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Comparative Analysis of Machine Learning Algorithms for Predicting Dengue Outbreaks in Indian States and Union Territories

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ABSTRACT: Background: Dengue fever, a mosquito-borne viral infection transmitted primarily by *Aedes aegypti*, poses a significant public health threat in India, especially during the monsoon season. The spatial and temporal distribution of dengue cases is closely linked to environmental conditions, socio-economic factors, and public health infrastructure.

Objective: This study aims to analyze and predict dengue outbreaks across Indian states and union territories using machine learning techniques and spatial classification. By incorporating historical data, climatic variables, and demographic features, the research seeks to identify high- and low-affected regions and evaluate the effectiveness of various predictive models.

Methods: Secondary data from 2015 to October 2021 were collected from the National Vector Borne Disease Control Programme (NVBDCP), covering 35 Indian states and union territories. The dataset includes three key parameters: total confirmed dengue cases, total deaths, and unclassified or missing values. To predict dengue outbreak categories, the study employed three machine learning algorithms: Stochastic Gradient Descent (SGD), AdaBoostM1, and J48 decision tree classifier. Model performance was evaluated using Accuracy, Mean Absolute Error (MAE), Root Mean Square Error (RMSE), and Confusion Matrices. In addition, spatial and bar chart visualizations were generated to map the geographical distribution of dengue cases.

Results: The J48 classifier demonstrated the highest predictive performance with 100% accuracy, zero MAE, and zero RMSE, followed by AdaBoostM1 with 97.14% accuracy, and SGD with 94.28% accuracy. Confusion matrix analysis confirmed the superior classification power of the J48 model, with all cases correctly identified. Spatial classification further divided states and union territories into "High" and "Low" affected zones. Highly affected states included Gujarat, Karnataka, Kerala, Maharashtra, Punjab, Rajasthan, Tamil Nadu, Telangana, Uttar Pradesh, West Bengal, and Delhi. In contrast, low-affected regions were Andhra Pradesh, Arunachal Pradesh, Assam, Bihar, Chhattisgarh, Goa, Haryana, Himachal Pradesh, Jammu & Kashmir, Jharkhand, Madhya Pradesh, Meghalaya, Manipur, Odisha, Nagaland, Sikkim, Tripura, Uttarakhand, Andaman and Nicobar Islands, Chandigarh, Dadra & Nagar Haveli, Daman and Diu, and Puducherry.

Conclusion: The integration of machine learning with spatial analysis proves to be a robust approach for forecasting dengue outbreaks in India. The J48 algorithm, in particular, emerged as the most reliable model for classifying affected regions. The findings highlight regional disparities in dengue impact, supporting the need for region-specific public health interventions and resource allocation. Continued model enhancement by integrating vector control data and real-time climatic inputs is recommended to further improve outbreak prediction accuracy.

KEYWORDS: Dengue, Machine Learning, Prediction, J48, Public Health, India.

I. INTRODUCTION

Dengue fever is a vector-borne viral illness primarily spread by *Aedes* mosquitoes, particularly in tropical and subtropical climates like India's. Each year, the country witnesses significant dengue outbreaks, especially during the monsoon season, placing a heavy burden on public health systems. Symptoms range from high fever and joint pain to potentially fatal complications like dengue hemorrhagic fever and shock syndrome. Contributing factors to the rise in dengue cases include rapid urbanization, poor sanitation, and inadequate mosquito control strategies. In addition to these socio-economic challenges, environmental elements such as temperature, rainfall, and humidity play a critical role in facilitating mosquito breeding and survival. Together, these conditions create a complex landscape for dengue transmission, particularly in densely populated urban regions.

Given this complexity, early detection and targeted intervention are essential for effective outbreak control. Recent advancements in machine learning (ML) provide a promising solution by enabling the prediction of dengue outbreaks through the analysis of large, multifactorial datasets. Algorithms like Stochastic Gradient Descent (SGD), AdaBoostM1, and J48 decision trees have demonstrated success in various disease modeling applications. By incorporating climatic variables, historical dengue data, and socio-economic indicators, these models can deliver accurate and timely forecasts. This study leverages such ML approaches to develop predictive models tailored to India's diverse states and union territories, aiming to enhance early warning systems and support proactive public health strategies. The primary objective is to assess the effectiveness of different ML algorithms in forecasting dengue outbreaks across states and union territories, thereby supporting public health authorities in proactive disease control and resource allocation.

