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Deep learning with LSTM networks for dengue disease forecasting and control

Tahmid Nowsher^{1†}, Shaiful Islam Arafat^{2*†} and Md. Kamrujjaman^{1,3*} 

[†]Tahmid Nowsher and Shaiful Islam Arafat have contributed equally to this work.

*Correspondence:
Shaiful Islam Arafat
shaifulislamarafat@gmail.com
Md. Kamrujjaman
kamrujjaman@du.ac.bd

¹Department of Mathematics,
University of Dhaka, Dhaka
1000, Bangladesh

²Department of Mathematics,
Comilla University, Cumilla
3506, Bangladesh

³Department of Applied
Mathematics and Data Science,
Asian University for Women,
Chattogram 4000, Bangladesh

Abstract

Accurate forecasting of infectious disease dynamics is essential for effective public health planning and early outbreak response. Traditional statistical models and modern deep learning approaches have both been widely used for epidemiological time-series forecasting. Dengue fever remains a major public health concern in Bangladesh, where seasonal outbreaks often produce sharp and unpredictable infection spikes. Reliable forecasting models are therefore important for anticipating infection trends and supporting early intervention strategies. This study investigates the performance of Long Short-Term Memory (LSTM) networks for predicting daily dengue infection counts in Bangladesh using surveillance data from 2010 to 2022. Multiple LSTM architectures were developed by varying the number of LSTM units, lookback window size, and data preprocessing strategies. A fixed time-based data split was used, with training data up to 30 September 2021 and testing on subsequent observations to avoid information leakage. The proposed LSTM models were compared with several baseline forecasting approaches, including Naive, Seasonal-Naive, and ARIMA models. Model performance was evaluated using standard forecasting metrics including Mean Absolute Error (MAE), Root Mean Square Error (RMSE), and Symmetric Mean Absolute Percentage Error (SMAPE). Experimental results indicate that classical statistical models remain strong benchmarks for dengue forecasting. Among all evaluated models, the ARIMA(2,1,2) model achieved the best predictive performance on the test dataset with MAE of 8.40 and RMSE of 14.72. The best-performing LSTM configuration produced competitive results with MAE of 8.92 and RMSE of 15.87, outperforming simple baseline approaches such as the Naive and Seasonal-Naive models. These findings suggest that while deep learning models are capable of capturing complex temporal patterns, their advantage over well-tuned statistical models is not guaranteed for this dataset. The results highlight the importance of benchmarking deep learning models against classical time-series approaches when forecasting epidemiological data. While LSTM networks demonstrate promising performance in modeling nonlinear temporal dynamics, the ARIMA model provided the most accurate predictions for the studied dengue dataset.

Keywords Deep learning, LSTM model, ARIMA model, Dengue, Time-series forecasting



1 Introduction

The study of infectious disease dynamics is critical in understanding and predicting the spread of pathogens, guiding public health interventions and informing policy decisions. The advent of sophisticated computational models has significantly enhanced our ability to analyze complex time-series data, which is pivotal in tracking infection trends and projecting future outbreaks. Among these models, Long Short-Term Memory (LSTM) networks, a specialized form of recurrent neural networks (RNNs), have emerged as powerful tools for handling sequential data due to their ability to capture long-term dependencies and manage temporal information effectively. In recent years, the world has witnessed unprecedented challenges posed by infectious diseases, ranging from seasonal influenza to the global COVID-19 pandemic. Accurate prediction models are indispensable for preparing and responding to such outbreaks. Traditional statistical methods, while useful, often fall short in handling the non-linear and intricate patterns inherent in epidemiological data. This limitation necessitates the adoption of more advanced machine learning techniques, such as LSTMs, which can accommodate the non-stationary nature of infection counts and the multifaceted factors influencing their trends.

The motivation for utilizing LSTM networks in infectious disease modeling stems from their architecture, which is adept at maintaining and forgetting information as needed, thereby providing a nuanced approach to sequence prediction. Unlike standard RNNs, which suffer from issues like vanishing and exploding gradients, LSTMs employ a gating mechanism that regulates the flow of information, making them particularly suitable for tasks requiring the modeling of dependencies over extended periods. This capability is crucial for anticipating surges in infection rates and implementing timely interventions.

AI and deep learning have been a phenomenon in forecasting any epidemic model. The number of research papers on predicting many diseases such as COVID-19, HIV etc using AI and deep learning is increasing [1–5]. Yang Z et al. [6] used modified SEIR for mathematical analysis of dengue diseases and used one of the famous deep learning methods LSTM (Long Short-Term Memory) neural networks to forecast the disease. They trained actual data and with the help of it, then predicted the data. The application of machine learning techniques, particularly Long Short-Term Memory (LSTM) networks, has gained significant traction in forecasting infectious diseases due to their ability to model complex temporal dependencies. LSTM, first introduced by Hochreiter and Schmidhuber [7], was designed to overcome the limitations of traditional Recurrent Neural Networks (RNNs) by addressing the vanishing gradient problem, making it particularly suited for time-series prediction tasks involving long-term dependencies [7]. This architecture has been applied successfully in various studies to model infectious disease outbreaks.

For instance, Chae et al. [8] demonstrated the efficacy of deep learning models, including LSTM, in predicting influenza outbreaks, showing significant improvements over traditional epidemiological models [8]. Similarly, Liu et al. [9] applied LSTM to predict the trajectory of COVID-19 cases in China, emphasizing the challenges of forecasting abrupt changes in infection trends [9]. Arora et al. [10] further explored the use of LSTM for COVID-19 case prediction in India, highlighting the advantages of deep learning for short-term forecasts but also pointing out the difficulty in capturing sharp spikes in

infection counts [10, 11]. Salman et al. [12] extended these findings by employing LSTM to predict COVID-19 cases in Egypt, showing that hyperparameter tuning, such as adding dropout layers, can enhance prediction accuracy and reduce overfitting [12]. Li et al. [13] incorporated multiple data sources into LSTM-based models, achieving more accurate predictions of infectious disease outbreaks, especially in recognizing seasonal variations and sudden infection surges [13]. Shastri et al. [14] conducted a comparative study between India and the USA, demonstrating the LSTM model's performance across different regions and the impact of data quality on forecasting accuracy [14]. In addition to this literature, numerous studies have focused on and forecasted disease modeling using stochastic analysis to control epidemics [15–17].

