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Benchmarking LSTM and Attention-Based Models for Climate-Driven Dengue Prediction in Lampung, Indonesia

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ABSTRACT

Dengue fever remains one of the most significant vector-borne diseases in tropical regions, with transmission dynamics strongly influenced by climatic variability. This study develops a data-driven deep learning framework to forecast monthly dengue incidence in Lampung Province, Indonesia, using Long Short-Term Memory (LSTM) networks. Monthly climatic variables i.e. temperature, rainfall, and relative humidity together with standardized dengue incidence data from 2015–2024 were analyzed. Cross-correlation analysis revealed 2–3-month lagged effects for rainfall and temperature, guiding the construction of lagged predictors. Three recurrent neural architectures i.e. LSTM, Stacked LSTM (S-LSTM), and Temporal-Attention LSTM (TA-LSTM) were optimized through a Genetic Algorithm (GA). Comparative evaluation against traditional models (SVR, MLP, and Random Forest) demonstrated that the S-LSTM with [42, 122] units achieved the best overall accuracy, with Mean Absolute Percentage Errors (MAPE) of 21.5 % (train) and 32.0 % (test), outperforming both simpler and more complex alternatives. The findings highlight that temporal depth and automatic architecture optimization significantly improve model generalization, capturing lagged nonlinear dependencies between climate and dengue incidence. This framework provides the first localized deep learning early-warning system for dengue in Lampung, offering a scalable basis for climate-informed public health surveillance across Indonesia.

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1. INTRODUCTION

Dengue fever (DF) is one of the most prevalent mosquito-borne viral diseases in tropical and subtropical regions and continues to pose a major global public health threat [16]. The disease is caused by the dengue virus, which is transmitted through the bites of infected female *Aedes aegypti* and *Aedes albopictus* mosquitoes. In 2019, dengue was listed by the World Health Organization as one of the ten greatest global health threats, and the number of cases reported in 2023 reached the highest level recorded to date [1]. This persistent burden underscores the

strong linkage between dengue transmission dynamics and environmental variability, particularly climate change.

The primary vector, *Aedes aegypti*, is highly sensitive to climatic conditions such as temperature, rainfall, and relative humidity. These factors influence the mosquito's life cycle and the efficiency of viral replication and transmission. Temperature accelerates mosquito development and viral incubation [8],[10], while humidity supports adult survival and increases biting frequency. Rainfall determines the availability of breeding sites, directly affecting larval density and vector abundance [2],[3],[13]. Consequently, climatic fluctuations exert a considerable impact on dengue incidence, both through short-term weather anomalies and longer-term climate patterns.

Empirical studies have shown that optimal humidity levels (66.67%–89.6%) are associated with an increase in dengue cases, often preceded by periods of intense rainfall or the onset of the wet season [3],[4],[14]. These climatic factors not only regulate mosquito reproduction and longevity but also influence the timing and intensity of dengue outbreaks. However, the effects of climate conditions are not immediate; rather, they are delayed due to the biological processes governing mosquito development and virus transmission. This delay—commonly referred to as the *time lag effect*—represents the period between changes in climatic variables and their observable impact on dengue incidence [5],[6],[7]. Considering this lag is essential for improving disease prediction accuracy, as climatic variations typically require several weeks to translate into measurable changes in case counts.

Previous climate-based dengue models in Indonesia have primarily focused on metropolitan or coastal regions such as Jakarta and Bali, where high-resolution datasets and long-term surveillance records are available. For example, studies such as DBDKlim successfully integrated climatic predictors into early-warning frameworks for those areas. In contrast, Lampung Province—despite being a key endemic region in southern Sumatra—has not yet been systematically analyzed using data-driven predictive approaches that incorporate lagged climate factors. This absence of localized modeling limits the capacity to design timely public health interventions in the province.

To address this research gap, the present study applies Long Short-Term Memory (LSTM) neural networks to explore the delayed influence of climatic variables on dengue incidence in Lampung Province, Indonesia. LSTM, a variant of recurrent neural networks specifically designed to capture long-term temporal dependencies in sequential data [9], provides a robust framework for modeling the nonlinear and lagged relationships between weather fluctuations and disease transmission patterns. By explicitly incorporating lagged climatic predictors including temperature, rainfall, relative humidity, and Dengue incidence. The model seeks to better represent the incubation-related delays inherent in dengue transmission dynamics.

Unlike previous works that primarily focused on national or city-level models such as the DBDKlim systems in Jakarta and Bali, this study represents the first localized data-driven modeling effort for Lampung Province. The research introduces a systematic approach that integrates empirically derived lag structures, LSTM-based temporal modeling, and genetic algorithm (GA)-based architecture optimization to improve predictive reliability under regional climatic and epidemiological conditions. The resulting framework is expected to support the development of a province-specific, climate-informed dengue early warning system, contributing to both scientific understanding and practical public health preparedness in Indonesia.

