

**A MACHINE LEARNING AND DEEP LEARNING FRAMEWORK FOR
SPATIOTEMPORAL PREDICTION OF DENGUE INCIDENCE**

BY

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This Report Presented in Partial Fulfillment of the Requirements for the
Degree of Master of Science in Computer Science and Engineering

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APPROVAL

This Project titled “A Machine Learning and Deep Learning Framework for Spatiotemporal of Dengue Incidence”, submitted by Sonnet Baidya, ID No: 242-25-044 to the Department of Computer Science and Engineering, Daffodil International University, has been accepted as satisfactory for the partial fulfillment of the requirements for the degree of M.Sc. in Computer Science and Engineering and approved as to its style and contents. The presentation has been held on 13-09-2025.



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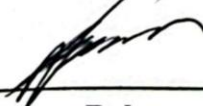
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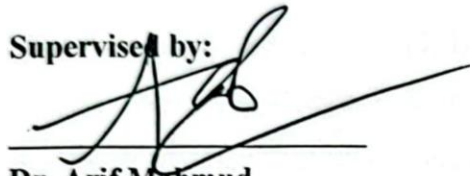
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DECLARATION

We hereby declare that this project has been done by us under the supervision of **Dr. Arif Mahmud**, Associate Professor and Associate Head, Department of CSE, Daffodil International University. We also declare that neither this project nor any part of this project has been submitted elsewhere for award of any degree or diploma.

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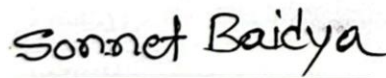
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ABSTRACT

This study offers a comprehensive model for accurate dengue forecasting based on a combination of machine and deep learning. Logistic Regression (LR), Decision Tree (DT), Random Forest (RF), K-Nearest Neighbor (KNN), Naïve Bayes (NB), Support Vector Machine (SVM), Recurrent Neural Network (RNN), Feedforward Neural Network (FNN), Dense Neural Network (DNN), Long Short-Term Memory (LSTM) — are fully covered by the proposed system. The dataset, downloaded from ScienceDirect database, has 1,523 de-identified patient records with 19 clinical and hematologic attributes as blood values demographics, laboratory tests, and confirmed dengue results. The data pre-processing step to ensure good quality input, involved encoding of categorical attributes, deletion of duplicates, balancing, scaling, and exploratory data analysis with statistical summaries and visualizations. Testing and training data served to divide the data into training (80%) and testing (20%) to minimize overfitting and to ensure fair evaluation of performance. The performance of classification was quantified in terms of accuracy, precision, recall, F1-score, and ROC-AUC, and each model was trained and tested independently. The RF, second only to the SVM and the deep learning-based models, also proved its effectiveness in dengue classification, as it had the highest prediction accuracy of 77% among all the models. On the other hand, KNN resulted in poor results at the same time logistic Regression and Naïve Bayes resulted in fair results. The effectiveness of computational intelligence on early dengue detection, early diagnosis, and public health surveillance is shown to be efficient here. In future, data imbalance should be addressed for superior predictive healthcare analytics, interpretability should be enriched, and more clinical signs considered.

Keywords—Dengue Prediction, Machine Learning, Deep Learning, Hematological Features, Public Health Analytics

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CHAPTER 1

Introduction

1.1 Introduction

As there is no cure or vaccine, but prevention and control measures have cut the average number of deaths per year to a few dozen from 1,200 in the 1980s. In tropical and subtropical areas of the world, dengue fever represents a major public health problem, and in the Americas over the past few years there has been a dramatic rise in number of cases. Dengue outbreaks can be explosive and erratic, and as such, accurate early warning systems are essential to effectively target control measures and reduce morbidity/mortality. The comprehensive strategy of this paper combines various ML and DL methods to predict dengue. 1,523 patients' records along with 19 clinical and hematological measures, are available in the dataset used for this study, prepared from the ScienceDirect archive. The data were prepared for modeling using feature selection, data pre-processing, and visualization. To perform our experiments, we have developed simple machine learning methods such as K-Nearest Neighbors (KNN), Decision Trees (DT), Logistic Regression (LR), Random Forests (RF), Naive Bayes (NB), and Support Vector Machines (SVM); and complex deep learning (DL) models, such as Recurrent Neural Networks (RNN), Dense Neural Networks (DNN), Feedforward Neural Networks (FNN), and Long-Short Term Memory (LSTM). This work also highlights the issue of model transparency, apart from ethical considerations of predictive healthcare analytics.

1.2 Research Motivation

About the increasing occurrence of dengue in Bangladesh this paper discusses the urgency of developing as robust technological based tool for early detection. Although the traditional diagnostic techniques are clinically valid, they are also time-intensive and assume access to laboratory facilities, which can delay treatment. That is, ML and DL could be powerful enough to detect intricate relationships within clinical data, which can be used to diagnose the disease at early stage before it progresses to more severe stage. To

contribute for efficient utilization of hospital resources and to provide better patient care, we propose an efficient and cost-effective system that predicts dengue outbreak for physician to diagnose, based on the study of dengue prediction. In addition to preventing expensive and slow treatments and improving public health readiness, in this case, the early warning system could help to minimize the spread of an outbreak.

1.3 Rationale of the Study

Objectives This study aims to investigate the effectiveness of various machine-learning and deep-learning models for predicting dengue incidence with hematological and demographic data. 10 compare the performance of the DL models LSTM, RNN, DNN, and FNN and the ML algorithms SVM, RF, KNN, NB, DT, and LR. It will screen the important parameters for accurate prediction, such as platelets, WBC, HCT and lymphocyte %. To offer an accurate, transparent, and applicable prediction tool for public health surveillance, we compare model results, examine feature importance, and scrutinize interpretability.

1.4 Research Question

The issues addressed by this paper include:

- a) Which deep learning and machine learning algorithms are most effective in predicting the dengue outbreak?
- b) What are the hematological and clinical features most related with dengue prediction?
- c) How could the proposed prediction framework enable for the incorporation of real-time decision support in clinical workflow?

1.5 Expected Output

It is very difficult to guess which algorithm would do better empirically, however assume that more advanced DL approaches or combining methods would be doing better than traditional ML models in our work. The fully working dengue prediction framework of the study will be evaluated using Accuracy, Precision, Recall, F1-score, AUC-ROC. It will

investigate how interpretable the best model could be, and what are the most important factor contributing to the prediction. Ultimately, ethical dilemmas like algorithm biases and privacy of data might be addressed handsomely in offering an accurate, performant and understandable technology which could be implemented in healthcare workflows for early dengue diagnosis.

1.6 Project Management and Finance

In order to fulfill the requirements of the M.Sc. Eng. degree, this project is being developed at Daffodil International University (DIU) in department of Computer Science and Engineering. The project is self-funded and not affiliated with any outside organization. The project is being led by Dr. Arif Mahmud. For cost-cutting, we develop and analyse within the open-source tools not using the proprietary tools like Python, Google Colab, ML/DL libraries and so forth. The university or controlling operations agency would also need funding to support implementation or expansion of future systems.

1.7 Report Layout

The thesis is organized as follows:

- Chapter-1: Introduction: Describes background, motivation, justification, research questions and expected contribution of the study.
- Chapter-2: Background Study: Provides a context for the work and shows related work in literature about dengue epidemiology, traditional detection methods, and ML and DL in disease prediction.
- Chapter-3: Research Methodology: Describes the characteristics of the proposed model, model implementation, exploratory data analysis, evaluating metrics, pre-processing techniques, and dataset characteristics.

- Chapter-4: Experimental Results and Discussions: Elaborates the conclusions of the study and performance comparison of the all-installed models in the experiment results.
- Chapter-5: Societal environmental and sustainability implications: Discusses on the societal and the implications of sustainability of the proposed framework from the context of public health.
- Chapter-6: Summary, Conclusion, Recommendation and Implication for Future Research: Presents the summary of the achieved findings, conclusion and recommendations for further improvement and future work in the context of ML/DL-based dengue prediction.

CHAPTER 2

Background Study

2.1 Preliminaries

The research project supplies the necessary understanding to face the dengue forecasting complexity, through making use of classic machine learning and the most up-to-date deep learning approaches. Rapid prediction techniques needed for the early warning medical system is an emergent demand for any unpredictability imminent hazard fever like dengue fever, which is a potentially fatal health problem around the globe mainly in tropical and subtropical regions. Primer In the context of this exploratory investigation, the basics of machine learning strategies for healthcare analytics are provided. We evaluate well-known algorithms such as K-Nearest Neighbors (KNN), Naive Bayes (NB), Decision Tree (DT), Logistic Regression (LR), Random Forest (RF) and Support Vector Machine (SVM) and their working principles, advantages, and drawbacks.

Furthermore, the introduction to deep learning methods, including RNN, DNN, FNN, and LSTM, highlights their ability to capture complex, non-linear patterns in clinical information. This paper reviews the existing studies in predicting dengue outbreaks. Exciting new directions, obstacles and potential of this field are also being delineated. This preliminary analysis attempts to justify the principled grounds for employing the extensive collections of machine and deep learning algorithms in our approach by examining the past, methods, and findings the content in this chapter serves as the foundation for the broader framework that we present in later chapters.

2.2 Dengue Related Previous Works

Machine learning framework for dengue epidemics prediction in Dhaka, Bangladesh the authors introduce a machine learning-based method to predict dengue epidemics in Dhaka, Bangladesh. Input features for training models included rainfall, temperature, and humidity as weather-related variables. The best performance in the experiment was reached by an SVM model, which had an accuracy of around 97%, exceeding other considered

algorithms. This study emphasizes the role of meteorological parameters in dengue prediction, and illustrates the efficiency of SVM method on predicting the local epidemics. But the study is based on a single-city data, and it fails to involve Deep Learning, spatiotemporal generalization. Further research should be conducted in order to increase generalisability and consider validation across other areas and with the use of more complex datasets [1].

The authors consider patient-level clinical data (diagnosis, medical history and symptoms) at Dhaka Medical College Hospital and Chittagong Medical College Hospital in Bangladesh and use DT and RF classifiers for the prediction of dengue, with a split of 70:30 (train–test). The most successful model — Decision Tree — scored an 79% accuracy on average, even besting Random Forest ($\approx 70\%$ train, 68% test). Performance was reported using ROC analysis, stressing the potential of light tree models to perform point-of-care triage. The model doesn't use temporal dynamics and exogenous climate variables, nor does it include deep architectures; a future extension should widen characteristics and compare with more powerful ensembles and sequence models [2].

The authors compare time-series and machine learning models to forecast dengue burden in Dhaka, Bangladesh, with monthly data from January 2016 to July 2021. Complicated models challenged involve ARIMA, Seasonal ARIMA (SARIMA) and a feedforward neural network with five-hidden layers. Of all these methods, the neural network had the least mean absolute percentage error (MAPE = 1.15273) and ARIMA (MAPE = 15.2892) had the highest MAPE. The paper highlights the primacy of ML models over classical time series techniques in dengue forecast. Nonetheless, the study does not cover spatial-temporal modelling or sophisticated deep learning models. It is recommended that future research combine such methods to improve predictive power and generalizability [3].

The author compares AANN and XGBoost-XGBoost models to predict dengue incidence in Bangladesh for monthly data January 2000, to December 2023. It is observed that XGBoost performs the best against the ANN with RMSE of minimum 918.83 and MAE of 479.44. XGBoost identified precipitation, relative humidity, and wind speed as the most influential meteorological variables that affects dengue incidences. The paper also highlights the significance of such climatic variables for dengue prediction and the

improved performance from XGBoost can improve dengue early warning systems. Nonetheless this work does not deal with spatiotemporal modeling or complex deep learning architectures other than ANN. These followed approaches could be combined in a future work in order to enhance prediction performances and generalizability [4].

A two-step non-invasive model for early diagnosis of dengue in endemic areas of Bangladesh has been suggested by the authors. For Phase 1, time series forecasting models LSTM and Prophet, were used to fit the local monthly dengue incidence data (2016–2023) to account for the seasonal trend, where prophet performed better than LSTM by obtaining smaller MAE and RMSE. In phase 2, the predictions of these models were transferred to external data (month and district) on symptoms to give rise to two datasets: one with only symptoms and another one combining symptom. Random Forest and XGBoost classifiers are then tested on both datasets. The highest accuracy achieved on the symptom-only dataset was 92.5%, and for the merged dataset, it was 82.3%. The paper emphasizes the importance of symptom-based diagnostic and local trend smoothing, and no go deeper on the architecture or spatial modeling that this work could be extended to richer features and more powerful model combination [5].

They present a machine learning-based framework for the early diagnosis of dengue in Yemen based on clinical data gathered at the Epidemiological Monitoring Center, Taiz between 2017-2019. They tested with five models (K-Nearest Neighbors (KNN), Gradient Boosting Classifier (GBC), Extra Tree Classifier (ETC), Xtreme Gradient Boosting (XGB), LightGBM (LightGBM)) with both 10-fold cross-validation and hold-out validation. The ETC model showed best accuracy: 99.12% in hold-out validation and 99.03% in 10-fold cross-validation, as well as good F1-score, precision, recall and AUC and short operating time. The work highlights the power of ensemble tree models and balanced preprocessing (SMOTE+ENN) in quick, accurate dengue detection at bedside, albeit constrained in geographical focus and deficit of deep learning exploration—further evaluation might be warranted using larger and wider datasets and state-of-the art architectures [6].

The authors propose an ensemble machine learning model for hybrid prediction model to predict dengue disease using symptom-based data from 110 patients with 21 features. They

used an Artificial Neural Network (ANN) with backpropagation (BPNN) as a classifier, tested via k-fold cross-validation with $k = 3, 5$, and 10 . The best performance was obtained with $k = 3$ with precision = 97.3%, recall = 97.3% and accuracy = 97.27%. The research explores the potential of ensemble-based hybrid methods that combine ML-DSS techniques with symptom data to cluster dengue (including DF, DHF, DSS), but does not consider climate inputs or spatial modeling. Integrating meteorological factors and widening the geographic and feature range would be helpful in further studies [7].

The authors examine the accuracy of prediction of dengue fever in Singapore by considering weekly dengue case counts (2012–2022) with several meteorological factors including temperature, rainfall, humidity, solar radiation, UV index, cloud cover, wind speed, and sea-level pressure. They benchmarked a group of algorithms – General Linear Model (GLM), Support Vector Machine (SVM), Gradient Boosting Machine (GBM), Decision Tree (DT), Random Forest, and eXtreme Gradient Boosting (XGBoost) with MAE, RMSE, and R^2 performance metrics. XGBoost provided the best model (MAE = 89.12, RMSE = 156.07, $R^2 = 0.83$), its most important predictors being time and cloud cover, with non-linear effects of 19 key predictors. The paper highlights the importance of complex machine learning models and meteorological variables into the dengue prediction with a view to analysing the possibility of future works on the spatial aspect and the real-time implementation [8].

They recommend employing machine learning and deep learning to forecast hospitalizations due to dengue fever, based on demographic, clinical and hospital data from hospitals in the dengue endemic areas. Several models (logistic regression, decision trees, random forests, support vector machines, and artificial neural networks) were calculated and tested with the deep neural network showing the best performance with an accuracy of 96.4%. Platelet count, hematocrit levels, and age were also found to be the most important factors associated with hospitalization risk. Although the study highlights the possibilities of ML/DL methods to assist in the planning of healthcare resource allocation, it is hindered by dataset coverage and lacks environmental or meteorological variables. Further research is needed to integrate data from other sources and more based-locations given a more generalizable framework [9].

An aggregate wavelet-type network (XEWNet) model is presented by the authors to predict the occurrence of dengue epidemics from climatic inputs. With wavelet transforms and exogenous climate variables (which are selected according to causality tests), the model was built to provide robust long-range prediction in three distinct locations: San Juan, Iquitos, and Ahmedabad. XEWNet outperformed the state-of-the-art statistical, machine learning, and deep learning methods in nearly 75% of short- and long-term forecasting scenarios. It shows that wavelet-based feature extraction information fusion with the ensemble neural networks and the meteorological-driven predictors may improve the performance of the proposed model for more reliable epidemic forecasting. It had only been tested on three geographical sites, and does not consider real-time deployment or wider generalisation. Validation in different regions, and integration into hybrid or mechanistic modeling frameworks is a potential future extension of our work [10].

The authors introduce RNN i.e. with Long Short-Term Memory (LSTM) architecture for prediction of dengue cases in Jodhpur, India. Their model reached an accuracy of 94%, they really improved forecast precision. The work highlights the importance of deep learning (Gao, 2015), particularly RNN (Lipton et al., 2015), in capturing temporal dynamics of dengue propagation. However, it is constrained in scope as a city-level model with no consideration of more general spatiotemporal generalization or incorporation of other sources of auxiliary information. Possible extensions of our approach might include checking the generalization of the approach to other geographical regions, the exploration of hybrid architectures, and additional richer environmental or social inputs to make predictions even more robust [11].

Authors compare classic and deep learning approaches: LSTM recurrent neural networks, Random Forest regression and LASSO regression to forecast weekly dengue incidence in 790 Brazilian cities, using multivariate time-series data and spatial information from epidemiologically similar cities. The LSTM model had the least prediction errors and outperformed the Random Forest and LASSO in out-of-sample forecasts for various sizes of cities. The research highlights the utility of deep learning models such as LSTM in modeling temporal and spatial variations in dengue transmission and could not be generalized, however, due to lack of wide model comparison (ensemble or hybrid models)

and lack of contextual environmental factors. Future research could improve generalizability by incorporating more comprehensive sources of data like climate factors and expanding validation to other geographic areas [12].

The authors introduce Dengue Disease Prediction and Diagnosis Model (DDPM), which integrates sentiment analysis and a number of machine learning models. Their model tested the performance of Support Vector Machines (SVM), Random Forest and Artificial Neural Networks (ANN), obtaining encouraging results in the early detection and forecast of dengue fever. Related: The world needs AI and big data now more than ever — and governments need to lead the charge The research highlights the importance of machine learning in developing tools helpful for healthcare professionals in combating public health crises. Nevertheless, the model is restricted to analyzing past records in only two cities—San Juan and Iquitos—and to comparing traditional machine learning algorithms. Further research could validate the approach in different geographical regions with different environmental conditions, and investigate the adoption of more complex hybrid or deep learning structures to improve predictive stability [13].

The authors propose a scheme of explainable AI in forecasting dengue outbreaks in Bangladesh based on eco-climatic, sociodemographic, and landscape explanatory variables observed between years 2000 and 2023. Applying models such as XGBoost and LightGBM, they rely on the SHAP and LIME methods to explain model predictions. Results The XGBoost model worked well with a satisfactory predictive performance (AUC = 0.89; Log Loss, 0.64). Identified key drivers include population density, precipitation, temperature, and land use, with LIME additionally highlighting the influence of relative humidity and minimum temperature. The research shows the potential of XAI to produce interpretable, actionable components that may be employed in an early warning system. However, it is limited in its retrospective modeling and could benefit from real-time implementation and validation across different settings. Applications of the framework that could have practical face-validity include implementation science on public health interventions developed in anticipation of future disease threats [14].

A new hybrid deep learning architecture, namely the CNN-LSTM, which combines Convolutional Neural Networks (CNNs) and Long Short-Term Memory (LSTM) networks

is proposed for weekly dengue incidence prediction in this work. This architecture used the CNNs for extracting the features of thumb motions, and the LSTMs for temporal sequence learning. The best performing architecture obtained 0.8772 accuracy in the forecasting task for Dengue surpassing other widely used deep learning models. The work demonstrates that the inclusion of CNN and LSTM as part of the model can significantly improve the predictive ability of epidemic forecasting. This is as opposed to a deep dive into just how and why it works, given that one study on a single dataset experiments can be quite limiting, particularly when it comes to generalizing the model across regions and other datasets to demonstrate robustness and usability [15].

