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Prediction of Dengue Outbreaks in Sri Lanka Using Machine Learning Techniques

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ABSTRACT

Dengue outbreaks pose a significant public health challenge in tropical and subtropical regions globally, necessitating effective predictive models for early detection and intervention. This study examines the complex nature of the disease by analyzing weather parameters such as temperature, wind speed, precipitation, and humidity. Through machine learning techniques, we successfully forecasted dengue outbreaks in nine districts in Sri Lanka and identified similar weather and dengue patterns in districts such as Gampaha, Colombo, Kandy and Kurunegala. These findings are important for developing an early warning system, optimizing public health measures, and efficiently allocating resources to minimize the negative impact on communities. Furthermore, the model offers valuable insights for epidemiological research on dengue spread and control.

Keywords: Dengue, Dengue outbreak prediction, Machine learning, Early warning system, Time series forecasting

INTRODUCTION

The Expanded Program on Dengue has emerged as a significant public health concern in many tropical and subtropical regions worldwide. It is estimated that about half of the world's population is at risk, with 100–400 million infections occurring annually (19). In 2023, over six million dengue cases and over 6,000 dengue related deaths were reported from 92 countries/territories (19). The highest burden of dengue was observed in the Americas, where all four-dengue virus (DENV) serotypes circulated

and caused outbreaks in several countries. Brazil, Bangladesh, Mexico, Peru, and Burkina Faso were among the countries with the most cases (Figure 1). Dengue also occurred in Africa, Asia, and Europe, where some locally acquired cases were reported in Italy, France, and Spain [20]. The disease is prevalent in tropical and subtropical climates, particularly in urban and semi-urban areas. While many DENV infected individuals remain asymptomatic or experience only mild symptoms, the virus can occasionally lead to severe dengue such as dengue hemorrhagic fever and dengue shock syndrome and the latter sometimes leads to death (19).



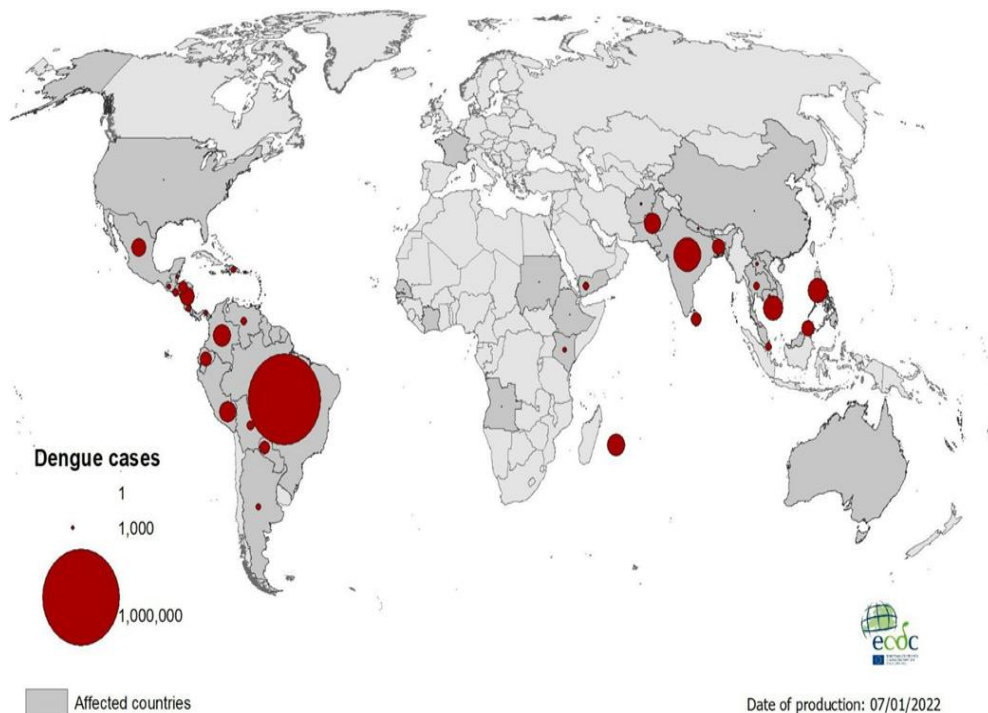


Figure1: Geographical distribution

Dengue, a mosquito-borne viral infection caused by four distinct but closely related dengue virus (DENV) serotypes (DENV-1, DENV-2, DENV-3 and DENV-4). Dengue poses a significant global health challenge. It is estimated that nearly 3.6 billion people are at risk, with approximately 390 million infections occurring annually, of which 96 million are symptomatic (21). The disease spectrum ranges from asymptomatic DENV infection to severe forms such as dengue hemorrhagic fever (DHF) and dengue shock syndrome (DSS), leading to around 21,000 fatalities each year (21).

Dengue is a complex and dynamic disease influenced by multiple factors at different scales. Some of the factors that affect the spread of dengue include the vector population, which determines the availability and distribution of the dengue mosquito vectors (22); urbanization, which creates favorable conditions for vector breeding and human exposure (22); climate change, which affects the ecology and behavior of the mosquito vectors and the DENV (23); travel and globalization, which can introduce new DENV strains or serotypes, or new mosquito vectors, to previously unaffected areas (24); population density, which affects the contact rate between

humans and mosquitoes; and herd immunity, which depends on the history and frequency of DENV infections, and the cross-reactivity and duration of the antibodies; and mutation and evolution of DENV, which can generate new variants with different virulence, transmissibility, and antigenicity.