2. MATERIALS AND METHODS

2.1. Study Area

Lampung Province lies at the southernmost part of Sumatra Island, Indonesia, between 3°45'–6°45' S and 103°40'–105°50' E. The province covers approximately 35,000 km² and has a tropical monsoon climate characterized by two distinct seasons: a wet season from November to April and a dry season from May to October. Average monthly temperatures range between 24 °C and 33 °C, with annual rainfall exceeding 2500 mm in several districts. Major urban centers such as Bandar Lampung, Metro, and Pringsewu record recurrent dengue outbreaks each year. Although dengue surveillance has been continuously conducted by the local health authorities, no previous data-driven climatic prediction system has been developed for the region—unlike the DBDKlim initiatives implemented in Jakarta and Bali. This research therefore represents the first systematic attempt to construct a localized LSTM-based climate–dengue forecasting framework for Lampung.

2.2. Data Description

Monthly dengue incidence data from January 2015 to December 2024 were obtained from the Lampung Provincial Health Office. The incidence was standardized per 100,000 population using interpolated mid-year census data from the Indonesian Bureau of Statistics (BPS). Climatic predictors i.e. average temperature ($^{\circ}\text{C}$), total rainfall (mm), and relative humidity (%) were sourced from the Meteorological, Climatological, and Geophysical Agency (BMKG).

Dengue and Climate Variables in Lampung (2015–2024)

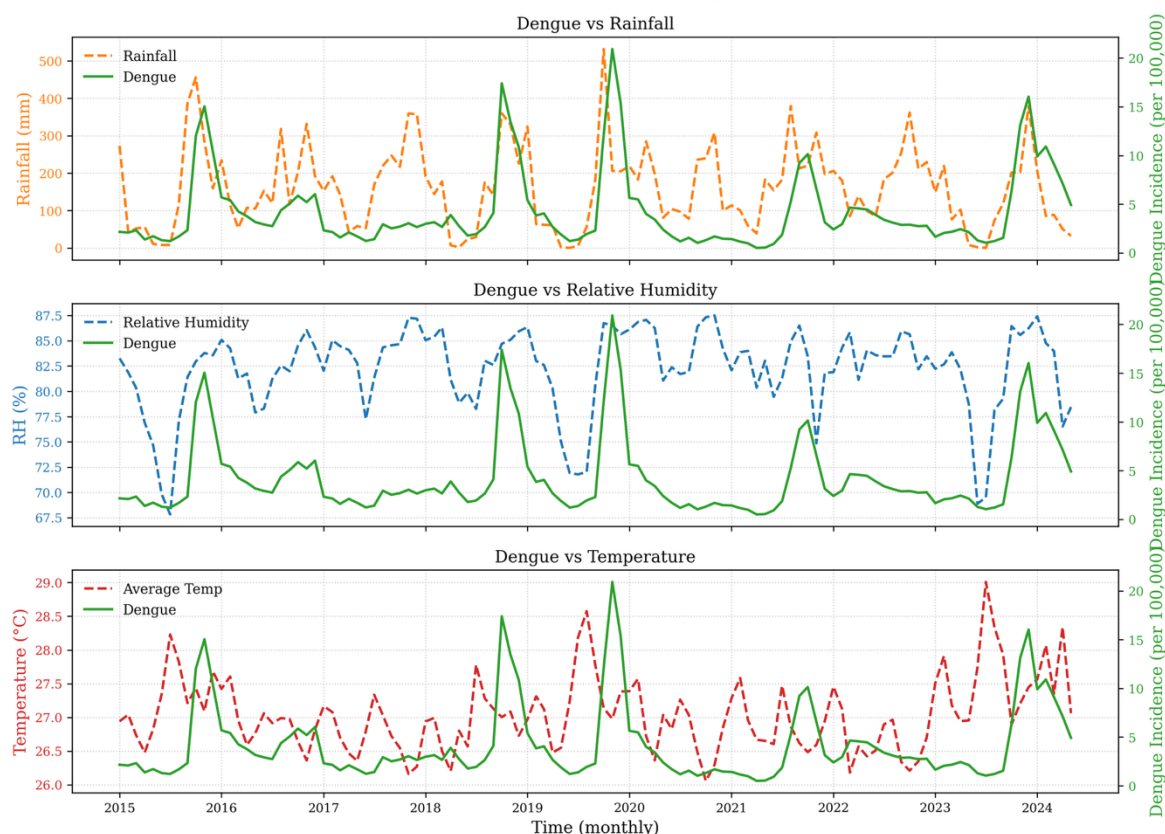


Figure 1. Dengue incidence and climate data in Lampung (2015–2024).

Figure 1 overlays monthly dengue incidence (indicated by right y-axis) with three climate variables (indicated by left y-axis) from Jan-2015 to 2024. In the rainfall data, major dengue surges (e.g., early-2016, late-2019/early-2020, and 2024) occur shortly after large rainfall peaks, suggesting a lagged, positive association consistent with increased vector breeding following wet months. The relative humidity data shows dengue tending to rise during periods of sustained higher RH (approximately 80–85%), again with a short delay, troughs in RH coincide with relatively lower dengue. The Temperature data exhibits a weaker pattern i.e. temperature varies within a narrow band (approximately 26–28.5 $^{\circ}\text{C}$), and dengue peaks visually do not align as tightly with short-term temperature fluctuations as they do with rainfall and humidity. Overall, the plots indicate stronger seasonality and lagged co-movement of dengue with rainfall and humidity than with temperature, motivating formal lagged or distributed-lag modeling in the analysis.