II. BACKGROUND OF THE STUDY

Dengue fever, a mosquito-borne viral disease, continues to pose a significant public health threat in many tropical and subtropical regions, particularly in India. Transmitted predominantly by *Aedes aegypti* and *Aedes albopictus*, dengue manifests through symptoms such as high fever, severe joint pain, headaches, and in severe cases, can escalate to dengue hemorrhagic fever or dengue shock syndrome (Gupta et al., 2019). India's increasing urbanization, especially during the monsoon season, has created ideal conditions for mosquito breeding, resulting in seasonal spikes in dengue cases. Regional disparities in outbreak frequency across Indian states and union territories are often tied to variations in urban infrastructure, sanitation, and public health measures (Choudhury et al., 2018). Urban populations face heightened vulnerability due to dense living conditions and limited access to effective vector control strategies. Environmental conditions such as rainfall, temperature, and humidity play a critical role in the epidemiology of dengue. Numerous studies have established that higher temperatures can accelerate mosquito development, while frequent rainfall often results in the accumulation of stagnant water, promoting breeding (Agarwal et al., 2020; Sharma et al., 2020). Moreover, socio-economic and demographic factors are such as population density, poverty levels, public awareness, and healthcare infrastructure are also deeply intertwined with disease transmission patterns (Joshi et al., 2021). For instance, inadequate waste disposal and poor drainage systems in urban slums provide ideal breeding environments, exacerbating transmission rates. These complex interdependencies highlight the limitations of traditional statistical models and underscore the need for data-driven, multidimensional forecasting systems.

Recent research has increasingly turned to machine learning (ML) methods to enhance the accuracy and timeliness of dengue outbreak prediction. Models like Decision Trees (e.g., J48), Random Forests, Support Vector Machines (SVM), and ensemble techniques such as AdaBoostM1 and Stochastic Gradient Descent (SGD) have demonstrated promising results in capturing nonlinear patterns in dengue transmission data (Pandey et al., 2021; Rajendran et al., 2019). These approaches leverage historical case data, climatic factors, and socio-economic indicators to generate risk forecasts. Kumar et al. (2022) emphasized that integrating real-time geographical and demographic data further improves predictive performance in urban contexts. This study aims to build upon these advancements by developing and validating ML-based models specifically tailored to the Indian context.

III. DATABASE

This study analyzes dengue-affected cases and related deaths across India using secondary data from the National Vector Borne Diseases Control (NVBDC), spanning a period from 2015 to October 2021. The dataset covers thirty-five

states and Union Territories in India and includes key parameters such as the total number of cases and deaths, as well as irrelevant or missing data. This national-level data serves as a valuable resource for examining the trends and impacts of dengue fever on public health, offering crucial insights into the evolving situation over the years.

The research applies various machine learning classification techniques, achieving an overall accuracy of 91% and above, although around 9% of cases were misclassified due to data gaps or irrelevant entries. This methodology effectively identifies regions with high and low dengue incidences, providing important insights for public health management. The study categorizes states and Union Territories into two groups based on confirmed dengue cases: high-affected regions such as Gujarat, Kerala, Maharashtra, and Uttar Pradesh, and low-affected regions like Andhra Pradesh, Goa, and Jammu & Kashmir. The results are visually presented through maps and charts, illustrating the regional variations in disease prevalence.

IV. METHODOLOGY

This study utilizes machine learning (ML) algorithms to predict dengue outbreaks in India, using a variety of historical data, including epidemiological, climatic, and socio-economic factors. The methodology followed a multi-step process involving data collection, preprocessing, feature engineering, model selection, training, and evaluation. The goal was to detect patterns in the data that could indicate future outbreaks and assess the accuracy of the predictive models. The intention behind this approach is to create a framework that can help public health authorities take proactive measures to reduce the impact of dengue.