DENV is transmitted to humans through the bite of infected mosquitoes, specifically a few species that act as vectors. A vector, often an arthropod like mosquitoes, ticks, lice, flies, or fleas, is an organism that carries and transmits a disease-causing microbe to its host. When a mosquito bites a person infected with the DENV virus, it becomes a carrier of the virus and can infect healthy individuals through subsequent bites. It's important to note that DENV don't spread directly from person to person; mosquitoes are essential for its transmission (25). DENV is primarily spread by the *Aedes aegypti* mosquito, which serves as the main vector for the virus. Other *Aedes* species, such as *Aedes albopictus*, *Aedes polynesiensis*, and *Aedes scutellaris*, can also carry the virus but to a lesser extent (25).

Dengue, a disease that can range from mild to severe, typically presents symptoms for 4-10 days

post-infection, lasting for 2-7 days. Common symptoms include high fever, severe headache, retro-orbital pain, muscle and joint pains, nausea, vomiting, swollen glands, and rash. A second infection can increase the risk of severe dengue. After the fever subsides, severe symptoms such as abdominal pain, persistent vomiting, rapid breathing, bleeding gums or nose, fatigue, restlessness, blood in vomit or stool, extreme thirst, pale and cold skin, and weakness may occur. Immediate medical attention is advised for these severe symptoms. Post-recovery, individuals may experience fatigue for several weeks (19).

Prevention and control of dengue are largely dependent on vector control to avoid mosquito bites. Despite the lack of a specific treatment for dengue and severe dengue, early detection and access to proper medical care can significantly reduce case fatality rates. Therefore, prevention strategies and timely medical intervention are crucial in managing dengue.

Sri Lanka, a lush tropical island in the Indian Ocean, home to 21 million people, has been besieged by the relentless scourge of dengue since the 1960s. Despite its seasonal nature, with epidemics primarily afflicting regions experiencing annual rainfall exceeding 2,500 mm, the situation escalated dramatically in 2017 (Figure 2). Prior to

1988, occurrences of the more severe DHF/DSS were sporadic. However, from 1991 to 2008, dengue epidemics became more pronounced, occurring every few years amidst endemic transmission. The year 2009 marked a grim milestone with over 35,000 suspected cases and 346 deaths, highlighting the severity of the crisis. Subsequent years saw a steady rise in cases, peaking in 2017 with a staggering 186,101 suspected cases and 440 deaths, marking it as the deadliest outbreak since dengue was classified as a notifiable disease in 1996.

The inefficiency of a robust public health surveillance system compounded the challenge, hindering efforts to track and monitor outbreaks effectively. This deficiency, coupled with limited accessibility to medical facilities, particularly in rural areas, exacerbated the crisis (14-16). High population density, especially prevalent in the Eastern Province, further fueled the rapid transmission of the virus, making containment efforts even more daunting. Furthermore, the absence of regular updates on confirmed cases exacerbated the difficulty in identifying trends and anticipating outbreaks (18). Urgent measures are needed to address this escalating public health crisis, including the implementation of predictive tools to anticipate outbreaks and monitor cases effectively (92).

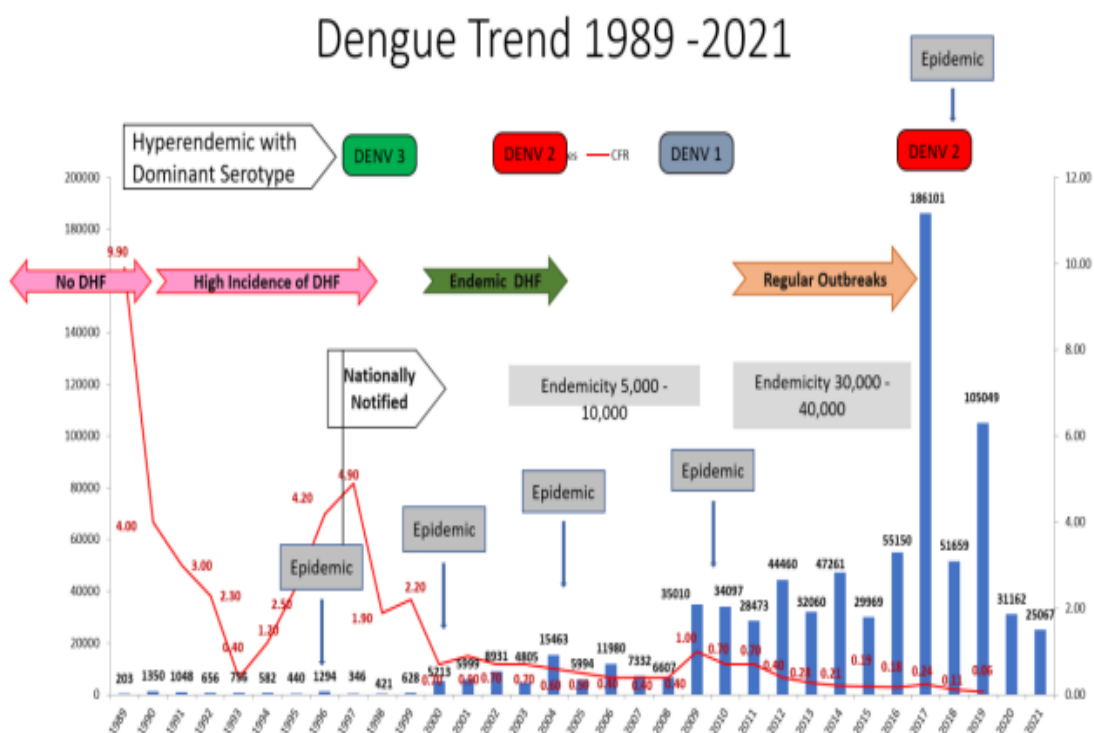


Figure 2: The Reported Dengue Infected Count in Sri Lanka from 1989 to 2021 [1].