2.3. Data Pre-processing

Prior to model development, all variables were synchronized to a common monthly timeline. Missing climate observations ($< 2\%$) were linearly interpolated. Each feature was then normalized to the range $[0, 1]$ using a Min–Max scaler fitted exclusively on the training subset to prevent data leakage. To reflect the temporal dependency of dengue transmission, input–output sequences were structured in a sliding-window format: for each month t , the previous p months of climate data were used to predict dengue incidence at $t + 1$. Lag selections of $p = 1 - 6$ were compared during model tuning.

The full dataset was divided chronologically into training (70 %), validation (15 %), and testing (15 %) sets, ensuring that future information did not leak into earlier periods. Performance stability was further checked using a rolling-origin cross-validation scheme.

2.4. Model Architecture

2.4.1 LSTM cells as computational unit

The Long Short-Term Memory (LSTM) network is a variant of the Recurrent Neural Network (RNN) designed to overcome the *vanishing gradient* problem commonly encountered in sequential or time-series data processing. Unlike conventional RNNs, which tend to lose information over long sequences, the LSTM architecture can selectively retain, update, and discard information across extended time spans, allowing it to capture complex temporal dependencies among variables in time-series datasets [23].

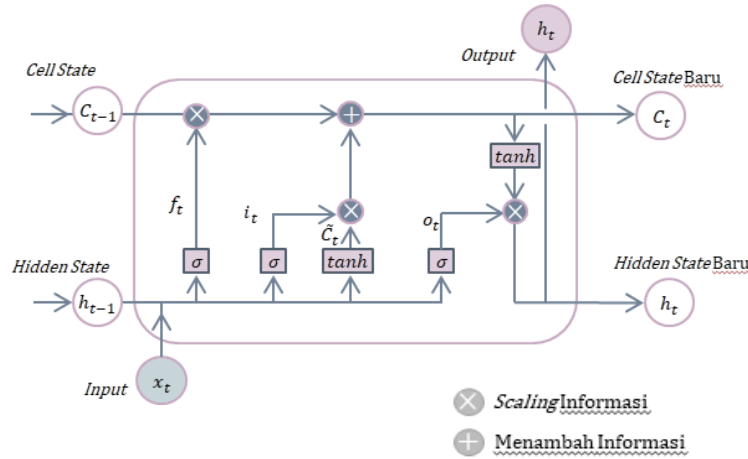


Figure 2. Illustration of an LSTM Cell

An LSTM network consists of a series of processing units known as *memory cells* (Figure 2), each containing three main gates: the forget gate, input gate, and output gate. The forget gate determines which information from the previous state should be discarded; the input gate regulates which new information should be stored in the cell; and the output gate controls which portion of the cell state is passed forward as the hidden output [24]. Through these mechanisms, the LSTM can maintain long-term dependencies in the data more stably and effectively than a standard RNN.

Mathematically, the internal structure of the LSTM cell can be described as follows.

- (a) Forget Gate: decides what portion of the previous information should be retained or discarded, based on the current input x_t and the previous hidden state h_{t-1}

$$\sigma(W_f \cdot [h_{t-1}, x_t] + b_f) \quad (2)$$

where f_t is the forget gate vector at time t , x_t is the input, h_{t-1} is the previous hidden state, W_f and b_f are the weight and bias terms, and σ denotes the sigmoid activation function.

- (b) Input Gate: regulates the information to be added to the current cell state using two activation functions (sigmoid and $\tanh$):

$$i_t = \sigma(W_i[h_{t-1}, x_t] + b_i) \quad (3)$$

$$\tilde{C}_t = \tanh(W_c[h_{t-1}, x_t] + b_c) \quad (4)$$

where i_t represents the input gate, $\tilde{C}_t$ is the candidate cell state, W_i and W_c are the respective weight matrices, b_i and b_c are the bias vectors, and $\tanh$ is the hyperbolic tangent activation.

- (c) Cell State Update: combines the retained information from the forget gate and the new candidate state to update the overall memory cell

$$C_t = f_t \cdot C_{t-1} + i_t \cdot \tilde{C}_t \quad (5)$$

where C_t and C_{t-1} denote the current and previous cell states, respectively.

- (d) Output Gate: determines the next hidden state h_t that serves as both the output and the recurrent input for the next time step

$$o_t = \sigma(W_o[h_{t-1}, x_t] + b_o) \quad (6)$$

$$h_t = o_t \cdot \tanh(C_t) \quad (7)$$

In this study, the LSTM model is applied to predict dengue incidence by learning the temporal relationships between climatic factors—rainfall, humidity, temperature, and sunshine duration—and the monthly number of dengue cases. By incorporating time-lagged climate variables, the LSTM can detect delayed effects between

environmental fluctuations and subsequent increases in dengue incidence, leading to more precise forecasting for disease monitoring and control [25].

