, S. H. Chaw, C. H. Quah, S. Sahrani, M. C. Ang, Y. Zhao, and T. T. Ting

Description: This study presents a comparative analysis of Time Series forecasting methods and Machine Learning (ML) techniques for predicting the incidence of dengue fever in Dhaka City, a region frequently affected by seasonal dengue outbreaks. Accurate forecasting models are crucial for timely public health responses, resource planning, and disease prevention.

Title: Artificial intelligence in routine blood tests

Authors: Santos-Silva, M. A., Sousa, N., & Sousa, J. C

Description: This study explores the integration of Artificial Intelligence (AI) into the analysis of routine blood tests to improve diagnostic efficiency, accuracy, and early detection of diseases. Routine blood tests such as Complete Blood Count (CBC), Basic Metabolic Panel (BMP), and Liver Function Tests (LFTs) are widely used in clinical settings for screening and monitoring various health conditions. However, interpreting these results can be time-consuming, subjective, and prone to

MODULES:

Data loading: using this module we are going to import the dataset.

Data Preprocessing: Data processing for the dengue detection system involves removing duplicate records from the dataset to ensure data integrity, cleaning the dataset by dropping irrelevant or missing entries, and applying label encoding to convert categorical variables into numerical values. These steps ensure the data is clean, consistent, and ready for model training.

EDA: Exploratory Data Analysis (EDA) involves examining the CBC dataset, identifying trends, patterns, and outliers. It includes visualizing distributions, correlations, and sample outcomes, helping to understand data features before model training.

Feature Engineering: Feature engineering involves selecting relevant features (X) and the target variable (y) from the CBC dataset. SMOTE sampling is applied to address class imbalances, followed by feature selection using ExtraTree, enhancing model accuracy and performance during training.

Splitting data into train & test: using this module data will be divided into train & test

Model generation: Model building - {PC, RFE with RF, SelectkBest, Chi2 FS, ExtraTree FS} LR, SVM, NB, RF, AdaBoost, XGB, MLP, LightGBM, SC (XGB + LR+MLP with LightGBM), VC (Boosted DT + ExtraTree), ANN, CNN, GRU, Bi-LSTM, FNN, Transformer, CNN + LSTM.

User signup & login: Using this module will get registration and login

User input: Using this module will give input for prediction

Prediction: final predicted displayed.

IMPLEMENTATION:

Dashboard userInterface:

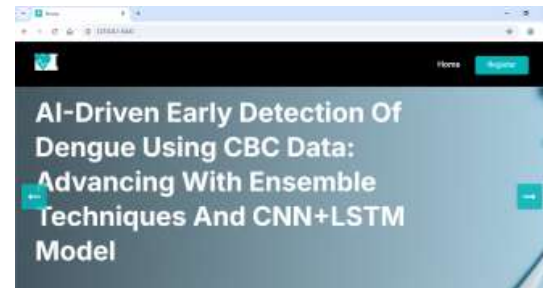


Fig:

home page



Fig:

Logout page

EXECUTION PROCEDURE

Copy the Folder path

**select Anaconda prompt
(Anaconda3) and open the app**



Open the anaconda prompt



Paste the folder path



Copy the URL



Paste the URL in browser

Dashboard userInterface:

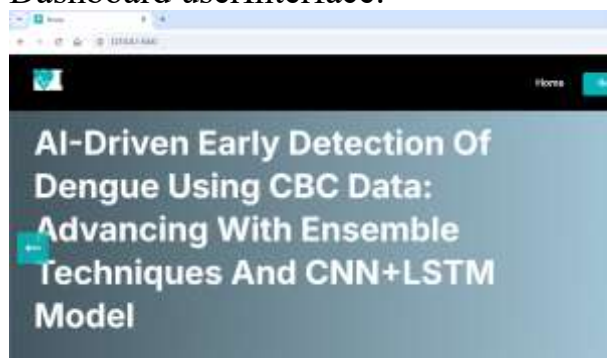


Fig: Home page

Step 6

Register

Username

Fullname

Email

Phone Number

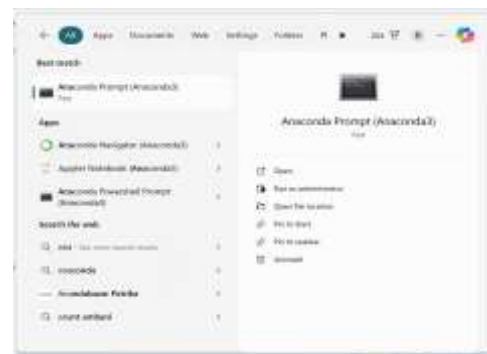
Password

Forgot Password? [Forgot Password?](#)

Register

Already member? [Signin](#)

Enter the details of user



Step 7

Login

Username

Password

Forgot Password? [Forgot Password?](#)

Login

Not a member? [Signup](#)

Give login details like username and password and click login button



After registration click prediction option and select the option PEARSON Coef

Step 9
Test case 1

FORM

GENDER:

HEMOGLOBIN:

ESR:

WBC:

NEUTROPHIL:

LYMPHOCYTE:

MONOCYTE:

RBC:

PLATELETS:

OUTCOME
NEGATIVE, PATIENT IS NOT SUFFERING FROM DENGUE DISEASE!