While the application of LSTM models in predicting infectious diseases has been widely explored, several important methodological challenges remain. Many previous studies focus primarily on deep learning architectures without performing systematic comparisons with classical time-series forecasting approaches. In addition, some studies rely on random data splits that may lead to information leakage in time-series prediction problems. Establishing rigorous forecasting evaluation frameworks and benchmarking deep learning models against statistical baselines therefore remains an important research need.

In this study, we investigate the use of Long Short-Term Memory (LSTM) networks for forecasting daily dengue infection counts in Bangladesh using national surveillance data. To ensure a realistic forecasting setting, we employ a strict chronological data split in which historical observations are used for training and later observations are reserved for testing. In addition to evaluating multiple LSTM configurations, the deep learning models are compared with classical forecasting benchmarks including the Naive model, the Seasonal Naive model, and the ARIMA model. This comparative framework allows us to assess the relative predictive performance of deep learning and statistical models for dengue time-series forecasting.

Figure 1a–d shows a comparative rise in infection counts over recent years, with the worst scenario occurring during the 2019 monsoon season.

The remainder of this paper is organized as follows. Section 2 describes the forecasting framework, dataset, model structures, and evaluation metrics used in this study. Section 3 presents the numerical results and compares the forecasting performance of the proposed LSTM models with classical baseline approaches. Section 4 provides additional residual diagnostic analyses and discusses their implications for epidemic forecasting. Finally, Sect. 5 concludes the paper and outlines potential directions for future research.

2 Forecasting framework and model structures

This section describes the dataset, forecasting framework, deep learning models, baseline statistical models, and evaluation metrics used in this study. The experimental design follows a strict chronological evaluation protocol to ensure that models are trained on historical data and evaluated on future unseen observations.

2.1 Dataset

Daily dengue infection data for Bangladesh were obtained from the Directorate General of Health Services (DGHS) surveillance reports [18]. The dataset spans the period from

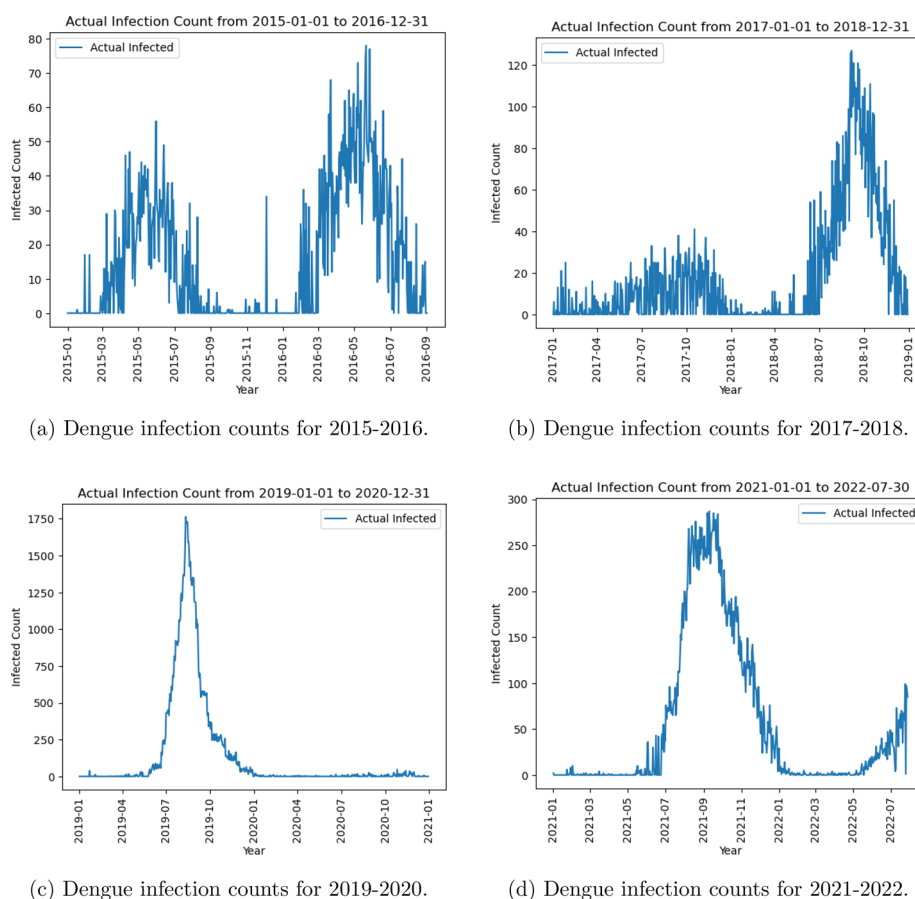


Fig. 1 Dengue infection trends over the years: a comparison of infection counts from 2015 to 2022 in four distinct periods

1 January 2010 to 30 July 2022 and contains the number of confirmed dengue infections reported each day. The temporal evolution of the infection counts is illustrated in Fig. 2. The data exhibit strong seasonal patterns associated with monsoon periods as well as large epidemic peaks during severe outbreak years.

To evaluate forecasting performance in a realistic setting, a fixed chronological split was applied. All observations up to 30 September 2021 were used for model training, while observations after this date were reserved for out-of-sample testing.

2.2 Forecasting workflow

The forecasting pipeline used in this study is illustrated in Fig. 3. The workflow consists of data preprocessing, sequence construction, model training, walk-forward forecasting, and performance evaluation. This framework ensures that models learn from historical infection trends and generate predictions for future observations without using information from the test period during training.