Related work

Over the past few decades, Sri Lanka has witnessed a significant number of recorded cases of dengue, marking it as one of the most dangerous infections in the country. Despite the gravity of the situation posed by dengue, there is a noticeable dearth of comprehensive data on DENV and dengue epidemiology coupled with machine learning (ML) prediction tools in Sri Lanka. Contrary to the considerable attention generated by dengue, revealing a significant research gap in understanding their epidemiology and the negative impact on the island.

In the context of dengue-related studies in Sri Lanka, several notable research gaps have been identified:

- A. Dengue Outbreak Prediction in Sri Lanka.
- B. Classification of Different Types of DENV Post Mutation.

Addressing these research gaps, this study focuses on predicting the dengue outbreaks while managing specific challenges associated with predicting.

A. Dengue Outbreak Prediction in Sri Lanka

Recent advancements in machine learning for dengue prediction have demonstrated success in other tropical regions. Hybrid CNN-LSTM models achieved 89% accuracy in Brazil by integrating urbanization indices (11), while gradient boosting machines in Indonesia incorporated waste management data to improve outbreak alerts (12). However, these approaches remain untested in Sri Lanka's unique socio-climatic context.

Furthermore, much of the research on dengue outbreak prediction has been conducted in the context of other countries, with limited attention given to Sri Lanka (3-5). The unique climatic, environmental, and socio-economic factors of Sri Lanka make it imperative to develop prediction models tailored to the local context. Our study bridges this gap by focusing specifically on Sri Lanka, leveraging local data to ensure higher relevance and accuracy.

By introducing an up-to-date and comprehensive system for dengue outbreak prediction in Sri Lanka, our work not only contributes to the body of knowledge but also provides a practical tool for

mitigating the impact of dengue outbreaks in the region.

Accessing genome data for dengue virus research remains a significant challenge due to limited resources and data availability in Sri Lanka (17). This lack of genomic information restricts the ability to incorporate valuable insights into virus evolution and transmission dynamics, which could greatly enhance the accuracy of outbreak predictions (6). If such data were more accessible, it could be integrated with environmental and socio-economic factors to develop more precise and comprehensive models, offering a deeper understanding of dengue outbreaks and enabling better-targeted preventive measures. SARIMAX model can address Sri Lanka's data limitations by:

1. Accommodating sparse genomic data through weather-driven temporal patterns
2. Capturing delayed mosquito life cycle effects better (13)

B. Classification of Different Types of Dengue Viruses Post Mutation

The use of machine learning for classifying and understanding Dengue viruses post-mutation marks a pioneering advancement in dengue research. While existing studies have detailed the serotypes DENV-1 to DENV-4 and their clinical manifestations, a notable gap remains in applying machine learning for classifying these strains after mutations (7). Traditional molecular techniques have provided critical insights into genetic variability, transmission pathways, and the role of DC-SIGN (CD209) in human dendritic cell infections, contributing to disease management and vaccine development (8-9).

Machine learning offers a transformative approach, enabling analysis of large datasets to uncover patterns, correlations, and predictive markers that conventional methods may miss (10). This capability could enhance subtype classification and inform disease control strategies. Additionally, the rise of severe secondary infections due to different serotypes highlights the need for robust classification models that integrate genomic, clinical, and

epidemiological data to predict outcomes and assess risks (7)

METHODOLOGY

Data Collection

This paper analyzes dengue outbreaks in selected Sri Lankan districts based on weather data, including precipitation, humidity, wind speed, and temperature. Weather data was sourced from the Sri Lanka Meteorological Department. Due to budget limitations, weather data was provided for some selected districts. Districts without sufficient data were excluded, leaving Batticaloa, Colombo, Galle, Jaffna, Katugastota, Katunayake, Kurunegala, Puttalam, and Ratnapura. Dengue epidemiological data (January 2007–April 2024) was obtained from the Ministry of Health's public epidemiological department official website. Weekly weather data would improve precision but is unfeasible due to budget limitations and limited time-series and granular socio-economic data, like population density and waste collection, hinders accurate dengue outbreak prediction in Sri Lanka.

Data Analysis

Exploratory Data Analysis (EDA) was carried out to gain a deeper understanding of the collected data. We visualized patient counts from 2007 to 2024 in Sri Lanka (Figure 3) and created a correlation matrix to assess relationships between weather parameters and patient count but found no strong correlations at this stage. Next, we analyzed patient counts for the nine selected districts individually (Figure 5) and observed a major spike in 2017, followed by a smaller spike in 2019.

