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PREDICTION OF DENGUE CASES AND DEATHS USING MACHINE LEARNING ALGORITHM

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ABSTRACT: This study presents a comprehensive analysis of machine learning algorithms in predicting Dengue deaths and cases using a dataset containing monthly records of Dengue occurrences per region in the Philippines from 2016 to 2020. The metadata, encompassing temporal and regional attributes, facilitates a nuanced exploration of Dengue dynamics, answering critical questions about peak months, regions with the highest average cases, and overall trends. The application of these predictive models holds significance in public health, offering insights for targeted interventions and resource allocation. The study employs various machine learning algorithms, including Random Forest, Random Tree, Linear Regression, MLP, and SVM Regression, and evaluates their performance using metrics such as correlation coefficients and error measures. Overall, SVM regression performs better and obtained 0.49 correlation coefficient score for the prediction of deaths due to dengue. In dengue disease prediction SVM regression performs better as it achieves highest scores in three evaluation measures. The dataset's richness and the chosen algorithms collectively form a powerful toolkit for understanding and responding to the complex dynamics of Dengue disease, showcasing the practical application of machine learning in addressing public health challenges.

***Index Terms*—**Dengue Disease Prediction, Machine Learning, SVM regression, Death Prediction.

I. INTRODUCTION

In the dynamic landscape of global health, infectious diseases continue to pose formidable challenges, demanding innovative approaches for effective management and prevention. Among these, Dengue fever stands out as a significant public health concern [1][2], with its prevalence expanding across regions with favorable climatic conditions for the Aedes mosquito vector [3][4]. As scientists grapple with the complexities of controlling Dengue outbreaks, the integration of cutting-edge technologies [5], particularly machine learning [6][7], emerges as a beacon of hope in fortifying human's defense against this relentless adversary.

This article delves into the realm of predictive analytics, harnessing the power of machine learning algorithms to forecast Dengue cases and fatalities [8] [9]. Traditional epidemiological models have played a crucial role in understanding the dynamics of Dengue transmission [10] [11], but the advent of advanced data science techniques opens new frontiers in enhancing our predictive capabilities. By leveraging vast datasets encompassing environmental, demographic, and epidemiological variables, this study embark on a journey to develop robust models capable of anticipating Dengue outbreaks and associated mortality rates [12].

As this study navigate to predict Dengue incidence, this article will scrutinize the pivotal role of machine learning in not only predicting the occurrence of Dengue cases but also forecasting the potential severity of outbreaks, providing valuable insights for public health practitioners, policymakers, and healthcare professionals. The integration of these predictive models into existing surveillance systems holds the promise of a proactive and targeted response, enabling timely allocation of resources and implementation of preventive measures to mitigate the impact of Dengue on vulnerable populations.

Dengue is a severe epidemic in several countries and it boost in specific months and regions of almost 129 countries for example Bangladesh, Brazil, Burkina Faso, Fiji, Pakistan, the Philippines, and Viet Nam according to WHO[1]. This study focus on a dataset[2] collected from Philippines seventeen regions from year 2016 to 2020. While efforts have been made to predict Dengue incidence, there remains a significant gap in our ability to forecast mortality rates accurately. Understanding the factors influencing Dengue-related deaths is crucial for prioritizing healthcare resources and implementing targeted interventions [13].

The application of machine learning algorithms in predicting Dengue cases and deaths holds transformative potential for enhancing the effectiveness of public health interventions [10]. By harnessing the power of advanced data analytics, these models offer a range of applications aimed at mitigating the impact of Dengue fever [7]. There are key areas where the

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[1] https://www.who.int/emergencies/disease-outbreak-news/item/2023-DON498

[2] https://www.kaggle.com/datasets/vincentgupo/dengue-cases-in-the-philippines/data

integration of predictive models can bring about significant improvements for example early warning system, resource allocation, targeted interventions, and severity of forecasting, adaptive response, and public health planning [9].

There are several researchers tried to address the problem of Prediction of Dengue Cases and Deaths by time series analysis, correlation studies, epidemiological models, spatial analysis, clinical and laboratory analysis. This study specifically address this problem by using machine learning techniques including Random Forest, Random Tree, Linear Regression, MLP (Multi-Layer Perceptron), and SVM Regression on the dataset of total 1,020 instances.