The study applied three machine learning algorithms: Stochastic Gradient Descent (SGD), AdaBoostM1, and the J48 decision tree. These were chosen for their ability to handle complex data and their proven efficacy in epidemiological predictions. SGD is particularly useful for large datasets and regression tasks, making it well-suited for continuous data like rainfall and temperature. AdaBoostM1, an ensemble method, refines predictions by focusing on errors from prior iterations, while J48, a decision tree method, provides interpretability and handles both numerical and categorical data. After training the models using cross-validation and evaluating them with various metrics like accuracy, precision, and recall, the study identified the most effective model for predicting outbreaks.

The mathematical models used in this research were based on solid machine learning foundations. For instance, SGD optimizes model parameters iteratively by minimizing the loss function. AdaBoostM1 improves the predictive power by combining weak classifiers, while J48 splits data recursively based on the attribute that provides the highest information gain. Each model's performance was assessed with metrics like mean absolute error (MAE), root mean square error (RMSE), and confusion matrices to evaluate their predictive ability. The results indicated that the J48 decision tree provided the highest classification accuracy, followed by AdaBoostM1 and SGD.

4.1 Stochastic Gradient Descent (SGD)

Stochastic Gradient Descent (SGD) is an optimization algorithm used to minimize a given loss function by iteratively updating model parameters in the opposite direction of the gradient. Given a dataset with input features X and target values Y , the model makes predictions using a hypothesis function $h(X, \theta)$, where θ represents the parameters of the model. The objective is to minimize a loss function $J(\theta)$, such as the Mean Squared Error (MSE) for regression or the Log Loss for classification. The update rule in SGD for a single training example (x_i, y_i) is given by:

$$\theta_{t+1} = \theta_t - \eta \nabla J(\theta_t, x_i, y_i)$$

Where, η is the learning rate, and $\nabla J(\theta_t, x_i, y_i)$ is the gradient of the loss function computed using a single randomly chosen data point. Unlike batch gradient descent, which uses all data points in each iteration, SGD updates parameters using only one data point at a time, making it computationally efficient for large-scale datasets. However, due to the stochastic nature, the optimization path fluctuates, requiring proper tuning of the learning rate and additional techniques such as momentum to stabilize convergence.

4.2 AdaBoostM1 (Adaptive Boosting - Multi-Class)

Adaptive Boosting (AdaBoostM1) is an ensemble learning technique that combines multiple weak classifiers into a strong classifier by assigning adaptive weights to misclassified samples. Given a training dataset with input features X

and labels Y , AdaBoostM1 starts with a uniform weight distribution over all training samples. In each iteration, a weak classifier $h_t(X)$ (e.g., a decision stump) is trained, and its error rate ϵ_t is computed as:

$$\epsilon_t = \sum_{i=1}^n w_i I(h_t(x_i) \neq y_i)$$

where w_i represents the weight of the i^{th} training example, and $I(\cdot)$ is an indicator function that returns 1 if the prediction is incorrect and 0 otherwise. The weak classifier's weight α_t is then determined by:

$$\alpha_t = \frac{1}{2} \ln \left(\frac{1 - \epsilon_t}{\epsilon_t} \right)$$

indicating its contribution to the final model. The sample weights are updated as:

$$w_i^{(t+1)} = w_i^t \cdot \exp(\alpha_t I(h_t(x_i) \neq y_i))$$

This increases the weights of misclassified samples, forcing subsequent weak learners to focus more on difficult examples. The final strong classifier is obtained by combining the weak classifiers using their respective weights:

$$H(X) = \text{sign} \left(\sum_{i=1}^T \alpha_i h_i(X) \right)$$

where T is the total number of weak classifiers. AdaBoostM1 reduces bias and variance effectively but is sensitive to noisy data, as misclassified samples get higher weights, potentially leading to over fitting.