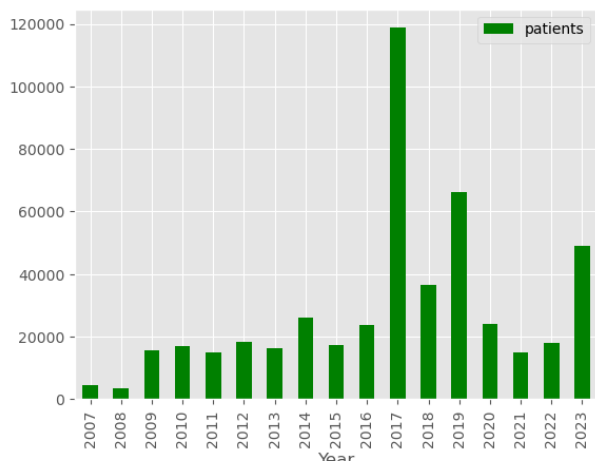


Figure 3: Distribution of patient counts in Sri Lanka from 2007 to 2023

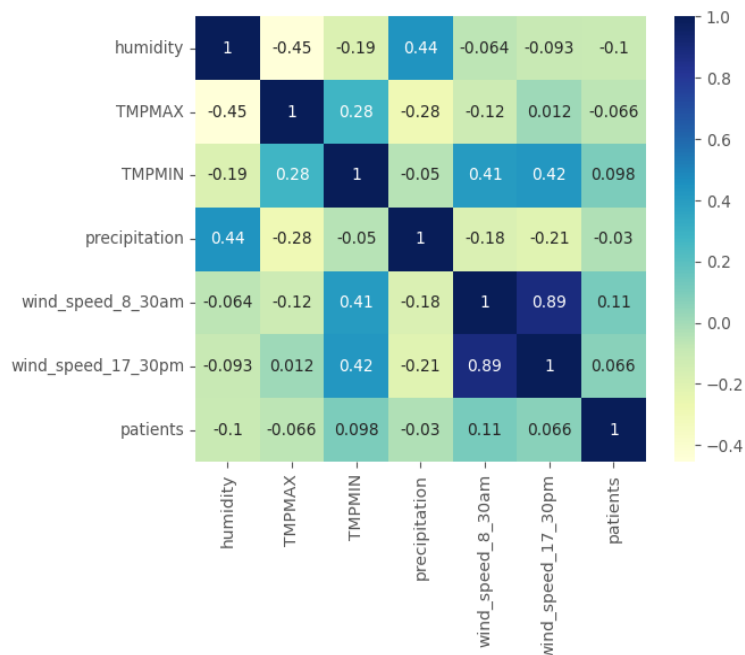


Figure 4: Heatmap Correlation Matrix

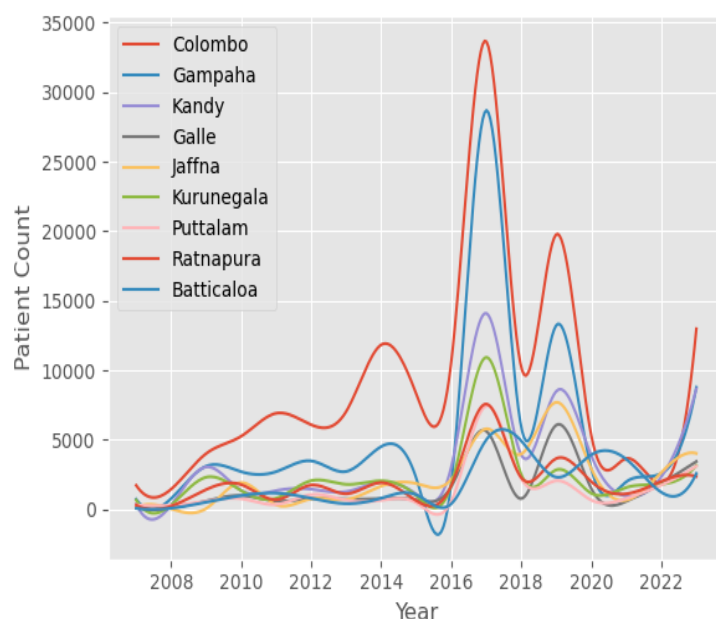


Figure 5: The district-wise distribution of patient counts from 2007 to 2023 in Sri Lanka

Colombo and Gampaha districts consistently recorded the highest patient counts each year, with similar distribution patterns (Figure 6). Additionally, Kandy and Kurunegala districts displayed a similar relationship in their patient count distributions over the years (Figure 7).

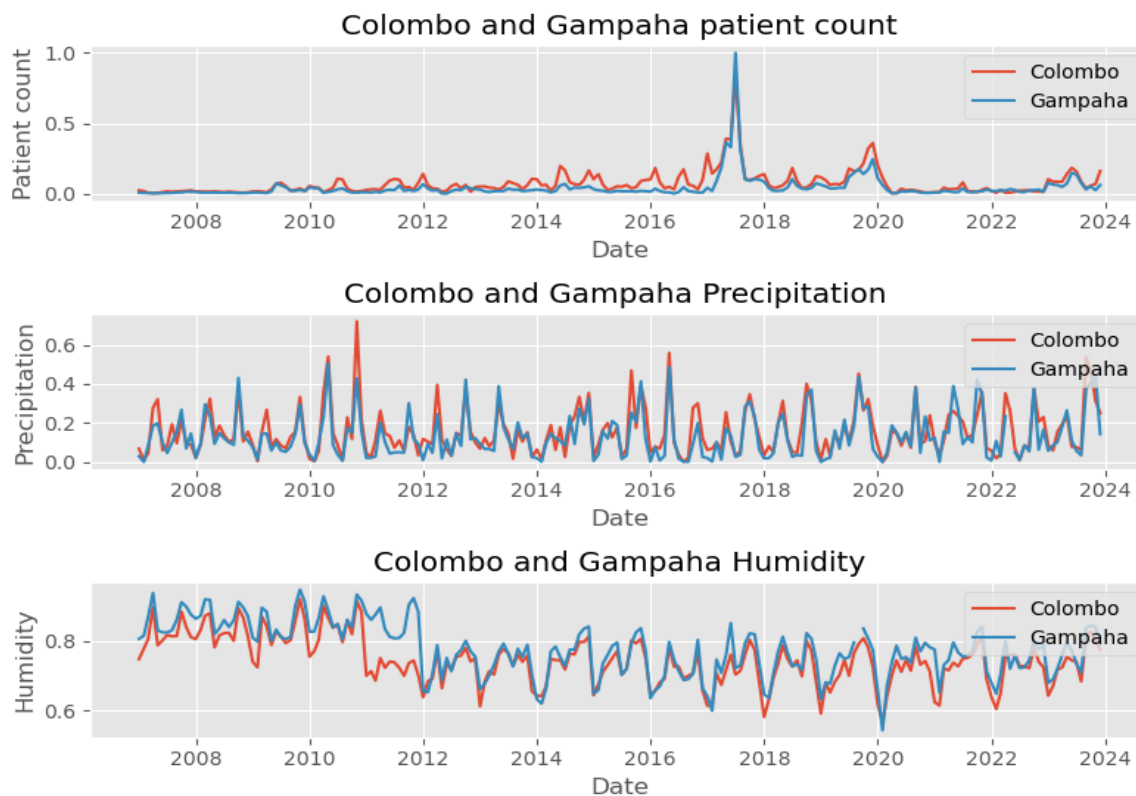


Figure 6: Comparison of Patient Count, Precipitation, and Humidity Data in Colombo and Gampaha Districts

