Comparative Analysis of Time Series Forecasting Methods for Dengue Fever in Thailand's EEC Zone

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***Abstract*— Dengue fever remains a persistent public health challenge in Thailand, with recurring outbreaks placing a heavy burden on health systems. The Eastern Economic Corridor (EEC), comprising Chachoengsao, Chonburi, and Rayong provinces, is particularly vulnerable due to rapid urbanization, industrial growth, and dense populations. Accurate forecasting of dengue cases is therefore critical for outbreak preparedness and effective interventions. This study compares two forecasting approaches—Autoregressive Integrated Moving Average (ARIMA) and Long Short-Term Memory (LSTM) neural networks—using dengue case data from 2012 to 2022 provided by the ASEAN–South Korea GFID platform. Model performance was evaluated under different data partitions using MAE, MSE, RMSE, and MAPE at regional and provincial levels within the EEC. Results show that ARIMA performs better in provinces with stable, linear patterns, such as Rayong, while LSTM provides greater accuracy in provinces with volatile and nonlinear trends, including Prachinburi and Chanthaburi. Findings indicate that no single model is universally superior; instead, model choice should align with local data characteristics. The study provides a comparative framework to support early-warning systems for dengue and suggests future directions involving hybrid models, external variables, and explainable AI for real-time epidemic preparedness.**

Keywords—Dengue Fever, Time Series Forecasting, ARIMA, LSTM, Eastern Economic Corridor (EEC), SDGs

I. Introduction

Dengue fever [1] is a mosquito-borne viral disease mainly transmitted by Aedes aegypti, common in tropical and subtropical regions including Thailand. Over the past decade (2012–2022), the country has faced recurring outbreaks that are difficult to predict and continue to strain the public health system. The Eastern Economic Corridor (EEC), covering Chachoengsao, Chonburi, and Rayong, is a rapidly developing region driven by industrial, transport, and residential growth. Such expansion, together with rising population density, has created favorable conditions for dengue transmission [2].

Accurate forecasting is essential for outbreak preparedness and resource allocation. Time series methods are widely applied in this field as they capture long-term trends, seasonal patterns, and fluctuations in historical data [3]. ARIMA (AutoRegressive Integrated Moving Average) is a classic statistical model effective for linear and stationary series, while LSTM (Long Short-Term Memory) neural networks can learn nonlinear and long-term dependencies, offering potential advantages in more complex epidemic patterns [4], [5].

This study compares ARIMA and LSTM models in forecasting dengue cases in the EEC using 2012–2022 data [6]. The objective is to evaluate their accuracy at both regional and provincial levels and provide a framework for selecting suitable forecasting tools. Such evidence can support local health management, early warning systems, and rapid responses to emerging diseases.

II. Related Work

A. Eastern Economic Corridor (EEC)

The Eastern Economic Corridor (EEC) is Thailand's flagship economic initiative aimed at driving competitiveness under the Thailand 4.0 policy. It promotes foreign investment, infrastructure development, and industrial expansion [7]. Key projects include the high-speed rail network, Laem Chabang Port Phase 3, and U-Tapao Airport [8], [9]. These developments have accelerated urbanization, land-use transformation, and population growth, which indirectly increase the risk of dengue transmission [10], [11]. Efficient infrastructure planning and public health strategies are therefore vital to mitigate these impacts [12].

B. Dengue Fever and Forecasting

Dengue fever remains a major public health challenge in tropical regions, with the WHO estimating 390 million infections annually [1]. In Thailand, outbreaks occur cyclically every 2–5 years [6], influenced by rapid urbanization, mobility, and climate conditions [2]. Forecasting has become a key tool for epidemic preparedness.

Statistical models such as ARIMA have been widely used to capture temporal and seasonal patterns of dengue incidence. Bhunia and Ghosh [13] demonstrated ARIMA's effectiveness in India, while Mahikul et al. [6] applied it successfully in Thailand. However, deep learning methods, particularly LSTM, have shown advantages in handling nonlinear and complex patterns. Wang et al. [14] reported improved performance of LSTM in China, and Jin et al. [5] confirmed its utility for predicting vector-borne diseases. Hybrid approaches have also emerged: Chae et al. [15] combined ARIMA and LSTM to improve accuracy in the Philippines.