In conclusion, the problem addressed by this study is determining the most effective machine learning algorithm for predicting dengue cases and deaths caused by the dengue virus that aims to provide timely treatment for patients. It identifies Support Vector Machine (SVM) and Linear Regression as the best approaches to tackle this problem. Also, this study not only contributes to predictive modeling for Dengue outcomes but also demonstrates the practical application of machine learning in addressing public health challenges. The dataset's richness and the chosen algorithms collectively form a powerful toolkit for understanding, predicting, and responding to the complex dynamics of Dengue disease in the Philippines.

II. RELATED WORK

The related work section of the study aims to contextualize and review existing research on the prediction of Dengue disease occurrences, particularly focusing on machine learning applications and spatiotemporal analyses. Numerous studies have delved into the use of predictive models for understanding and forecasting Dengue outbreaks, leveraging diverse datasets and methodologies.

In 2023 a research study focuses on predicting dengue fever cases in Malaysia using machine learning, employing various LSTM models [14]. Utilizing a dataset spanning 2010 to 2016, including climate, geography, and demographics of five states. This dataset is provided by Malaysia Open Data website. In this study six LSTM models were developed and compared. The LSTM with spatial attention (SA-LSTM) model, demonstrated superior performance with an average RMSE of 3.17 across all lookback periods. This model uses eight layers including input layer, batch normalization, LSTM, spatial dropout, spatial attention, dropout, dense and prediction layer. In comparison to benchmark models (SVM, DT, ANN), it exhibited significantly lower RMSE. Spatial attention models generally outperformed temporal ones, and the SSA-LSTM model excelled across different states and prediction horizons, affirming its efficacy in dengue prediction in Malaysia.

Another study presented by [15] addresses the challenge of predicting dengue fever caused by Aedes mosquito-borne dengue viruses, a significant public health concern with an increasing global incidence. Dengue hemorrhagic fever, a severe form, can lead to dengue shock syndrome, posing fatal risks. Early and accurate differentiation of dengue and its subcategories is crucial for providing timely care. Predicting infectious diseases like dengue is challenging, and existing forecast systems are in early stages. This study uses a dataset consists of 1872 instances in which 1456 used in training and 416 in testing. The study proposes the construction of a machine learning method for forecasting dengue fever, utilizing data from microarrays and RNA-Seq. By using Random Forest they achieve 8.72 mean score. This approach aims to enhance predictive accuracy and facilitate early diagnosis, potentially saving lives by enabling timely intervention.

Another effort done by [16] in 2022 to address the problem of dengue risk assessment. This study proposed a dataset of 312 instances given on the website (União CGU 2021). Machine learning techniques, including logistic regressions, linear discriminant analyses, Naive Bayes, decision tree, and random forest classifiers, to assess dengue fever risk. Focused on the municipality of São Luís do Maranhão, Brazil, the models use oversampling techniques due to the region's smaller size. Utilizing data on dengue cases, climatic factors, and environmental variables from 2014 to 2020, the DBSMOTE-trained Random Forest classifier yields the best results, achieving a 75.1% AUC, 75.43% sensitivity, and 60.53% specificity. The approach aims to create effective public health policies based on localized mathematical models for disease prevention.

Another study investigates the progression of severe dengue, aiming to predict and prevent shock development in patients using machine learning [17]. The proposed dataset consisted on 170 instances in which 70% used in training and 30% used in testing. Patient data from a medical center is analyzed, and various algorithms, including logistic regression, decision trees, support vector machines, and neural networks, are assessed for predictive performance. Ensemble learning techniques like bagging and boosting are applied to enhance results. The bagging algorithm emerges as the most effective, showing a 14.5% improvement over individual decision trees. Actually bagging is an ensemble learning method which is specifically used in noisy dataset. Notably, day 2 hemoglobin levels in the full blood count (FBC) are identified as a robust predictor for severe dengue occurrence. These findings contribute to early detection and treatment strategies for severe dengue infections, enhancing patient outcomes.