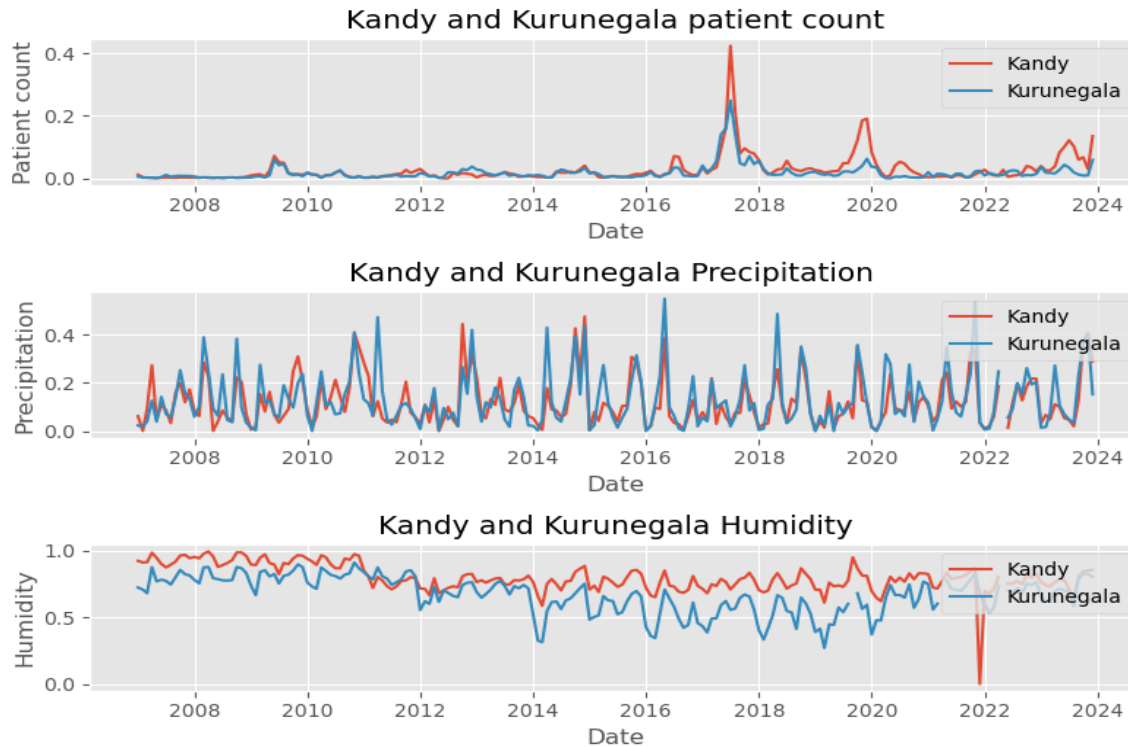


Figure 7: Comparison of Patient Count, Precipitation, and Humidity Data in Kandy and Kurunegala Districts

- **Data Preparation and Integrity Checks**

The dataset comprised monthly dengue case counts (2007–2024) and corresponding meteorological parameters (temperature, humidity, precipitation, wind speed) across nine Sri Lankan districts. Initial preprocessing involved systematic aggregation of heterogeneous data formats into a unified temporal framework. Districts exhibiting >10% missing weather records were excluded to mitigate sampling bias, while linear interpolation addressed sporadic gaps in temperature and humidity measurements.

- **Temporal and Spatial Trend Analysis**

Longitudinal visualization of nationwide patient counts (Fig. 3) facilitated identification of multiyear epidemiological patterns. District-level profiling through kernel density estimation (Fig. 5) revealed heterogeneous case distribution dynamics, with Colombo and Gampaha demonstrating near-identical temporal trajectories. Cross-correlation analysis using Spearman's rank coefficients between weather variables and case counts yielded insignificant immediate relationships, prompting investigation of delayed effects.

- **District-Level Comparative Analysis**

Spatiotemporal mapping of case trajectories (Figures 6–8) uncovered two distinct district clusters:

- 1 Urban Corridor (Colombo-Gampaha)
- 2 Inland Plateau (Kandy-Kurunegala)

Then, we had to search for another criterion to find any relationship between the patient count and weather parameters. We decided to consider the life cycle of the *Aedes aegypti* mosquito, hypothesizing that it might offer insights into the observed trends. Given the life cycle of the *Aedes aegypti* mosquito and the delayed effect of weather parameters on dengue outbreaks, we hypothesized that there might be a correlation between the patient count for a given month and the weather data from previous months. To test this hypothesis, we shifted the data accordingly and re-analyzed it (Figure 9, Figure 10). This new analysis revealed considerable improvements in the correlation factors, supporting our hypothesis

and demonstrating the importance of considering the time lag effect of weather parameters in predicting dengue outbreaks using machine learning.