2.3 Data transformation and sequence construction

Because dengue infection counts are non-negative and often exhibit large outbreak spikes, a variance-stabilizing transformation was applied using $z_t = \log(1 + y_t)$. The transformed series was then normalized to the range $[0, 1]$ using a MinMax scaling procedure fitted only on the training data.

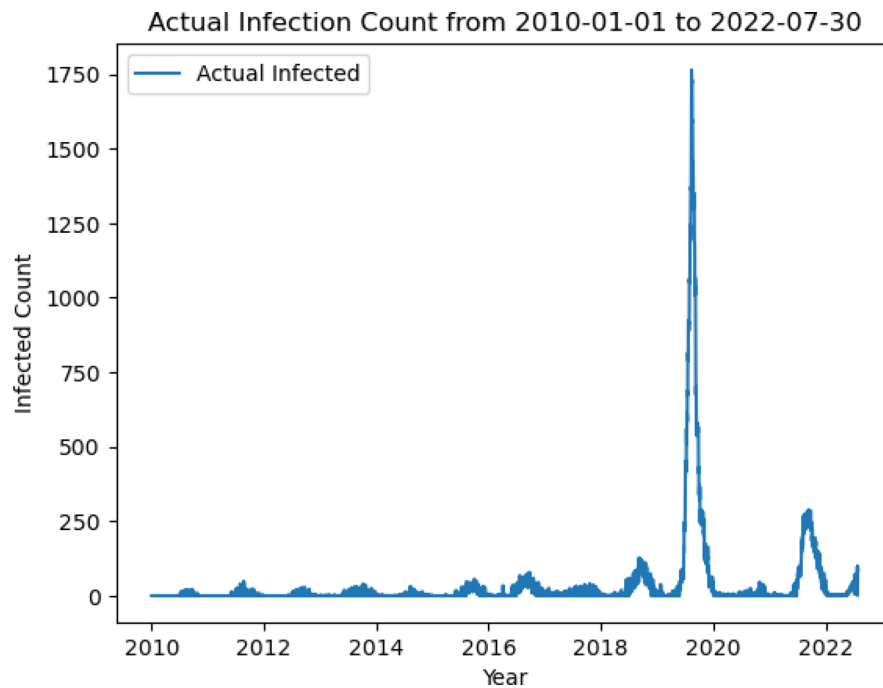


Fig. 2 Daily dengue infection counts in Bangladesh from 2010-01-01 to 2022-07-30

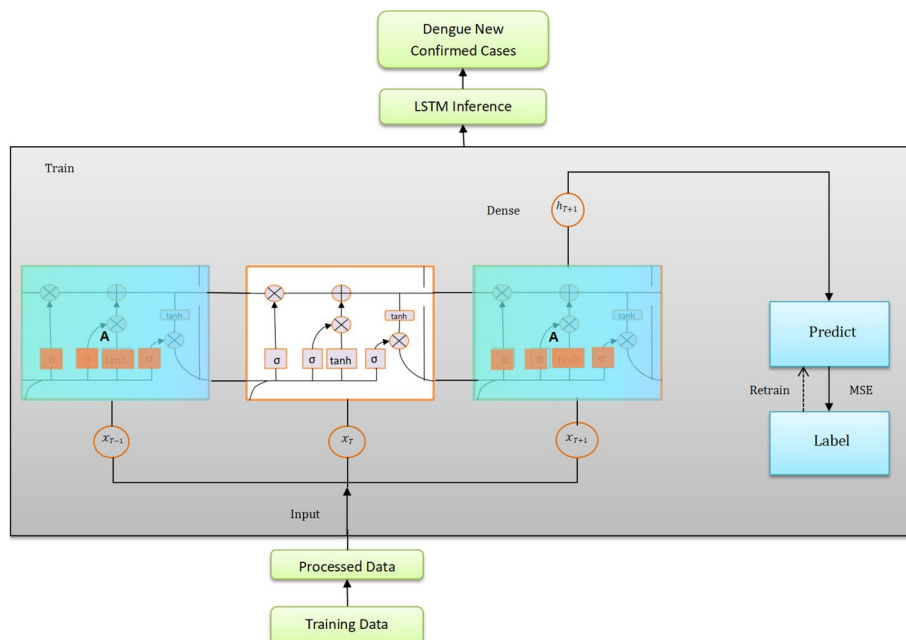


Fig. 3 Forecasting workflow used in the experimental framework

For LSTM training, the time series was converted into supervised learning sequences using a sliding window approach. For a lookback window length L , the input consists of the previous L observations $(z_{t-L}, \dots, z_{t-1})$, and the target output is z_t . Two lookback window sizes were investigated in this study: $L = 30$ and $L = 60$, allowing the model to learn either short-term or longer temporal dependencies in the infection time series.

2.4 LSTM model architectures

Deep learning models were implemented using stacked Long Short-Term Memory (LSTM) networks. The architecture of the forecasting network is illustrated in Fig. 4. Each network consists of two LSTM layers followed by dropout regularization and a dense output layer:

$$\text{LSTM}(u, \text{return_sequences} = \text{True}) \rightarrow \text{Dropout}(0.2) \rightarrow \text{LSTM}(u/2) \rightarrow \text{Dropout}(0.2) \rightarrow \text{Dense}(1).$$

Two model capacities were evaluated by setting the number of units in the first LSTM layer to $u = 50$ and $u = 64$. The second LSTM layer therefore contains 25 and 32 units respectively. This stacked architecture enables the network to capture hierarchical temporal patterns in dengue infection dynamics.

The models were trained using the Adam optimizer with mean squared error (MSE) loss. Each model was trained for up to 150 epochs with a batch size of 16. To preserve the temporal ordering of the data, shuffling was disabled during training. A time-aware validation split was created by reserving the final 10% of the training sequences for validation. Early stopping with patience equal to 10 epochs was applied to prevent overfitting and restore the model parameters corresponding to the lowest validation loss.