The authors develop a machine learning application (Dengue Forecasting) for dengue case predictions in Bandung City, Indonesia using climatic factors (sun exposure, temperature, humidity, wind speed, and precipitation) and container index (Angka Bebas Jentik/ABJ). It simplifies dengue recording and utilizes data from Indonesia's Ministry of Health and its Meteorological, Climatological and Geophysical Agency. R programming language 4.2.2 with packages such as (caret, shiny, io) and the linear regression model which predicted most accurately, with RMSE = 68.32 (Mean Absolute Error (MAE) = 164.1), in the predictions of dengue fever cases and outbreaks. The instrument is developed to help district policy makers as an additional tool to early warning and response systems to predict and prevent dengue outbreaks, particularly in Bandung City [16].

The authors present an investigation of applying machine learning for predicting dengue outbreaks, specifically working to help governments to make predictions quickly and confidently about the future of the disease. Their study demonstrates that the inclusion of nature-mimicking algorithms could enhance predictive models. But they recognize that traditional machine learning methods may struggle with such encodings of long-range dependencies using time-series which are necessary for accurate dengue case predictions. This study highlights the utility of machine learning in the estimation of risk factors for severe dengue and suggests a need for models which are capable of emulating such long-range dependencies [17].

The authors suggested a hybrid model based on deep learning approach combining LSTM networks with spatial attention mechanisms to predict dengue fever in Malaysia. They

proposed and compared six LSTM-based models (e.g., stacked LSTM (S-LSTM), temporal attention LSTM (TA-LSTM), and spatial attention LSTM (SA-LSTM)) for predicting weekly dengue cases of 2010–2016. The SSA-LSTM with stacked LSTM and spatial attention achieved the best performance, with an average RMSE of 3.17 across all lookback periods. The model also outperformed benchmark support vector machine (SVM), decision tree (DT), as well as artificial neural network (ANN) models. The study of dengue prediction also demonstrates that integrating spatial attention mechanism can improve the prediction performance by LSTM model, which indicates that spatial feature is considered to be of great importance in outbreak prediction [18].

The authors develop deep learning models—convolutional neural network (CNN), transformer, long short-term memory (LSTM), LSTM with attention mechanisms (LSTM-ATT) for dengue fever occurrences prediction in Vietnam using the meteorological data from 1997 to 2016 in the 20 provinces. The predictive accuracy of the LSTM-ATT model was better and the average ranks of RMSE and MAE were 1.60 and 1.95, respectively, which were superior over the other models in 13–14 of the 20 provinces. It predicted dengue with lead time of up to 3 months corresponding to the ability of robust prediction in the long-term. This study demonstrates the potential of using deep learning approach, such as the LSTM-ATT, to enhance early-warning dengue systems under the influence of climate changes [19].

Aturi (2020) introduced dengue forecasting model with machine learning approach and gave importance to data preprocessing, clustering, and fuzzy-based decision systems. The study demonstrates value of K-means clustering for forming patient clusters, leading to better prediction accuracy. It is also demonstrated that the employment of fuzzy logic can improve decision build-up in uncertainty of fever symptoms classification. Although the method shows promise in early detection and better preventable control on outbreaks, it is heavily dependent on traditional sources of data and lack of effort made on hybrid or deep learning models lead hinder broad adoption. Future studies can further expand this work by adding additional real-time information sources, using more complex spatiotemporal models and testing performance on various environments [20].

Machuca et al. (2023) for improving dengue prediction using LSTM across 217 Paraguayan cities. They first experimented with both raw clustering and feature-based clustering before concluding that hierarchical clustering with Spearman correlation, when used across an entire time series, gives the most sensible clusters. With these clusters, they developed LSTM models with weekly dengue cases and meteorological data. The LSTM models were clustered trained on non-interpolated energy series and outperformed single series LSTM models with a decrease in root-mean-square error of $19.48 \pm 18.80\%$. The analysis demonstrates the power of data-based aggregation to bolster epidemic prediction in a heterogeneous environment. However, it is limited in that it is limited to Paraguay and does not consider generalization over a wider geographical area or incorporation of auxiliary information e.g., demographic or mobility information. Extension of this cluster-based method to other regions where high-resolution data are scarce, to dynamic clustering approaches, or to richer environmental or social data would potentially increase robustness and applicability [21].

Overview Fathima & Hundewale (2012) compare two fundamental machine learning classifiers (Support Vector Machine and Naïve Bayes) for differentiating between dengue cases and non-dengue cases and demonstrate the use of various datasets in the context of one of India's largest outbreaks of arboviral diseases. The outcome shows that the proposed model SVM performs better than Naïve Bayes and it provides better global classification results. Nevertheless, hyperparameters tuning via Grid Search did not help to push the sensitivity of SVM higher than 47%, while the sensitivity of Naïve Bayes came at the price of a very poor ability to distinguish the classes (~17% specificity and 12% accuracy. The results of this study spotlight the complexity of the trade-offs between class separation and balanced prediction reliability of model type, yet are constrained by its binary (dengue or non-dengue) nature.” The binary (dengue vs. non-dengue) and lack of multi-class classification is a constraint of their model. Future work might consider more than just a binary classification of diagnosis, compare to other arboviruses, rely on richer data sets, and assess ensemble/hybrid models that may offer better sensitivity and specificity in different epidemiological settings [22].

Nirob, Sharkar et al. (2025) have presented a detailed hematology database for dengue in Bangladesh primarily based on clinical and laboratory features obtained from patient blood profiles. The dataset, scraped from Jamalpur Medical College Hospital, comprises 1,523 cases and 19 demographic, hematological and diagnostic features that serves as a potential resource for clinical and computational practices. The significant differences between both the dengue positive and negative cases (especially in WBC, RBC, Hb, monocyte counts) supports their role as being diagnostic of dengue cases. The dataset has significant utility in predictive modeling and surveillance of illness but the single-center nature of the dataset constrains wider generalization; additionally, the lack of complex predictive modeling would benefit from future work. In addition, computer-aided methods such as the hybrid or deep learning models and the spatiotemporal patterns of dengue could be a part of the future studies to improve the prediction performance and clinical application on multi-center, or real-world data [23]

2.3 Comparison Study of Dengue Related Previous Works

Table 2.3 shows a variety of ML and DL techniques have been used to the dengue prediction. Classic models including Decision Tree, and Random Forest obtained average correctness of (79%) and (92.5%) respectively; yet, more advanced ensemble models advanced as XGBoost, and Extra Tree Classifier gave better correctness in which the correctness of XGBoost and Extra Tree Classifier 2019ElsevierB.V9776 Abdualgalil et al. (2022) having the highest accuracy of 99.12% on a hold-out dataset. Deep learning method such as ANN, LSTM as well as combination of both hybrid ensemble-networks also performed well in prediction, where DNN model provides 96.4% accuracy and LSTM model giving lesser predictive error due to their capacity to encapsulate temporal dependency. Nevertheless, in spite of the advances, a number of limitations were inherent to these studies, including dependence on small- or symptom-only data, potential overfitting owing to lack of cross-validation, and complex model whose interpretation was limited. In conclusion, although ensemble and deep learning algorithms provide improved predictive performance compared to traditional methods, future work will need to focus on

generalizability, interpretability, and validation across multiple diverse real-world clinical datasets to make results clinically useful.

Table 2.3: Comparison Study of Dengue Related Previous Works

Study No.	Author(s)	Model(s) Used	Best Performance Metric	Research Gap
[1]	Sarwar & Mamun (2022)	SVM, RF, DT, KNN	SVM – Accuracy: 97%	Focused only on limited classifiers; lacks deep learning integration.
[2]	Sarma et al. (2020)	DT, RF	Decision Tree – Accuracy: 79%	Performance relatively low; no advanced models applied.
[3]	Akter et al. (2024)	ARIMA, SARIMA, Feedforward NN	NN – MAPE: 1.15273	Limited to time-series; does not integrate hybrid learning.
[4]	Chowdhury (2025)	ANN, XGBoost	XGBoost – RMSE: 918.83, MAE: 479.44	High RMSE and MAE values; lacks optimization techniques.
[5]	Syfullah et al. (2024)	RF, XGBoost	RF – Accuracy: 92.5% (symptom-only dataset)	Dataset limited to symptoms; excludes environmental/temporal data.
[6]	Abdualgalil et al. (2022)	KNN, GBC, ETC, XGB, LightGBM	ETC – Accuracy: 99.12% (hold-out)	Overfitting risk due to hold-out testing; lacks real-time validation.
[7]	Gangula et al. (2023)	ANN (BPNN) Ensemble	Accuracy: 97.27%, Precision: 97.3%, Recall: 97.3%	Ensemble focused only on ANN; hybridization with other models missing.
[8]	Tian et al. (2024)	GLM, SVM, GBM, DT, RF, XGBoost	XGBoost – MAE: 89.12, RMSE: 156.07, R²: 0.83	Performance limited by feature selection; interpretability not addressed.
[9]	Lalitha et al. (2023)	Logistic Regression, DT, RF, SVM, ANN, DNN	Deep NN – Accuracy: 96.4%	Computationally expensive; lacks explanation of feature contribution.
[10]	Panja et al. (2023)	XEWNNet (Ensemble NN + Wavelet)	Superior performance – ~75% of cases	Complex structure; generalization to diverse datasets not validated.

[11]	Chovatiya et al. (2019)	RNN (LSTM)	Accuracy: 94%	Limited to sequential modeling; ignores hybrid methods.
[12]	Mussumeci & Coelho (2020)	LSTM, RF, LASSO	LSTM – Lowest predictive error	Evaluation lacks detailed metrics; dataset constraints.
[13]	Gupta et al. (2023)	SVM, RF, ANN (DDPM model)	Encouraging results (not exact metric reported)	No clear quantitative benchmark provided.
[14]	Rahman & Shiddik (2025)	XGBoost, LightGBM with XAI	XGBoost – AUC: 0.89; Log Loss: 0.64	High complexity; explainability applied but limited interpretability.
[15]	Zhao et al. (2023)	CNN–LSTM (Hybrid)	Accuracy: 87.72%	Accuracy moderate; requires further tuning with larger datasets.
[16]	Nasir et al. (2024)	Linear Regression	RMSE = 68.32; MAE = 164.1	Simple regression; lacks advanced learning models.
[17]	Aziz & Aziz (2021)	ML overview (SVM, RF, DT, ANN)	Not reported (conceptual emphasis)	Theoretical only; no practical validation.
[18]	Majeed et al. (2023)	LSTM variants (S-LSTM, TA-LSTM, SA-LSTM, SSA-LSTM)	SSA-LSTM – RMSE: 3.17 (avg)	Performance comparison provided, but lacks real-world application.
[19]	Nguyen et al. (2022)	CNN, Transformer, LSTM, LSTM-ATT	LSTM-ATT – RMSE rank: 1.60, MAE rank: 1.95	Computationally intensive; requires optimization for deployment.
[20]	Saturi (2020)	K-means clustering + Fuzzy system	Not reported	No quantitative results; lacks benchmarking with ML models.
[21]	Machuca et al. (2023)	Cluster-based LSTM	Error reduced by $19.48 \pm 18.80\%$	Performance varies widely; dataset dependency.
[22]	Fathima & Hundewale (2012)	SVM, Naive Bayes	SVM – Sensitivity: 47% (best among tested)	Low sensitivity; outdated dataset and methods.
[23]	Nirob, Sharker et al. (2025)	Not employ any models	Only descriptive statistics analysis	Need to employ machine learning modes

2.4 Scope of the Problem

The primary aim of this research is to apply machine learning and deep learning approaches to construct and evaluate models that predict the incidence of dengue by spatiotemporal, clinical, and environmental characterizations. The problem's precise scopes are—

a) Data-Preprocessing

- Take appropriate step after investigation of any missing or lopsided data.
- Ensure that all the encoded features such as gender, result, and others should correspond to the categorical data.
- Think about the significance of attributes and possible dimensionality reduction.
- Think about outliers handling

b) Machine learning model development

- The hyperparameter of successive approach also be optimized for best performance of dengue prediction: Random Forest Naive Bayes Decision Tree Logistic Regression KNN SVM.
- Re-consider what algorithm A1 does and what algorithm A2 does in terms of recall, accuracy, precision, F1-score and any other known relevant measure.

c) Modelling for deep learning

- Optimizing deep learning models suitable for dengue prediction: They consisted in Feedforward Neural Networks (FNN), Recurrent Neural Networks and Long Short-Term Memory (LSTM), and Deep Neural Networks (DNN).
- DNN is selected as simulating very complex nonlinear relationships in large datasets may have a lot of fine detail features ignored by simpler topologies.
- Examine the performance of deep learning models with that of the prominent machine learning models.
- Bring in disease or domain specific epidemiological knowledge to the model architecture being used and used better features if available.

d) Model interpretation and explainability

- Analyze the models in order to understand the most important variables for forecasts and understand how decisions were made.
- Evaluate whether the model is relevant to public health decision-making and comprehensible to epidemiologists and policymakers.

e) Generalization and validation

- Assess the best models with external validation sets and cross-validation.
- Limitations of the study should be mentioned.
- Investigate the influence of temperature, precipitation, and population density on the predictions of dengue outbreak.
- Consider how you would adapt the models for a risk assessment conducted at another location.
- Evaluate the feasibility and potential benefits to use the models for real surveillance systems.

2.5 Challenges

There are several obstacles during conducting this study:

- Data quality:** Environmental and epidemiological datasets may have missing data or inconsistencies or measurement errors. Preparing and cleaning data can be very hard and requires domain knowledge.
- Data size and complexity:** One major challenge with spatiotemporal datasets is their size which can cause high computation overheads, requiring efficient techniques for data processing and storage.
- Class unbalance:** In case dengue incidence data is unbalanced, there are lesser number of outbreak cases than that of non-outbreak which may make models difficult to capture minority patterns.
- Heterogeneity:** This is hard to model do to variations in environmental factors, population density and immunization levels in location.

- e) **Temporal dependency:** Dengue patterns change over time due to climate variations and human movement, requiring models that capture time-series dependencies.
- f) **Choosing the right algorithm:** Each algorithm has its pros and cons, and now and then, the right solution to a problem is to try more than one algorithm.
- g) **Overfitting:** To circumvent overfitting of training data, strong regularization and validation methods are required so as to keep in check complex models such as deep learning models; the likes of LSTM and DNN.
- h) **Interpretability:** It may be more challenging for public health authorities to trust and utilize the deep learning models, particularly DNN and LSTM, for acting as "black boxes."
- i) **Generalizability:** As a model trained over data from one city or region may not apply well along others due to the difference in the environment and demographics.
- j) **Ethical issues:** Privacy, bias and fairness should be considered in using AI for public health surveillance.
- k) **Clinical and operational integration:** Predictive models must be integrated into healthcare and public health system processes to have an impact.
- l) **Cost effectiveness:** A cost benefit analysis is needed before large-scale implementation since developing, deploying, and maintaining model is costly.

CHAPTER 3

Research Methodology

3.1 Proposed Model

The block diagram given in Figure 3.1 explains the prime aim of the proposed work that is to develop effective prediction models of Dengue Fever utilising distinct machine learning and deep learning methodologies. The classical classification models widely used for performance evaluation include KNN, NB, DT, LR, RF, SVM, RNN, DNN, FNN and LSTM. The optimal dengue prediction model is selected from among the most suitable and robust models based on separate training and validation.

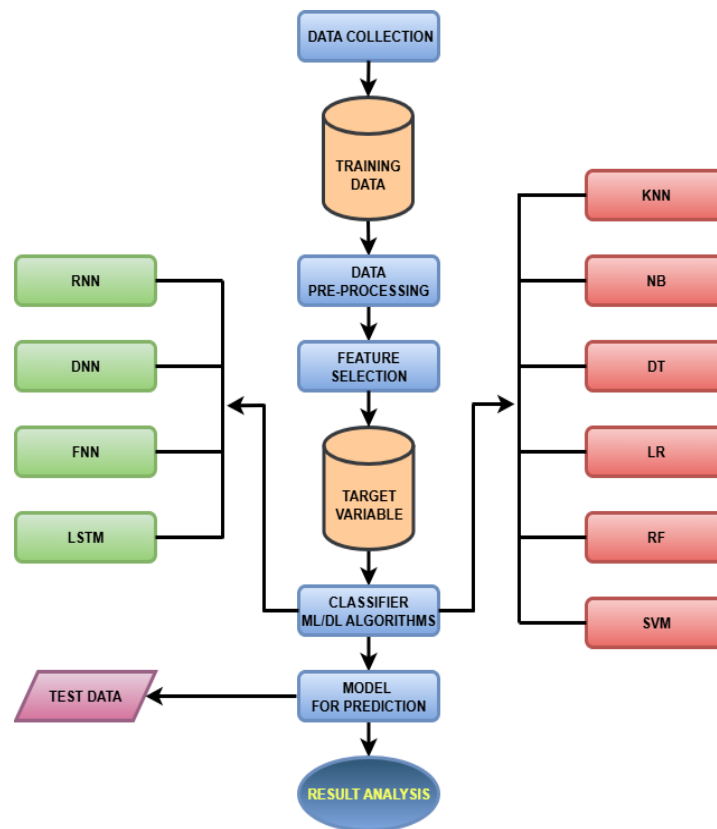


Figure 3.1: Diagram for Dengue Prediction System

3.2 Dataset Collection

The first phase of this study is data gathering. Data, comprising 19 hematological and clinical features of dengue patients admitted in Jamalpur Medical College Hospital of Jamalpur, Mymensingh, Bangladesh, were also obtained from ScienceDirect named “Dengue Fever Hematological Dataset: Clinical Insights for Improved Diagnosis and Patient Management” [23]. There are 1523 patient-bracelet records in the data set. All other of these characteristics are quantitative, only two attributes, Gender and Result, are nominal (object type). While in the result column, the dengue status is shown as positive and negative, the Gender column includes values such as male and female. Since our patient data were gathered for study purposes from a number of centers, they were anonymised for the purpose of this study.

3.3 Data Pre-processing

"Pre-processing" is the processing that the data goes through before you enter the aforementioned algorithm. With different pre-processing methods, in this step, raw data is transformed to a well-organized and understandable state. Raw data from multiple sources is unfit for immediate analysis. In order to enable them to be used as inputs of the machine learning and deep learning models, the categorical values of the two attributes in the dataset applied in this study were converted to numerical values. We found when we looked for repeated values and removed them. No missing data were missing in the dataset as determined by missing value analysis. After cleaning, the set was "fit for" further re-organization, like balancing and scaling of the features, to achieve the best model performance.

The data pre-processing steps are illustrated in Figure 3.3 below-



Figure 3.3: Data Pre-processing System Diagram

3.4 Dataset Description

There are several types of wood texture features in the dataset. The sample contains 1523 observations and 19 variables. These parameters are gender, age, hemoglobin, neutrophils, lymphocytes, monocytes, eosinophils, hematocrit (HCT), mean corpuscular volume (MCV), mean corpuscular hemoglobin (MCH), mean corpuscular hemoglobin concentration (MCHC), red cell distribution width-coefficient of variation (RDW-CV), the platelet count, mean platelet volume (MPV), platelet distribution width (PDW), plateletcrit (PCT), the WBC count, and overall hemoglobin. There is also column "Gender" which are categorical. There are numbers, in other columns. Gender is associated with a whole bunch of things, like male and female. Second, the column status-result has two categories (positive/negative) to know whether a patient is a dengue case or not.