III. Methodology

In this research, the methodology for conducting the study is divided into four main parts: (1) Data Collection and Preprocessing, (2) Statistical Analysis, (3) Prediction Model, and (4) Validation for the Prediction Model. The framework is illustrated in the figure below.

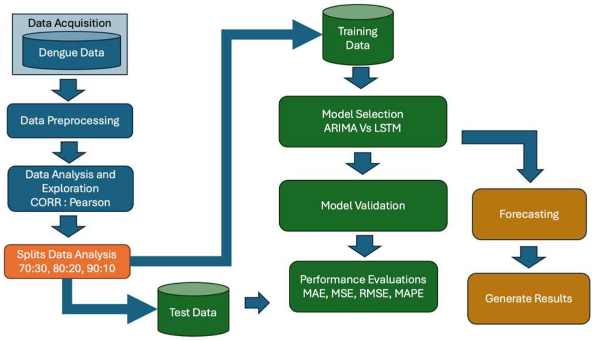

Fig. 1. Research Framework

A. Data Collection

Data collection and data use in the research experiments used Open Data from the ASEAN-South Korea Collaborative Platform for GFID Project Digital Information Sharing Platform for Global Disease Epidemics at the website https://aida.informatics.buu.ac.th/, which is a collaborative website for collecting data on epidemics in Thailand, Indonesia, and South Korea. The research used Dengue Virus data in 2012-2022 in the experiments, which can be accessed from the website as shown in the figure below.

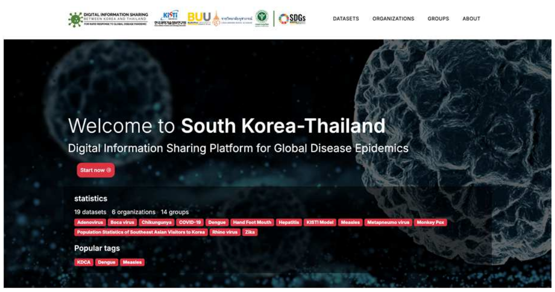

Fig. 2. Figure showing the website page for information on epidemic dissemination.

As illustrated in Fig. 2, we used Dengue Virus data from 2012 to 2022 in the experiment. The data can be displayed according to the number of Dengue Virus infections in Thailand as a whole and separated by region into six regions as follows:

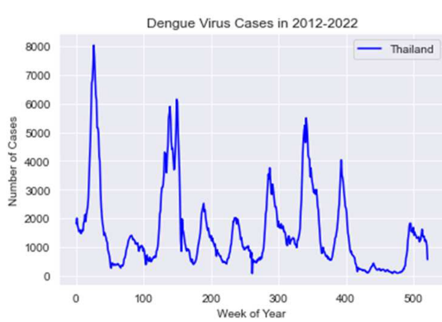

Fig. 3. The figure shows the total number of infected people in Thailand.

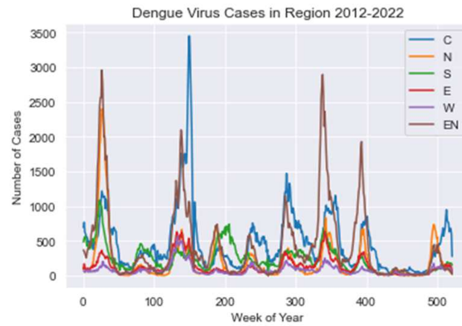

Fig. 4. Dengue virus cases by region in Thailand from 2012 to 2022.

As illustrated in Fig. 4, the number of dengue virus cases in Thailand between 2012 and 2022 was grouped and analyzed by region. The Central (C) region includes 22 provinces, the Northern (N) region 9 provinces, the Southern (S) region 14 provinces, the Western (W) region 5 provinces, the Eastern (E) region 7 provinces, and the Northeastern (EN) region 19 provinces. The figure highlights the temporal trends of infection across these regions, showing seasonal fluctuations and recurring outbreak peaks. For further analysis, Pearson's correlation was employed to examine the similarity of infection patterns between regions, using the number of reported cases in each period as the primary variable. To analyze the similarity of dengue infection patterns between two regions, denoted as u_a and u_b, we employed Pearson's correlation coefficient. This measure evaluates the degree of linear relationship between the time series of reported cases in each region.Let $r_{u,i}$ represent the number of infected individuals in region u during time period i, and let$\bar{r}_u$ denote the mean number of cases in region uuu over the observation period. The similarity between two regions, u_a and u_b, is then calculated as follows

$$sim(u_a, u_b) = \frac{\sum_{h=1}^{n}(r_{u_a,i_h} - \bar{r}_{u_a})(r_{u_b,i_h} - \bar{r}_{u_b})}{\sqrt{\sum_{h=1}^{n}(r_{u_a,i_h} - \bar{r}_{u_a})^2}\sqrt{\sum_{h=1}^{n}(r_{u_b,i_h} - \bar{r}_{u_b})^2}} \quad (1)$$