The delayed effect of certain weather parameters, such as precipitation and humidity, on the patient count can be attributed to the life cycle of the *Aedes aegypti* mosquito, the primary vector of dengue. These mosquitoes typically lay eggs in containers or places that hold water about 10 days after a rainfall event. It then takes approximately 14 days for these eggs to develop into adult mosquitoes. The lifespan of an adult mosquito is usually between 56 and 60 days. When a dengue mosquito bites a human, it takes about 4 to 10 days for the disease to be detectable.

Therefore, on average, it takes about 2 to 3 months to observe an increase in the patient count following a significant rainfall event. This time lag is crucial to consider when predicting dengue outbreaks using machine learning techniques, as it reflects the biological and environmental factors influencing dengue transmission. Based on the above analysis and findings, we decided to train nine separate models, one for each district, rather than combining districts. Combining districts in a time series analysis could lead to unsuccessful predictions, as the model would struggle with two different sequences being fed into it. Additionally, we are applying the time-shifting technique to each model to further enhance the predictive accuracy.

Data Preprocessing

- 1) Patient Data Preprocessing: Weekly records were combined into monthly summaries, and any missing or wrong entries were corrected.
- 2) Weather Data Preprocessing: Missing weather values were filled in using the KNN method, and all numbers were normalized between 0 and 1 to ensure fairness by mitigating bias.

Model Training

Following three time-series forecasting models trained and evaluated using RMSE (Root Mean Squared Error), which measures how far the predicted values are from the actual values, with lower values indicating more accurate predictions.

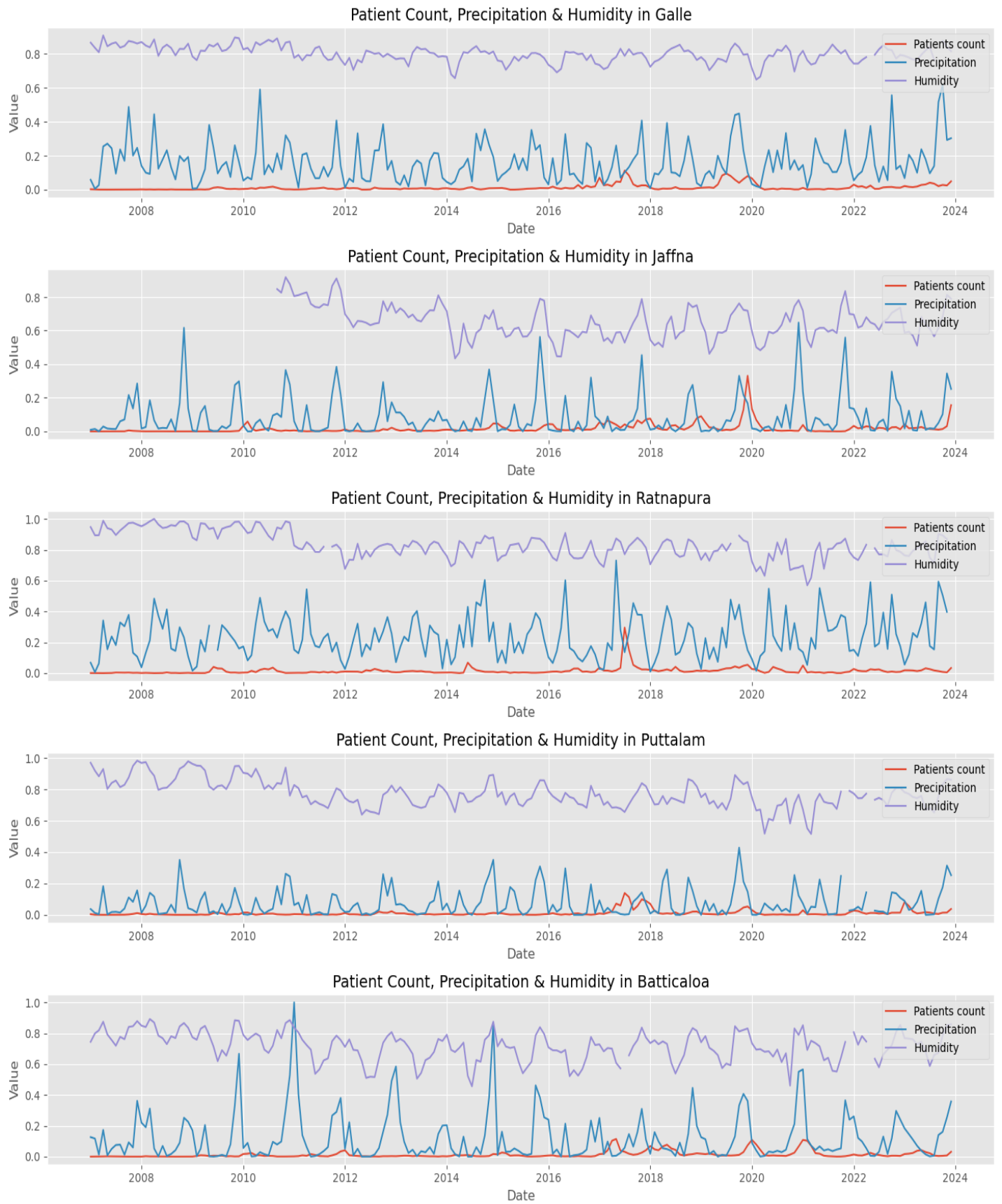


Figure 8: Comparison of Patient Count, Precipitation, and Humidity Data in Other Districts