A study focuses on predicting Dengue fever cases in 11 districts of Bangladesh using machine learning models, namely Multiple Linear Regression (MLR) and Support Vector Regression (SVR) [18]. The DengueBD dataset is created, considering factors like temperature, rainfall, and humidity, divided by 80% training set and 20% testing set. The research observes a seasonal trend with a decrease in Dengue cases during the winter and an increase during the rainy season. Both MLR and Support Vector Regression (SVR) models demonstrate accuracy (67% and 75%, respectively) and low Mean Absolute Error (MAE). The analysis suggests that Dhaka, the capital, will experience the highest number of Dengue cases. Overall, the study emphasizes the potential of machine learning algorithms in predicting Dengue epidemics based on environmental factors, providing insights for public health planning.

Another study addresses the challenge of early prediction of Dengue prevalence in Kerala, India, using various data modeling approaches in 2023 [19]. The dataset is taken from 2003 to 2017, and from analysis they found that almost 24000 total cases were reported in Thiruvananthapuram. Vector Auto Regression, Generalized Boosted Models, Support Vector Regression, and Long Short-Term Memory (LSTM) are applied to predict Dengue cases, considering weather variables as independent factors. Among these models, LSTM outperforms others with superior prediction capabilities (RMSE: 0.345, R2: 0.86). While all models capture the trend, LSTM excels in predicting outbreak periods. The results offer valuable insights for public health agencies and policymakers to implement timely control measures against Dengue. The proposed LSTM model can serve as a guide for other states in India, emphasizing the potential of advanced modeling for accurate Dengue predictions and control.

The [11] study addresses the development of predictive models for monitoring Dengue transmission rates using machine learning algorithms (ML). Unlike previous works focusing on specific variables and algorithms, this study incorporates vector indices and meteorological data as predictors. Seven ML algorithms, including ensemble methods like XG Boost, AdaBoost, and Random Forest, were trained and validated. Results indicate that ensemble ML methods outperform logistics regression, Naïve Bayens, decision tree, and support vector machine (SVM), with XGBoost showing the highest AUC, accuracy, and F_1 score. Variable importance analysis identifies the container index as the least important, and removing it improves ML model performance by at least 6% in AUC and F_1 score. The findings offer a framework for future studies aiming to develop early warning systems for Dengue using predictive models.

Dengue, caused by Aedes mosquito-borne dengue viruses, poses a global health threat with millions of infections reported annually [20]. Timely prediction of dengue outbreaks is crucial for effective care due to the lack of vaccines and antiviral drugs. This study focuses on Bangladesh, where dengue cases surged in recent years, aiming to predict dengue fever using a machine learning approach. A patient dataset was constructed from real-time data collected at medical colleges in Bangladesh. It consists of 70% training set and 30% test set for experiments. Machine learning algorithms, specifically decision tree (DT) and random forest (RF), were applied in a classification model. The decision tree achieved an average accuracy of 79%, surpassing the random forest in predicting dengue cases. This research underscores the potential of machine learning for accurate and timely dengue outbreak predictions, offering valuable insights for public health planning and management.

FIGURE 1. Model illustration from input to output

In 2010 a research study produced by [21] focuses on predicting dengue-confirmed cases using Artificial Neural Networks (ANNs) based on real data from the Singaporean National Environment Agency. The study utilizes physical parameters such as mean temperature, mean relative humidity, and total rainfall to model the behavior of dengue cases. Analyzing 14,209 confirmed dengue cases with ANNs yielded promising results. The study identified mean temperature, mean relative humidity, total rainfall, and the total number of dengue confirmed cases as crucial features for predicting dengue cases effectively. Artificial Neural Network (ANNs) prove to be highly efficient processing systems for modeling and simulating dengue-confirmed cases, offering a prediction model applicable globally and at any time, as it doesn't rely on time information during construction. This approach holds significant potential for dengue surveillance and management worldwide.

In summary, the related work section outlines the landscape of previous research, highlighting key methodologies, findings, and existing gaps. This contextualization sets the stage for the current study, demonstrating its relevance and potential contributions to the broader field of Dengue prediction and control.

III. Model Description

This section describe the model briefly, including machine learning models settings implemented, dataset description, and evaluation measures.