2.4.2 Time Attention Mechanism

Let an input window $X = (x_1, \dots, x_L)$, $x_t \in \mathbb{R}^d$. An LSTM encodes the sequence into hidden states $h_t \in \mathbb{R}^H$ (and cells c_t), e.g.

$$\begin{aligned} i_t &= \sigma(W_i x_t + U_i h_{t-1} + b_i), f_t = \sigma(W_f x_t + U_f h_{t-1} + b_f), \\ \tilde{c}_t &= \tanh(W_c x_t + U_c h_{t-1} + b_c), c_t = f_t \odot c_{t-1} + i_t \odot \tilde{c}_t, \\ o_t &= \sigma(W_o x_t + U_o h_{t-1} + b_o), h_t = o_t \odot \tanh(c_t). \end{aligned}$$

Instead of using only the last state h_L , temporal attention learns data-driven weights over all $\{h_t\}_{t=1}^L$ and forms a context vector c by a convex combination:

$$c = \sum_{t=1}^L \alpha_t h_t, \quad \alpha_t = \frac{\exp(e_t)}{\sum_{j=1}^L \exp(e_j)}, \quad \alpha_t \geq 0, \quad \sum_t \alpha_t = 1$$

The “energy” (or score) e_t measures how relevant h_t is for the current prediction. Two common choices:

- Additive attention

$$e_t = v^T \tanh(W_h h_t + W_q q + b),$$

- Dot-product attention

$$e_t = \frac{1}{\sqrt{H}} h_t^T q.$$

Here the query q summarizes “what we are looking for.” In sequence forecasting, a standard and effective choice is

$$q = W_c h_L \text{ (query derived from the last LSTM state),}$$

though q can also be a learned vector or another function of $\{h_t\}$. Finally, the model predicts from c (optionally concatenated with h_L):

$$\hat{y} = W_y c + b_y$$

Interpretation. The weights α_t are time-step importances: large α_t means the model relies more on month t in the look-back window. Because α_t form a probability simplex, the mechanism yields an interpretable, normalized attribution over past times. Training minimizes a loss (e.g., MSE) and backpropagates through the softmax, jointly learning the encoder (LSTM) and the attention scorer ($W_h, W_q, v, \dots$).

2.4.3 Proposed LSTM Architecture

Figure 3 compares three sequence-modeling pipelines used for one-step-ahead dengue prediction from a look-back window of monthly observations. All variants share the same input and output scaffold: the input sequence is first normalized with Batch Normalization to stabilize training; the final prediction is produced by a linear Dense head, with Dropout before the head for regularization. The LSTM baseline (left) uses a single recurrent layer whose last hidden state summarizes the window. The Stacked LSTM (center) deepens the temporal encoder by feeding a second LSTM with the full sequence of states from the first, enabling higher-order temporal interactions. The LSTM + Temporal Attention model (right) retains the full sequence of LSTM states, applies Spatial Dropout (channel-wise) as stronger regularization, and then a Temporal Attention block that learns importance weights over past months to form a context vector, from which the Dense head predicts the next value. This design isolates the effects of depth (Stacked LSTM) and data-driven time weighting (Attention) while keeping preprocessing and heads identical.