The sample of data frame below is the column headers Sample of column headers of data below (Table 3.4.1 & Table 3.4.2) -

Table 3.4.1: Dataset Columns Header (Before encoding)

	Gender	Age	Hemoglobin(g/dl)	Neutrophils(%)	Lymphocytes(%)	Monocytes(%)	Eosinophils(%)	RBC	HCT(%)	MCV(fl)	MCH(pg)	MCHC(g/dl)	RDW-CV(%)	Total Platelet count(/cumm)	MPV(fl)	PDW(%)	PCT(%)	Total WBC count(/cumm)	Result
0	Male	21	14.800	48	47	3	2	5	48.00	96.0	29.60	30.80	11.60	112000	10.70	15.40	0.120	5100	positive
1	Male	30	15.000	47	49	6	3	5	49.80	96.1	28.40	29.50	11.80	96000	10.60	15.80	0.121	4500	positive
2	Male	51	16.300	41	48	4	5	5	50.10	93.5	31.30	32.70	13.50	184000	10.40	16.40	0.130	6000	negative
3	Female	26	12.300	46	49	7	5	5	44.00	90.0	30.50	30.50	14.70	167000	8.10	17.10	0.110	5000	negative
4	Male	35	16.100	45	46	4	4	5	50.53	91.0	29.12	29.20	15.20	155000	10.52	12.34	0.150	4600	negative
5	Male	67	13.500	50	44	2	2	5	47.00	89.0	28.30	29.80	11.10	84000	9.70	14.60	0.101	4100	positive
6	Female	45	12.400	43	42	3	4	4	39.00	84.0	27.90	29.13	12.30	92000	10.30	13.60	0.183	4700	positive
7	Female	34	13.400	42	40	3	3	4	40.20	88.0	28.31	31.40	13.20	90000	8.90	13.60	0.111	4200	positive
8	Female	56	14.700	45	48	7	5	5	44.50	93.0	30.45	33.61	13.80	177000	10.23	16.10	0.141	5500	negative
9	Female	26	14.100	42	45	3	4	4	45.00	85.0	31.00	32.35	14.15	220000	10.00	17.60	0.170	6000	negative
10	Male	55	15.700	45	49	3	5	6	49.00	91.0	30.00	32.78	15.60	230000	10.80	15.80	0.140	5000	negative
11	Female	40	11.900	50	41	2	3	4	38.64	97.0	27.08	29.80	12.00	80000	9.40	14.39	0.133	4050	positive
12	Female	23	15.400	44	46	5	4	5	44.50	86.0	31.04	32.13	14.00	160000	10.37	16.70	0.180	5300	negative
13	Male	47	14.500	47	49	5	5	5	41.06	90.0	28.44	29.70	13.40	159000	10.20	14.50	0.150	4800	negative
14	Male	33	16.670	47	48	3	4	6	51.15	99.0	30.65	31.70	14.54	170000	10.71	16.21	0.100	5400	negative
15	Male	37	15.900	44	47	4	5	6	49.50	86.0	29.90	30.60	15.00	160000	10.44	17.12	0.160	5700	negative
16	Male	46	17.400	45	41	2	2	5	46.17	91.0	30.17	31.84	14.30	132000	10.23	15.32	0.162	4400	positive
17	Male	29	16.300	49	42	3	2	5	45.55	85.0	28.30	29.43	12.14	120000	9.80	14.10	0.192	4500	positive
18	Male	28	15.439	43	46	3	4	5	47.70	95.0	29.50	30.67	13.80	164000	10.40	16.20	0.200	6500	negative
19	Male	31	15.700	42	48	4	5	5	49.62	99.0	31.10	32.78	14.57	187000	10.20	15.70	0.160	5000	negative

Table 3.4.2: Dataset Column Headers (After Encoding)

	Age	Hemoglobin(g/dl)	Neutrophils(%)	Lymphocytes(%)	Monocytes(%)	Eosinophils(%)	RBC	HCT(%)	MCV(fl)	MCH(pg)	MCHC(g/dl)	RDW-CV(%)	Total Platelet count(/cumm)	MPV(fl)	PDW(%)	PCT(%)	Total WBC count(/cumm)	Gender	Result
0	21	14.800	48	47	3	2	5	48.00	96.0	29.60	30.80	11.60	112000	10.70	15.40	0.120	5100	1	1
1	30	15.000	47	49	6	3	5	49.80	96.1	28.40	29.50	11.80	96000	10.60	15.80	0.121	4500	1	1
2	51	16.300	41	46	4	5	5	50.10	93.5	31.30	32.70	13.50	184000	10.40	16.40	0.130	6000	1	0
3	26	12.300	46	49	7	5	5	44.00	90.0	30.50	30.50	14.70	167000	8.10	17.10	0.110	5000	0	0
4	35	16.100	45	46	4	4	5	50.53	91.0	29.12	29.20	15.20	155000	10.52	12.34	0.150	4600	1	0
5	67	13.500	50	44	2	2	5	47.00	89.0	28.30	29.80	11.10	84000	9.70	14.60	0.101	4100	1	1
6	45	12.400	43	42	3	4	4	39.00	84.0	27.90	29.13	12.30	92000	10.30	13.60	0.183	4700	0	1
7	34	13.400	42	40	3	3	4	40.20	88.0	28.31	31.40	13.20	90000	8.90	13.60	0.111	4200	0	1
8	56	14.700	45	48	7	5	5	44.50	93.0	30.45	33.61	13.80	177000	10.23	16.10	0.141	5500	0	0
9	26	14.100	42	45	3	4	4	45.00	85.0	31.00	32.35	14.15	220000	10.00	17.60	0.170	6000	0	0
10	55	15.700	45	49	3	5	6	49.00	91.0	30.00	32.78	15.60	230000	10.80	15.80	0.140	5000	1	0
11	40	11.900	50	41	2	3	4	38.64	97.0	27.08	29.80	12.00	80000	9.40	14.39	0.133	4050	0	1
12	23	15.400	44	46	5	4	5	44.50	86.0	31.04	32.13	14.00	160000	10.37	16.70	0.180	5300	0	0
13	47	14.500	47	49	5	5	5	41.06	90.0	28.44	29.70	13.40	159000	10.20	14.50	0.150	4800	1	0
14	33	16.670	47	48	3	4	6	51.15	99.0	30.65	31.70	14.54	170000	10.71	16.21	0.100	5400	1	0
15	37	15.900	44	47	4	5	6	49.50	86.0	29.90	30.60	15.00	160000	10.44	17.12	0.160	5700	1	0
16	46	17.400	45	41	2	2	5	45.17	91.0	30.17	31.84	14.30	132000	10.23	15.32	0.162	4400	1	1
17	29	16.300	49	42	3	2	5	45.55	85.0	28.30	29.43	12.14	120000	9.80	14.10	0.192	4500	1	1
18	28	15.439	40	46	3	4	5	47.70	95.0	29.50	30.67	13.80	164000	10.40	16.20	0.200	6500	1	0
19	31	15.700	42	46	4	5	5	49.62	99.0	31.10	32.78	14.57	187000	10.20	15.70	0.160	5000	1	0

Feature index is given below-

- Gender: Indicates the biological sex of the patient, male or female.
- Age: Age of the patient which is in year.
- Hemoglobin(g/dl): Hemoglobin of blood, in grams per deciliter.
- Neutrophils(%): This percentage reflects the ratio of the number of neutrophils to the total number of white blood cells.
- Lymphocytes (%): WBC count in which the lymphocytes are the number of white blood cells that are lymphocytes.
- Monocytes (%): Percentage of monocytes in the total WBC count.
- Eosinófilos (%): Proporción de glóbulos blancos del tipo eosinofilo, sobre el total de glóbulos blancos en la muestra.
- RBC (mill/cumm): red blood cells in millions per cubic mm of blood.
- HCT (%): Hematocrit percentage is the measure of the proportion of red blood cells in the Blood.

- MCV (fl): The mean corpuscular volume measures the average size of a red cell in femtolitres.
- MCH (pg): The mean corpuscular hemoglobin – the quantity of hemoglobin per red blood cell, expressed in picograms.
- MCHC (g/dl): Mean corpuscular hemoglobin concentration: It is the average amount of hemoglobin in a red cell.
- RDW-CV (%): Red Blood Cell distribution width, this is a measure of the variation in the size of blood cells.
- Total Platelet Count (/cumm): the no of platelets per cubic mm of blood volume.
- MPV (fl): Mean Platelet Volume (fl), The Mean size of the platelet.
- PDW (%): Platelet distribution width, indicates variation in platelet size.
- PCT (%): plateletcrit, demonstrating the platelet volume percentage in the blood.
- Total WBC Count (/cumm): Daily Total number of WBC in blood per cubic millimeter.
- Results: target variable which denotes “positive” or “negative” dengue status.

The count, mean, max, and standard deviation for the values in the data sheet are also been computed. The table is displayed below-

Table 3.4.3 Descriptive Statistics of the Dataset

	count	mean	std	min	25%	50%	75%	max
Age	1523.0	40.310571	15.286190	5.00000	28.000	39.000	53.000	78.000
Hemoglobin(g/dl)	1523.0	14.513451	1.627142	10.40000	13.200	14.600	15.800	17.500
Neutrophils(%)	1523.0	44.484570	4.344736	29.00000	42.000	45.000	48.000	60.000
Lymphocytes(%)	1523.0	43.559422	4.972815	29.00000	41.000	44.000	47.000	56.000
Monocytes(%)	1523.0	3.270519	1.209507	2.00000	2.000	3.000	4.000	9.000
Eosinophils(%)	1523.0	3.083388	1.000791	1.00000	2.000	3.000	4.000	9.000
RBC	1523.0	4.765594	0.722874	4.00000	4.000	5.000	5.000	7.000
HCT(%)	1523.0	45.189280	3.566435	36.30000	42.595	45.550	47.840	51.980
MCV(fl)	1523.0	89.815561	5.515619	80.00000	85.100	89.700	94.200	100.000
MCH(pg)	1523.0	29.897225	2.026022	22.90000	28.400	30.000	31.400	34.000
MCHC(g/dl)	1523.0	32.050271	1.551697	27.08000	30.900	32.000	33.200	35.000
RDW-CV(%)	1523.0	13.635792	1.430746	11.00000	12.400	13.800	14.700	21.330
Total Platelet Count(/cumm)	1523.0	173127.170716	64832.681751	56000.00000	114907.000	167385.000	228649.500	299803.000
MPV(fl)	1523.0	9.588806	0.848706	7.50000	8.900	9.660	10.283	11.235
PDW(%)	1523.0	15.312966	1.405457	8.40000	14.230	15.260	16.400	17.990
PCT(%)	1523.0	0.289080	5.992864	0.00002	0.106	0.141	0.173	234.000
Total WBC count(/cumm)	1523.0	5483.024951	1137.344040	3500.00000	4626.000	5397.000	6131.500	14900.000
Gender	1523.0	0.471438	0.499348	0.00000	0.000	0.000	1.000	1.000
Result	1523.0	0.684176	0.464996	0.00000	0.000	1.000	1.000	1.000

Key details from descriptive analysis-

Number of samples: 1523 samples for each feature.

Numerical features (with units where applicable):

- a) Age – Ranges from 5 to 78 years, mean ≈ 40.31 .
- b) Hemoglobin (g/dl) – Ranges from 10.4 to 17.5 g/dl, mean ≈ 14.51 .
- c) Neutrophils (%) – Ranges from 29% to 60%, mean ≈ 44.48 .
- d) Lymphocytes (%) – Ranges from 29% to 56%, mean ≈ 43.56 .
- e) Monocytes (%) – Ranges from 2% to 9%, mean ≈ 3.27 .
- f) Eosinophils (%) – Ranges from 1% to 9%, mean ≈ 3.08 .
- g) RBC – Ranges from 4.0 to 7.0 million/ μ l, mean ≈ 4.77 .
- h) HCT (%) – Ranges from 36.3% to 51.98%, mean ≈ 45.19 .
- i) MCV (fl) – Ranges from 80 to 100 fl, mean ≈ 89.82 .
- j) MCH (pg) – Ranges from 22.9 to 34 pg, mean ≈ 29.90 .
- k) MCHC (g/dl) – Ranges from 27.08 to 35 g/dl, mean ≈ 32.05 .
- l) RDW-CV (%) – Ranges from 11% to 21.33%, mean ≈ 13.64 .
- m) Total Platelet Count (/cumm) – Ranges from 56,000 to 299,803, mean $\approx 173,127.17$.
- n) MPV (fl) – Ranges from 7.5 to 11.235 fl, mean ≈ 9.59 .
- o) PDW (%) – Ranges from 8.4% to 17.99%, mean ≈ 15.31 .
- p) PCT (%) – Ranges from 0.00022% to 234%, mean ≈ 0.29 (the high max suggests an outlier).
- q) Total WBC Count (/cumm) – Ranges from 3,500 to 14,900, mean $\approx 5,483.02$.

Categorical features:

- a) Gender – Encoded numerically (0 = Female, 1 = Male). Mean ≈ 0.47 , indicating a balanced gender distribution.
- b) Result – Binary target variable (0 or 1), mean ≈ 0.68 , suggesting about 68% positive cases.

3.5 Histogram Visualization

One of the essential visualisation techniques used to understand numerical data distribution in histogram. It provides a pictorial representation of data that is grouped into intervals (bins) by displaying the frequency of the data in each interval. A histogram is essentially an estimate of a continuous variable's frequency distribution. This display method makes it is easier to identify whether there are areas containing higher or lower values concentration, the data structure, as well as patterns. The y-axis indicates how many values of a particular amount exists in the set, and the x-axis represents the range of the dataset.

For each feature, the histograms are shown below in figure 3.5-



Figure 3.5: Histograms for Each Feature

In figure 3.5, represents the before predictive modeling, the histogram scenarios provide valuable insight about the center of the tendency, the variability, and the asymmetry of the distribution patterns of each of the attributes in dengue data sets. There are more observations between 20 and 40 years than the alternative edges up to about 70 years, so Age is slightly right skewed. Most of the patients' hemoglobin (g/dl) results fall in the range of 13–16 g/dl (normal range) as shown. The percentages of immune cell types are relatively constant; neutrophils (%) range mostly between 40 and 50%, and lymphocytes (%) are predominantly focused on 40–55%. B: Eosinophils (%), monocytes (%) Both eosinophils (%) and monocytes (%) have got significant left-skewed, and most of patients show the proportion of eosinophils and monocytes in the range of 2–4%. HCT (%) is well distributed with a normal range between 40 and 50 percent and RBC count (million/ μ L) have a concentration between 4.5 and 5.5 million/ μ L, MCHC (g/dl) symmetric formation surrounding the 33 g/dl, MCV (fl) generally series from 82 to 96 fl and MCH (pg) très abordables significations with concentration of 28 to 32 pg. It varies significantly but the Total Platelet Count (/cumm) is commonly between 100,000 to 250,000 reflecting infection related variations as well as RDW-CV (%) which peaks between 12 to 14%. Though, PDW (%) do not show such large variation and ranges primarily from 14 to 16%, MPV (fl) values are more or less around 8.5 to 10 fl. Most patients have a low PCr and the distribution of the PCT (%) is very skewed towards the left. The Total WBC Count counts (cells/ μ L) in the second pair of histograms explo at 4,000–6,000 cells/ μ L a narrow distribution of values Between the classes for the Result property which classifies dengue, is an example of class imbalance where positive far exceeds the negatives and Gender which provides a nearly equal proportion of male and female patients to maintain demographic balance.

3.6 Box Plot Visualization

Box Plot (aka Box-and-Whisker Plot) can be created to visualize the distribution and summarize the distribution of a dataset by showing the median of the dataset, lower and upper quartiles, and any outliers. They are commonly used for validating the integrity of the data prior to modelling, comparing distributions of features and detecting anomalies in data in machine learning. Box plots (or box and whisker plots) are used to visualize the

distribution of the values of a dataset's numeric input variables to identify outliers. Middle line in the box of the plot is median (50th percentile) and lines on bottom and top of the box are 25th (Q1) and 75th (Q3) percentiles respectively. The “whiskers” are the minimum and maximum not-outlier values, data points outside the “whiskers” are explicitly marked by a symbol. Box charts are therefore useful especially to get a fast impression of dataset variance, outliers.

There are box-plots for each individual feature below in the figure 3.6-

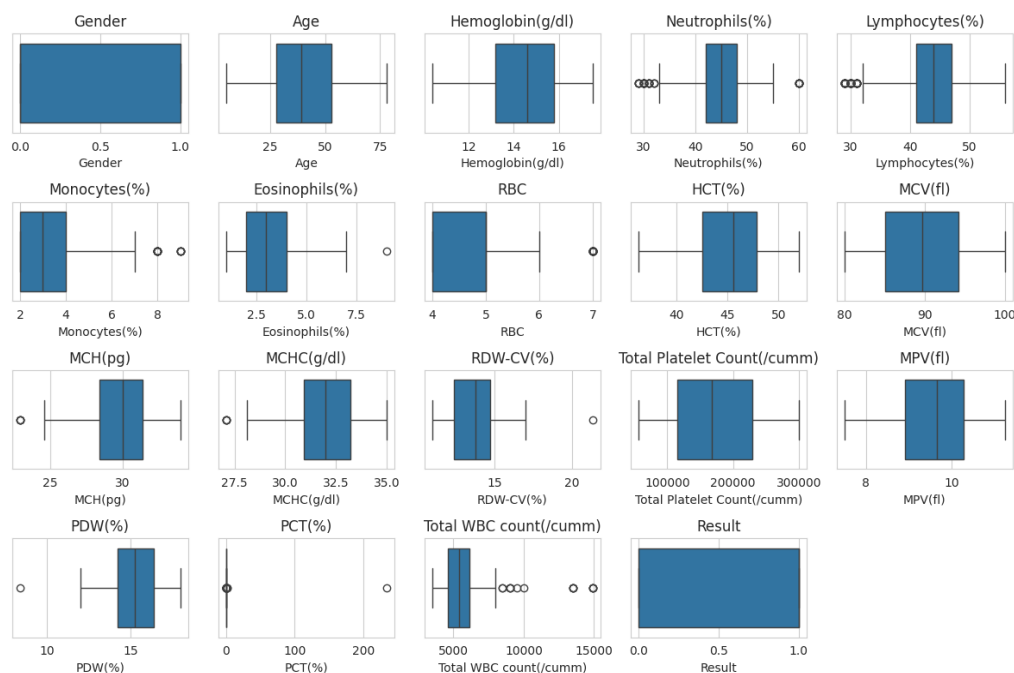


Figure 3.6: Box Plots for Each Feature

The box plot of the dataset is employed to display distribution profiles, the central trend and the presence of outliers for each variable. Figure 3.6 shows a balanced representation (unequal numbers) on Gender with two of its level (values), 0 and 1, whereas no incidence of outliers in the plot. "Age" is quite normally distributed with median ~mid-40's but there are few outliers although it is quite well centered. median "Hemoglobin (g/dl)" is near to 14.5 with not so much IQR with no any significant outliers. " Lymphocytes (%)" also falls around the mid-40s but includes some low-valued outliers, while " Neutrophils (%)" has a

median around 45 with few low-end outliers. Except a few high-end exceptions, "Monocytes (%)" and "Eosinophils (%)" are both closely notited. There is one clear high outlier, but the "RBC" count is peaked at 5.2 with a small IQR. The values of both "MCV (fl)" and "HCT (%)" appear to be normally distributed without any marked changes. (6–9)) While both MCH and MCHC contain one very low outlier on the low side, red blood cell indices "MCH (pg)" and "MCHC (g/dl)" are centered, with small spreads. "RDW-CV (%)" Nothing interesting is noticeable. Total Platelet Count (/cumm) : There is 1 low extreme outlier and median is near about 200,000. The "MPV (fl)" is robust against outliers. There are general conformities between "PDW (%)" and "PCT (%)" in most of their data, but "PCT (%)" has a highHlstat, "P " " value outlier, and "PDW (%)" has a low Hlstat, "P " " value outlier. "Aandas" As there are high value outliers with greater than 12,000, median of "Total WBC count (/cumm)" is almost 7,000. Finally, because there is no variation in two outcomes (0 and 1), the binary "Result" variable is both displayed. Most variables are reasonably well-centered and are within what might be considered to be normal clinical ranges, based on this overview of the distribution. But neutrophils, lymphocytes, monocytes, eosinophils, red blood cells, PLT, PCT, and WBC have some outliers, which might reflect special clinical cases or input errors. They must be intensely verified during the preprocessing for the model robustness.

3.7 Training Data and Test Data

80% of data were utilized for training and 20% were used to test for fair evaluation and to avoid overfitting. This division also preserved a representative subset for testing while leaving a sufficient sample for learning patterns. This data separation should keep intact with the model's ability to generalize the transfer and predict on new instances, accounting for the real on the ground forecast performance on real cases of dengue.