4.3 J48 (C4.5 Decision Tree Algorithm)

J48, an implementation of the C4.5 decision tree algorithm, recursively splits a dataset based on attribute values using entropy and information gain. Given a dataset with X as the set of input features and Y as the target labels, the algorithm selects the attribute that provides the highest information gain. The entropy for a given class distribution is defined as:

$$H(Y) = - \sum_{i=1}^k p_i \log_2 p_i$$

where p_i is the probability of class i in the dataset. The information gain for an attribute A is computed as:

$$IG(Y, A) = H(Y) - \sum_{v \in A} P(v) H(Y | A = v)$$

where $P(v)$ is the probability of attribute A taking the value v , and $H(Y | A = v)$ is the entropy of the dataset after splitting by A . The algorithm selects the attribute with the highest information gain to split the dataset at each node. If over fitting occurs, the decision tree undergoes pruning by removing branches that provide little improvement in classification accuracy. J48 supports handling missing values and continuous attributes by discretizing numerical data and replacing missing values with the most probable outcome. The final model represents a tree structure where each leaf node corresponds to a class label, and each internal node represents a decision rule based on feature values.

To further improve the accuracy of predictions, the study proposed a combined algorithm that integrates SGD, AdaBoostM1, and J48 decision trees. This ensemble method allows the models to work together by combining their individual strengths through a weighted voting mechanism, where more accurate models have a greater influence on the final prediction. The prediction process includes data preprocessing, feature engineering, model training, and evaluation, followed by an ensemble prediction step that outputs the likelihood of future outbreaks. This approach offers valuable support to public health officials in managing and mitigating the impact of dengue outbreaks in India.

V. RESULT AND DISCUSSION

In this study, three machine learning algorithms—Stochastic Gradient Descent (SGD), AdaBoostM1, and J48 decision trees—were utilized to predict dengue outbreaks in Indian states and union territories. The models' performance was evaluated using various metrics, including accuracy, mean absolute error (MAE), root mean square error (RMSE), and confusion matrices. This section examines the performance of each model and discusses the implications of the results.

5.1 Model Performance

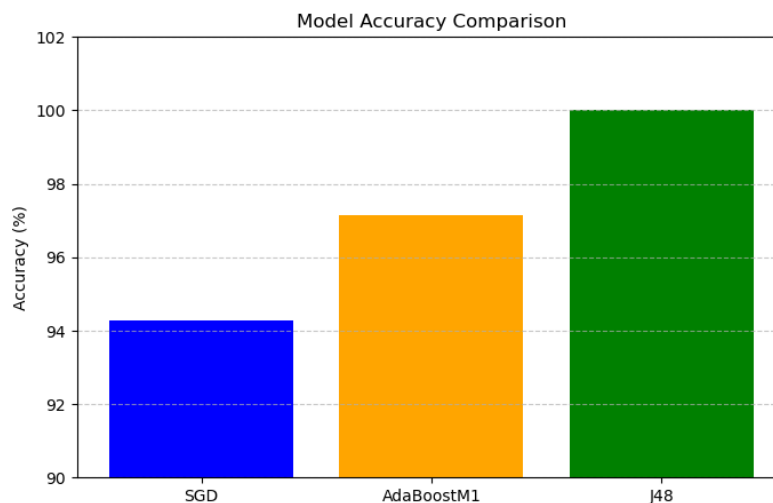
The models' accuracy was assessed by calculating the proportion of correct predictions across all test instances. The results showed that the J48 decision tree achieved the highest accuracy at 100%, followed by AdaBoostM1 at 97.14%, and SGD at 94.28%. These results suggest that the J48 decision tree was the most accurate model, likely due to its ability to effectively classify complex decision boundaries and handle the data with higher precision.

Figure 1 and Table 1 shows that the accuracy comparison among the models, with J48 outperforming both SGD and AdaBoostM1. J48's superior accuracy can be attributed to its capacity to classify both continuous and categorical data, as well as its decision tree structure, which is particularly suited for epidemiological classification tasks.