Out-of-sample predictions were generated using a one-step-ahead walk-forward forecasting strategy. At each step, the model predicts the next day's infection count using the most recent L observations. The input window is then updated using the actual observed value from the test dataset, allowing the model to sequentially forecast the entire test horizon.

2.5 Baseline forecasting models

To provide meaningful benchmarks for evaluating deep learning performance, three classical forecasting models were implemented.

Naive model: The Naive forecasting model predicts the next observation using the most recently observed value, i.e., $\hat{y}_t = y_{t-1}$. Predictions are generated sequentially using a walk-forward procedure.

Seasonal Naive model: The Seasonal Naive model predicts each observation using the value observed one seasonal period earlier. Because dengue outbreaks often follow annual seasonal patterns, a lag of 365 days was used, i.e., $\hat{y}_t = y_{t-365}$.

ARIMA model: An autoregressive integrated moving average (ARIMA) model was selected using a grid search over (p, d, q) combinations with $p \in \{0, 1, 2\}$, $d \in \{0, 1\}$, and

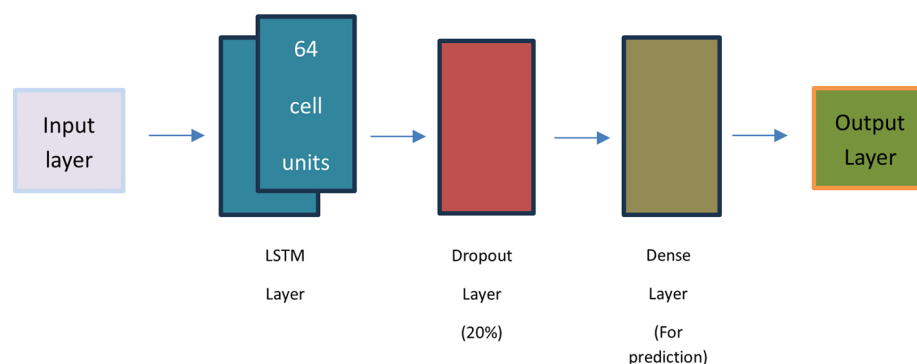


Fig. 4 Stacked LSTM architecture used for dengue infection forecasting

$q \in \{0, 1, 2\}$. Model selection was performed using a validation subset consisting of the final 10% of the training data. The best-performing ARIMA configuration was then refitted on the full training dataset and evaluated on the test period using one-step-ahead walk-forward forecasting.

2.6 Evaluation metrics

Forecasting accuracy was evaluated using four widely used performance metrics: Mean Absolute Error (MAE), Root Mean Square Error (RMSE), coefficient of determination (R^2), and Symmetric Mean Absolute Percentage Error (SMAPE). Let y_t denote the observed value at time t , $\hat{y}_t$ denote the predicted value, and n denote the number of observations in the test dataset.

The Mean Absolute Error (MAE) measures the average magnitude of prediction errors and is defined as

$$\text{MAE} = \frac{1}{n} \sum_{t=1}^n |y_t - \hat{y}_t|.$$

The Root Mean Square Error (RMSE) penalizes larger prediction errors more heavily and is defined as

$$\text{RMSE} = \sqrt{\frac{1}{n} \sum_{t=1}^n (y_t - \hat{y}_t)^2}.$$

The coefficient of determination (R^2) measures the proportion of variance in the observed data explained by the forecasting model:

$$R^2 = 1 - \frac{\sum_{t=1}^n (y_t - \hat{y}_t)^2}{\sum_{t=1}^n (y_t - \bar{y})^2},$$

where $\bar{y}$ represents the mean of the observed values.

Finally, the Symmetric Mean Absolute Percentage Error (SMAPE) provides a scale-independent measure of forecasting accuracy and is defined as

$$\text{SMAPE} = \frac{100}{n} \sum_{t=1}^n \frac{2|y_t - \hat{y}_t|}{|y_t| + |\hat{y}_t|}.$$

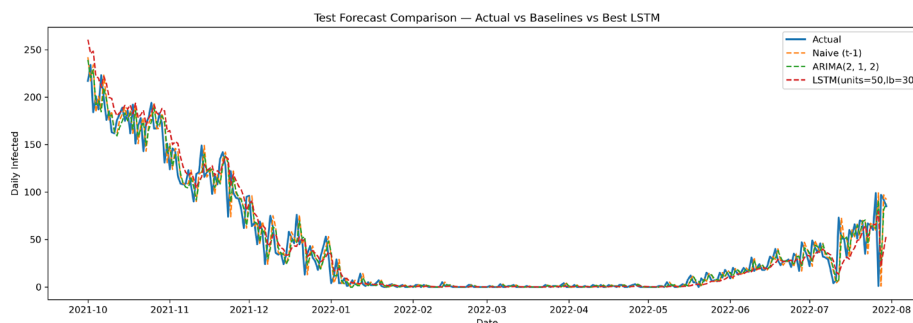
These complementary metrics provide a comprehensive assessment of forecasting performance by measuring both absolute prediction error and relative model explanatory power.

3 Numerical results and model comparison

This section presents the forecasting results obtained from the deep learning models and baseline statistical approaches described in Section 2. The objective of the analysis is to evaluate the predictive performance of the models on unseen test data and compare their ability to capture the temporal dynamics of dengue infections.