3.8 Feature Selection

In this research, a dual step feature selection approach was adopted to find out the windows that will contain most relevant nuggets of information from the dataset. Correlation was

further explored to determine the independent variable(s) most strongly associated with the dependent variable. Redundant, bulky and uninformative features were eliminated that served as a way of reduction in noise and complexity of the model. Model allowed further filtering based on feature importance rank. By inspecting the relative importance of each features in the model prediction, you can rank the most informative feature and prune out the less useful ones. In addition to improving the predictive power of the models, this rigorous selection enabled interpretation of predictive patterns. Features of the data were Gender, Age, Hemoglobin (g/dl), Neutrophils (%), Lymphocytes (%), Monocytes (%), Eosinophils (%), RBC (lacs/cumm), HCT (%), MCV (fl), MCH (pg), MCHC (g/dl), RDW-CV, Total Platelet Adequacy (/cumm), MPV (fl), PDW (%), PCT (%) and Total WBC count (/cumm). All of these characteristics were included in the model building without the Result in order to achieve the most accurate prediction.

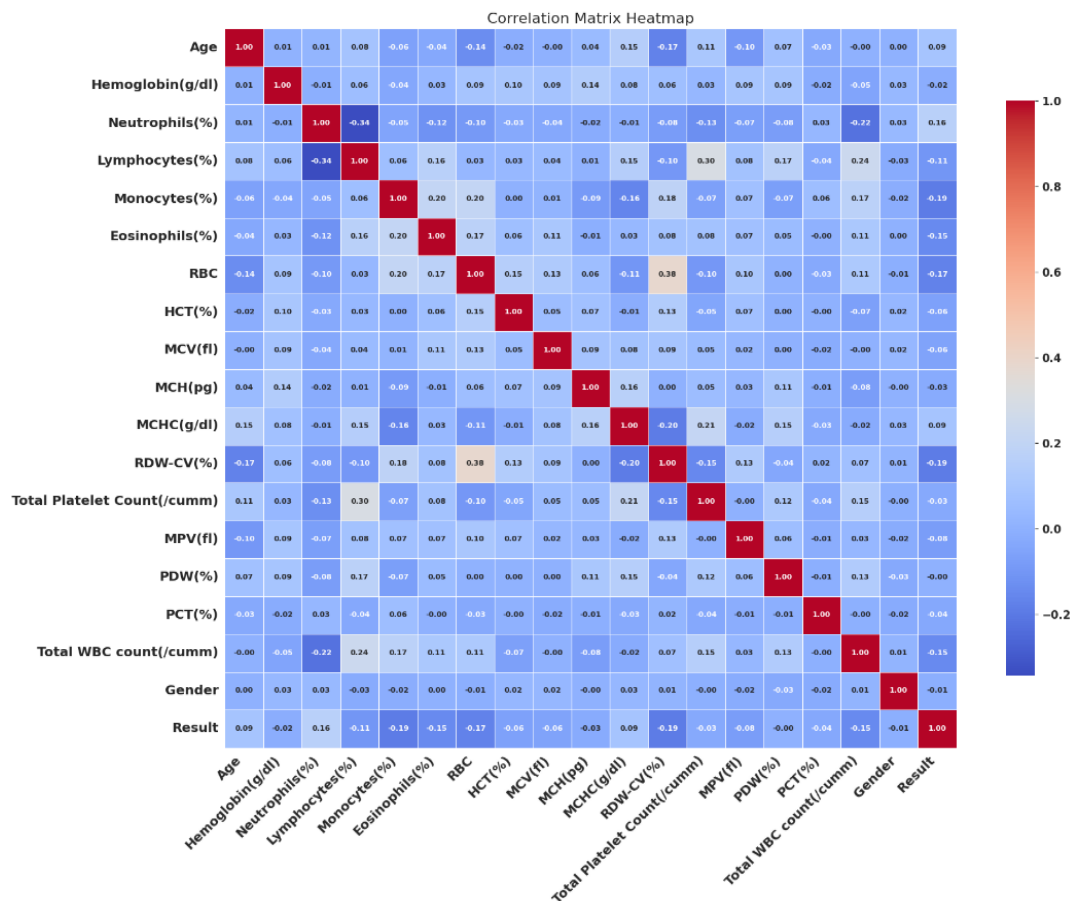


Figure 3.8: Correlation Matrix Heatmap

Figure 3.8 results on a correlation matrix heatmap between the Pearson correlation coefficients of all demographic and laboratory characteristics and the diagnosis of dengue. The correlation and a color-coded intensity scale are shown in each cell and strong and weak associations are shown by deep red and light shades of blue, respectively. Each diagonal feature is perfectly correlated (1.00) with all other features. Strong positive correlations between Hemoglobin & Hematocrit and MCV & MCH respectively, indicating redundancy for these red cell parameters. The moderate negative relationship between neutrophils and lymphocytes reflects the usual immunological response to an infection. Multivariate modelling is required as most predictor variables have small to modest correlations with the Result variable, suggesting that no single trait is a good strong linear predictor for dengue status.

3.9 Target Variable

The final result of the study is the study variable Result that takes the values zero or one, according to the presence or absence of the dengue disease in the patient. A positive-dengue case was assigned a value of 1 and a negative-dengue case was assigned a value of 0. It is the variable 'Y' in any of the classification model, created in the study. According to correlation analysis, there is weak linear relationship in between Result and constructs. It is significant to note a single parameter from the clinical and laboratory findings is inadequate to predict the dengue status. Therefore, to capture the complicated patterns in the data, multi-variable need to be incorporated and we should take multivariate and non-linear modeling in the classification. In this setting, DENV diagnosis is the subject of this clinical prediction challenge. The training of the model relies on this critical outcome variable with significant clinical repercussions as it identifies people who are highly probable to develop this lethal disease or to be affected by this. By thoroughly examining a large pool of predictors, the model seeks to find a strong association between these predictors and the presence of dengue. This will afford HCPs crucial information with which to treat, intervene earlier, and improve patient outcomes. Finally, the predictive knowledge provided by the model should help in clinical decision-making and resource allocation support in health-care institutions.

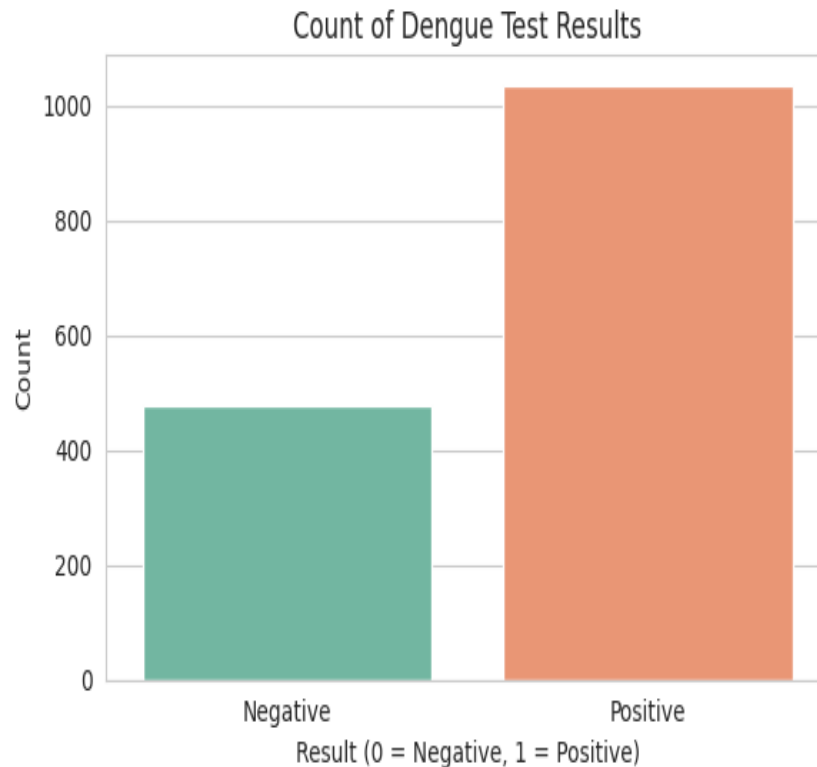


Figure 3.9: Count Plot for Result Column

Figure 3.9 depicts a bar chart named “Count of Dengue Test Results” plotting the distribution of positive and negative dengue cases in the dataset. The number of cases is plotted on the vertical axis and the test result, with "Negative" being 0 and "Positive" being 1, is plotted on the horizontal axis. There are over 1,000 more positive cases — far more than the 500 negative cases — than negative cases, according to the chart. This difference suggests that the dataset is biased towards patients with dengue, and so we need to consider this when we design and evaluate prediction model, because it may influence the bias and performance of model.

3.10 Used Machine Learning and Deep Learning Algorithms

The model was not tuned to achieve the best it could on dengue test results early prediction and rather made the model to pass through a trial and error to get a small set of good performing algorithms. We applied a set of machine learning classifiers in this study. It is

possible to understand what algorithms might be best for this classification task by observing the data visualization plots. Training data is that which is used to teach models to recognize patterns, and test data to evaluate the quality of the trained model with respect to prediction. In this work, the forecast performance is assessed with respect a number of criteria through machine learning based comparisons of the forecasted quantities for the evaluation dataset vs. the ground truth.

In this study, Ten machine learning and deep learning algorithms are being tested by the model. These models are listed below:

- 1) K-Nearest Neighbor (KNN)
- 2) Naive Bayes (NB)
- 3) Decision Tree (DT)
- 4) Logistic Regression (LR)
- 5) Random Forest (RF)
- 6) Support Vector Machine (SVM)
- 7) Recurrent Neural Network (RNN)
- 8) Dense Neural Network (DNN)
- 9) Feedforward Neural Network (FNN)
- 10) Long Short-Term Memory (LSTM)

K-Nearest Neighbor (KNN)

K-Nearest Neighbor, or KNN, is one of the simplest and popular machine learning algorithms for both regression and classification problem. It finds the K data points from the new data point that are the most nearby (its neighbors) and makes them vote to predict the class of the new data point. As far as dengue is concerned, detection process of KNN is like a medical detective searching for fresh patients based on previous patients. Selecting the K most similar patients from previous cases, with the aid for example of fever duration, platelets, and hematocrit values, it checks for similarities. The probability of a new patient testing positive or negative for dengue is computed using the results of these similar cases

using K-nearest neighbor. However, KNN requires fine scaling of features, as well as tuning of the parameters to perform reasonably well.

Naive Bayes (NB)

As probability model in classification tasks the Naive Bayes family of classifiers are often used. This is probably not true in reality but it assumes that all features are independent. Under the dengue prediction setting, one way to think of Naive Bayes as a diagnosis process is to look at each health signal (like temperature, WBC count and possibility of rash happening) in isolation and find the probability of dengue if the health signal occurs. By aggregating these different probabilities, a final prediction is provided. For example, in a medical investigation, Naive Bayes treats the platelet count and the duration of fever as separate clues although they are related. For dengue prediction, this is a nice cheap and cheerful model to kick us off as it's fast, it's easy, and weirdly it works really well for a range of medical data.

Decision Tree (DT)

The decision tree is a versatile machine learning approach to classification as well as regression problems. The data is split by feature values, resulting in branch nodes that ultimately arrive at leaf nodes that denote predictions. The Decision Tree acts like a doctor asking series of yes/no questions such as "Is platelet count below a certain value?" until it has determined whether a patient has dengue or not. or "Is duration of fever more than five days?" Its tree-based model is easy to interpret and reason about, giving doctors insight into the exact logic behind a diagnosis. But if Decision Trees are not regularized, they can easily overfit the training data, so it is important to use depth control and pruning in order for a Decision Tree to work well. Decision trees are suitable for a number of medical data sets as they can process both numerical and qualitative data. They are easy to model as you don't need to spend too much of time on data cleaning and filling missing values of data is not required for a number of models. They can also be learned quickly, even on large datasets, and are computationally efficient. They have the downside of tending to be biased

when processing data that is not balanced, however. But despite these limitations, Decision Trees form the foundation for some of the most powerful machine learning methods used today, like Random Forests and Gradient Boosting Machines.

Logistic Regression (LR)

Logistic regression is a statistical model for binary classification problems. It is a linear model in that it predicts the probability of belonging to a particular class on the basis of weighted combinations of input information. In case of dengue, Logistic Regression gives a probability score in between [0-1] which actually represents the probability to have the dengue by taking the features such as Body temperature, Platelets and Hematocrit etc. This technique is valuable in situations where you need to understand the impact of each feature since it is simple and interpretable. Medical decision-making could benefit from knowing, for example, the platelet count which has the highest coefficient for a measure substantial association with dengue positive.

Random Forest (RF)

A machine learning technique known as Random Forest builds multiple tree models in a predictive model and takes the average of their predictions to achieve a final result. In order to ensure diversity and to avoid overfitting, each of the trees in the forest is trained with a random subset of the features and data. Random Forest by Random Forest scans through patient information in a manner that a panel of clinicians would and votes on whether the patient is positive for negative for dengue. Random Forest is a good choice for this classification task because it often has better accuracy than a single Decision Tree, by using so-called collective wisdom.

Support Vector Machine (SVM)

Help in a feature space, SVMs find the optimal hyperplane (decision boundary) to discriminate the classes. For SVM, a line or surface that best separates the positive and

negative cases is found so as to maximize the margin between them in dengue diagnosis. The maximum margin principle makes SVM optimal in term of generalization to unknown data. SVM fares well in non-linear relationships through the use of kernel functions thus, it is relevant to complex, non-linearly separable dengue data patterns.

Recurrent Neural Network (RNN)

Recurrence comes from deep learning models that are made to work with sequential or time-based data, namely recurrent neural networks. RNNs can be applied to dengue prediction provided that patient data is available with temporal information such as fever temperature over a few days, or daily platelet count. By “remembering” previous points in the sequence, the model could potentially pick up patterns in the course of the disease that a static model may miss. Here this sequential learning feature could provide an early warning before the problem deteriorates.

Dense Neural Network (DNN)

Each neuron of a densely connected neural network is linked to every unit in the layer above. DNNs can learn complex and highly non-linear relationships between hematological and clinical parameters in dengue forecasting. Hierarchical feature representations are learned by stacking the network with multiple hidden layers and activation functions, and obtain improved accuracy over shallow models. Unlike SVMs, in order to avoid overfitting and ensure good generalization, we must be careful to set for DNNs hyperparameters (like the number of the layers, the number of the neurons and the learning rate).

Feedforward Neural Network (FNN)

Processing incoming data through several connected layers of nodes, a feedforward neural network moves forward only. An FNN processes the static patient data (lab results, symptoms, etc.) using y layers to find complex nonlinear relationships between the

covariates and dengue case status. Final output layer provides both positive and negative classifications. The architecture of the FNN is good at collecting all kind of feature interaction for an observation, although it forgets the sequential input.

Long Short- Term Memory (LSTM)

A special class of RNN, namely LSTM network is introduced to overcome the vanishing gradient problem and to model long range dependencies over data sequences. Since LSTMs are able to sense very small changes over time which might indicate the onset of the disease, they are particularly useful to dengue identification, where health conditions of patient were checked over days. For instance, they might learn to recognise a warning profile of dengue through seeing a gradual fall in platelets accompanied by an extended duration of fever. While LSTMs are more computationally expensive than FNNs, they can perform better than FNNs in time-series prediction application for medical data.

CHAPTER 4

Experimental Results and Discussion

4.1 Experimental Setup

This research train and validate the developed dengue prediction model using 1,523 patient data (articles) retrieved from the ScienceDirect database in this experiment. Data set contains 19 hematological, clinical and response variable shows dengue status (positive/negative). A set of preliminary data preprocessing steps is performed to encode categorical features, eliminate duplicates, scale the features, and balance the samples to allow the improved factorization model even more “leverage”. In this study, several machine learning and deep learning are adopted, such as DT, RF, KNN, NB, SVM, LR, FNN, DNN, CNN, RNN and LSTM. To have a fair assessment, we use 80-20% train:test split of the data set. To assess the model, we compute the following popular metrics precision, recall, F1-score, and accuracy, and report the confusion matrices.

4.2 Experimental Results and Analysis

Precision:

‘Precision’ is a concept in machine learning and deep learning to check the correctness of a classification model when we talk about it in a binary classification case. One can test the stability of the model through how accurate the positive prediction is. It is the ratio of true positive bullying to the sum of true positive bullying and false positive bullying. Precision is TP on $TP + FP$. A true negative model that is classified as being positive is known as a false positive. In other words, precision can be formally denoted as:

$$\text{Precision} = \frac{TP}{TP + FP} \quad (1)$$

Recall:

The recall is a performance measure in machine learning, deep learning to show how well the model is, particularly used in binary classification problems. It is also known as the true positive rate or sensitivity. It is defined as number of true positive predictions divided by true positives plus false negatives. In other words, it gauges what fraction of relevant occurrences that a dataset actually contains. Recall is calculated as the TP rate divided by the sum of TP and FN. Where the recall formula is:

$$\text{Recall} = \frac{\text{TP}}{\text{TP} + \text{FN}} \quad (2)$$

F1- Score:

F1 score is one of the most common metrics in machine learning and deep learning to judge performance of classification model. It becomes more handy when you have an imbalance dataset, where there are more samples in one of the class than the others. F1 score is the harmonic average of the precision and recall. Two important measures that illustrate different aspects of categorization performance are recall and precision. If you have a class imbalance (i.e more true positives than negatives in this case) and you want to strike a balance between recall and precision, you can use F1 Score. The following defines the recall formula:

$$\text{F1-Score} = 2 * \frac{\text{Precision} * \text{Recall}}{\text{Precision} + \text{Recall}} \quad (3)$$

Accuracy:

Another common metric to evaluate the overall performance of classification model is deep learning and machine learning is accuracy. It represents the percentage of accurately classified instances vs all instances in the dataset. To be specific, the accuracy formula is: Accuracy = (Number of Correct Predictions) / (Total Number of Predictions). Accuracy is

generally assumed as an easy and informative measure of performances of a model, given a balanced dataset. Nevertheless, accuracy may not be the whole story in terms of the effectiveness of a model, especially in an unbalanced class setting where minority classes may be neglected. As a result, they frequently use accuracy together with precision, recall and F1-score to evaluate performance more thoroughly. Where the accuracy formula is:

$$\text{Accuracy} = \frac{\text{TP} + \text{TN}}{\text{TP} + \text{TN} + \text{FP} + \text{FN}} \quad (4)$$

Machine Learning Models Outcome

K-Nearest Neighbor (KNN)

Table 4:2:1 shows the classification report of proposed dengue prediction framework- Precision, Recall, F1-Score, Training Accuracy and Testing Accuracy. This comprehensive evaluation illustrates the efficiency of the models by focusing on their accuracy in detecting dengue-positive cases, recall in detecting all relevant cases, F1-Score in trade of both and accuracy in sustaining a constant performance across the training and testing datasets.

Table 4.2.1: Classification Report for KNN Model

	Accuracy	Precision	Recall	F1-Score	Support
Negative		0.38	0.26	0.31	99
Positive		0.69	0.79	0.74	204
Accuracy				0.62	303
Macro (AVG)		0.54	0.53	0.52	303
Weighted (AVG)		0.59	0.62	0.60	303
Training	0.77				303
Testing	0.62				

The true positives, true negatives, false positives, and false negatives are shown in the KNN model's confusion matrix, providing a comprehensive view of the classification results in

Figure 4.2.1. Apart from the overall model performance, this representation offers additional perspective on how accurate and inaccurate predictions are distributed by showing how well the model discriminates between dengue positive and dengue negative cases.