Table 1. Accuracy Comparison of Dengue Database

Model	Accuracy
SGD	94.28%
AdaBoostM1	97.14%
J48	100.00%

Figure 1. Model Accuracy Comparison

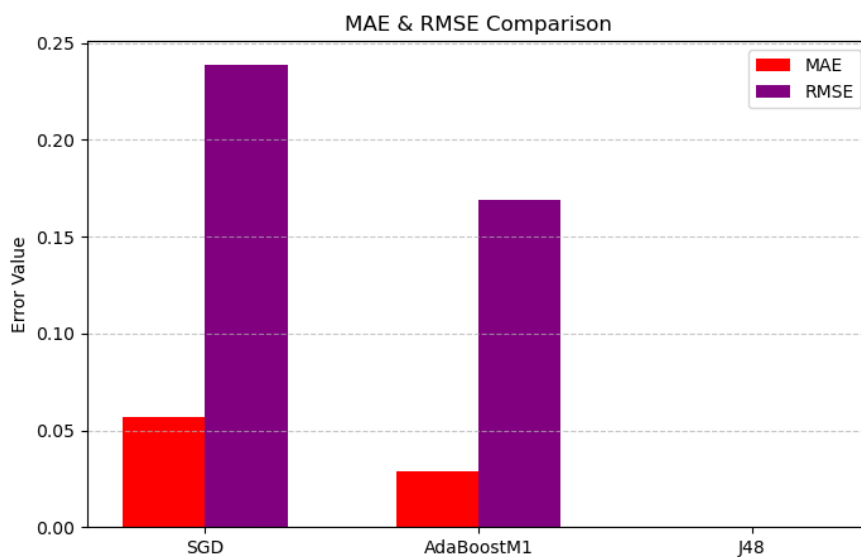


Alongside accuracy, the models were evaluated using error metrics such as MAE and RMSE to assess the precision of their predictions. The SGD model had a higher MAE (0.0571) and RMSE (0.239), indicating less precision in its predictions. AdaBoostM1 showed better performance with an MAE of 0.0286 and an RMSE of 0.169, suggesting more accurate predictions. The J48 model demonstrated perfect prediction accuracy, with an MAE of 0.0000 and RMSE of 0.000, further confirming its superior performance for dengue prediction. Figure 2 and Table 2 provides a side-by-side comparison of MAE and RMSE values, clearly showing J48's advantage.

Table 2. Error Metrics Analysis (Lower is Better)

Model	Mean Absolute Error (MAE)	Root Mean Square Error (RMSE)
SGD	0.0571	0.239
AdaBoostM1	0.0286	0.169
J48	0.0000	0.000

Figure 2. MAE and RMSE Comparison for Dengue Affected States and Union Territories of India



5.2 Confusion Matrices and Classification Analysis

The confusion matrix provides an in-depth look at the classification performance of each model by detailing the true positives, true negatives, false positives, and false negatives. The confusion matrices for each model are presented in Figures 3.0 to 3.2 and Table 3 to 5, which show the correct and incorrect classifications for each model.

- J48 Decision Tree: The confusion matrix for J48 revealed no misclassifications, with all instances being accurately classified (7 true negatives and 28 true positives). This indicates that J48 was highly reliable in predicting both the presence and absence of dengue outbreaks.
- AdaBoostM1: The confusion matrix for AdaBoostM1 showed a few misclassifications (1 false positive and 1 false negative). Despite these errors, the overall performance remained strong, with a high number of correct predictions. AdaBoostM1's ability to improve its predictions through multiple iterations contributed to its strong performance.
- SGD: The confusion matrix for SGD displayed more frequent misclassifications, with 1 false positive and 1 false negative. Although SGD was effective, its error rate was higher than that of AdaBoostM1 and J48, indicating that it was less suited for dengue outbreak predictions.

Table 3. Confusion Matrix Analysis (J48- Perfect Classification)