	C	N	S	E	W	EN
C	1.000	0.448	0.397	0.769	0.725	0.554
N	0.448	1.000	0.588	0.530	0.422	0.784
S	0.397	0.588	1.000	0.466	0.310	0.620
E	0.769	0.530	0.466	1.000	0.872	0.830
W	0.725	0.422	0.310	0.872	1.000	0.605
EN	0.554	0.784	0.620	0.830	0.605	1.000

Fig. 5. Similarity of dengue infection patterns between six regions of Thailand (2012–2022) using Pearson's correlation.

As shown in Fig. 5, dengue infection patterns across six regions of Thailand were compared using Pearson's correlation. Values close to 1 indicate strong similarity, while lower values suggest weaker associations. The Eastern (E) and Western (W) regions show the highest correlation (r = 0.872), followed by Eastern (E) and Northeastern (EN) (r = 0.830), indicating similar epidemic dynamics. In contrast, the Southern (S) and Western (W) regions have the lowest correlation (r = 0.310), reflecting distinct outbreak patterns. These results emphasize regional differences that should guide targeted surveillance and control strategies.

B. Statistical Analysis

1) Time Series: Data collected sequentially over time, such as daily, monthly, or yearly, can reflect trends, seasonal patterns, and uncertainties. Time series analysis is therefore an important technique used in many fields, such as economics, energy, finance, and epidemiology, particularly in forecasting infectious diseases that tend to change seasonally, such as dengue fever [2].

2) ARIMA (AutoRegressive Integrated Moving Average): It is a statistical data forecasting method that is popular and widely used, especially when the data is linear and has a trend. ARIMA consists of 3 main parts: (1) AR (AutoRegressive): using the values of past data to create a model, (2) I (Integrated): making the data stationary and (3) MA (Moving Average): using the values of errors from the past to adjust the values in the present. From research by Mahikul et al. [6] ARIMA was found to be able to predict infectious disease trends in Thailand satisfactorily, especially in areas with consistent epidemic patterns.

$$Y_t = c + \sum_{i=1}^{p} \emptyset_i Y_{t-i} + \sum_{j=1}^{q} \theta_j \varepsilon_{t-j} + \varepsilon_t \quad (2)$$

By Y_t: The actual value of the data at the time position t ,$\emptyset_i$: Coefficient of AR term (Auto Regression), θ_j : Coefficient of MA term (Moving Average) , ε_t: White noise, p: AR sequence, d : Number of times of differencing, q : MA sequence, and c : Constant.

3) LSTM (Long Short-Term Memory): is a Recurrent Neural Network (RNN) that is designed to learn long-term sequence relationships using a "memory" structure consisting of control functions such as forget gate, input gate, and output gate, allowing the model to retain and forget past data based on its importance [16].

Forget gate

$$f_t = \sigma\left(W_f \cdot [h_{t-1}, x_t] + b_f\right) \quad (3)$$

Input gate

$$i_t = \sigma(W_i \cdot [h_{t-1}, x_t] + b_i) \quad (4)$$

$$\tilde{c}_t = tanh(W_c \cdot [h_{t-1}, x_t] + b_c) \quad (5)$$

Update cell state

$$c_t = f_t \odot c_{t-1} + i_t \odot \tilde{c}_t \quad (6)$$

Output gate

$$o_t = \sigma(W_o \cdot [h_{t-1}, x_t] + b_o) \quad (7)$$

Hidden state output

$$h_t = o_t \odot tanh(c_t) \quad (8)$$

By x_t: Input at t time, h_{t-1}: hidden state from the past, c_t : Cell state at t time, σ: sigmoid function, and $\odot$: Element-wise multiplication.