Table 1 Forecasting performance comparison of baseline and LSTM models on the test dataset

Model	MAE	RMSE	R^2	SMAPE(%)
ARIMA(2,1,2)	8.395	14.721	0.937	84.198
LSTM(units=50, lb=30)	8.920	15.866	0.927	83.305
Naive (t-1)	9.264	16.227	0.924	60.576
LSTM(units=64, lb=60)	14.558	24.971	0.819	90.663
LSTM(units=50, lb=60)	27.225	48.458	0.318	106.648
LSTM(units=64, lb=30)	29.226	52.188	0.209	108.840
Seasonal Naive (t-365)	38.759	68.245	-0.353	132.430

**Fig. 5** Comparison of observed dengue infections with forecasts produced by Naive, ARIMA, and the best-performing LSTM model over the entire test period

3.1 Model comparison

The final comparison table was constructed by combining the forecasting metrics obtained from the baseline models (Naive, Seasonal Naive, and ARIMA) and the LSTM models with different architectural configurations. The models are evaluated using four metrics: Mean Absolute Error (MAE), Root Mean Square Error (RMSE), coefficient of determination (R^2), and Symmetric Mean Absolute Percentage Error (SMAPE).

Table 1 presents the complete comparison of all models sorted by RMSE. Lower RMSE and MAE values indicate better forecasting accuracy, while higher R^2 values indicate stronger explanatory power.

The results indicate that the ARIMA(2,1,2) model achieves the lowest RMSE and MAE among all models, making it the most accurate forecasting model in this study. The best-performing LSTM model corresponds to the configuration with 50 units and a lookback window of 30 days. This model achieves forecasting accuracy comparable to the ARIMA model but slightly underperforms in terms of RMSE and R^2 .

These findings suggest that while deep learning models can effectively capture nonlinear temporal dependencies in dengue infection data, classical statistical models such as ARIMA may still perform competitively when the underlying time series exhibits strong autoregressive structure.

3.2 Forecast visualization

To further illustrate the forecasting performance of the models, Fig. 5 presents a comparison between the observed infection counts and the predictions generated by the Naive model, the ARIMA model, and the best-performing LSTM model. The figure covers the entire test period.

From Fig. 5, it can be observed that all models generally follow the overall trend of dengue infection counts. However, the ARIMA model appears to capture the short-term

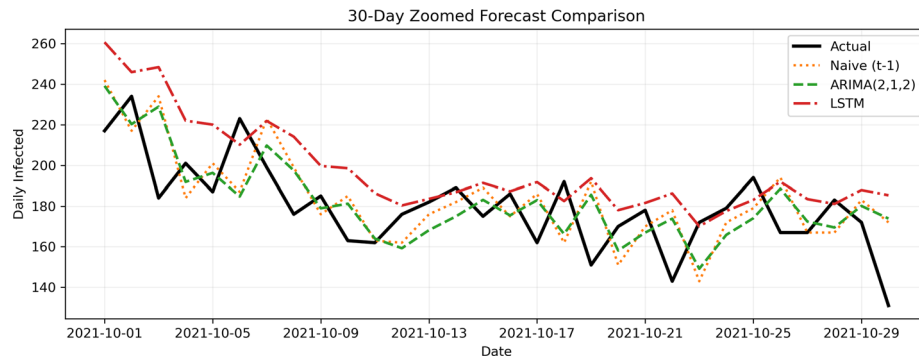


Fig. 6 Thirty-day zoomed comparison of forecasting performance between Naive, ARIMA, and LSTM models

Table 2 Residual diagnostic statistics for forecasting models

Model	Mean Residual	Std Residual	Lag-1 Autocorr	Ljung–Box p-value
Naive (t-1)	− 0.518	16.245	− 0.477	6.81×10^{-12}
ARIMA(2,1,2)	− 0.139	14.745	− 0.332	2.22×10^{-5}
LSTM (Best)	− 1.631	15.808	0.139	1.05×10^{-10}

fluctuations more accurately, particularly during periods of rapid increases or decreases in infection counts.

Because the full test horizon contains a large number of observations, visual interpretation can be challenging. Therefore, a zoomed view of the first 30 days of the test period is provided in Fig. 6.

The zoomed visualization clearly demonstrates that the ARIMA model tracks the observed infection counts more closely than the other models. The LSTM model follows the general trajectory but occasionally underestimates sudden changes in infection counts. The Naive model exhibits larger deviations due to its reliance on the most recent observation only.

3.3 Error and residual analysis

To further evaluate the statistical properties of the prediction errors, residual diagnostics were performed for the Naive, ARIMA, and best-performing LSTM models. Residuals were defined as the difference between the observed and predicted infection counts, i.e., $e_t = y_t - \hat{y}_t$. Ideally, a well-specified forecasting model should produce residuals with mean close to zero and minimal autocorrelation.

Table 2 summarizes several key diagnostic statistics of the residual series, including the mean residual, standard deviation, lag-1 autocorrelation, and the Ljung–Box test p-value for serial correlation.

The results indicate that the ARIMA model produces residuals with the smallest standard deviation and a mean residual closest to zero, suggesting more stable prediction errors compared to the other models. In contrast, the Naive model exhibits the strongest negative lag-1 autocorrelation, indicating systematic error patterns caused by its simplistic forecasting assumption.

The LSTM model demonstrates moderate residual variance but exhibits positive lag-1 autocorrelation, implying that some temporal dependence remains unexplained by the neural network predictions. The Ljung–Box test results further indicate that all models

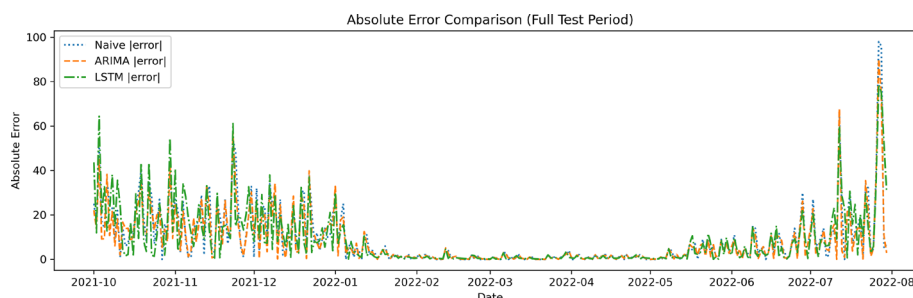


Fig. 7 Absolute error comparison of Naive, ARIMA, and LSTM models over the full test period