In this study, the model implemented has five steps, in firstly data is input to given machine learning models. Secondly, the machine learning algorithms were employed to predict Dengue deaths and cases based on a dataset spanning from 2016 to 2020, encompassing monthly records per region in the Philippines. For this in third step these models are trained on 76% of total data.

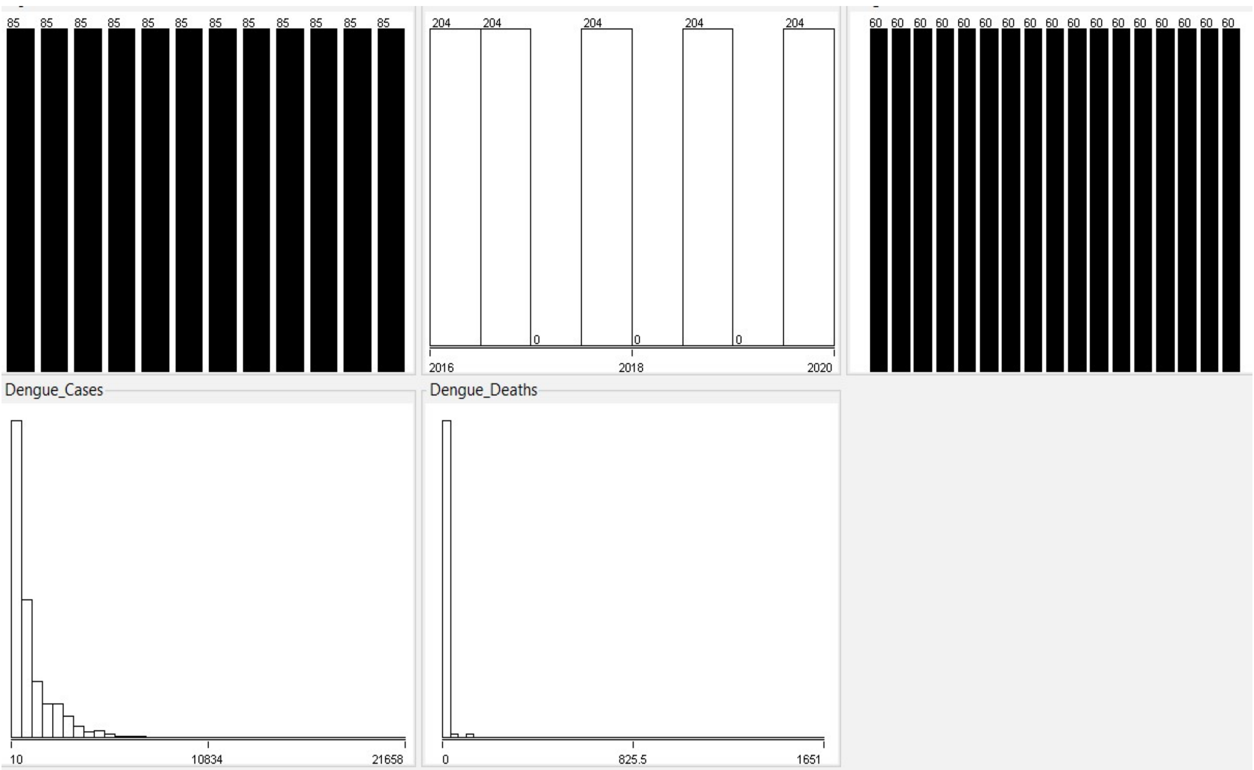

FIGURE 2. Dataset statistics

The models applied include Random Forest, Random Tree, Linear Regression, MLP (Multi-Layer Perceptron), and SVM Regression. Figure 1 illustrates the workflow of the predictive modeling process. The dataset, featuring metadata such as month, year, region, Dengue cases, and Dengue deaths, serves as the foundational input for training and testing the models. Each algorithm undergoes a training phase, learning from historical data, and subsequently, in fourth step testing phase to assess its predictive performance. At the last step evaluation metrics, including correlation coefficients, mean absolute error, root mean squared error, and relative errors, and provide quantitative insights into the accuracy and precision of each model. The chosen models collectively contribute to a comprehensive understanding of Dengue dynamics, enabling proactive measures and targeted interventions in public health.