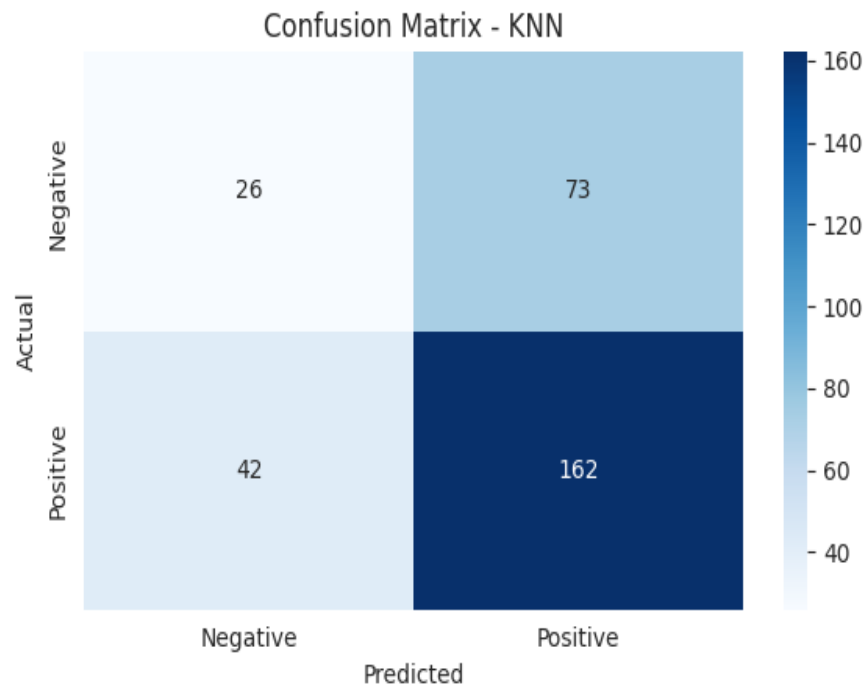


Figure 4.2.1: Confusion Matrix (KNN)

The confusion matrix for KNN model is also shown in Figure 4.2.1 which represents the aggregate of the successful and non-successful predictions of dengue. The model misclassified 73 negative samples to positive, and 42 positive to negative, whereas, the real 26 negative and 162 positive samples to positive were detected under the total. Despite the relatively large number of fabricated positive predictions, these results also show that the KNN model is more precise in predicting a dengue status positive, rather than a negative, for patients. In summary, the confusion matrix helps to visualize the limitations of the model for non-dengue case discrimination and of dengue cases detection.

In figure 4.2.2, displays the ROC curve for the KNN average model, which gives the true positive rate against the false positive rate for different true positive rates. Discussion of

how well the model is able to classify dengue-positive and dengue-negative is covered in detail. The better a curve lies in the upper-left corner of the plot (higher sensitivity at lower false positive rates), the better is the classification. And that is why we prefer an evaluation metric like the ROC curve where how it is put in order is not just get form the accuracy to measure more broadly KNN's model discriminative quality.

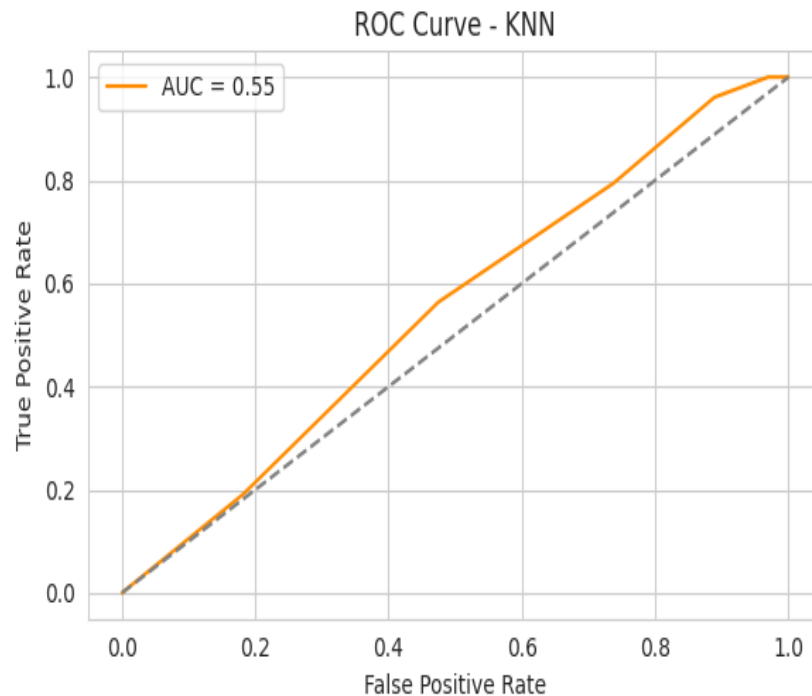


Figure 4.2.2: ROC- Curve (KNN)

The KNN model ROC curve is illustrated in Figure 4.2.2, which is the plot of the true positive rate against the false positive rate for different cut-off values. An AUC value of 0.55 indicates that the curve nearly coincides with the diagonal-reference line. The KNN classifier, which models the maximum information over all learning distances, does not perform well in discriminating to dengue positive or dengue negative patients albeit slightly better than chance. The model is in general very non-discriminative among classes as it's pretty low AUC (absolute low), though it can only find some few true positives. This indicates that KNN does not capture enough of the feature distribution characteristic of the dataset. The performance differential suggests the model is inappropriate to confidently

guide clinical decision-making. Therefore, either more complicated classifiers or the ensemble strategies are the prerequisites for improving the prediction performance.

Naive Bayes (NB)

Results The performance of the NB model in terms of accuracy, precision, recall, and F1-Score measures can be seen in Table 4.2.2. Through this evaluation, the variables that combined could demonstrate how good the NB model performs in classifying dengue at an efficient rate. Recall is an explanation of how well does the model find all the positive cases and precision helps in knowing how many of the positive predictions made by the model were actually positive, and the F1-Score signifies a very good trade-off between recall and precision. Overall, these indicators provide a full picture on the predictive performance of the NB model between dengue incidence and total accuracy.

Table 4.2.2: Classification Report for NB Model

	Accuracy	Precision	Recall	F1-Score	Support
Negative		0.77	0.24	0.37	99
Positive		0.72	0.97	0.83	204
Accuracy				0.73	303
Macro (AVG)		0.75	0.60	0.60	303
Weighted (AVG)		0.74	0.73	0.68	303
Training	0.74				
Testing	0.73				

In Figure. 4.2.3, confusion matrix generated for NB model is plotted, and gives preliminary idea of the classification outcome for the dengue prediction done by model. The diagram visualizes how well the model separates the distribution of true positive, true negative, false positive and false negative with respect to the dengue-positive and negative cases. It enables obtains a more complete perspective of the model advantage and disadvantage in the practical diagnostic application, it make to discover the positive cases that were successfully classified, the general errors of the model that happened, etc. It tests whether the model has a bias towards getting more false negatives (which could delay life-saving treatment) or more false positives (causing unnecessary health anxiety) from tests. Some

performance measures including accuracy, precision, recall and f1-score are reported by using the confusion matrix. It is also practical information for clinicians, reminders that sensitivity versus specificity in the diagnosis of dengue is always a compromise. While a better choice of feature selection or else adjusting the prior of the NB model basing on the error patterns may offer significant improvement. This analysis also demonstrates that the Naive Bayes is very simple and understandable to deal with health classification problems. At last, the confusion matrix acts as a diagnostic tool for model as well as approaches to improve predictive performance.

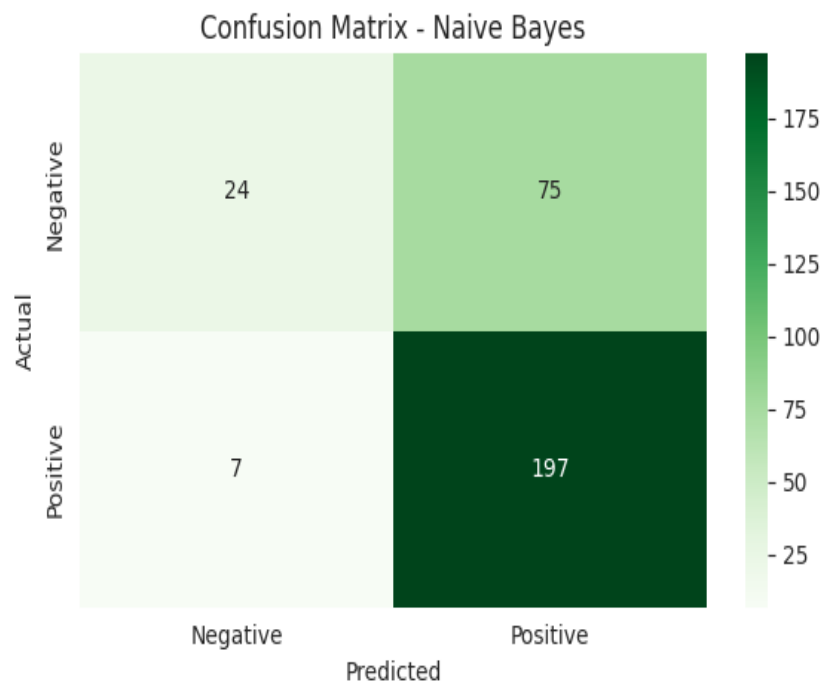


Figure 4.2.3: Confusion Matrix (NB)

Confusion matrix in Figure 4.2.3 shows how well the classifier predicts cases for dengue-positive and dengue-negative using the Naive Bayes (NB) model. A relatively small percentage of false-positives could be observed from the fact 24 of the real negative cases were correctly classified as negative and 75 were misclassified as positive. But the model identifies dengue positive cases quite well with 197 true positive cases and only 7 cases being falsely classified as negative. This indicates that a NB model is less powerful in SP, since more negative patients misclassified, but it has a good ability of SE to grab the

authentic patients. As a whole, Figure 4.2.3 indicates the weakness of the model in correctly localizing negatives, and the strength in detecting positive examples.

The Receiver Operating Characteristic (ROC) curve for the Naive Bayes (NB) model is shown in figure 4.2.4, the ROC curve is a plot of the true positive rate versus the false positive rate at 'various threshold settings. The ROC curve that describes these rates offers a global picture of the model's capability to discriminate between dengue positive and dengue negative cases. A curve closer to the top-left indicates a better model. This discrimination ability can also be measured by the AUC, and the higher the AUC, the more predictive the model. Therefore, Figure 4.2.4 provides with useful information: NB even sucks in terms of accuracy but the classification of a large number of instances (852815) is really good.

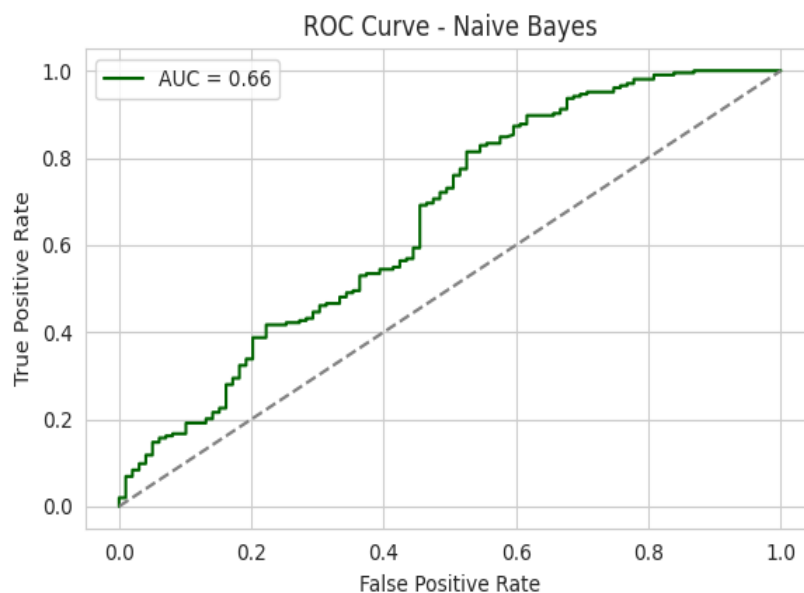


Figure 4.2.4: ROC- Curve (NB)

Figure 4.2.4 demonstrates the ROC curve of the NB model, which is a graph illustrating the ability of the model to discriminate power at different thresholds representing the true positive and false positive rate, ranging from 0 to 1. It performs better than chance as the curve is above the diagonal reference line, which represents random classification. The low discriminative accuracy of the model to discriminate dengue-positive from dengue-

negative patients is demonstrated by an AUC of 0.66. This curve shows that the NB model provides a fair compromise between sensitivity and specificity, which means that it is an acceptable technique for accurately diagnosing dengue cases, but its result is not that very strong.

Decision Tree (DT)

Table 4.2.3 compares accuracy, precision, recall and F1-Score of the Decision Tree (DT) model from the classification performance. By analysing the DT model's precision (the number of positive predictions/positive class), recall (the total number of true positive and false negative) and F1-Score (a measure of a test's accuracy that considers precision and recall), the evaluation demonstrated the ability of the model to properly classify issues. Table also presents the model performance on the overall accuracy, which helps to get a complete picture on whether the DT algorithm can be considered a good model for predicting dengue cases relative to other models used.

Table 4.2.3: Classification Report for DT Model

	Accuracy	Precision	Recall	F1-Score	Support
Negative		0.54	0.53	0.53	99
Positive		0.77	0.78	0.78	204
Accuracy				0.70	303
Macro (AVG)		0.66	0.65	0.66	303
Weighted (AVG)		0.70	0.70	0.70	303
Training	1.00				
Testing	0.70				

The confusion matrix of the DT model is presented in Figure 4.2.5 that will provide a “big picture” view of the classification performance of the model, by comparing the model fit to the actual data. The true positive (TP), true negative (TN), false positive (FP) and false negative (FN) rates are highlighted which allows a straightforward overview of how much the DT algorithm is effective in identifying patients with and without dengue. It is important as a diagnostic tool for the overall soundness of the model: it enables one to see that the models make the right choices when the opportunity is there but that they are

penalized when they betray themselves by unforced classification errors. Another important aspect when considering the model for medical decisions is to understand whether the model is biased towards predicting a particular class. We can also optimize the performance of the model by adjusting parameters (max depth, pruning method, etc) based on the confusion matrix. The aim was to improve the predict performance of the DT model ultimately and to make it applicable in the future real medical practices.

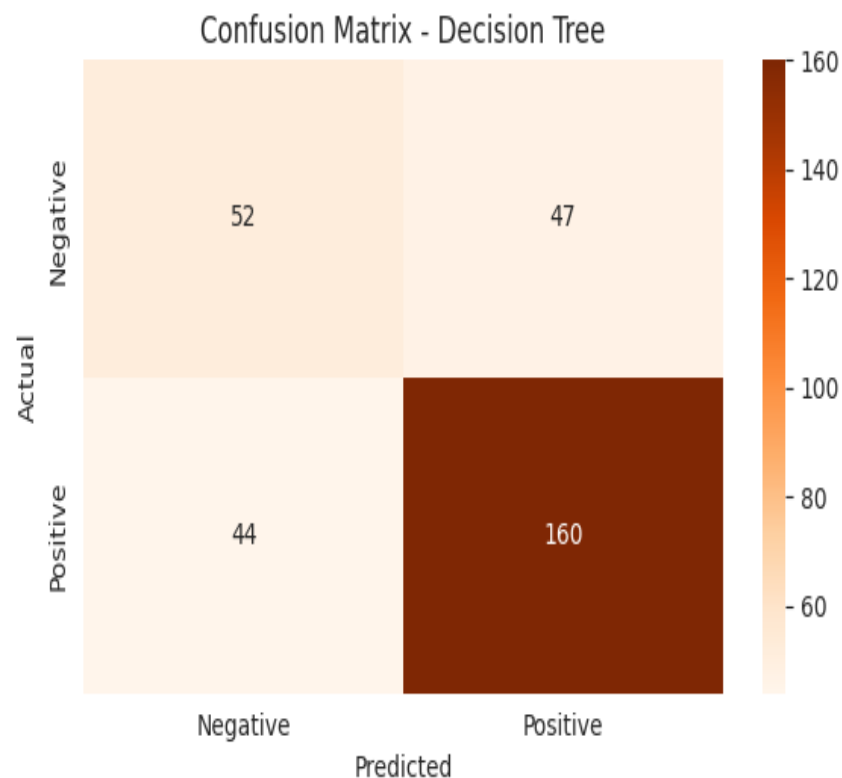


Figure 4.2.5: Confusion Matrix (DT)

The confusion matrix of the Decision Tree model for identifying the effectiveness of correctly predicting case as dengue-positive and dengue-negative can be seen at Figure 4.2.5. For adverse event, the mode misclassified 47 negative phenomenon to positive but correctly classified 52 specimens as negative phenomenon. It appears that the DT model did actually predict the data of 160 positive cases as positive and that of 44 positive cases as negative. Even with some misclassification in both classes that provokes some confusion to the model's global trade-off between sensitivity and specificity, it seems that, as have

demonstrated these results, even if not great, the model is effectively good in predict the positive dengue case.

Figure 4.2.6 shows the ROC curve of the DT model, at alternate threshold levels, which represents the relationship between true positive and false positive terms. A detailed analysis of the predictive power for a person to be or not to be a case (as quantified by AUC is the ROC curve: a curve that traces these rates. The curve approaches the top-left corner when the categorization is more and more perfect. A higher value implies better predictive capability and the Area Under the curve (AUC) assesses the classification performance of this classifier.

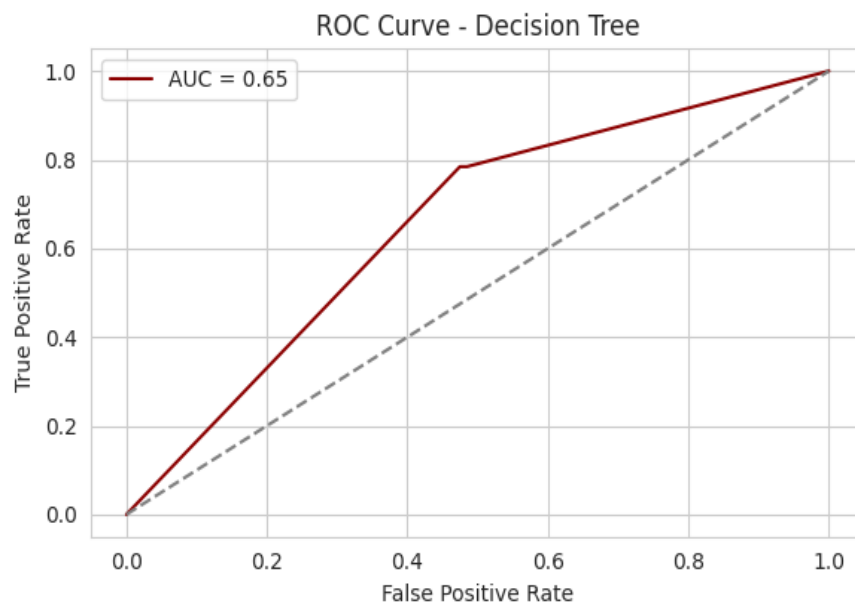


Figure 4.2.6: ROC- Curve (DT)

The ROC curve of the Decision Tree model (Figure 4.2.6) has an operations characteristic (AUC) of 0.65 exceeding the diagonal line. This also shows that the DT model lacks discrimination power between dengue positive and negative cases. The AUC was low, suggesting that the discriminative performance of the model is not as good as it could be, but the upward trajectory suggests that the model can correctly identify many true positives. If DT is really sensitive, classification mistakes could make the model's performance, mediocre this time and not really good prediction power as well.

Logistic Regression (LR)

The classification report of the (LR) model as its precision, recall, F1-score, and support is shown in Table 4.2.4 for Dengue-Positive and Dengue-Negative cases. The talk about training and test accuracies and those kinds of metrics paints a very clear picture of the global behaviour and the global ability of generalization of a model.

Table 4.2.4: Classification Report for LR Model

	Accuracy	Precision	Recall	F1-Score	Support
Negative		0.74	0.28	0.41	99
Positive		0.73	0.95	0.83	204
Accuracy				0.73	303
Macro (AVG)		0.73	0.62	0.62	303
Weighted (AVG)		0.73	0.73	0.69	303
Training	0.75				
Testing	0.73				

The comparison of true vs false classification of dengue is shown in Figure 4.2.7 below where confusion matrix results of LR model are plotted.