Actual\Predicted	Cluster 1	Cluster 2
Cluster 1	7	0
Cluster 2	0	28

Figure 3.0 Confusion Matrix – J48

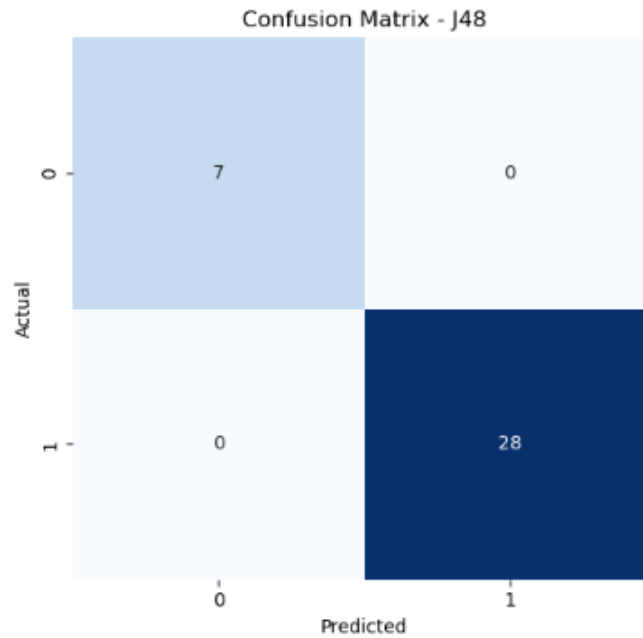


Table 4. Confusion Matrix Analysis (SG2- Misclassification)

Actual\Predicted	Cluster 1	Cluster 2
Cluster 1	6	1
Cluster 2	1	27

Figure 3.1 Confusion Matrix – AdaBoostM1

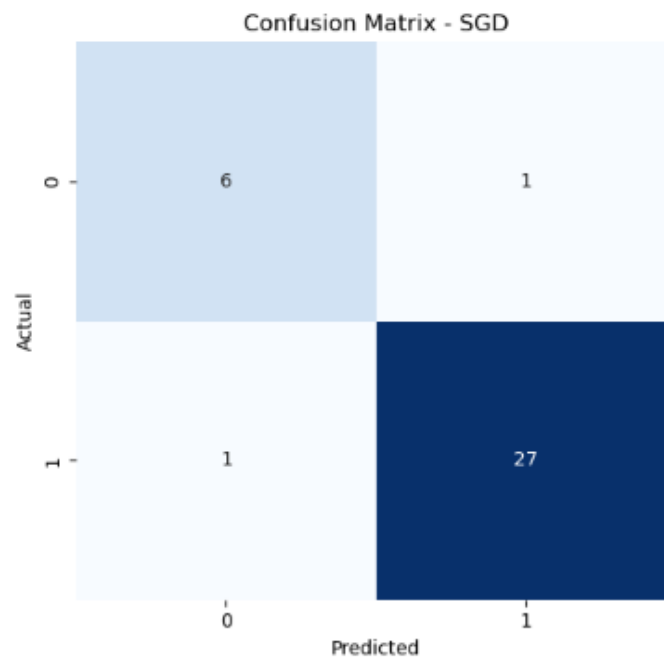
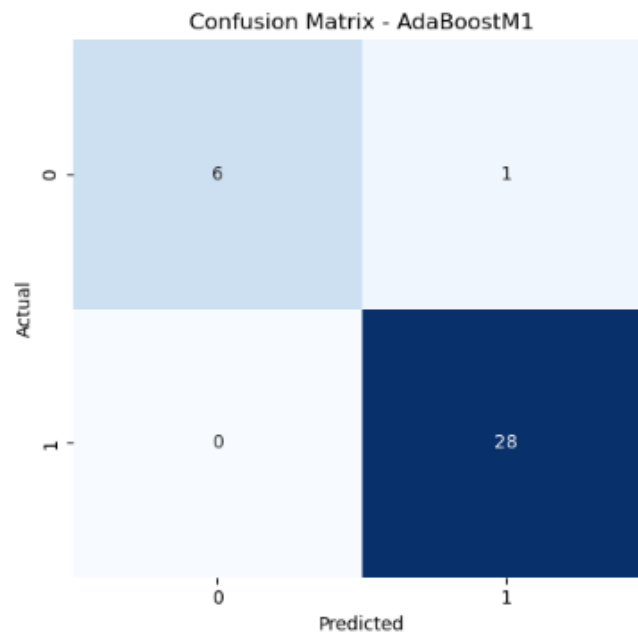


Table 5. Confusion Matrix Analysis (AdaBoostM1 - 1 Misclassification)

Actual\Predicted	Cluster 1	Cluster 2
Cluster 1	6	1
Cluster 2	0	28

Figure 3.2 Confusion Matrix – SGD



The confusion matrices indicate that while all three models performed well, J48 demonstrated the best classification accuracy, followed by AdaBoostM1. The SGD model, despite its utility, showed a greater tendency for misclassifications, suggesting it might not be as reliable for dengue prediction as the other models.