A. DATASET

The dataset under consideration in this study comprises a total of 1,021[3] instances, with 347 instances allocated for testing purposes. These instances represent monthly records of Dengue occurrences per region in the Philippines from the years 2016 to 2020. The dataset's richness is evident in its temporal granularity, featuring metadata such as the month, year, region, Dengue cases, and Dengue deaths. The division into testing instances, amounting to 347, underscores the meticulous approach to model evaluation, allowing for a robust assessment of predictive performance. The dataset's comprehensive nature enables a thorough exploration of spatiotemporal trends, contributing to a nuanced understanding of Dengue dynamics over the specified five-year period. This dataset forms the cornerstone of the study, providing the necessary inputs for training and testing machine learning models and facilitating evidence-based insights into Dengue disease patterns in the Philippines.

B. EVALUATION MEASURES

To evaluate the regression problems in machine learning mostly relative errors are reported [14], [15], [16]. So, for this study according to this problem's nature we also used correlation coefficient, Mean Absolute Error, Root Mean Squared Error, Relative Absolute Error, and Root Relative Squared Error[4]. The formulas and description of all these evaluation measures are given below.

The correlation coefficient (ρ) measures the linear relationship between predicted (X) and actual (Y) values [22]. The formula is given in equation 1.

$$\rho_{XY} = \frac{Cov(X,Y)}{\sigma_X \sigma_Y} \qquad (1)$$

The second evaluation measure is mean absolute error (MAE) that is an average absolute difference between predicted (Ŷ) and actual (Y) values [23]. It formula is given in equation 2.

$$MAE = \frac{\sum |Y - \hat{Y}|}{n} \qquad (2)$$

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[3] https://www.kaggle.com/datasets/vincentgupo/dengue-cases-in-the-philippines Last visited: 27-12-2023

[4] https://indhumathychelliah.com/2020/12/16/correlation-coefficient%E2%80%8A-%E2%80%8Aclearly-explained/

The third evaluation measure calculated is root mean squared error (RMSE). It is the square root of the average squared differences between predicted (Ŷ) and actual (Y) values [23]. Its formula is given in equation 3.

$$RMSE = \sqrt{\frac{\left(\sum\left(Y-\hat{Y}\right)^{2}\right)}{n}} \qquad (3)$$

The fourth evaluation measure is relative absolute error (RAE) in percentage. It is a mean absolute error expressed as a percentage of the mean of actual (Y) values [24]. The formula is given in equation 4. In this equation MAE is mean absolute error.

$$\mathrm{RAE} = \left(\frac{\mathrm{MAE}}{\mathrm{mean(Y)}}\right) \times 100 \qquad (4)$$

The fifth evolution measure is root relative root mean squared error also in percentage. It is a percentage of the root mean squared error of actual (Y) values [25]. The equation 5 represents the formula of root relative squared error.

$$\mathrm{RRMSE} = \left(\frac{\mathrm{RMSE}}{\sqrt{\mathrm{mean}(\mathrm{Y}^2)}}\right) \times 100 \qquad (5)$$

The next section explain the results obtained by the machine learning algorithm to predict the dengue cases and deaths with the help of above discussed evaluation measures.

III. RESULTS AND ANALYSIS

This section describes the results obtained from five machine learning models on the dataset discussed in the previous section. Table 1 outlines the predictive performance of various machine learning algorithms in forecasting deaths attributed to Dengue disease. Five evaluation measures are employed to analyze the machine learning models more in-depth. The following paragraphs explain each one.

Firstly, the correlation coefficient (ρ) measures the linear relationship between predicted (X) and actual (Y) values. A higher value indicates better learning. In this regard, SVM regression outperforms all other ML models with an obtained value of 0.4900. Conversely, Random Tree obtains a value of 0.2519, indicating poor performance in this problem.

The second evaluation measure is mean absolute error, representing the average absolute difference between predicted (Ŷ) and actual (Y) values. A lower value suggests a better model. In the prediction of deaths due to Dengue disease, SVM obtains a value of 738.9404, while MLP performs poorly, yielding 1041.0691.

