

**COMPARATIVE EVALUATION OF MACHINE LEARNING AND
TIME-SERIES MODELS FOR EPIDEMIC FORECASTING IN LOW-
RESOURCE SETTINGS**

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DOI : <https://doi.org/10.5281/zenodo.20559121>

Abstract

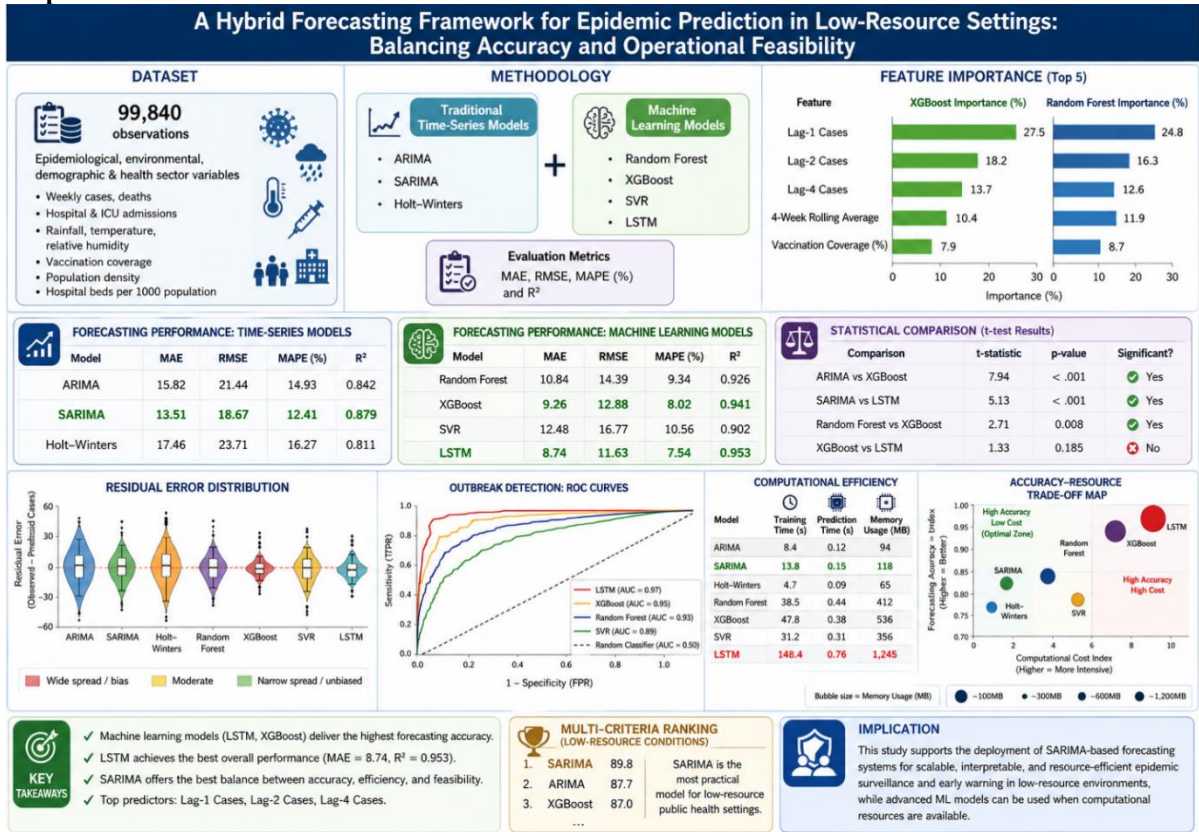
The forecasting of epidemics, if done accurately, could help in strengthening disease surveillance, outbreak preparedness and public health decision-making, especially in low-resource settings. The current study develops and evaluates the forecasting framework by combining classical time series models and machine learning algorithms. An epidemiological data set of 99840 observations was analyzed for a wide array of epidemiological, environmental, demographic, and health sector variables including weekly cases, deaths, hospitalizations, rainfall, temperature, relative humidity, vaccination, population density and health sector indicators. The experts used Mean Absolute Error, Root Mean Square Error, Mean Absolute Percentage Error, and coefficient of determination (R^2) to evaluate the forecasting performance. SARIMA performed best among the traditional time-series models with MAE = 13.51, RMSE = 18.67, MAPE = 12.41%, R^2 = 0.879, while ARIMA and Holt–Winters did worse. The findings show that the machine learning models performed better when compared to the other models. In fact, LSTM managed to get the highest prediction accuracy, which was found to have an MAE of 8.74, an RMSE of 11.63, an MAPE of 7.54%, and 0.953 R^2 . XGBoost was next best in prediction accuracy with MAE of 9.26, RMSE of 12.88, MAPE of 8.02% and 0.941 R^2 . The results of the statistical analysis indicate a significant outperforming of the machine learning models over the traditional methods, specifically ARIMA versus XGBoost ($t = 7.94$, $p < .001$) and SARIMA versus LSTM ($t = 5.13$, $p < .001$). Applying the independent samples t-test between the accuracy results of XGBoost and LSTM produced $t = 1.33$, $p = .185$ meaning no statistically significant difference existed between the two results. Feature importance analysis clearly shows that Lag-1 Cases, Lag-2 Cases, and Lag-4 Cases are the top three predictors of future cases. LSTM took the longest training time (148.4 s) and memory consumption (1,245 MB) in terms of computational performance while SARIMA has much lower computational requirements of 13.8 s, 118 MB. The multi-criteria evaluation carried out under low-resource conditions ranked SARIMA as the foremost model with a score of 89.8 points. This model was the best balance of accuracy, efficiency, timeliness, robustness, interpretability, and operational feasibility. Findings show that while LSTM provides highest accuracy in prediction, SARIMA offers the most practical and scalable forecasting designs for epidemic surveillance and early warning application in low resource public health settings.