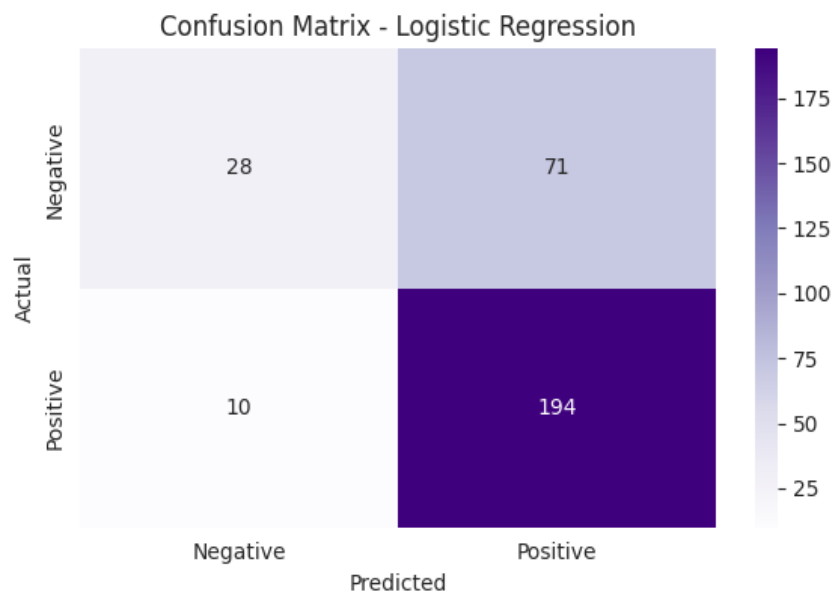


Figure 4.2.7: Confusion Matrix (LR)

The confusion matrix as shown in the below Figure 4.2.7 demonstrates that the results of dengue negative and dengue positive were predicted correctly for 28 cases and 194 cases by the LR model. However, 10 samples dengue positives were called as dengue negatives (false negatives) and 71 samples dengue negatives were called as dengue positives. The model's sensitivity is high for identifying positive dengue cases but the specificity is very low, resulting in a high rate of false positives, the findings suggest. The LR model tends to produce more positive detections at the expense of lower accuracy of the negative classification, which is not suitable for gas disease monitoring works.

Figure 4.2.8 represents the plot of Receiver Operating Characteristic (ROC) of Logistic Regression (LR) model which illustrates the how well the true positive rate (TPR) is trade-off the false positive rate (FPR) compared to various decision thresholds. In addition to accuracy being squeezed, this curve holds an added information regarding the discriminating power of the model, how well it is capable of differentiating dengue-positive and dengue-negative patients.

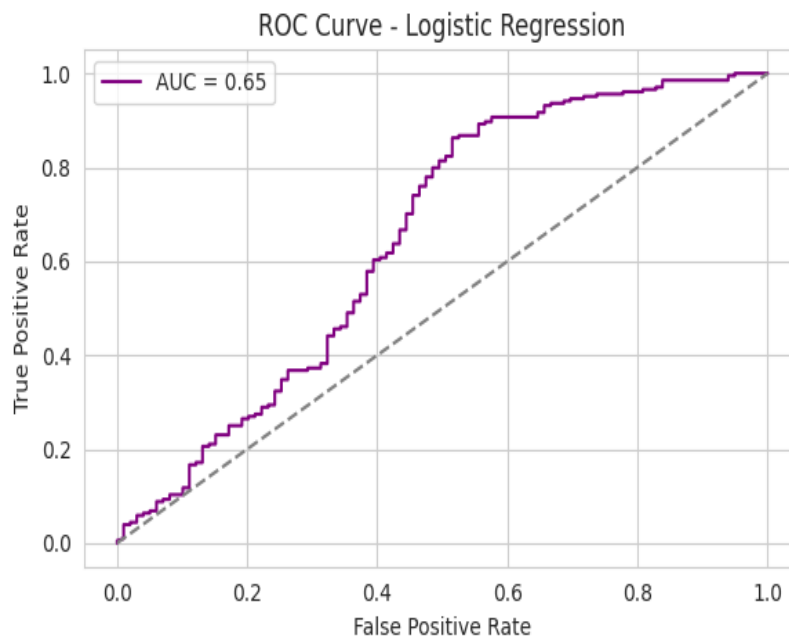


Figure 4.2.8: ROC- Curve (LR)

The ROC curve of the LR model in Figure 4.2.8 indicates that the model prediction is superior to random classification as the curve is above the reference line of the diagonal. Its discriminative power is fair, with an AUC of 0.65. Despite the fact that the curve suggests good recognition of positive cases by the model, the relatively low AUC value reveals that the prediction performance is rather modest. On the whole, the LR model has a fair sensitivity and specificity, and it is useful for dengue prediction, but it is not ungenuine.

Random Forest (RF)

The classification report of Random Forest (RF) model, in terms of precision, recall, F1-score, and support, of dengue-positive and dengue-negative can be found in Table 4.2.5. The training and test accuracies are also reported for a more complete view of the performance of the model and generalization ability, in addition to those performance measures. In this work, we have demonstrated that the RF model can aggregate multiple decision trees to improve predictive ability (mitigate overfitting) at the same time of providing well-balanced classification performance.

Table 4.2.5: Classification Report for RF Model

	Accuracy	Precision	Recall	F1-Score	Support
Negative		0.77	0.43	0.55	99
Positive		0.77	0.94	0.85	204
Accuracy				0.77	303
Macro (AVG)		0.77	0.69	0.70	3033
Weighted (AVG)		0.77	0.77	0.75	303
Training	1.00				
Testing	0.77				

The confusion matrix of the Random Forest (RF) model (Figure 4.2.9) is used to present the distribution between correct (accurate) and incorrect (inaccurate) dengue categorization predictions. This plot visualizes true positive, true negative, false positive, and false negatives, to make it very obvious, how well a model, performed in terms of classification trouble, way, way beyond accuracy.

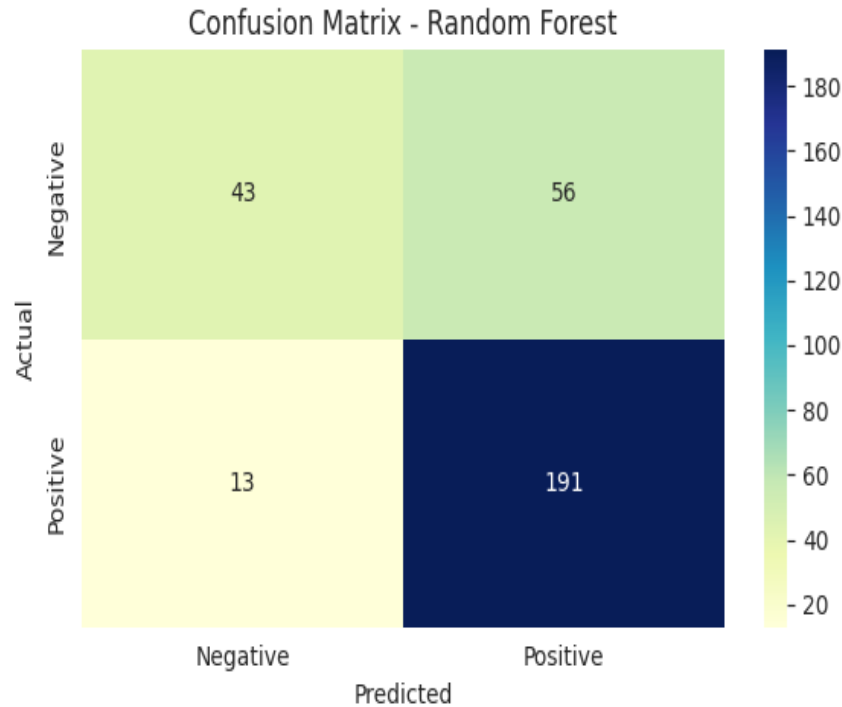


Figure 4.2.9: Confusion Matrix (RF)

191 (true positive) cases and 43 dengue-negative patients were correctly identified (true negative) by the RF model are shown in (Figure 4.2.9). Nevertheless, it falsely predicted 13 positive dengue cases as negative (false negative) and 56 negative dengue patients as positive (false positive). These data demonstrate that despite a loss in specificity (higher false positive rate), the sensitivity of the RF model is excellent, correctly predicting nearly all dengue-positive individuals. Overall, confusion matrix shows that, even though RF model's performance is low for negative prediction, it tends to invest much on the diagnosis of dengue positives (i.e., on the need to forecast the illness).

The ROC curve of RF is available to illustrate the trade-offs between true positive (sensitivity) and false positive rate at various decision thresholds (Figure 4.2.10). This ROC curve is just a plot that can show you really good how much better a model actually separate dengue-positive from dengue-negative than the “conventional standard” of predictive accuracy. The evident positive bend of the RF ROC that further verifies its superior discrimination over simpler classifiers.

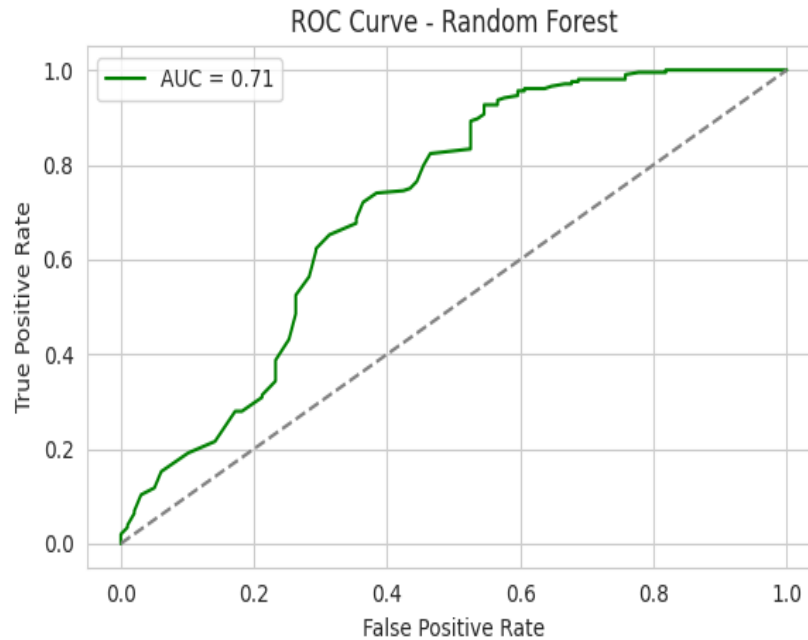


Figure 4.2.10: ROC- Curve (RF)

From Figure 4.2.10, it is clear that the ROC curve of RF model is all reversal hanged above the diagonal line – the reference line, which indicates that the model has better interpreting power than random guess. The AUC value was 0.71, indicating a relatively good discriminatory power to predict dengue cases. This reliable predictive impending value means that the RF model is equally sensitive as specific. The quick steepness of the curve shows that the model is good enough at identifying dengue-positives while at the same time mitigating the number of dengue-negatives falsely classified, still, using the confusion matrix, false positives persist. The performance of the Random Forest classifier is superior to that of several baseline models in this study, as shown in the ROC curve (apparent equal predictive ability).

Support Vector Machine (SVM)

The classification report on precision, recall, and F1-score, and Support Vector Machine (SVM) model is presented in Table 4.2.6 for dengue positives and dengue negatives. Together with this measure, we also provide train and test accuracies for a complete understanding of the model's overall performance and generalizable capacity for new data.

Table 4.2.6: Classification Report for SVM Model

	Accuracy	Precision	Recall	F1-Score	Support
Negative		0.79	0.33	0.47	99
Positive		0.75	0.96	0.84	204
Accuracy				0.75	303
Macro (AVG)		0.77	0.64	0.65	303
Weighted (AVG)		0.76	0.75	0.72	303
Training	0.79				
Testing	0.75				

An overall accounting of the classification performance of the SVM model for the dengue prediction is presented in the confusion matrix displayed in Figure 4.2.11. In addition to the overall accuracy, the confusion matrix gives a more intuitive picture of the capability of the SVM model to differentiate dengue positive from dengue negative cases by presenting true positive, true negative, false positive, and false negative cases.

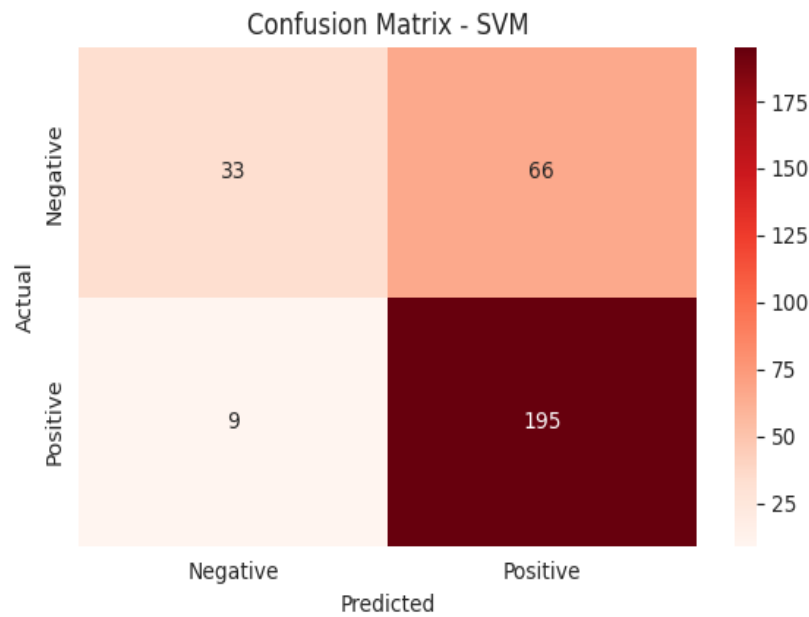


Figure 4.2.11: Confusion Matrix (SVM)

Out of the samples in its entirety, straight 33 cases and 195 dengue-positive patients reported by SVM model were improve All results in Figure 4.2.11. 66 negative cases were

erroneously labeled as positive (false positive) and the converse was the case for 9 positive cases (false negative). According to these results, the SVM model possesses quite poor specificity for the dengue-negative cases, but very good sensitivity for the dengue-positive cases. In order to assess the dependability of SVM classifier for real diagnosis of dengue, we show in the confusion matrix both the global recognition of true dengue patients with the model as well as the local regions where some misclassifications were observed.

The ROC curve of the SVM follows (Figure 4.2.12) indicating the true positive rate against the false positive rate over different cut-off values. The ROC curve is a good method of quantifying the discriminative power of the classifier alongside another measure (the accuracy). A curve that goes close to the top left corner is indicative of a better classification and the diagonal line corresponds to the case of random guessing.

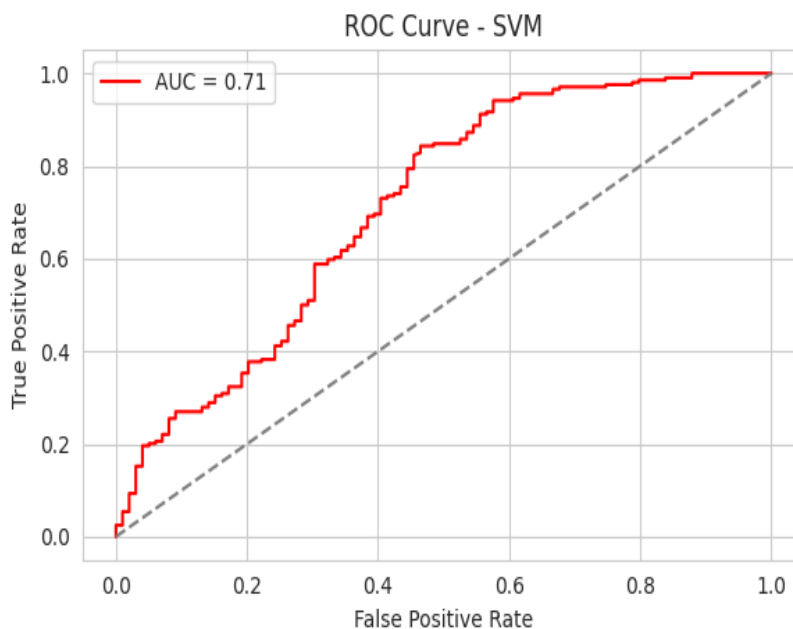


Figure 4.2.12: ROC- Curve (SVM)

The SVM model has a ROC curve (AUC = 0.71), above the diagonal line of equality (Figure 4.2.12). This implies that the (discriminate) of a dengue-positive case and a dengue-negative case using the model is fair. The orientation of the curve at the upper left corner indicates that it has high sensitivity which predicts true positives quite well. Some

specificity albeit with low specificity was, however, indicated by a confusion matrix due to false positives. The ROC curve shows that the classification of SVM model yields a good compromise between sensitivity and specificity for dengue prediction and it is superior to random classification.

Deep Learning Models Outcome

Recurrent Neural Network (RNN)

Table 4.2.7 RNN model classification report showing how well it predicts dengue cases. The report also shows three scores: precision, recall, F1-score, and support, for the dengue-positive and dengue-negative class. This full analysis shows how good the RNN model is at capturing the sequential dependencies in the data and informs us how predictive it is in comparison to other models.

Table 4.2.7: Classification Report for RNN Model

	Accuracy	Precision	Recall	F1-Score	Support
Negative		0.74	0.28	0.41	99
Positive		0.73	0.95	0.83	204
Accuracy				0.73	303
Macro (AVG)		0.73	0.62	0.62	303
Weighted (AVG)		0.73	0.73	0.69	303
Training	0.74				
Testing	0.73				

The confusion matrix of RNN model is listed in Figure 4.2.13 that vividly demonstrates a detailed compilation of classification results for the dengue cases prediction. Besides accuracy which is a generic metric, the confusion matrix also shows true positives, true negatives, false positives, false negatives and hence the ability of the model to discriminate between dengue patients and non-dengue patients. It provides deeper insights into model strengths and weaknesses by revealing exactly where misclassifications occur. Such analysis is essential to understand whether the RNN is more prone to false alarms or missed detections, which directly impacts its clinical reliability.

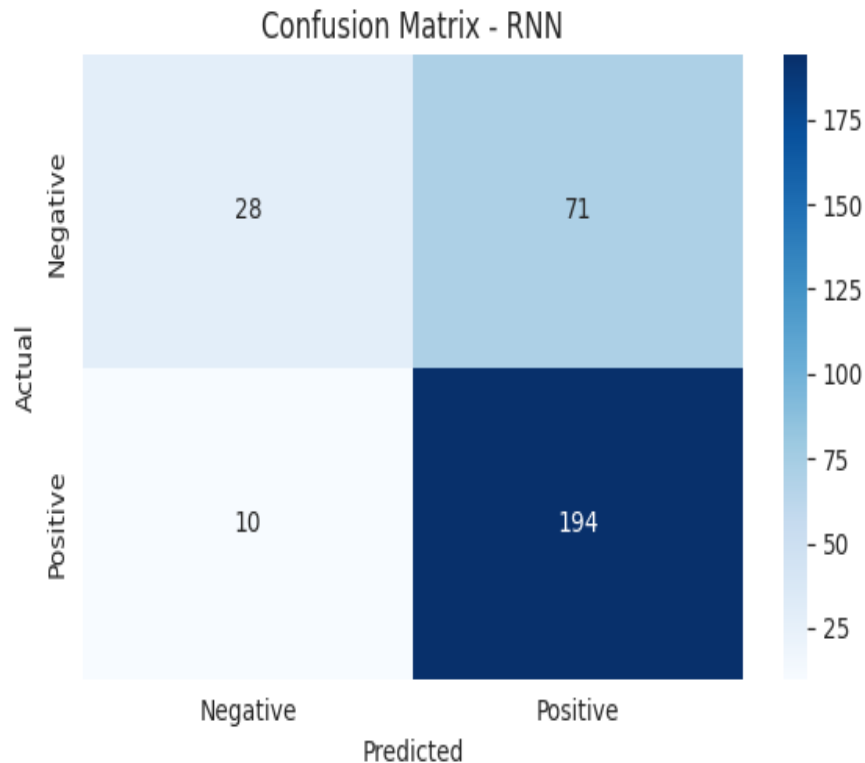


Figure 4.2.13: Confusion Matrix (RNN)

As can be seen from Figure 4.2.13, The RNN model indeed predicted correctly 194 dengue positive case (TP) and 28 dengue negative case (TN). Falsely positive diagnoses were 71 negatives erroneously diagnosed as positive and 10 positives as echocardiographic numbers but diagnosed as negatives (false negatives). A good number (78.7%) of positive dengue patients were successfully identified by the algorithm indicating that the algorithm was highly sensitive for finding individuals who were positive. Some individuals who do not have dengue may wrongly test positive for the disease (false positive- higher false positive rate) i.e, the specificity will be low. Although the proposed RNN model works reliably for finding warm positive dengue cases, it is not so effective at finding cold negatives, as indicated in the confusion matrix. This result demonstrates that sensitivity is dominated by specificity, which could be an advantage in medical testing, for example, because of the worse consequences of failing to detect the positive case. However, additional factors/optimizations/balancing may be achieved for improving the diagnostic reliability, and for reducing false positives.