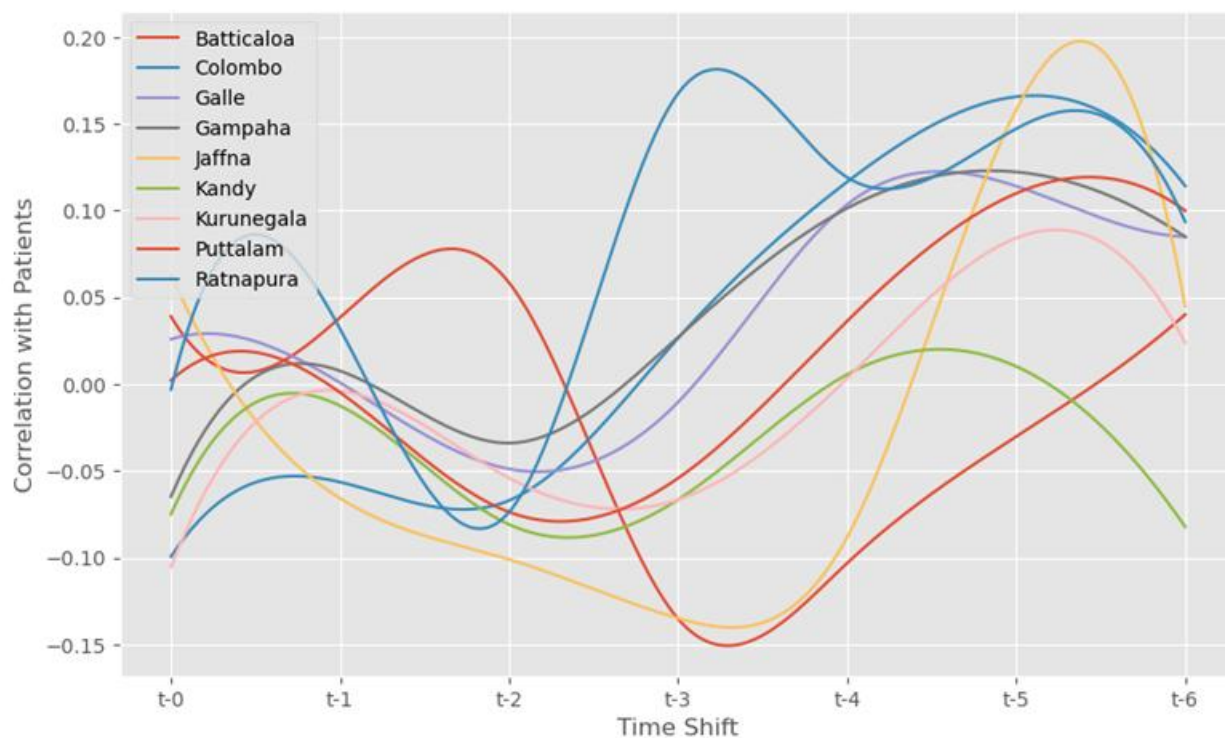


Figure 9: Correlation Between Shifts in Precipitation and Patient Count

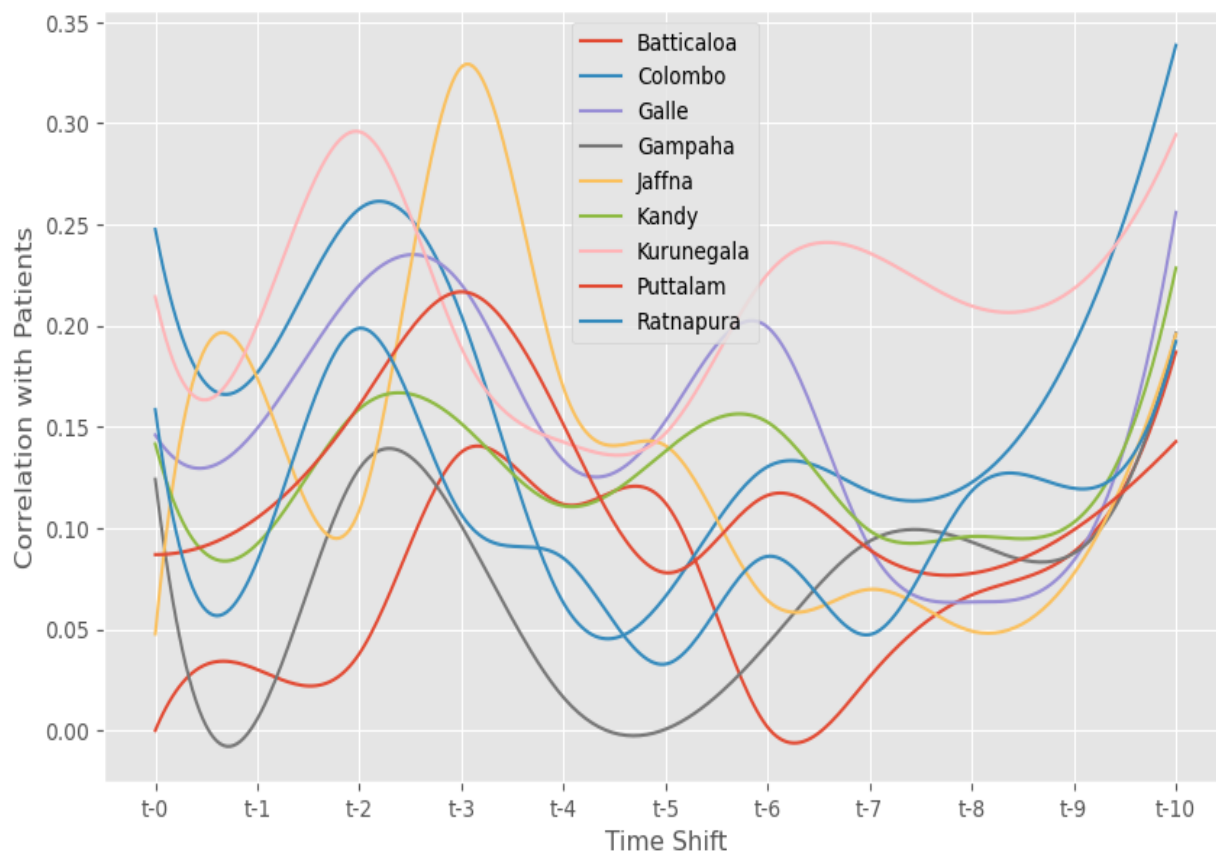


Figure 10: Correlation between Shifts in humidity and patient count

1 CNN (RMSE = 258.12)

A deep learning model that automatically learns patterns from data using layers. This produced high errors, indicating poor predictive performance.