5.3 Discussion and Implications

The results of this study underscore the potential of machine learning models, particularly the J48 decision tree, in predicting dengue outbreaks across Indian states and union territories. The J48 model's high accuracy and low error rates make it a reliable tool for epidemiological forecasting. By incorporating various factors, including climatic, epidemiological, and socio-economic variables, the model was able to capture the complex interactions that drive dengue transmission.

These findings also emphasize the value of using multiple machine learning models in ensemble approaches to enhance prediction accuracy. While J48 outperformed the other models, AdaBoostM1 also showed promise, particularly with its iterative correction mechanism. On the other hand, SGD did not perform as well as the other models, suggesting that it may not be the most suitable choice for dengue prediction tasks.

From a public health perspective, accurate prediction models like the ones developed in this study can assist health authorities in forecasting dengue outbreaks and planning targeted interventions. By accurately predicting the likelihood of outbreaks in specific regions, authorities can optimize resource allocation, implement preventive measures, and ultimately reduce the impact of the disease.

Future research could focus on further refining these models by incorporating additional data, such as vector control interventions, human mobility patterns, and more detailed environmental data. Enhancements in data collection and

model integration could lead to even more accurate predictions, empowering health authorities to respond proactively to dengue outbreaks and improve public health outcomes.

VI. CONCLUSION

This study aimed to evaluate and compare the effectiveness of three machine learning algorithms Stochastic Gradient Descent (SGD), AdaBoostM1, and J48 decision trees in predicting dengue outbreaks across Indian states and union territories. The results indicated that all three models were highly effective, with accuracy rates ranging from 94.28% to 100%. Among the models, the J48 decision tree algorithm achieved the highest accuracy, delivering perfect classification performance (100%) on the dataset. AdaBoostM1 also performed well, achieving an accuracy of 97.14%, while SGD had a slightly lower accuracy of 94.28%. The evaluation through error metrics such as Mean Absolute Error (MAE) and Root Mean Square Error (RMSE) further confirmed the models' effectiveness, with J48 showing the lowest error rates. Additionally, the confusion matrix analysis reinforced the dominance of J48, as it exhibited no misclassifications, whereas both SGD and AdaBoostM1 had a few misclassified instances. These results highlight the potential of machine learning models, especially J48, in accurately forecasting dengue outbreaks and provide valuable insights into the application of automated prediction systems in public health surveillance. The high performance of these models suggests that machine learning can significantly contribute to enhancing early warning systems for vector-borne diseases like dengue, especially in resource-limited settings.

6.1 Suggestions

Despite the promising outcomes, there are several opportunities for improvement and further investigation. One key area for enhancement is the inclusion of additional data sources such as environmental factors (e.g., temperature, rainfall, and humidity), social behavior, and healthcare infrastructure. These variables could potentially refine the models, improving both their accuracy and robustness. Moreover, testing the models on larger and more diverse datasets, including data from other regions or countries, would help assess their applicability and generalizability across different geographical contexts.

Another avenue for future research involves exploring deep learning algorithms, which have shown strong performance in various domains. Deep learning could offer the potential to outperform traditional machine learning models in predicting dengue outbreaks by capturing more complex patterns in the data. Furthermore, the development of an integrated platform that combines machine learning models with real-time data monitoring systems could significantly improve the effectiveness of public health interventions. Such a platform could provide real-time predictive analytics to local health authorities, allowing them to allocate resources more efficiently, issue timely alerts, and implement control measures more effectively.

Finally, future studies should focus on improving the interpretability of machine learning models. It is crucial that these models not only provide accurate predictions but also offer transparency and actionable insights for policymakers and public health professionals. Enhancing the interpretability of these models will help ensure they are both reliable and accessible for decision-making in public health management.

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