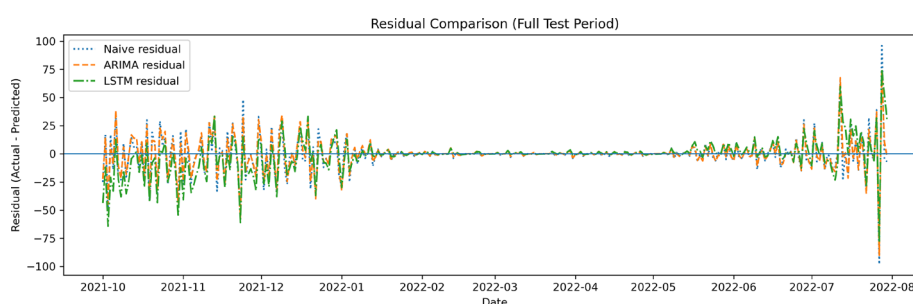


Fig. 8 Residual comparison for Naive, ARIMA, and LSTM models over the full test period

retain some degree of serial correlation in the residuals, although the ARIMA model reduces this dependence more effectively than the other approaches.

Additional diagnostic analyses, including residual histograms and QQ plots, were examined to assess the distributional properties of the prediction errors.

4 Residual diagnostics

This appendix presents additional diagnostic analyses used to evaluate the statistical properties of the forecasting errors. These analyses complement the residual statistics reported in Section 3.3 and provide a more detailed visual assessment of model performance.

Fig. 7 shows the absolute prediction errors for the Naive, ARIMA, and LSTM models over the entire test period. The figure illustrates that the ARIMA model generally produces smaller and more stable prediction errors compared with the other approaches.

The residual time series for each forecasting model are shown in Fig. 8. Residuals are defined as the difference between observed and predicted infection counts. Ideally, residuals should fluctuate randomly around zero without exhibiting systematic patterns.

The distribution of residuals for each model is further examined using histograms shown in Figs. 9, 10 and 11. These plots provide insight into the spread and symmetry of prediction errors.

To further assess the distributional properties of residuals, quantile–quantile (QQ) plots are shown in Figs. 12, 13 and 14. These plots compare the empirical distribution of residuals with a theoretical normal distribution and help identify potential deviations from normality.