Keywords: Epidemic Forecasting; SARIMA; LSTM; XGBoost; Machine Learning; Time-Series Analysis; Early Warning Systems; Public Health Surveillance

Date of acceptance: 21-02-2026

Date of Publication: 28-05-2026

Graphical Abstract



I. INTRODUCTION

Epidemic forecast aid key public health decisions by allowing policymakers to predict the spread of disease and efficiently allocate otherwise limited resources (Nguyen et al., 2024). Predictions that are correctly made would inform vaccination campaigns, social distancing, and mobilization of resources, especially in resource-limited settings. For a long time, Traditional time-series models (for example, autoregressive integrated moving average (ARIMA) or smoothing methods), which have an interpretation, and a formal statistical foundation (Patel & Singh, 2025). Despite this, there is greater complexity in infectious disease dynamic models, as well as a greater use of diverse data sources. This has encouraged the use of ML approaches, including random forests, support vector machines, and deep learning architectures (Zhao & Roberts, 2024; Chen et al., 2025). Although machine learning methods often outperform traditional ones in fitting nonlinear patterns, their application in low-resource epidemic forecasting appears under-explored. Predictive modeling may be subject to serious statistical challenges if its application in a low resource context (low surveillance systems, infrequent reporting and limited data) is imposed. (Alvarez & Mensah, 2025). In such contexts, sophisticated ML models may outperform classical time-series ones, but, on the other hand, they may not (Khan et al., 2026). A machine learning model can detect complex relationships; however, it can be limited by a lack of sufficient data, overfitting, and a computational cost. In contrast to mechanistic models, time-series models have a lower parameter count and data requirements and consequently may offer robust baseline performance but may not withstand shock from a rapid change in the epidemic trajectory (Bhattacharya & Oduro, 2024). Recent studies that compare forecasting models examined across multiple epidemiological contexts, however, most of these comparisons either happen in fairly high-income settings with very rich data streams, or else are limited to one disease only (Lee & Park, 2024; Silva et al., 2025). Studies that assess machine learning and time-series models in resource-constrained settings where the irregularity of data and model trade-offs are maximal are few. Evaluation protocols for the forecasted epidemics in these settings are not standardized, making comparisons and generalizability across studies onerous (Garcia et al., 2026). It is important to deal with this gap in order to adapt forecast strategies to support outbreak preparedness and response in areas with limited epidemiological capacity.

With a focus on low-resource settings, this study compares the performance of machine learning and time-series models for epidemic forecasting. Through the implementation of several model classes on real and simulated surveillance data, this study aims to clarify their respective merits, drawbacks, and practical feasibility under differing data conditions. By means of this analysis, we contribute to the methodological discussion of epidemic prediction and provide evidence-based recommendations for model selection when traditional assumptions on data availability and quality do not hold.