2 XGBoost (RMSE = 142.36)

An ensemble method that builds many decision trees and combines them to improve prediction accuracy. This model can capture complex, non-linear relationships from weather data and previous dengue cases, resulting in moderate accuracy.

3 SARIMAX (RMSE = 94.94)

A time series forecasting model that captures seasonal trends and incorporates external factors. It achieved the lowest error and the best overall performance.

RESULTS

Our initial exploratory analysis revealed (For a more detailed explanation, please refer to the data analysis section) that the patient count distributions and their fluctuations were very similar in the paired districts of Colombo and Gampaha (Figure 6), as well as in Kandy and Kurunegala (Figure 7). This observation indicates that the temporal variations in patient numbers follow comparable patterns across these district pairs, suggesting that underlying factors may be influencing them in a similar manner.

The most significant outcome of our study is that the SARIMAX model performed relatively well in forecasting dengue outbreaks in Sri Lanka. The performance of the model was quantitatively assessed using the Root Mean Squared Error (RMSE), a standard metric for measuring the accuracy of predictions by indicating how far the predicted values are from the actual values, with lower values indicating more accurate predictions. The RMSE values obtained for each district are summarized in Table 1.

Notably, districts like Ratnapura, Puttalam, Kurunegala, Batticaloa and Galle exhibited the lowest RMSE values, indicating a higher predictive

Table 1: RMSE values for SARIMAX model predictions across different districts

District	RMSE Value
Colombo	93.92
Gampaha	106.33
Kandy	95.68
Kurunegala	61.07
Ratnapura	46.2
Galle	65.97
Puttalam	52.74
Batticaloa	63.78
Jaffna	266.77

accuracy in these regions. Conversely, the district of Jaffna showed a significantly higher RMSE, suggesting challenges in model accuracy there. Based on these RMSE values, we can establish a confidence interval for the forecasts, providing a quantifiable measure of certainty in the model's predictions.

DISCUSSION

This study highlights the potential of machine learning techniques, particularly the SARIMAX model, in predicting dengue outbreaks in Sri Lanka. The significant correlations identified between weather patterns and dengue incidence underscore the importance of considering the time lag effect of weather parameters in forecasting outbreaks (For a more detailed explanation, please refer to the data analysis section). Our findings demonstrate that the SARIMAX model can effectively predict dengue incidence across different districts, providing a valuable tool for health authorities to anticipate and prepare for potential outbreaks.

However, several limitations impacted the model's accuracy. One key limitation was the low sensitivity of weather parameters due to the use of monthly weather data, limiting its ability to capture detailed patterns in the data. Accessing weekly weather data could potentially improve the accuracy and timeliness of predictions by capturing more granular weather patterns that influence mosquito breeding cycles. Moreover, the model did not account for certain socio-environmental factors that could have influenced dengue outbreaks, such

as population density and garbage disposal practices.

Another limitation was the accuracy and relevance of weather data for specific districts. For example, in the Gampaha district, the model relied solely on data from the Katunayake weather station, despite significant weather variations across other towns in the district. This may have reduced the precision of the model's predictions in areas where weather conditions differed markedly from those observed at Katunayake.

CONCLUSION

In conclusion, this research has demonstrated the feasibility of using machine learning techniques, specifically the SARIMAX model, to predict dengue outbreaks in Sri Lanka. By analyzing historical dengue cases and weather parameters, we have shown that considering the time lag effect of weather parameters is crucial in forecasting dengue incidence. The SARIMAX model achieved promising results, with low RMSE values in several districts, indicating its potential as a tool for health authorities to anticipate and mitigate dengue outbreaks.

Author declaration

Acknowledgement

Grateful to the Sri Lanka Department of Meteorology for providing the weather data used in this study, under the restriction of use for educational purposes. Special thanks to the Sri Lankan Ministry of Health for making the dengue case data publicly accessible, facilitating the epidemiological analysis crucial to this research.

Authors' contributions:

Conceptualization: HUU, KMSLK, GDRM, SNK, FN; Methodology: HUU, KMSLK, GDRM; Investigation: HUU, KMSLK, GDRM; Validation: HUU, GDRM; Software: HUU; Data Curation: HUU; Formal Analysis: KMSLK; Visualization: GDRM; Writing – Original Draft: KMSLK, GDRM; Writing – Review & Editing: HUU; Supervision: SNK, FN, IE; Project Administration: KMSLK; Resources: SNK.

Conflicts of interest:

The authors declare that there is no financial or non-financial conflict of interest.

Funding statement:

This study was supported by publicly available data sources, and no external funding was received.

Ethics statement:

Before we began our research, we sought approval from a lecturer panel, who considered our topic ethically sound. As a result, we felt it unnecessary to conduct further research on the ethical aspects of our study. Ethical clearance was granted, and informed consent was obtained from all participants, ensuring they understood the study's objectives, procedures, and their right to withdraw at any time without consequence.

Statement on data availability:

Some of the data supporting the findings of this study are publicly available at <https://www.epid.gov.lk/weekly-epidemiological-report/weekly-epidemiological-report>. Additional data that are not publicly available can be obtained upon request from the corresponding author, subject to any necessary ethical or legal considerations.

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