Figure 4.2.14 displays the ROC Curve and Training History of RNN models for Dengue Prediction. The ROC curve on the right illustrates the trade-off between the true positive and the false positive rates, and the training history chart on the left shows the accuracy and loss of model on training and validation dataset of several epochs. Taken together, these images paint a comprehensive picture of the categorization performance and learning dynamics of the RNN.

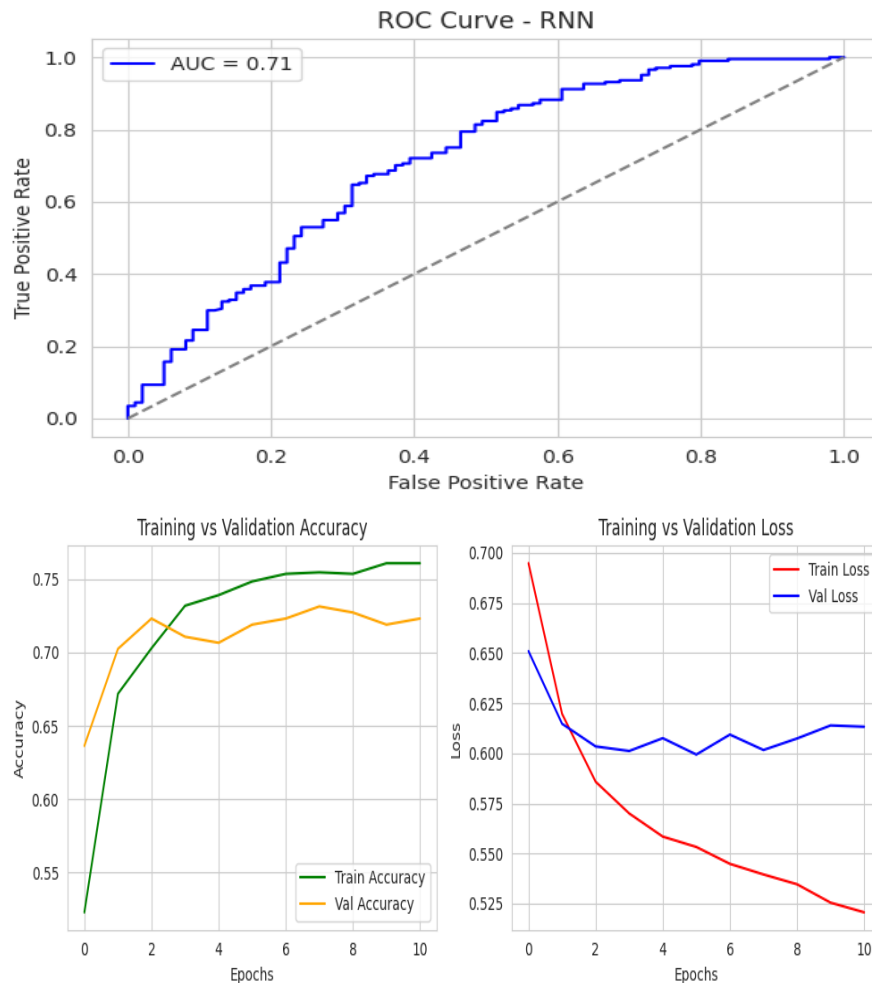


Figure 4.2.14: ROC- Curve and Training History (RNN)

A more detailed examination of the RNN model classification was also quantified in Figure 4.2.14 (up) through ROC curve. The model has a good AUC above-the-diagonal (AUC = 0.71), indicating that it is better than just random guessing. The curve is a clear bimodal with very strong sensitivity to dengue (with some limits to specificity). Overall, the ROC

curve provides evidences to the conclusion that the RNN presents a relatively good but fair discriminative performance on dengue prediction.

The histories to model performance and its association will be presented in the plot of training (Figure 4.2.14 down). The above model was generalizing pretty well albeit with a slight overfit and the training accuracy slowly rose up and eventually converged around the 0.76, while the validation accuracy hovered around 0.72–0.74. This value also converge at validation loss 0.60, then, the learning process is closed by the model and the training loss is slowly decreased over the epochs.

Dense Neural Network (DNN)

The classification report of the DNN model for dengue case prediction is presented in Table 4.2.8. Besides macro and weighted average, the table presents key statistics for both dengue-positive and dengue-negative close, precision, recall, f1-score, and accuracy. Generalization of the model to new data can be seen from the training and testing accuracies. This extensive review offers important perspective on the trade-off capacity of the DNN to provide a balance between sensitivity vs. specificity dengue discrimination characteristics.

Table 4.2.8: Classification Report for DNN Model

	Accuracy	Precision	Recall	F1-Score	Support
Negative		0.79	0.33	0.47	99
Positive		0.75	0.96	0.84	204
Accuracy				0.75	303
Macro (AVG)		0.77	0.64	0.65	303
Weighted (AVG)		0.76	0.75	0.72	303
Training	0.77				
Testing	0.76				

Figure 4.2.15 This is the confusion matrix of Deep Neural Network with the True Positive, True Negative, False positive, False negative Dengue prediction of DNN model. Such a

matrix offers an intuitive interpretation of how DNN categorizes and emphasizes its advantages and disadvantages in detecting true and false cases.

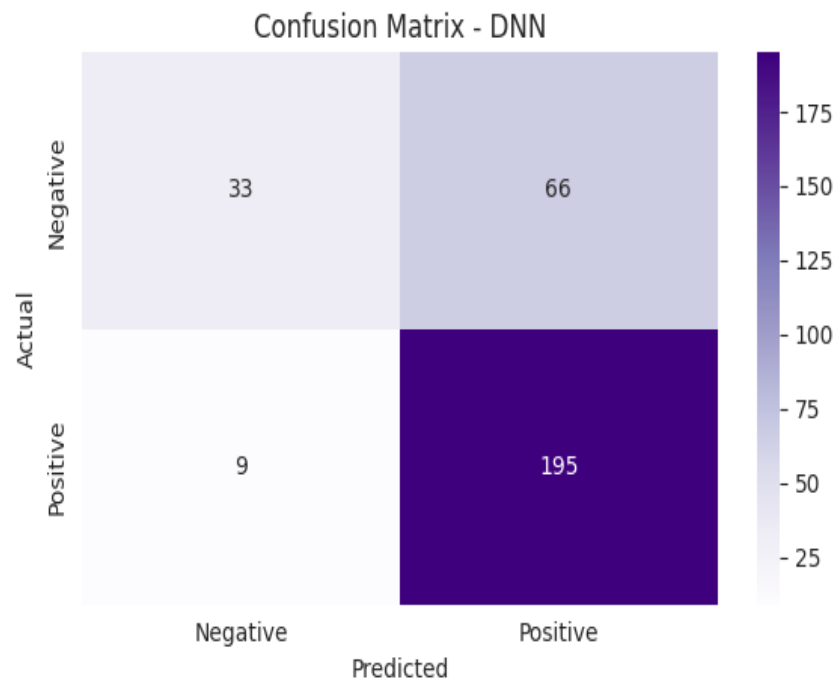


Figure 4.2.15: Confusion Matrix (DNN)

The DNN model calculated for 33 dengue-negative (true negatives) cases and for 195 dengue-positive patients (true positives) as shown in Figure 4.2.15. But there were just nine positive cases erroneously classified as negative (false negatives) and 66 negative cases that were falsely classified as positive (false positives). As these results demonstrate, DES-FDN-A has good sensitivity and will be able to identify most of effective Dengue+ individuals in medical diagnosis. But the high proportion of false positive also indicates a low specificity, preferring some non-dengue patients. By and large, the confusion matrix analysis indicates that the DNN model tends to focus on capturing dengue-positive cases at the expense of some mis-classification on the negative ones.

Relationship of parameters and dengue outcome the training history and ROC curve of DNN model for predicting dengue outcome are presented in Figure 4.2.17. The discriminatory performance of the model is expressed by true positive rate versus false

positive rate in the right ROC curve. And on the left, we see the model accuracy and loss over epochs for training and validation set in the training history plot. As a whole, just hope that this illustration helps the reader develop an intuition about the learning and predictive capacity of DNN.

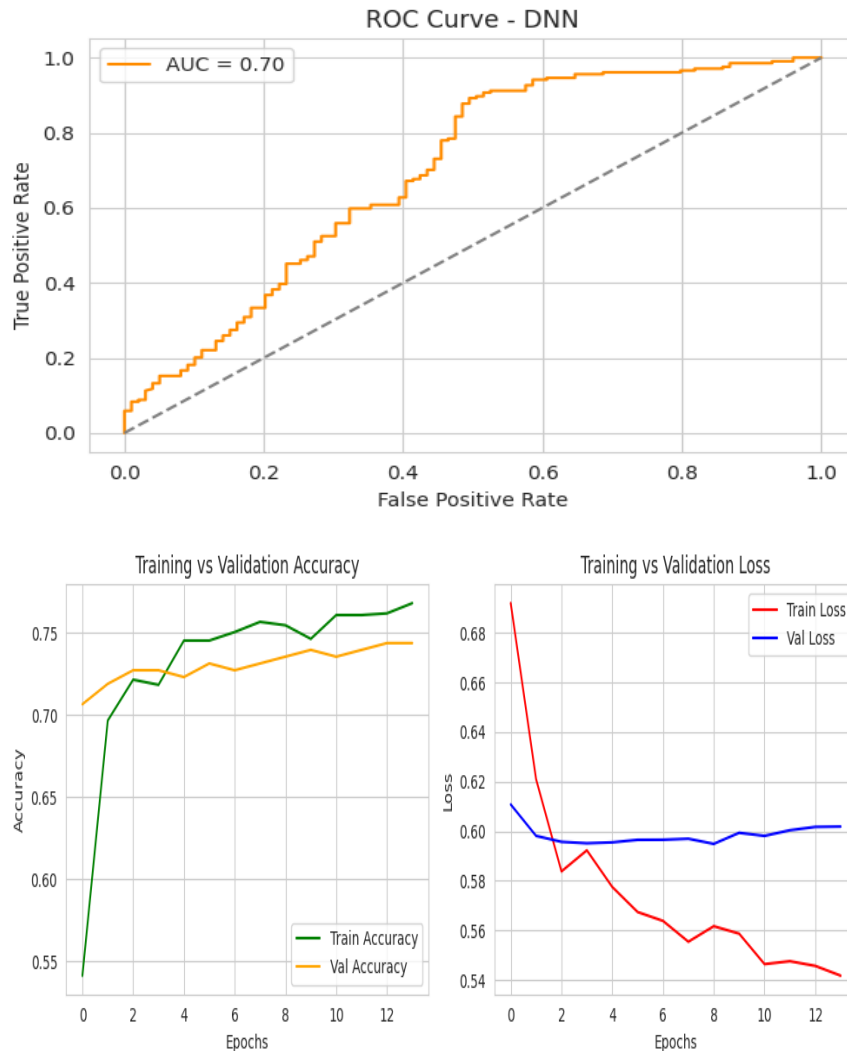


Figure 4.2.16: ROC- Curve and Training History (DNN)

As can be observed from the ROC Curve (up) of only Figure 4.2.16, the DNN is only marginally successful to distinguish between dengue-positive and dengue-negative cases with an AUC of 0.70. The less diagonal of DNN compared to random with reliable sensitivity but decreased specificity demonstrates that DNN is better than guessing the

random. The DNN demonstrates mainly a relatively smooth learning curves and high power of dengue predictive classification.

The validation accuracy stays in 0.72–0.74 range, and the training accuracy keeps increasing to settle at 0.77 in the training history plot in Figure 4.2.16 (below), indicating that the model has the ability to generalize without seeing a severe overfitting. This is a good sign of a converging model as you see the validation loss flatten out around 0.58-0.60 while the training loss is falling with epochs.

Feedforward Neural Network (FNN)

The classification report of referring to dengue prediction with FNN model is shown in Table 4.2.9. For each dengue positive and dengue negative case, precision, recall, F1-score and support are provided for the multi-label learning case for each class, while overall accuracy, weighted average and macro averages are given. Training and testing accuracies are also presented in Table for generalization comparison. All of these numbers combined are a powerful demonstration for the FNN's capability of modeling non-linear feature interactions, but also robustness regarding the trade-off between sensitivity and specificity, and consistency across the train–test split.

Table 4.2.9: Classification Report for FNN Model

	Accuracy	Precision	Recall	F1-Score	Support
Negative		0.75	0.36	0.49	99
Positive		0.75	0.94	0.84	204
Accuracy				0.75	303
Macro (AVG)		0.75	0.65	0.66	303
Weighted (AVG)		0.75	0.75	0.72	303
Training	0.75				
Testing	0.75				

The confusion matrix for dengue prediction with FNN model is also shown in Figure 4.2.17. The confusion matrix offers a nice visualization for the percentage of examples that are correctly/incorrectly classified into the positive/negative class to give an overall

classification birds-eye view of the model. This is a bit more information to the confusion matrix: it shows the model's strength and weakness in separating dengue positive cases from non-positive cases.

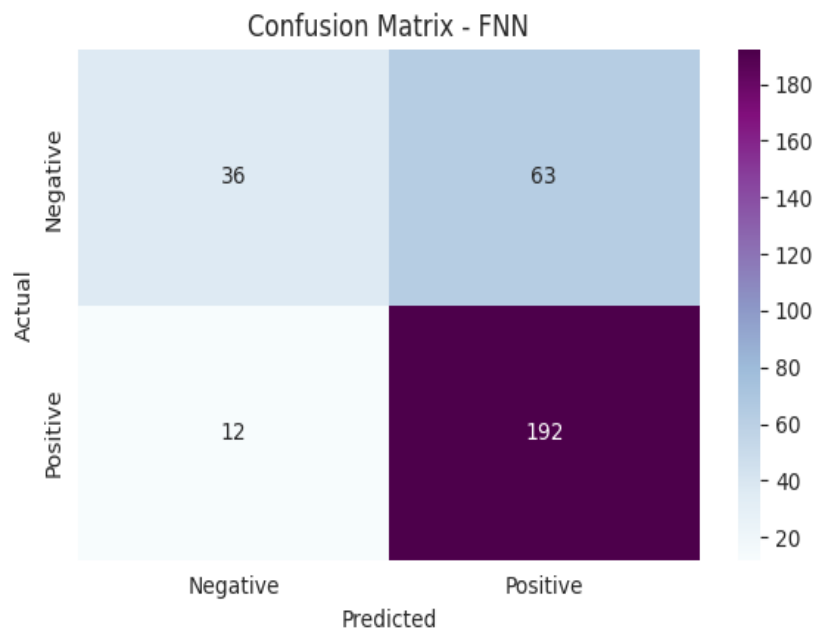


Figure 4.2.17: Confusion Matrix (FNN)

As can be seen in Figure 4.2.17, there were 12 positive samples that were incorrectly classified as negative (false negatives) when fitted by the FNN model, 63 negative samples that were incorrectly classified as positive (false positives), 192 positive and 36 negative samples were correctly classified. The large number of true positives suggests that model has good predictive capability for dengue-positives, despite that is far from flawless in discriminating negatives. The sensitivity for the dengue detection is highlighted by the FNN model, which is essential in an early diagnosis and prevention, also from the overall confusion matrix.

The dengue ROC and historical training are shown in Figure 4.2.18 for the FNN model. Left: Training/testing accuracy/loss history plot of epochs; Right: The ROC curves of the TPR and FPR. In general, these examples present a full exhibition on the learning and classifying performance of the FNN. By looking at the ROC curve, a trade-off between

sensitivity and specificity can be observed which is necessary to use in accessing the performance of the model. In addition, the training history can be utilized for detection of over fitting or under fitting, which is useful in the process of model optimization and improvement.

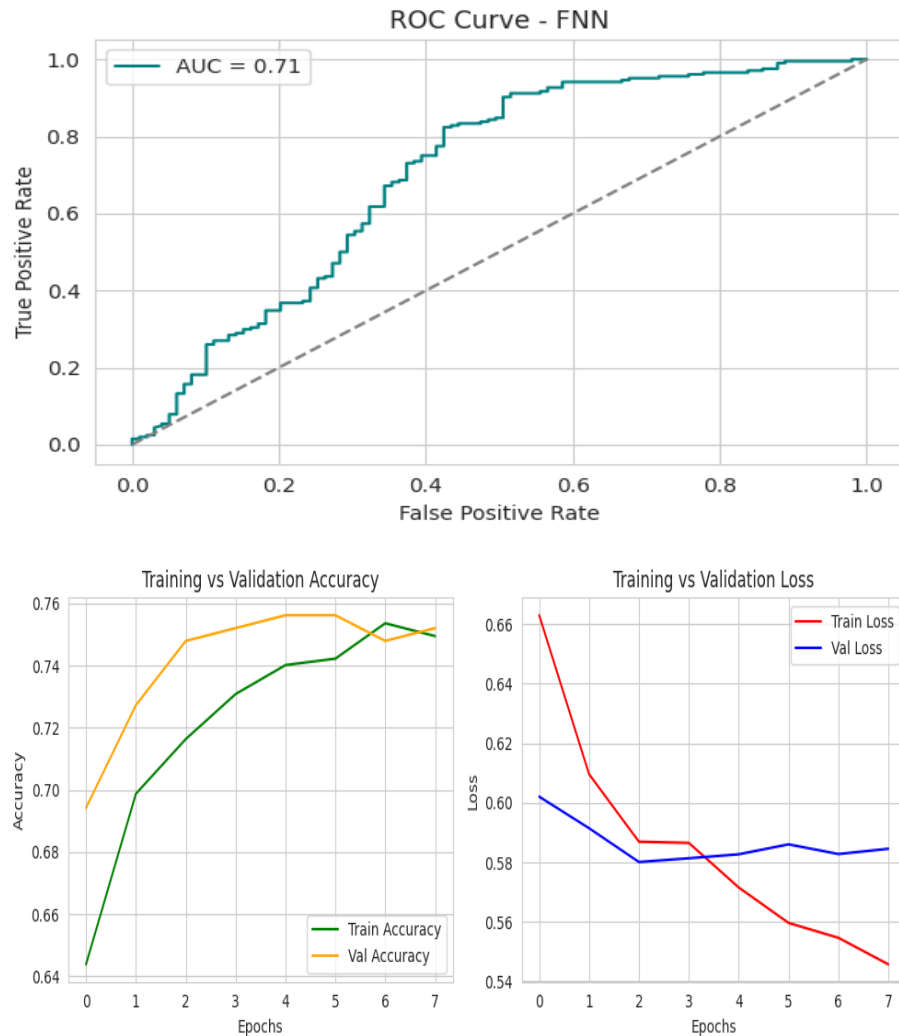


Figure: 4.2.18: ROC- Curve and Training History (FNN)

The classification performance of the FNN model is visualized by using a ROC curve in Figure 4.2.18 (below). 54 Performance of the Model 55 The high AUC value above diagonal reference line of 0.71 means that the model is performing better than the random guess. Sensitivity is high for now although specificity is low, the curve indicates that the

relative specificity will be high in detecting dengue positive cases. The relative equity of this FNN in discriminating within the dengue is also summarized in the total ROC curve.