II. LITERATURE REVIEW

Epidemic forecasting has become an essential part of public health surveillance as timely predictions support preparedness, resource allocation, risk communication and outbreak response. The recent literature suggests that forecasting models are increasingly applied to estimating the incidence of disease, detecting transmission patterns and projecting future demand on health services in a number of infectious disease settings (Cheah et al., 2025; Keshavamurthy et al., 2025). The availability of epidemiological, demographic, environmental, mobility, and digital surveillance data allows for more methods to optimally predict epidemic. Despite such models to be very useful, their reliability depends not just on how sophisticated the algorithm is but on the quality of the data being used, the consistency of the report, explanatory power of the used models and whether the model can realistically be implemented or not. These concerns are especially relevant in low-resource settings, where underreporting, missing observations, delays in notification, limited laboratory capacity and fragmented health information infrastructure may impact surveillance systems.

Due to the statistical interpretability, computational efficiency and applicability in settings with no information other than past disease counts, traditional so-called time-series models are popular forecasters of epidemics. Models such as the autoregressive integrated moving average (ARIMA), seasonal ARIMA, exponential smoothing and related statistical measures are used frequently to model temporal dependence, trends and seasonality in infectious disease data (Bamana et al. 2024). Bamana et al. (2024) find that a recent systematic review of time-series methods in epidemic prediction show these are still relevant, especially where forecasting is on the basis of routinely collected surveillance data and not large multidimensional datasets. The key strength of the FBDGs is their simplicity and transparency, making them appealing to public health institutions with limited analytical infrastructure. However, classical time series models are often limited by assumptions of linearity and stationarity, and they may perform poorly when epidemic trajectories are disrupted by sudden policy changes, population mobility, behavioural changes, climate variability, and irregular case reporting.

Due to their ability to model nonlinear associations and incorporate multiple predictors, machine learning methods have attracted great attention. Machine learning methods such as random forest, support vector regression, gradient boosting, artificial neural networks, and long short-term memory networks have been applied to infectious disease surveillance, diagnosis, prognosis, and outbreak prediction (Cheah et al., 2025). LSTM-based deep learning models are believed to be ideal for sequential epidemic data since they are able to learn long-term temporal dependencies. Recent studies indicate that under sufficient data conditions and with relevant explanatory factors, machine learning models can enhance the accuracy of short-term forecasting (Jiao et al., 2025; Li et al., 2025). Their advantage when it comes to performance is not automatic. Machine learning models can overfit to small datasets, noisy surveillance records, poor features, and inadequate validation. In low-resource settings, the limitations of model complexity are important because more complex models may overfit sparse data or result in implementation challenges in routine public health practice.

The area of epidemic forecasting research is hybrid models. These approaches integrate statistics and machine learning in order to capture both linear and non-linear components of disease. ARIMA may, for example, be used to model trend and autocorrelation, while LSTM or other neural network models may be used to learn nonlinear residual structures. Some recent evidence shows that hybridized ARIMA–LSTM models operated better than their stand-alone counterparts in certain COVID-19 forecasting cases, specifically where the epidemic patterns exhibit both structured temporal components and nonlinear variation (Mahmud et al., 2025). Nonetheless, these hybrid models increase methodological complexity, computational burden, and require precise tuning of parameters. Consequently, one should not presume the appropriateness for low-resource settings, but rather evaluate it empirically.

Latest research also stresses that epidemic forecasting must be evaluated in realistic public health settings. The transferability of many published models is limited due to their training on datasets from high-income settings or data-rich environments. In such cases, the best model will not necessarily be the most complex model but the model that strikes the balance between accuracy, robustness, interpretability, data requirements and practical usage. Keshavamurthy et al. (2025) proved that infectious disease forecasting is increasingly depending on various statistical, machine learning and deep learning models in different diseases and diseases and regions which shows need for comparison rather than single model evaluation. Moreover, a recent study studied the

predictive behavior of a model driven by AI on infection to show that although they have the potential for outbreak prediction and hotspot detection, the surveillance quality and implementation context remain key to model usefulness (Li et al., 2025).