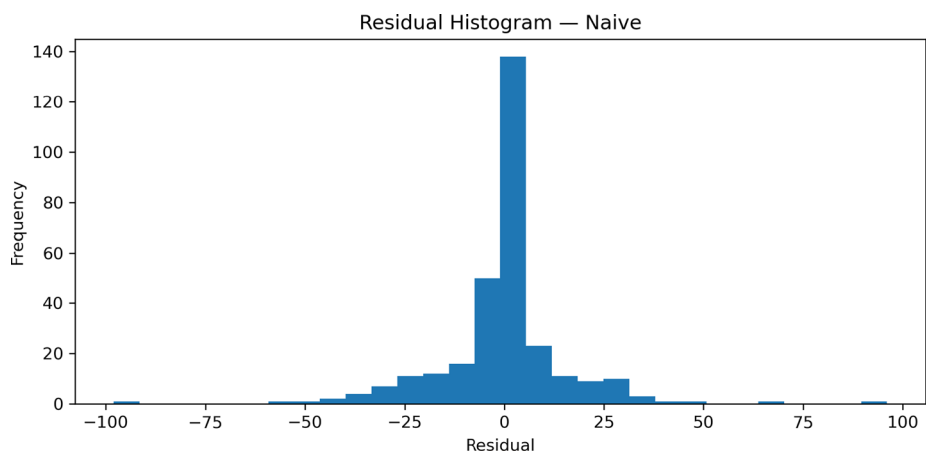


Fig. 9 Histogram of residuals for the Naive forecasting model

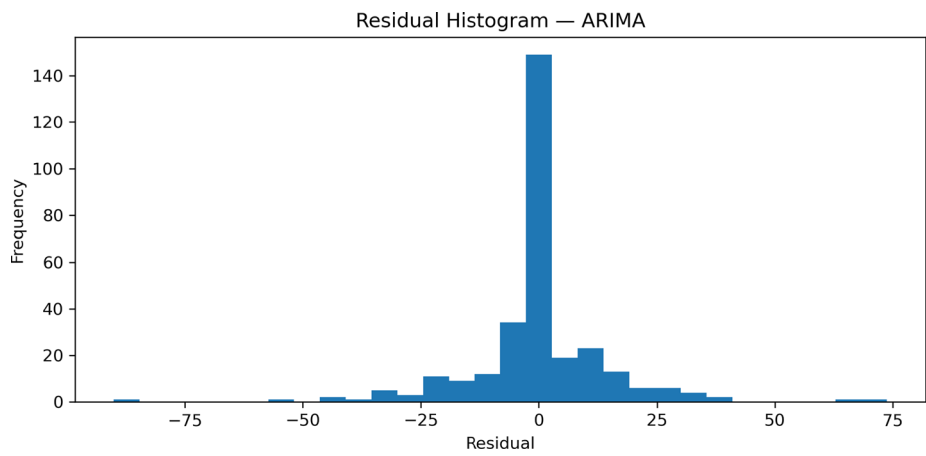


Fig. 10 Histogram of residuals for the ARIMA forecasting model

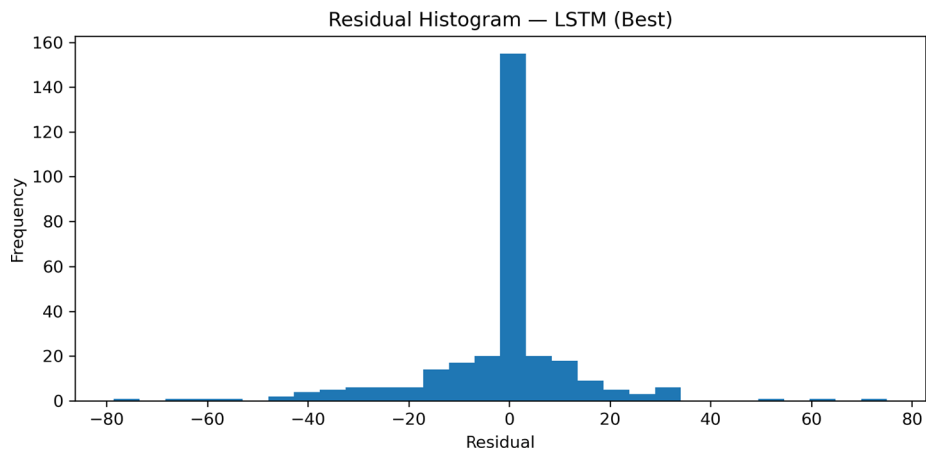


Fig. 11 Histogram of residuals for the best-performing LSTM model

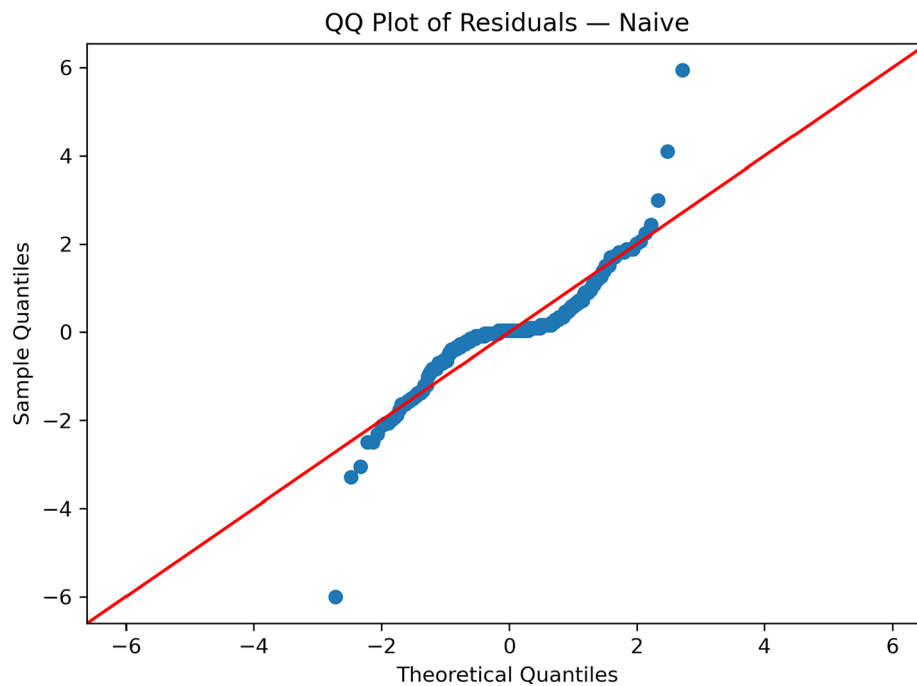


Fig. 12 QQ plot of residuals for the Naive forecasting model

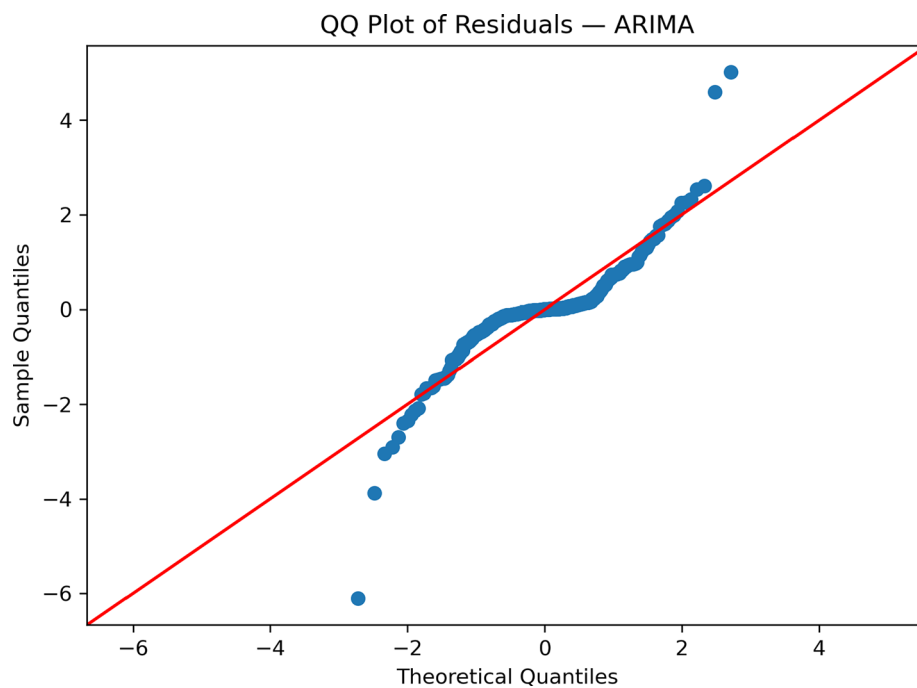


Fig. 13 QQ plot of residuals for the ARIMA forecasting model

4.1 Implications for epidemic forecasting

The forecasting results presented in this study provide several insights relevant to epidemic prediction and public health monitoring. First, the strong performance of the ARIMA model suggests that dengue infection counts in Bangladesh exhibit significant