The training history (below) is the graph of epochs versus performance; in Figure 4.2.18. The acc of validation remained around 0.74 and 0.76 and the acc of train was in the middle of the both and isn't increased after and almost the same as acc validation, it means that this model wasn't overfit. Similarly, over epochs, the training loss is steadily decreasing and the validation loss gradually staggers to a range between 0.58 and 0.60, suggesting that learning and generalization activities are managed efficiently.

Long Short- Term Memory (LSTM)

The classification report of the LSTM model for dengue prediction is illustrated in Table 4.2.10. Table presents a detailed view of the model's performance in detecting the dengue cases by improving the significant performance indicators like precision, recall, F1-score, and the support result for each class. Reporting training and testing accuracy also gives a hint of how well the LSTM model learned the dependencies present in the sequence and how well it generalized to the rest of the data that it never saw during training.

Table 4.2.10: Classification Report for LSTM Model

	Accuracy	Precision	Recall	F1-Score	Support
Negative		0.77	0.34	0.48	99
Positive		0.75	0.95	0.84	204
Accuracy				0.75	303
Macro (AVG)		0.76	0.65	0.66	303
Weighted (AVG)		0.76	0.75	0.72	303
Training	0.75				
Testing	0.75				

The confusion matrix plot of dengue prediction using LSTM is shown in Figure 4.2.19 which reflects the performance of classification. This matrix is a depiction of the true positives/negatives and the false positives/negatives. This nicely demonstrates how the model is able to pick up the dengue positive cases more effectively than the negative cases.

In addition to aggregate accuracy, this summary helps to understand the bias in the diagnostic potential of the LSTM model. It also identifies areas in which the model may categorize cases incorrectly, which could guide additional model development. The matrix can also help to navigate threshold settings and other tools to optimize the trade-off between sensitivity and specificity.

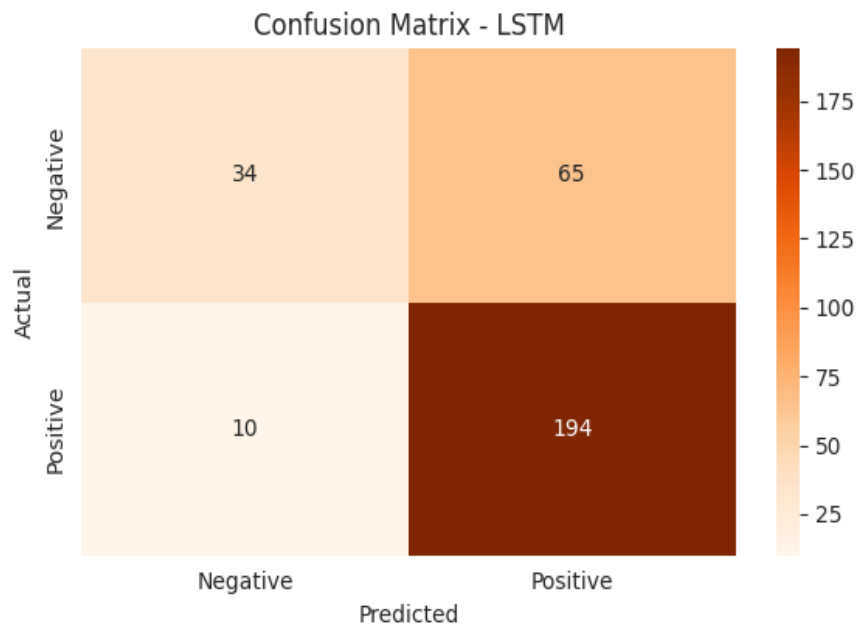


Figure 4.2.19: Confusion Matrix (LSTM)

Figure 4.2.19 According to Figure 4.2.19, the LSTM was able to correctly identify 34 non-dengue cases (true negatives) & 194 dengue cases (true positives). The false positive rate, 65 dengue-negative patients were misclassified as positive and the false negative rate, 10 dengue-positive patients wrongly classified as negative. The model captures the majority of the individuals who are dengue positive, indicating the model is highly sensitive, an important characteristic for early warning of disease in these results. More non-dengue cases will thus incorrectly be classified as positive, because when more true negatives become false positives, there is necessarily a reduction in the specificity. Lastly, the confusion matrix shows the hypothesis that the LSTM model is mistakenly incorporating some of the negative examples in the misclassification and is attracting some of the dengue positive cases.

The training process and ROC curve of the dengue prediction by the LSTM is shown in Figure. 4.2.20. Although the rightmost chart — an ROC curve — shows the pay-off between the true positive binary classification and the false positive rate, the loss and accuracy plots are the most interesting, since they show how well/poorly the accuracy and loss fluctuations over the number of epochs across both the training and validation set. Collectively, these figures present a comprehensive view over the learning dynamics and classification performance of the LSTM.

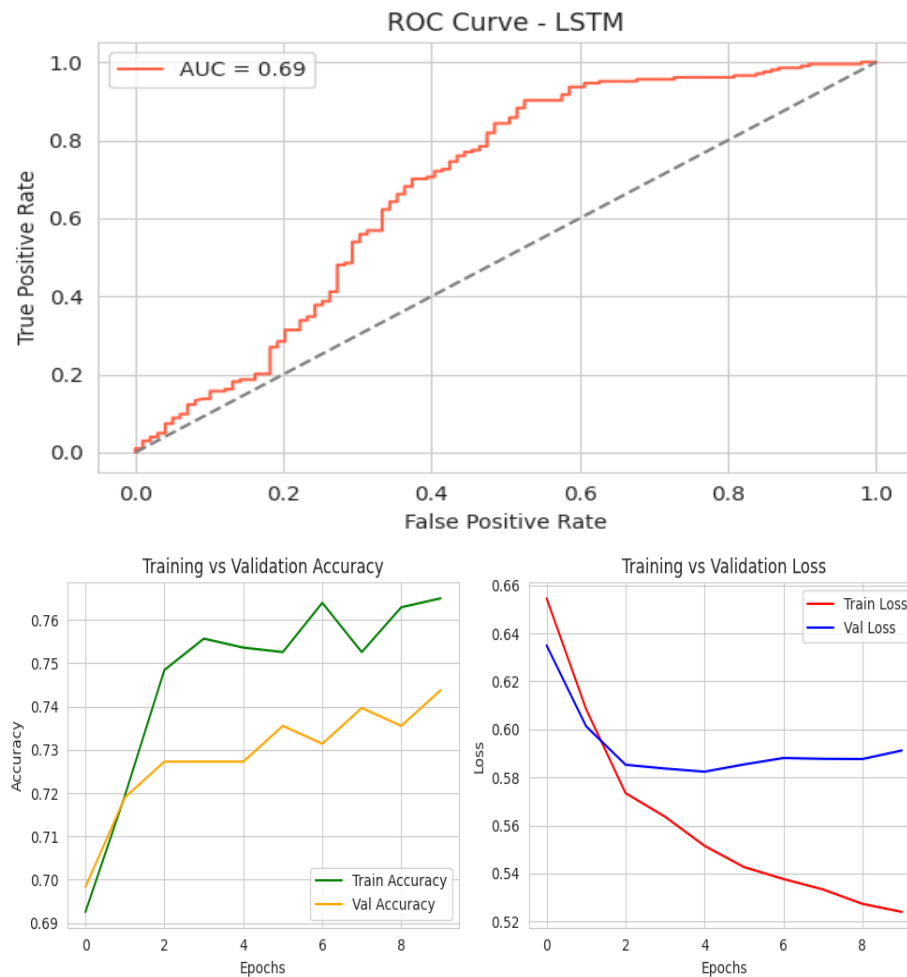


Figure 4.2.20: ROC- Curve and Training History (LSTM)

The ROC curve above (See Figure 4.2.20) shows the summary of the over-all classification performance of the LSTM model. It has a low Area Under the Curve (AUC) value (0.69), which equals random guess. Although specificity is still low, the shape of the curve shows

massive sensitivity to discriminate dengue positives, indicating the fine functioning of our LSTM in marking the true-positives as high priority for early detection purpose.

Complicating the even more picture between epochs and model performance is that there is a history of training that we can visualize with plot training history (below, see Figure 4.2.20). This is sign that the model did generalize quite well, without it being over-fitted to an unreasonable extent. The training Data's accuracy don't even taper off, and was ≈ 0.77 , capping off at around 74% for the test portion. Furthermore, the validation loss decreased a lot first then kind of flatten at $\sim 0.58-0.59$, and the training loss decreased as well over the epochs which let us know that the model learnt quite well.

4.3 Discussion

Table 4.3 displays the recapitulates relative performances of several machine learning and deep learning models for dengue prediction. Using hematological and clinical data, it is shown that there are system-dependent significant differences in the efficacy of classification of these algorithms and potential vulnerabilities of each approach are demonstrated.

Table 4.3: Analysis of Classification Result (ML/DL Models)

Model	Accuracy	Precision (Avg)	Recall (Avg)	F1-Score (Avg)	AUC
KNN	62%	0.59	0.62	0.60	0.55
NB	73%	0.74	0.73	0.68	0.66
DT	70%	0.70	0.70	0.70	0.65
LR	73%	0.73	0.73	0.69	0.65
RF	77%	0.77	0.77	0.75	0.71
SVM	75%	0.76	0.75	0.72	0.71
RNN	73%	0.73	0.73	0.69	0.71
DNN	75%	0.76	0.75	0.72	0.70
FNN	75%	0.75	0.75	0.72	0.71
LSTM	75%	0.76	0.75	0.72	0.69

The Random Forest (RF) classification had the accuracy, precision, recall, F-1 score, and AUC values of 77%, 0.77, 0.77, 0.75, and 0.71 points, respectively, better than those of the

others. This superior performance is attributed to its ensemble learning approach where multiple decision trees are aggregated through a bagging. RF also enhances generalization, reduces overfitting, and decreases variance by voting predictions of a number of weak learners. RF performed better in this study than single ML models as well as DL architectures due to its resistance. The four models SVM, DNN, FNN, and LSTM achieved 75% accuracy around RF with a balanced columns_precision_recall_F1_scores were in the range 0.72–0.76. These observations suggest that deep learning methods and traditional machine learning models are in a competitive position for predicting dengue. The DNN and LSTM exploited the sequential dependencies and nonlinear feature representations for classification improvement, while the SVM achieved good performance mainly due to its ability to maximize class separation in the high-dimensional feature space. But as these models were employed individually rather than in teams, they may have had limited predictive power. On the other hand, the KNN model had the worst performance, in which AUC and precision were 0.55 and 0.59, respectively, and the accuracy was only 62%. This is why the curse of dimensionality, overlapping clinical features, and KNN's sensitivity to noisy input often negatively affect the reliability of the networks in medical prediction tasks. Likewise, the 70% accurate DT model was also overfitting that is common for use with small or imbalances datasets. The NB and LR models had moderate consistency at the 73% accuracy. Their relatively balanced metrics indicate the good generalization ability, albeit inferior to the best one. In situations where speed, interpretability, and computational efficiency are valued over fine-tuning of forecast accuracy, such models remain attractive candidates.

The results as a whole show that, by averaging many learners for better stability and accuracy, ensemble learning methods like Random Forest have a competitive advantage in dengue detection. The deep learning methods were competitive as well. however, they were less superior due to the lack of ensemble. Additional work might consider hybrid ensemble methods combining machine learning and deep learning classifiers to improve the prediction quality as reflected in the close difference of RF and the best deep learning models. Importantly, Random Forest is the best predictor model of dengue, being both robust and achieving high accuracy.

The Random Forest model features importance analysis, for dengue prediction is shown in Figure 4.3. The contribution of individual clinical and haematological characteristics to the likelihood of having or not having of dengue is apparent in the figure. By prioritizing these features based on their predictive importance, the visualization presents to the observer an indication of what factors most heavily affect how the data points are being classified.

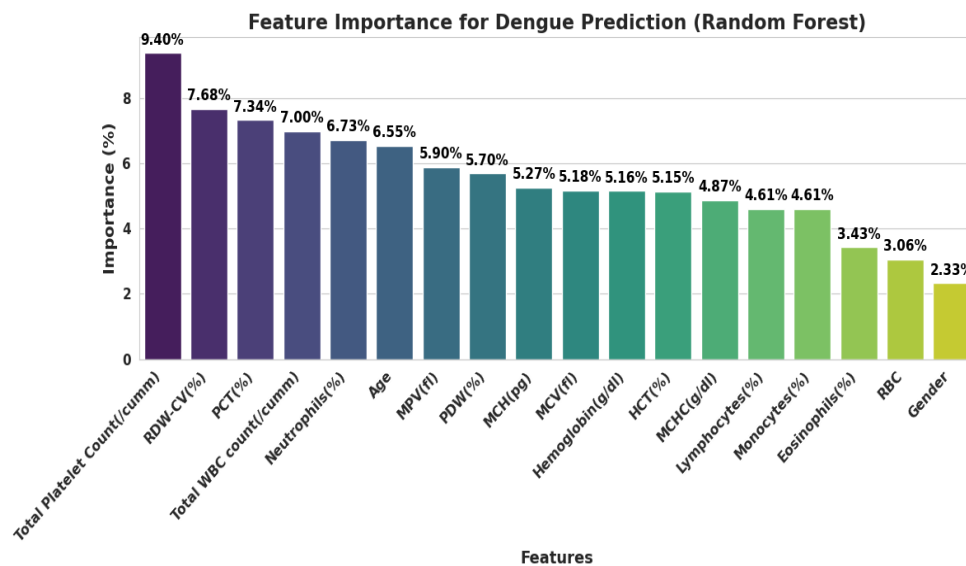


Figure 4.3: Feature Importance for Proposed Model (RF)

Total Platelet Count became the most important predictor with a contribution of 9.40% (Figure 4.3) which is also inline to the clinical understanding that decrease in platelet count is one of the major indicators of dengue infection. Other very significant variables emerged as well that can be used as critical hematological parameters related to the progression of the disease, such as RDW-CV (7.68%) which appeared retained, PCT (7.34%) (included) and Total WBC count (7.00%) (included). Features like Neutrophils (6.73%), Age (6.55%), MPV (5.90%), PDW (5.70%) were shown to have moderate importance in predictions. However, Gender (2.33%) and RBC (3.06%) contributed least to the model, suggesting that these features exerted relatively less influence in the classification of dengue.

Overall, the analysis shows that blood-related parameters, particularly platelet and WBC indices, are crucial predictors for the accurate dengue forecast through the Random Forest method.

CHAPTER 5

Society, Environment, and Sustainability Implications

5.1 Impact on Society

The proposed model of forecast dengue has vital social implications, particularly in health promotion. The occurrence of dengue can be forecast in a timely manner and accurately, providing policymakers and health workers an opportunity to enhance their response using the advanced warning period for disease surveillance, resource allocation, and implementation of prevention activities. This instantly helps contain outbreaks of dengue, cuts down on hospitalizations, and ultimately, saves lives. In addition, the framework strengthens local RO communities by increasing knowledge of risk factors and enabling focused interventions in high-risk areas. Machine learning and deep learning models could potentially firm up healthcare decision-making, improve patient outcomes and increase trust in technology based solutions for the public.

5.2 Impact on Environment

While the framework itself does not directly impact natural ecosystems, it has a major indirect environmental footprint. Damage to nature as with chemical spraying is not anymore, a problem then with the regional level, if the dengue is foreseen and handled well. The technology enables eco-friendlier and sustainable measures for controlling diseases as it now allows proactive management approach to dengue instead of a reactive one. Further, through its emphasis on evidence-based approaches that leverage available resources and minimize unnecessary interventions, the framework also minimizes ecosystem disturbance.

5.3 Ethical Aspects

The practical ethical implications of AI in healthcare are highly sensitive. Privacy and discretion are critical as patient medical records are accessed. And also, an ethical utilizing of the proposed model is needed by complying with the data privacy regulations and

applying right procedures for the processing and storage of data. The fairness and bias of the model should also be examined, because the case of misclassification rate might be larger for the disadvantaged group. It also depends on the predictability of the forecasts and on the transparency of the model judgements for maintaining the trust of patients, healthcare workers and policy makers.

5.4 Sustainability Plan

The developed framework's adaptability, scalability, and ability to be incorporated into existing healthcare infrastructures is crucial to its sustainability. In addition to daily retraining to avoid prediction failures, long term performance requires prediction accuracy to be preserved. Government offices, providers and academic institutions will further support sustainable implementation together. The system should have not only the infrastructure for user-training and community-awareness programs, but should also be cost-effective to deploy. Open-source development and cloud-based deployment may additionally enhance accessibility, making the framework applicable to low-resource settings. The sustainability strategy aims to build and sustain an equitable, self-renewing, and ethical dengue control program.

CHAPTER 6

Summary, Conclusions, Recommendations and Suggestion for Further Studies

6.1 Summary of the Study

Hematological and clinical parameters were utilized for the construction and assess the machine and deep learning tool for prediction of dengue patients. For model validation, 1,523 patients were encoded, scaled and balanced in a dataset. This study, there are used and analyzed a few algorithms like Decision Tree, Naive Bayes, K-Nearest Neighbor, Support Vector Machine, Random Forest, Logistic Regression, RNN: recurrent neural network, DNN: dense neural network, FNN: feedforward neural network and LSTM: long short-term Memory. Results Random Forest 77%, then by SVM and deep learning models 75%, based on experimental evidence outcomes.

6.2 Conclusion

The present study was successful in generating a prediction model that may classify dengue cases reasonably. The experimental results show how ensemble models, and specifically Random Forest, outperform isolated machine and deep learning techniques, in terms of robustness and generalization. Simpler models like Naive Bayes and Logistic Regression are however useful alternatives while interpretability and computational efficiency are the most important factors of consideration, even though they are less accurate. The study demonstrates the need for adoption of cutting-edge computational tools in health decision-making in order to positively impact the patient treatment and disease surveillance, epidemiological analysis, and outbreak control. Second, the results suggest that further improving disease prediction performance and reliability could be achieved by integrating hybrid methods or the fusion of multiple models. Overall, the research is illustrative of the utility of machine learning and deep learning techniques in helping to support proactive, evidence-based public health management strategies. The Random Forest model perform better than others model.

6.3 Recommendation

- **Implementation in Health Systems:** Machine learning-based dengue prediction models can be embedded in routine diagnostic practice to aid timely clinical decisions.
- **Government and Policy Support:** Public health authorities should spend money on AI-based surveillance systems to optimize resource allocation and improve epidemic preparedness.
- **Data Encouragement and Sharing:** Researchers and institutions are encouraged to promote larger, more diverse datasets by supplementing with clinical, demographic, and environmental information to enable trusting models.
- **Model Interpretability:** Despite the effectiveness of complex models, simpler, more interpretable tools should be considered for frontline healthcare applications in which interpretability is paramount.
- **Build Capacity:** Predictive systems will be accepted and utilized if public health and health care professionals have training in AI methodologies.
- **Sustainable Implementation:** Deployment plans need to prioritise scale, affordability and ethical use to equally benefit communities.

6.4 Implication for Further Study

Although the proposed framework gave promising results, there are several issues that need to be further studied:

- **Larger and more diverse data:** Model generalization will be improved by integration of real-time as well as multi-geographic data.
- **Build up hybrid ensemble models:** Hybrid ensemble strategies Cross-fusing deep learning and machine learning models could offer way better predictive ability.
- **Explainable AI (XAI):** For future work, we need more focus on interpretability to ensure doctors can understand and trust in predictions.
- **Linking to IOT and GIS platforms:** Linking predictions to climate, environmental and spatial data could enhance predictions of an outbreak.

- **Mobile and cloud deployment:** Developing low power applications can allow benefits of dengue prediction systems to reach the low resource and remote regions.

Overall, this study lays a sound groundwork for healthcare systems based on AI, and besides future endeavour may improve public health, support sustainable disease control, and contribute to readiness for global pandemic prevention.

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