4) MAE (Mean Absolute Error): is a measure of the difference between the actual value and the value estimated from the model. If the MAE value is low, it means that the model can estimate the value close to the experimental result.

$$MAE = \frac{1}{S}\sum_{i,j}\left|R_{i,j} - \hat{R}_{i,j}\right| \quad (9)$$

By $R_{i,j}$: is the actual value, $\hat{R}_{i,j}$: The predicted value obtained from the model, and S : Amount of data used in the model.

5) MSE (Mean Squared Error): Mean Squared Error values give special attention to values with large deviations.

$$MSE = \frac{1}{S}\sum_{i,j}\left(R_{i,j} - \hat{R}_{i,j}\right)^2 \quad (10)$$

By $R_{i,j}$: is the actual value, $\hat{R}_{i,j}$: The predicted value obtained from the model, and S : Amount of data used in the model.

6) RMSE (Root Mean Squared Error): is the square root of MSE, which still gives high weight to the error value and has the same units as the real data. It is a measure of the error which has the same characteristics as the square root of the mean standard deviation. If it is small, it means that the model can estimate the value close to the real value. It has the equation.

$$RMSE = \sqrt{\frac{1}{S}\sum_{i,j}\left(R_{i,j} - \hat{R}_{i,j}\right)^2} \quad (11)$$

By $R_{i,j}$: is the actual value, $\hat{R}_{i,j}$: The predicted value obtained from the model, and S : Amount of data used in the model.

7) MAPE (Mean Absolute Percentage Error): The average error is a percentage, suitable for comparing model performance across areas or different data units.

$$MAPE = \left(\frac{1}{S}\sum_{i,j}\frac{|R_{i,j} - \hat{R}_{i,j}|}{|R_{i,j}|}\right) * 100 \quad (12)$$

By $R_{i,j}$: is the actual value, $\hat{R}_{i,j}$: The predicted value obtained from the model, and S : Amount of data used in the model.

C. Prediction Model

In the research process, we have studied the data division for use in the experiment. In the research on Dengue Virus, a survey on the data division was conducted for use in this research. The research used the following data division techniques: Split data (1) Training data 70% Test data 30% (31.25%) (2) Training data 80% Test data 20% (15.63%) (3) Training data 90% Test data 10% (9.38%) Cross validation (1) 5 folds cross validation (3.13%) (2) 10 folds cross validation (65.63%). The research employed the ARIMA Model to determine the optimal data division for the experiment, utilizing the total number of infected people in Thailand as the test data. The experimental results of the data division are as follows.

Table I shows the results of the test of splitting the data. The Data were collected according to the specified proportions, namely 70:30, 80:20, and 90:10. The ARIMA Model was then used to forecast the number of infected people and evaluate their efficiency, with the results shown in the image below.

TABLE I. EVALUATION OF DATA SPLITTING STRATEGIES (ARIMA)

Type	Split 70:30	Split 80:20	Split 90:10
RMSE	127.677	97.439	130.215
MAE	77.341	58.627	87.506
MSE	16301.445	9494.415	16956.018
MAPE	0.123	0.136	0.127

The Fig. 6-8 shows the results of splitting the data into different periods used in the experiment using the ARIMA model for the entire country. Therefore, the 80:20 data split is the most appropriate for this research.

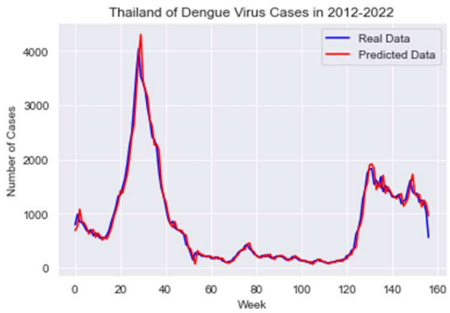

Fig. 6. Dengue virus cases in Thailand (2012–2022) with a 70:30 train–test data split.

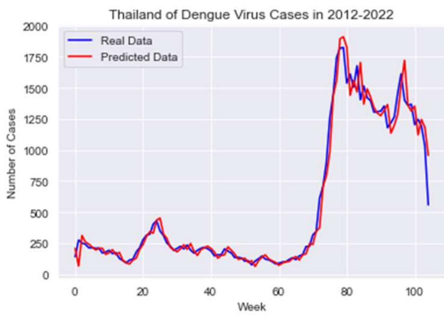

Fig. 7. Dengue virus cases in Thailand (2012–2022) with a 80:20 train–test data split.