The third evaluation measure is root mean square error. In this evaluation, linear regression models obtain a value of 1546.4007, which is better than all other models. Conversely, Random Tree obtains a value of 1971.9126, indicating worse performance for this problem.

According to the relative measure, SVM regression achieves the highest performance with a lower error value of 72.0474%. In contrast, MLP performs poorly, obtaining the highest relative error of 101.5052%.

Finally, in relative square error, the linear regression model obtains a value of 87.5667%, performing the best among these machine models. In this context, Random Tree performs worse, obtaining a relative square error of 111.6618%.

SVM regression demonstrates a relatively high correlation coefficient of 0.49, the lowest mean absolute error at 738.9404, and the lowest relative absolute error at 72.0474%, suggesting superior predictive accuracy among the considered algorithms. This comprehensive evaluation aids in discerning the strengths and weaknesses of each model, facilitating informed choices for Dengue mortality predictions.

TABLE I
PREDICTION OF DEATHS DUE TO DENGUE DISEASE

ML Algorithm	Correlation. Coefficient	Mean Absolute Error	Root Mean Square Error	Relative Absolute Error	Relative Square Error
Random Forest	0.3772	839.0581	1717.7684	81.809%	97.2706%
Random Tree	0.2519	922.6818	1971.9126	89.9624%	111.6618%
Linear Regression	0.4865	846.7783	**1546.4007**	82.5617%	**87.5667%**
MLP	0.4622	1041.0691	1714.853	101.5052%	97.1055%
SVM Regression	**0.4900**	**738.9404**	1574.9494	**72.0474%**	89.1833%

Table 2 provides an overview of the performance of machine learning algorithms in predicting Dengue cases, using various evaluation metrics. The algorithms considered are Random Forest, Random Tree, Linear Regression, MLP (Multi-Layer Perceptron), and SVM Regression. The correlation coefficient measures the linear relationship between predicted and actual values, with linear regression having a coefficient of 0.3176, indicating the highest level of learning. In contrast, random tree obtained a value of -0.0053, indicating worse performance.

In terms of mean absolute error, SVM regression outperforms all other ML algorithms, achieving a value of 19.5832. On the contrary, MLP performs the worst, obtaining a value of 48.9441.

In the third evaluation, root mean square error, linear regression exhibits the best performance, with a value of 121.4203, while MLP shows poor performance with a value of 147.0069.

According to the third evaluation, relative absolute error, SVM regression again outperforms others, obtaining a 73.2268% error value for predicting Dengue cases. Conversely, MLP performs poorly, achieving a 183.0150% error value.

In terms of relative square error, SVM regression performs better, achieving a value of 100.3627%, while MLP performs worse than other models, obtaining a value of 115.6068%.

Overall, we have assessed that SVM regression learns better than other ML algorithms, and MLP performs worse. The table helps assess the predictive capabilities of each algorithm, considering factors such as correlation, absolute errors, and relative errors in predicting Dengue cases.

TABLE II
PREDICTION OF DENGUE CASES

ML Algorithm	Correlation. Coefficient	Mean Absolute Error	Root Mean Square Error	Relative Absolute Error	Relative Square Error
Random Forest	0.0935	27.2368	129.8068	101.8457%	102.0806%
Random Tree	-0.0053	27.9248	135.1168	104.4182%	106.2564%
Linear Regression	**0.3176**	31.21	**121.4203**	116.7025%	95.4854%
MLP	0.1348	48.9441	147.0069	183.015%	115.6068%
SVM Regression	0.088	**19.5832**	127.6223	**73.2268%**	**100.3627%**

IV. CONCLUSION

In summary, the evaluation of machine learning algorithms for predicting deaths and Dengue cases yields distinct insights. SVM Regression excels in predicting Dengue-related deaths, displaying the highest correlation coefficient and the lowest mean absolute error. Meanwhile, for Dengue cases prediction, Linear Regression and SVM Regression stand out with the lowest root mean squared error and mean absolute error, respectively. The diverse performance metrics underscore the need for a nuanced evaluation approach. Ultimately, the findings provide valuable guidance for selecting appropriate algorithms tailored to specific predictive objectives in the context of Dengue disease.

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