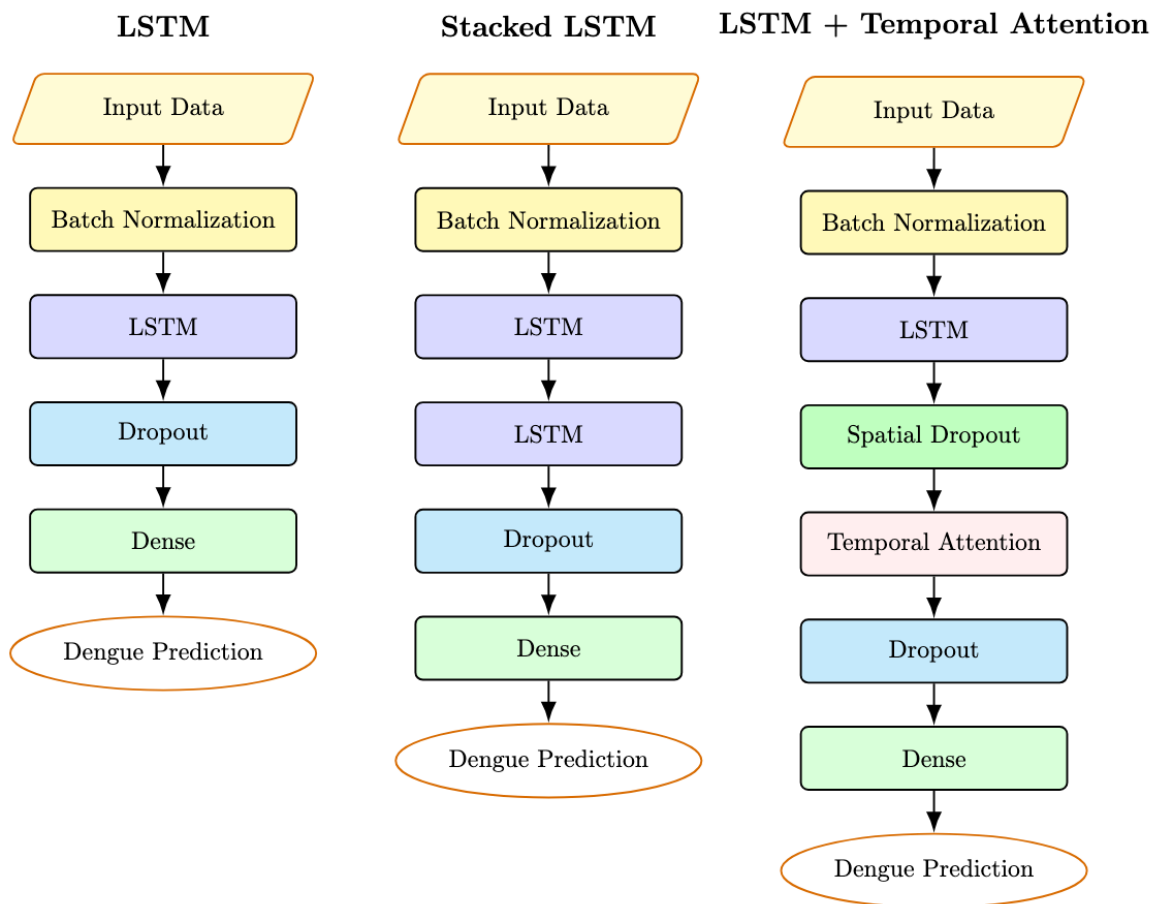


Figure 3. Architectures evaluated for dengue prediction—(left) LSTM, (center) Stacked LSTM, and (right) LSTM with Temporal Attention. Each pipeline receives an input sequence, applies batch normalization, encodes with one or two LSTMs, regularizes (dropout), and predicts through a dense layer; the attention model additionally learns per-time-step weights before the prediction head

2.5. Benchmark and Evaluation

For comparison, three traditional models frequently used in epidemiological forecasting were implemented as benchmarks: Support Vector Regression (SVR) with radial-basis-function kernel, Decision Tree Regressor (DT), and a simple Artificial Neural Network (ANN) with two hidden layers (32–16 neurons). Each baseline was tuned through grid search on the validation subset.

Model performance was evaluated using Mean Absolute Percentage Error (MAPE), Mean Absolute Error (MAE), Root Mean Squared Error (RMSE), and the coefficient of determination (R^2). Lower error values and higher R^2 indicate better predictive accuracy. Statistical significance between models was assessed using the Diebold–Mariano test on forecast errors.

The Mean Absolute Percentage Error (MAPE) is expressed as

$$MAPE = \frac{100\%}{N} \sum_{t=1}^N \frac{|y_t - \hat{y}_t|}{|y_t|} \quad (8)$$

where y_t represents the actual value at time t , $\hat{y}_t$ denotes the predicted value at time t , and N is the total number of observations.

MAPE quantifies the average prediction error as a percentage, thereby providing an intuitive measure of how far predicted values deviate from the observed data. The interpretation of MAPE values is summarized in Table 1.

Table 1. Range MAPE values

Range MAPE	Interpretation
------------	----------------

$MAPE \leq 10\%$	<i>Highly accurate forecasting</i>
$10\% < MAPE \leq 20\%$	<i>Good forecasting</i>
$20\% < MAPE \leq 50\%$	<i>Reasonable forecasting</i>
$MAPE > 50\%$	<i>Inaccurate forecasting</i>

Source : [30]

Meanwhile, the Mean Squared Error (MSE) is employed as the loss function during model training, as it imposes a larger penalty on greater deviations, thereby guiding the model to minimize the difference between predicted and actual values. The MSE is defined as [26]:

$$MSE = \frac{1}{n} \sum_{i=1}^n (y_t - \hat{y}_t)^2 \quad (9)$$

$$RMSE = \left(\frac{1}{n} \sum_{i=1}^n (y_t - \hat{y}_t)^2 \right)^{1/2} \quad (10)$$

where y_i denotes the actual value at the i -th observation, $\hat{y}_i$ is the corresponding predicted value, and N represents the total number of observations. The loss function used in this study is MSE i.e. equation 9. This loss is applied throughout the training process to update the neural network's weights.

2.6. Genetic Algorithm for Hyper-parameter Tuning

To select the hyper-parameters of each LSTM variant (number of cells per layer, and—when applicable—both layers), we use a Genetic Algorithm (GA) run separately for each look-back L . Each candidate solution is an integer vector of hyper-parameters θ (e.g., $\theta = [u_1]$ for one LSTM layer or $\theta = [u_1, u_2]$ for a stacked model). A population of such candidates is evolved across generations. For a given θ , we train the model on the inner training split with early stopping and evaluate the validation RMSE as fitness; lower is better. In each generation we (i) keep a small set of elites (best candidates), (ii) create offspring by selection (tournament or probability proportional to quality), crossover (per-gene mixing from two parents), and mutation (small random integer steps with clipping to bounds), and (iii) repeat until a fixed number of generations or convergence. The best θ is then retrained on (almost) the full training data and finally evaluated on the held-out test block.

Let $\mathcal{P}^{(t)} = \{\theta_i^{(t)}\}_{i=1}^N$ be the population at generation t .

Fitness

The fitness function can be any real valued function depending on the problem. For this case of Dengue prediction we will minimize the RMSE of the prediction i.e. equation 10.

Selection. With quality $q_i^{(t)} = \frac{1}{f(\theta_i^{(t)})}$, select parent indices with

$$p_i^{(t)} = \frac{q_i^{(t)}}{\sum_{k=1}^N q_k^{(t)}}, \text{Parent} \sim \text{Categorical}(p_1^{(t)}, \dots, p_N^{(t)}),$$

(or tournament selection in practice).