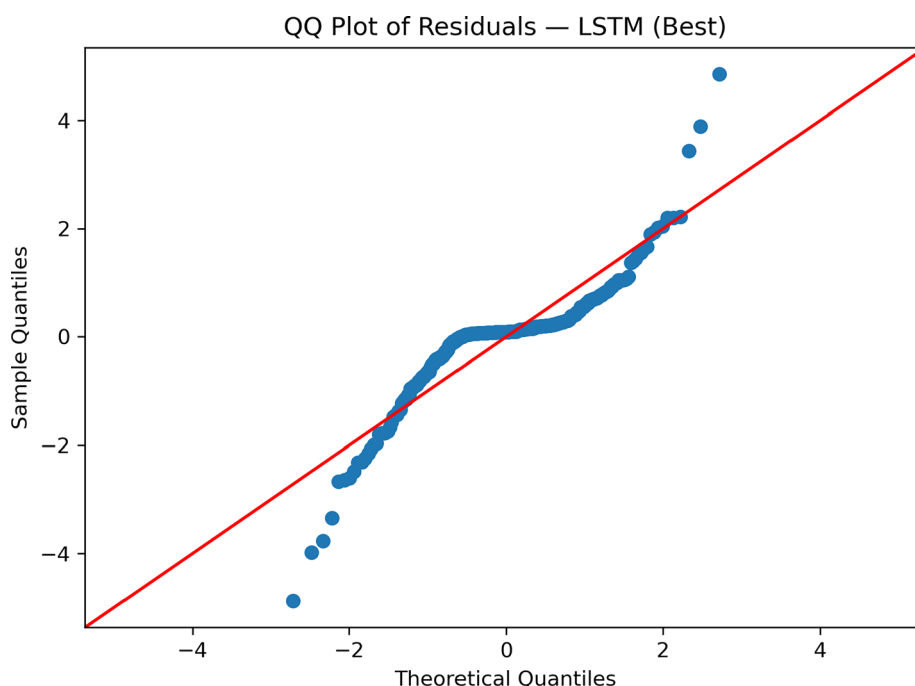


Fig. 14 QQ plot of residuals for the best-performing LSTM model

autoregressive and seasonal dynamics. These patterns arise from recurring climatic conditions, mosquito population cycles, and periodic outbreak behavior.

Second, although the LSTM models capture nonlinear relationships within the time series, their performance does not surpass the classical ARIMA approach when only historical infection counts are used as input. This observation highlights an important limitation of purely data-driven neural network models when the available dataset is relatively small or lacks additional explanatory variables.

Nevertheless, the LSTM framework remains promising for epidemic forecasting because of its ability to incorporate multiple predictors simultaneously. In practical epidemiological applications, environmental factors such as rainfall, temperature, humidity, and population mobility often influence dengue transmission dynamics. Integrating such covariates into multivariate LSTM architectures may further enhance prediction accuracy.

From a public health perspective, reliable short-term forecasting models can assist policymakers in anticipating outbreak surges and allocating healthcare resources more efficiently. Accurate prediction of dengue infection trends can support early warning systems, targeted vector control strategies, and improved preparedness during high-risk transmission periods.

5 Conclusion and future work

In this study, we investigated the problem of forecasting daily dengue infection counts in Bangladesh using both deep learning and classical time-series modeling approaches. A stacked Long Short-Term Memory (LSTM) network was developed and evaluated alongside baseline statistical models including the Naive, Seasonal Naive, and ARIMA models. The models were trained using historical infection data and evaluated on an

out-of-sample test period using multiple forecasting metrics, including MAE, RMSE, R^2 , and SMAPE.

The experimental results demonstrate that the ARIMA(2,1,2) model achieved the best overall forecasting accuracy among the models considered in this study. In particular, the ARIMA model produced the lowest RMSE and MAE values and exhibited more stable residual behavior compared with the Naive and LSTM models. The best-performing LSTM configuration, consisting of 50 units with a lookback window of 30 days, achieved forecasting accuracy close to the ARIMA model but slightly underperformed in terms of RMSE and R^2 . Residual diagnostics further revealed that the ARIMA model produced prediction errors with lower variance and weaker autocorrelation compared with the other models, indicating that it captured the temporal structure of the dengue infection series more effectively. These findings suggest that the dengue infection time series exhibits strong autoregressive characteristics that can be effectively modeled using classical statistical approaches.

Although the LSTM model did not outperform the ARIMA model in this univariate forecasting setting, the deep learning framework remains promising for epidemic prediction tasks. Neural network models are particularly advantageous when multiple explanatory variables are available and complex nonlinear relationships exist between predictors and disease transmission dynamics. Future research may extend this work by incorporating additional epidemiological and environmental factors, such as temperature, rainfall, humidity, and mosquito population indicators, into multivariate forecasting models. Hybrid approaches combining statistical and deep learning models may also improve prediction performance. Furthermore, probabilistic forecasting and uncertainty quantification techniques could provide more informative early warning tools for public health decision-making. These results highlight the importance of carefully benchmarking modern deep learning approaches against well-established statistical models in epidemiological forecasting applications.

The forecasting framework presented in this study provides a systematic approach for evaluating machine learning and statistical models for epidemic prediction. Accurate short-term forecasting of dengue infections can contribute to improved outbreak preparedness, targeted vector control strategies, and more efficient allocation of healthcare resources.

Acknowledgements

This project received partial funding from the University Grants Commission of Bangladesh and the University of Dhaka. I have not received a number for this grant.

Author contributions

Tahmid Nowsher: Conceptualization, Data curation, Formal analysis, Methodology, Software, Validation, Writing—original draft. Shaiful Islam Arfat: Conceptualization, Data curation, Formal analysis, Methodology, Software, Validation, Writing—original draft. Md. Kamrujjaman: Conceptualization, Validation, Resources, Investigation, Funding acquisition, Software, Supervision, Writing—review and editing. All authors have read and agreed to the published version of the manuscript.

Data availability

The data used in this study are publicly available and were obtained from the following source, which is publicly available: https://dashboard.dghs.gov.bd/pages/heoc_dengue_v1.php. There is no human participants in this study.

Declarations

Ethics approval and consent to participate

Not applicable.

Consent for publication

Not applicable.

Competing interests

The authors declare no competing interests.

Received: 4 January 2026 / Accepted: 29 June 2026

Published online: 17 July 2026

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