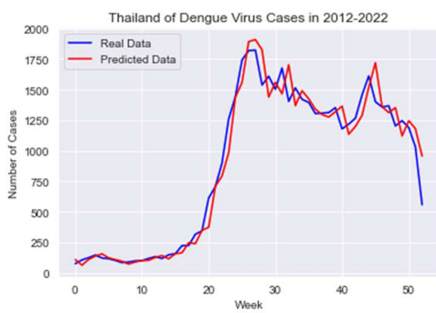

Fig. 8. Dengue virus cases in Thailand (2012–2022) with a 90:10 train–test data split.

As illustrated in Figs. 6–8, the dengue case data from 2012 to 2022 were divided into different training and testing ratios, namely 70:30, 80:20, and 90:10, to evaluate the performance of the forecasting models. The blue line represents the actual reported cases, while the red line shows the predicted values generated by the ARIMA model. Among the three scenarios, the 80:20 split (Fig. 7) demonstrated the most consistent alignment between predicted and actual values, indicating better model stability and generalization. Therefore, this proportion was selected as the optimal data division for building and testing both the ARIMA and LSTM forecasting models.

D. Validation for the Prediction Model

Validation for the Prediction of the research used ARIMA model and LSTM model to predict infection at the regional level and in each province in the Eastern region, which is a province in the EEC area, as shown below.

1) ARIMA MODEL: Using the ARIMA MODEL to forecast and test the performance of the forecast, the performance results are shown in Fig.9.

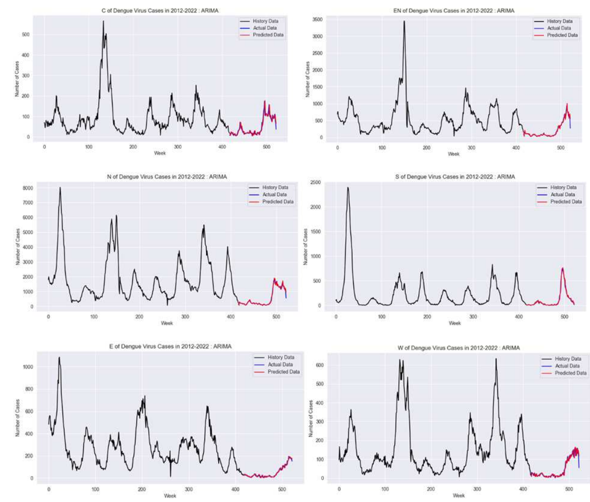

Fig. 9. Forecasting results of dengue virus cases in six regions of Thailand (2012–2022) using the ARIMA model.

As illustrated in Fig. 9, the ARIMA model was used to forecast dengue virus infections across Thailand's six regions. The graphs compare the actual number of reported cases with the predicted values, allowing for an assessment of model accuracy in different regional contexts. To quantitatively evaluate forecasting performance, four error metrics—MAE, MSE, RMSE, and MAPE—were calculated, with the results summarized in Table II.

TABLE II. REGIONAL FORECASTING PERFORMANCE (ARIMA)

Region	MAE	MSE	RMSE	MAPE
TH	18.74	1122.252	33.5	0.281
N	58.627	9494.415	97.439	0.136
W	9.032	191.37	13.834	0.354
E	7.472	100.635	10.032	0.306
S	17.12	915.768	30.262	0.416
EN	30.796	2922.903	54.064	0.196
C	9.952	207.602	14.408	0.33

When evaluating the efficiency of predicting the number of infected people by province in the Eastern region using the ARIMA MODEL, the results are shown in Table III.

TABLE III. PROVINCIAL FORECASTING PERFORMANCE (ARIMA)

Province	MAE	MSE	RMSE	MAPE
Sa Kaeo	0.82	2.328	1.526	6.6845E+14
Prachinburi	1.471	4.85	2.202	1.2293E+15
Chachoengsao	0.886	1.502	1.226	1.0779E+15
Chonburi	1.46	5.212	2.283	1.5092E+15
Rayong	6.422	93.388	9.664	0.538
Chanthaburi	3.377	29.382	5.42	5.9422E+14
Trat	1.211	3.203	1.79	6.7703E+14

2) LSTM MODEL: Using the LSTM model to forecast and test its performance, the results are presented in Fig.10.