Crossover (per-gene mask). For parents θ_a, θ_b and Bernoulli mask $\mathbf{m} \in \{0,1\}^d$,

$$\theta_{\text{child}} = \mathbf{m} \odot \theta_a + (1 - \mathbf{m}) \odot \theta_b.$$

Mutation (integer step with clipping).

$$\tilde{\theta} = \theta_{\text{child}} + s \xi, \xi_k \in \{-2, -1, 1, 2\} \text{ with prob. } \rho, \text{ else } 0,$$

for each component k ,

$$\theta'_k = \min(\max(\tilde{\theta}_k, \ell_k), u_k).$$

If mutation pushes below ℓ_k , it's set to ℓ_k ; if it exceeds u_k , it's set to u_k . Where ℓ, u are lower/upper bounds (e.g., units $\in [8, 128]$) and s is the step size (e.g., multiples of 8 cells).

Elitism and next generation.

Let $\mathcal{P}_t = \{\theta_1^{(t)}, \dots, \theta_N^{(t)}\}$ be the size- N population of candidate hyper-parameters at generation t . The update

$$\mathcal{P}_{t+1} = \text{Top}_K(\mathcal{P}_t) \cup \text{Children}_{N-K} \quad (11)$$

Stopping. Stop when $t = T_{\text{max}}$ or when

$$\min_{\theta \in \mathcal{P}^{(t)}} f(\theta) \text{ fails to improve by more than } \varepsilon \text{ for } G \text{ generations.}$$

This GA framework yields, for each look-back L and each architecture (LSTM, Stacked LSTM, LSTM+Attention), a data-driven choice of the number of cells that minimizes validation RMSE while respecting integer/bounded constraints.

2.7. Implementation Workflow

The workflow comprised the following steps:

- Data preparation. Assemble a single monthly dengue incidence series, clean missing values, and align timestamps (order preserved).
- Windowing (look-back construction). For each $L \in \{1, \dots, 6\}$, convert the series into supervised samples $(\mathbf{x}_{t-L+1:t}, y_t)$, where $\mathbf{x}_{t-L+1:t} \in \mathbb{R}^L$ are the last L values and y_t is the next step.
- Split the windowed data into train (80%) and test (20%) without shuffling.
- Model families. Define three architectures: LSTM (1 layer), Stacked LSTM (2 layers), and LSTM with temporal attention (attention applied to LSTM outputs with `return_sequences=True`). All models use Adam (10^{-3}) and MSE loss.
- Genetic-Algorithm (GA) tuning (per model, per L).
- Selection & reporting. For each model and L , record the best units (lowest validation RMSE) and tabulate RMSE by look-back across the three models.
- Outputs & inspection. Report the RMSE table and the chosen unit counts per model/look-back.

3. RESULT AND ANALYSIS

3.1 Lead-Lag Structure between Climate and Dengue

We quantify how far in advance climate signals anticipate dengue by computing Pearson cross-correlations between current Dengue incidence and (i) Dengue incidence past values and (ii) lagged rainfall, relative humidity, and average temperature at 2 and 3 months. Incidence is moderately persistent at 2 months ($r \approx 0.36^*$) but largely fades by 3 months. Rainfall shows a clear positive link at 2 months ($r \approx 0.36^*$), while average temperature is positively associated at both 2 and 3 months ($r \approx 0.33^*, 0.57^*$). Relative humidity is weak at 2 months and negative at 3 months ($r \approx -0.29^*$). The asterisks symbol denote significance for $p < 0.05$.

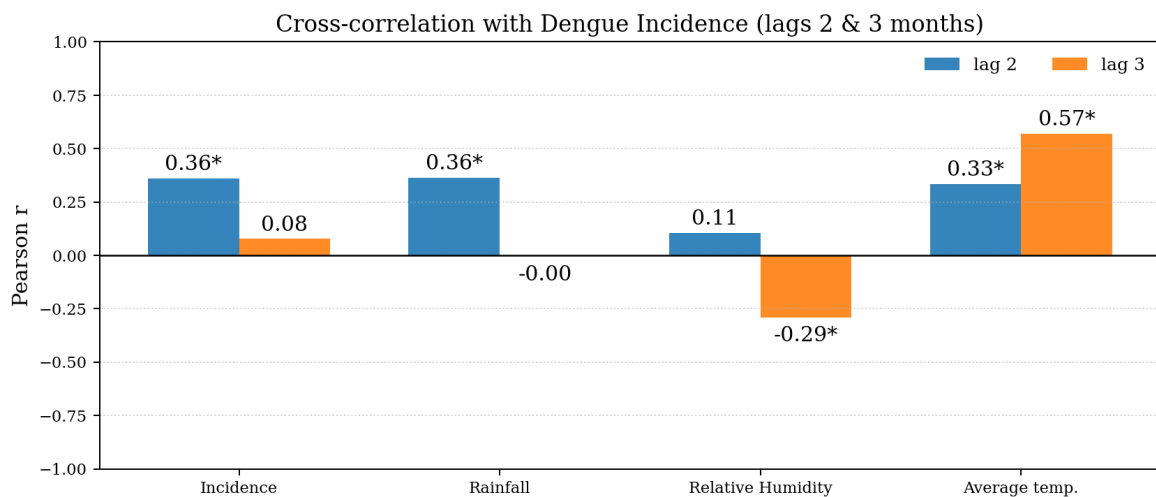


Figure 4. Cross-correlation of current dengue incidence with incidence (autocorrelation), rainfall, relative humidity, and average temperature at lags of 2 and 3 months for 2015–2024 (asterisks indicate statistical significance at $p < 0.05$)