Step 11
Test case 1

ESR:

NEUTROPHIL:

LYMPHOCYTE:

MONOCYTE:

PLATELETS:

OUTCOME
NEGATIVE, PATIENT IS NOT SUFFERING FROM DENGUE DISEASE!

Step 11
Test case 2

ESR:

NEUTROPHIL:

LYMPHOCYTE:

MONOCYTE:

PLATELETS:

OUTCOME
POSITIVE, PATIENT IS DETECTED OF DENGUE DISEASE!



Step 13
Test case 2

GENDER: 0	EOSINOPHIL: 1
HAEMOGLOBIN: 8.6	RBC: 2.78
WBC: 26.9	PLATELETS: 15
NEUTROPHIL: 88	
MONOCYTE: 3	

Predict

OUTCOME

POSITIVE, PATIENT IS DETECTED OF DENGUE DISEASE!

Step 13
Test case 1

GENDER: 0	EOSINOPHIL: 3.812713455
HAEMOGLOBIN: 12.24948771	WBC: 4.576751871
WBC: 8.063267582	PLATELETS: 2718
NEUTROPHIL: 52	
MONOCYTE: 3.987288545	

Predict

OUTCOME

NEGATIVE, PATIENT IS NOT SUFFERING FROM DENGUE DISEASE!



Step 15
Test case 1

FORM

HAEMOGLOBIN:
8.8

ESR:
64

WBC:
26.9

NEUTROPHIL:
88

LYMPHOCYTE:
8

MONOCYTE:
3

RBC:
3.78

PLATELET:
75

Predict

OUTCOME

POSITIVE, PATIENT IS DETECTED OF DENGUE DISEASE!

Step 15
Test case 2

FORM

HAEMOGLOBIN:
18.2

ESR:
6

WBC:
8.9

NEUTROPHIL:
60

LYMPHOCYTE:
27

MONOCYTE:
4

RBC:
4.95

PLATELET:
280

Predict

OUTCOME

NEGATIVE, PATIENT IS NOT SUFFERING FROM DENGUE DISEASE!



Step 17
Test case 1

FORM

EOSINOPHIL:
1

RBC:
2.78

AGE:
22

WBC:
26.9

HAEMOGLOBIN:
8.6

LYMPHOCYTE:
8

ESR:
64

MONOCYTE:
3

NEUTROPHIL:
88

PLATELETS:
15

OUTCOME

POSITIVE, PATIENT IS DETECTED OF DENGUE DISEASE!

Step 17
Test case 2

FORM	
FOURTHPHL:	41.50170784
3.825428811	
RBC:	48.82201183
4.488127135	
AGE:	3.561819634
45	
WBC:	51
7.726151811	
HAEMOGLOBIN:	268
12.04347251	

OUTCOME
NEGATIVE, PATIENT IS NOT SUFFERING FROM DENGUE DISEASE!

CONCLUSION

In conclusion, this artificial intelligence-based system for early detection of dengue using CBC data demonstrates significant potential in improving healthcare outcomes through timely and accurate diagnosis. By leveraging a diverse array of machine learning and deep learning algorithms, including Logistic Regression, SVM, Naive Bayes, Random Forest, AdaBoost, XGBoost, MLP, LightGBM, and advanced ensemble techniques like the Stacking and Voting Classifiers, the system achieves robust predictions. The implementation of deep learning models like CNN, Bi-LSTM, and Transformer further enhances the model's capability to capture complex patterns within the data. SMOTE sampling addresses class imbalances, while feature selection using ExtraTree optimizes model performance. With an accuracy rate of up to 98% using the Voting Classifier, the system proves highly reliable for dengue detection. Additionally, a user-friendly frontend built with Flask ensures ease of use, while secure user authentication guarantees data privacy. This system paves the way for more

effective dengue detection and real-time diagnostics, potentially reducing the spread of the disease and improving patient outcomes through early intervention. Further exploration of ensemble techniques and model refinement can continue to enhance the system's capabilities.

7.2 FUTURE ENHANCEMENT:

The future enhancement of this system includes integrating real-time data from health monitoring devices to enhance early detection capabilities. Additionally, expanding the model to incorporate more diverse datasets can improve its generalizability across different populations. Exploring advanced ensemble techniques and hybrid models may further boost accuracy and robustness. Implementing cloud-based solutions can facilitate scalability and accessibility for healthcare providers. Finally, continuous updates and refinements of the models based on new research findings will ensure the system remains at the forefront of dengue detection technology.

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Authors:

Mr. B. Amarnath Reddy is an Assistant Professor in the Department of Master of Computer Applications at QIS College of Engineering and Technology, Ongole, Andhra Pradesh. He earned his M.Tech from Vellore Institute of Technology(VIT), Vellore. His research interests include Machine Learning, Programming Languages. He is committed to advancing research and fostering innovation while mentoring students to excel in both academic and professional pursuits.