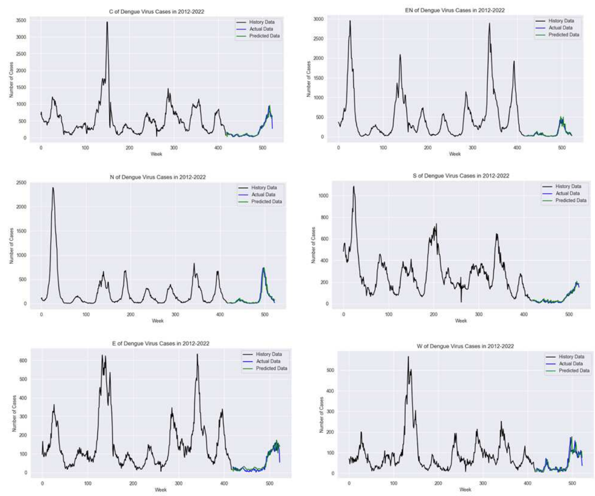

Fig. 10. Forecasting results of dengue virus cases in six regions of Thailand (2012–2022) using the LSTM model.

As illustrated in Fig. 10, the LSTM model was applied to forecast dengue virus infections across the six regions of Thailand. The plots compare actual reported cases with the predicted values, highlighting the model's ability to capture nonlinear and fluctuating outbreak patterns. To assess forecasting accuracy, the results were evaluated using MAE, MSE, RMSE, and MAPE, with detailed values presented in Table IV.

TABLE IV. REGIONAL FORECASTING PERFORMANCE (LSTM)

Region	MAE	MSE	RMSE	MAPE
TH	88.189	20413	142.87	0.199
N	31.402	3853.7	62.078	0.525
W	13.216	376.21	19.396	0.387
E	12.284	376.37	19.4	0.561
S	9.561	168.25	12.971	0.332
EN	73.924	9623.2	98.098	2.66
C	39.49	4576.9	67.652	0.256

When evaluating the efficiency of predicting the number of infected people by province in the Eastern region using the LSTM MODEL, the results are as shown in the table V.

TABLE V. PROVINCIAL FORECASTING PERFORMANCE (LSTM)

Province	MAE	MSE	RMSE	MAPE
Sa Kaeo	1.412	4.51	2.124	1.3874E+15
Prachinburi	0.996	1.96	1.4	1.2747E+15
Chachoengsao	1.51	5.291	2.3	1.2428E+15
Chonburi	8.232	169.874	13.034	0.64
Rayong	3.981	44.426	6.665	1.122E+15
Chanthaburi	1.244	3.792	1.947	8.8414E+14
Trat	1.05	2.215	1.488	2.1837E+15

IV. RESULT AND DISCUSSION

The results show that ARIMA and LSTM models have different performance in forecasting the number of dengue fever patients in the Eastern Economic Corridor (EEC) and different regions of Thailand, considering the MAE, MSE, RMSE, and MAPE indicators.

A. Regional comparison results

For regional comparison results, we have measured the performance of the prediction results with the values of MAE, MSE, RMSE, and MAPE as shown in the table VI.

TABLE VI. REGIONAL COMPARISON OF MAE (ARIMA VS. LSTM)

REGION	ARIMA:MAE	LSTM:MAE
TH	18.74	88.189
N	58.627	31.402
W	17.12	13.216
E	7.472	12.284
S	9.032	9.561
EN	9.952	73.924
C	30.796	39.49

TABLE VII. REGIONAL COMPARISON OF MSE (ARIMA VS. LSTM)

REGION	ARIMA:MSE	LSTM:MSE
TH	1122.252	20412.637
N	9494.415	3853.719
W	915.768	376.212
E	100.635	376.366
S	191.37	168.251
EN	207.602	9623.241
C	2922.903	4576.854

TABLE VIII. REGIONAL COMPARISON OF RMSE (ARIMA VS. LSTM)

REGION	ARIMA:RMSE	LSTM:RMSE
TH	33.5	142.873
N	97.439	62.078
W	30.262	19.396
E	10.032	19.4
S	13.834	12.971
EN	14.408	98.098
C	54.064	67.652

TABLE IX. REGIONAL COMPARISON OF MAPE (ARIMA VS. LSTM)

REGION	ARIMA:MAPE	LSTM:MAPE
TH	0.281	0.199
N	0.136	0.525
W	0.416	0.387
E	0.306	0.561
S	0.354	0.332
EN	0.33	2.66
C	0.196	0.256

The results from the table show that the ARIMA model gives lower error values MAE and RMSE than many regions, especially the Eastern and Central regions, indicating its suitability for forecasting linear and stationary data. The LSTM model also shows better performance in some areas, such as the Northern and Southern regions, which have fluctuating data patterns and are non-linear.