Ecologically, these patterns are consistent with Dengue vector, i.e. *Aedes* dynamics. Heavy rain creates breeding sites; allowing for larval development, adult emergence, virus extrinsic incubation, and reporting delays yields a compounded lag near 2 months. Warmer conditions accelerate development, biting, and viral replication, sustaining an effect out to 3 months. The negative relative humidity at 3 months likely reflects seasonal transitions and behavior (e.g., pre-rainfall water storage increasing container habitats) and/or collinearity with rainfall—hence it should be interpreted within a multivariate, distributed-lag model rather

than as an isolated causal driver. Overall, the 2–3-month lead in rainfall and average temperature supports their use in early-warning systems.

3.2 Genetic Algorithm Settings for Hyperparameter Tuning

We tuned the number of LSTM units for three models—(i) LSTM, (ii) Stacked LSTM, and (iii) LSTM with Attention—separately for each look-back $L = 1, \dots, 6$. Data were split in time (80% train, 20% test). From the training block, the last 20% served as a validation fold used only to choose hyper-parameters. Inputs/targets were standardized using training statistics to avoid leakage. The score we minimize is the validation RMSE in equation 10.

A candidate (a “chromosome”) is the number of units in each LSTM layer: LSTM: (n_1) , TA-LSTM: (n_1) , and Stacked LSTM: (n_1, n_2) . Each n_i is an integer between 8 and 128. For a candidate, we train the model on the inner-train split with early stopping (max 50 epochs) and take its RMSE_{val} .

We use a small population and few generations to keep compute practical: population $P = 8$, generations $G = 5$.

1. Start with P random candidates.
2. Evaluate each: train briefly, record RMSE_{val} .
3. Keep the best half (elitism) and create children by mixing parent genes (single-point crossover) and randomly changing one gene with prob. 0.3 (mutation).
4. Repeat steps 2–3 for G generations.

A concise update view is done by employing i.e. equation 11, the next population is the best half plus offspring from crossover+mutation. After G rounds we pick the best settings θ^* , refit them on (almost) all training data, and then report test RMSE.

3.3 LSTM Model Evaluation

The comparative results of RMSEs across different lookback windows (1–6 months) are summarized in Table 2.

2. The GA process converged to three optimal architectures:

- i. LSTM: 124 hidden cells (single layer)
- ii. S-LSTM: [42, 122] cells (two stacked layers)
- iii. TA-LSTM: 56 hidden cells with temporal attention

All models show consistent improvement as the lookback period increases, indicating that longer historical windows enhance the model’s ability to capture seasonal dengue patterns.

Tabel 2. Performance of LSTM architectures for Dengue prediction in Lampung

Look-back	Model		
	LSTM	S-LSTM	TA-LSTM
1	0.650966	0.680614	0.642907
2	0.629018	0.669973	0.645560
3	0.650406	0.599910	0.615789
4	0.552365	0.579632	0.576324
5	0.562718	0.557892	0.574051
6	0.505699	0.530938	0.544635
Min	0.505699	0.530938	0.544635
Max	0.650966	0.680614	0.645560
Average	0.591862	0.603160	0.599878
Std. Dev.	0.054977	0.055215	0.037562

All models show steady improvement as the look-back period increases, confirming that incorporating longer historical windows improves the network’s ability to capture seasonal dengue patterns. Among the tested variants, the S-LSTM achieved the lowest average $\text{RMSE}=0.603$ and maintained a relatively stable deviation (0.055), suggesting that a deeper two-layer recurrent structure yields better generalization than both the baseline LSTM and TA-LSTM.

Although the TA-LSTM theoretically provides higher expressive capacity via its attention mechanism, it did not outperform the simpler stacked configuration. This outcome differs slightly from Majeed et al. (2023), who reported that spatial-temporal attention improved dengue forecasting accuracy in Malaysia. In the present work, the limited sample size and local-scale data may have constrained the benefits of attention.

The findings underscore an important insight: model simplicity coupled with automatic architecture optimization can outperform more complex attention-based designs when the dataset is region-specific and moderate in size.