B. Provincial-level comparison results in the EEC area

Provincial level comparison results, we have measured the performance of the prediction results with the values of MAE, MSE, and RMSE as shown in the table XI - XII.

TABLE X. THE PROVINCE'S MAE VALUE OF ARIMA AND LSTM .

Province	ARIMA:MAE	LSTM:MAE
Sa Kaeo	0.82	1.412
Prachinburi	1.471	0.996
Chachoengsao	0.886	1.51
Chonburi	1.46	8.232
Rayong	6.422	3.981
Chanthaburi	3.377	1.244
Trat	1.211	1.05

TABLE XI. THE PROVINCE'S MSE VALUE OF ARIMA AND LSTM .

Province	ARIMA:MSE	LSTM:MSE
Sa Kaeo	2.328	4.51

Province	ARIMA:MSE	LSTM:MSE
Prachinburi	4.85	1.96
Chachoengsao	1.502	5.291
Chonburi	5.212	169.874
Rayong	93.388	44.426
Chanthaburi	29.382	3.792
Trat	3.203	2.215

TABLE XII. THE PROVINCE'S RMSE VALUE OF ARIMA AND LSTM .

Province	ARIMA:RMSE	LSTM:RMSE
Sa Kaeo	1.526	2.124
Prachinburi	2.202	1.4
Chachoengsao	1.226	2.3
Chonburi	2.283	13.034
Rayong	9.664	6.665
Chanthaburi	5.42	1.947
Trat	1.79	1.488

From the performance evaluation results table, it can be seen that in many provinces, such as Prachinburi, Chanthaburi, and Trat, the LSTM model gives lower error values than ARIMA, reflecting the potential of LSTM in dealing with complex Time Series data, while in some provinces, such as Rayong, the ARIMA model still has higher accuracy.

Overall, ARIMA is suitable for linear and uniform data, while LSTM is suitable for non-linear and volatile data. This finding is consistent with previous research that indicates that LSTM is better at learning long-term relationships in data, but it is sensitive to parameter settings and requires a large amount of data for learning. Appropriate application of both methods in each context may improve the accuracy of forecasting and epidemic management planning in the EEC area. This shows that no single model is best in all contexts. Instead, the choice of ARIMA or LSTM should depend on the data characteristics and local environment. This finding is essential for future policy management and dengue early warning systems.

V. CONCLUSION AND FUTURE WORK

This study compared ARIMA and LSTM models for forecasting dengue fever cases in Thailand's Eastern Economic Corridor (EEC) using data from 2012–2022. Results show that ARIMA provides higher accuracy in provinces with stable and linear trends, such as Rayong, while LSTM performs better in provinces with more volatile and nonlinear patterns, such as Prachinburi and Chanthaburi. These findings confirm that no single model is universally optimal; instead, model selection should be guided by the nature of local data and outbreak dynamics. The comparative framework presented here can inform evidence-based public health planning and strengthen dengue early-warning systems in the EEC, supporting timely interventions and efficient resource allocation.

Future research should prioritize three directions. First, hybrid approaches that combine ARIMA, LSTM, or other advanced techniques may improve predictive accuracy by leveraging both short-term linear and long-term nonlinear patterns. Second, integrating exogenous factors—such as rainfall, temperature, and socioeconomic indicators—can enhance forecasting reliability and provide actionable insights for outbreak prevention. Third, developing explainable and real-time forecasting platforms will allow policymakers and health professionals to better interpret predictions and respond rapidly to epidemics. Beyond technical improvement, the adoption of sustainable forecasting systems contributes to the United Nations Sustainable Development Goals (SDGs), particularly SDG 3 on ensuring healthy lives and SDG 11 on building resilient, sustainable communities. Embedding such systems into long-term health governance frameworks can promote resilience, reduce the social and economic costs of outbreaks, and ensure preparedness for future vector-borne and emerging diseases across Thailand and the ASEAN region.

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