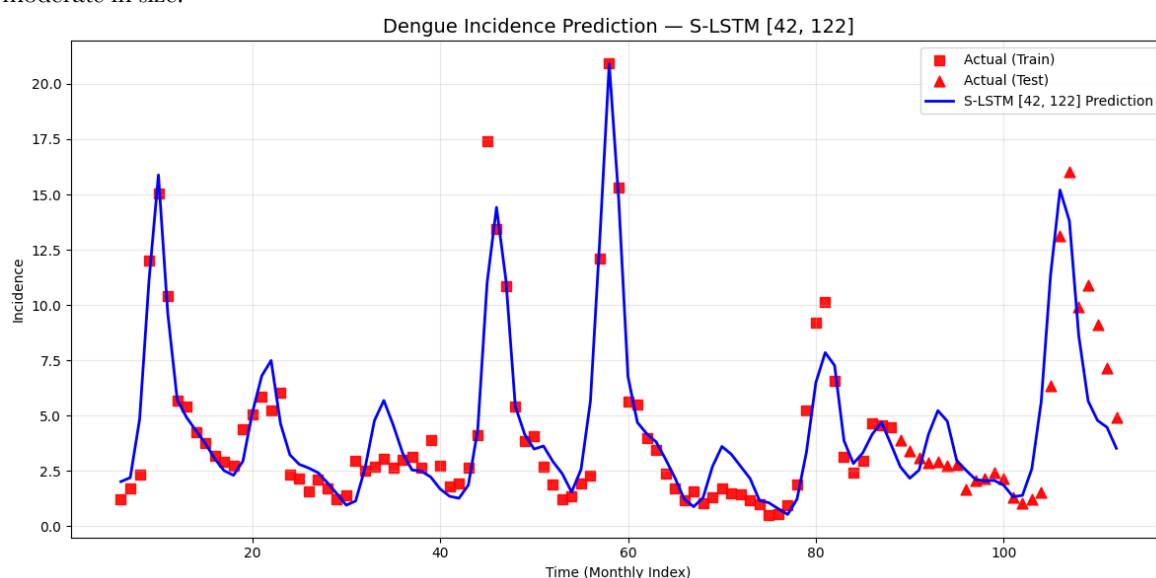


Figure 5. Comparison between actual and predicted monthly dengue incidence in Lampung Province using the Stacked LSTM (S-LSTM) model with [42, 122] units

Table 3 summarizes the Mean Absolute Percentage Error (MAPE) achieved by four predictive models—S-LSTM, support vector regression (SVR), multi-layer perceptron (MLP), and random forest—on both training and testing datasets. The S-LSTM with [42, 122] stacked cells yielded a Train MAPE = 21.54 % and a Test MAPE = 31.99 %, outperforming all baselines in generalization accuracy. Although the SVR achieved a lower training error (6.24 %), its test error rose sharply (38.04 %), showing overfitting and poor adaptability to unseen data. The MLP and Random Forest models exhibited even higher test errors (50.00 % and 70.01 %), indicating that static, non-sequential learners struggle to capture dengue’s temporal patterns.

Table 3. Comparison of Model Accuracy (MAPE %) for Dengue Incidence Prediction

Model	Train MAPE (%)	Test MAPE (%)
S-LSTM [42,122]	21.537	31.986
SVR	6.236	38.041
MLP (64)	10.137	50.004
Random Forest (500)	11.764	70.012

In contrast, the S-LSTM effectively learned lag-based temporal dependencies between climatic factors and dengue incidence, enabling stable performance across both phases. The network’s recurrent structure allowed it to model delayed nonlinear effects in climatic variables, an essential property for diseases with incubation-related dynamics. Thus, while simpler regressors and feed-forward networks failed to generalize, the S-LSTM demonstrated the best trade-off between fit quality and predictive robustness, confirming its suitability for medium-term dengue trend forecasting.

4. CONCLUSION

This study presents the first localized deep learning framework for climate-based dengue forecasting in Lampung Province, Indonesia, integrating climatic and epidemiological data through recurrent neural

architectures. The research successfully implemented a Genetic Algorithm (GA) for automatic optimization of Long Short-Term Memory (LSTM) configurations and compared three neural variants i.e. LSTM, Stacked LSTM (S-LSTM), and Temporal-Attention LSTM (TA-LSTM), alongside traditional machine learning benchmarks (SVR, MLP, Random Forest).

The results consistently demonstrate that temporal depth and automatic hyperparameter tuning significantly enhance predictive accuracy. Among the tested models, the Stacked LSTM (S-LSTM) with [42, 122] units achieved the lowest average RMSE (0.603) and the best overall MAPE performance (Train = 21.54 %, Test = 31.99 %), outperforming both the simpler single-layer LSTM and the more complex attention-based TA-LSTM. While the Time-Attention variant theoretically offers richer temporal representation, its performance plateaued under Lampung's limited dataset size. This suggests that attention mechanisms may require larger and more diverse data to fully realize their potential.

In contrast, the S-LSTM captured the lagged, nonlinear dependencies between rainfall, humidity, and dengue incidence more effectively, showing stronger generalization and reduced overfitting compared to SVR, MLP, and Random Forest. The findings highlight an important practical insight that simple models, when paired with intelligent architecture search such as GA, can outperform more complex attention-based designs in localized, data-limited epidemiological forecasting.

This conclusion aligns with ecological understanding i.e. rainfall and humidity effects on dengue transmission exhibit 2–3 month lags, consistent with vector lifecycle and incubation delays. This confirms that well-structured recurrent models can exploit these dependencies for reliable early-warning dengue prediction.

Future extensions may include integrating spatial features (inter-district spread) and hybrid attention mechanisms as larger regional datasets become available. Nonetheless, the present study establishes a foundational methodological framework for data-driven, region-specific dengue forecasting in Lampung, demonstrating the feasibility and value of deep learning in public health surveillance.

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First author's Photo (3x4cm)	Xxxx (9 pt)
Second author's photo (3x4cm)	Xxxx (9 pt)