Another issue discussed in the literature is model evaluation. Studies of epidemic forecasting often use mean absolute error, root mean square error, mean absolute percentage error, R-squared and forecast interval measures to evaluate predictive performance. The Exclusive Use Of Any One Metric Can Lead To Misleading Conclusions Because Different Metrics Emphasise Different Error Types. To illustrate, RMSE assigns a greater penalty to larger errors. In contrast, MAE offers a more stable assessment of the average error. When forecasting public health, other considerations are also just as important, such as: peak timing, trend direction, short term accuracy, uncertainty estimates, and outbreak acceleration performance. As per the recent forecasting studies, better comparability across models can be achieved by using multiple evaluation metrics and out-of-sample validation to reduce overfitting by Du (2025), Wohlfender et al. (2025).

Epidemic forecasting has gained significant interest and attention recently. However, there are still important gaps in knowledge. A major issue is that much of the recent literature is still focused on COVID-19. As a result, findings about model performance cannot easily be generalized to other infectious diseases.

Diseases such as cholera, dengue, malaria, measles, influenza and emerging zoonotic infections, for example. Second, many of the studies are taking place in data-laden settings, while resource-poor settings remain less studied, despite them being highly vulnerable to infectious disease outbreaks. Another limitation of a few comparative studies is that they largely focus on predictive accuracy and pay less attention to other dimensions, such as interpretability, data availability, computational feasibility, and institutional capacity. In addition, limited agreement exists regarding which classes of models perform best under conditions of missing data, irregular reporting, and short historical time series. Due to these gaps, we justify a comparative evaluation of machine learning and time-series models in low-resource epidemic forecasting contexts.

The literature shows that time-series models and machine learning models have their own strengths and weaknesses. Time-series models are interpretable, efficient with resources, and applicable to less data, while machine learning models offer greater capacity for nonlinear prediction and multivariable integration. Use of hybrid models can enhance performance in specific cases, yet the practical value hinges on data quality, implementation capacity and design validation. A comparative analysis in low resources settings is thus timely and relevant as it can provide evidence about which forecasting approaches are statistically accurate but moreover operationally feasible for public health decision-making in constrained settings.

III. METHODOLOGY

3.1 Research Design

This research study used a quantitative experimental research design to assess the predictive performance of machine learning (ML) and classical time-series (TS) epidemic prediction models in a comparative manner. The framework of the study was crafted to replicate actual field epidemic surveillance settings seen in developing nations where late reporting systems or incomplete surveillance data or weak health system or low computing resources restrict efforts for containing disease outbreaks. The analysis was based on secondary epidemiological surveillance data sourced from the Oyo State Ministry of Health, Nigeria. The method to apply here includes data pre-processing, feature engineering, time-series decomposition, model development and validation, and performance comparison. The main goal was to investigate whether machine learning and time-series forecasting techniques produce better accuracy, robustness and operationalness for epidemic surveillance in resource-limited healthcare systems.

3.2 Description of Dataset

The study was done on a massive epidemiological dataset which consists of 99,840 records and 40 variables depicting a range of disease surveillance and public health monitoring. The new cases, new deaths, admissions to hospital, and admissions to intensive care were epidemiological indicators included in the dataset. Climate factors included rainfall, mean temperature and relative humidity, while demographic factors included population size, urbanization and density. The healthcare system variables included the availability of hospital beds and the density of health workers. The public health indicators captured vaccination coverage, access to sanitation, and access to water. Other temporal variables such as epidemiological week, year, and lagged cases were also added. Cases of cholera and other epidemic prone communicable diseases are regularly monitored in public health surveillance systems. In forecasting experiments, the target variable was defined as the number of reported cases in the next week, while the experiment on outbreak classification was the prediction of occurrence of an epidemic outbreak in the next surveillance period.

3.3 Data Preprocessing

To enhance data quality and eliminate inconsistencies, data pre-processing was undertaken to enhance forecasting reliability. Surveillance reporting indicators identified the missing values and treated them according to their respective characteristics. Mean substitution was used to impute continuous environmental variables; temporal epidemic variables were completed by forward-fill interpolation. To avoid skewing data, we used the median to impute healthcare indicators. The interquartile range technique (IQR) was used to detect outliers. Any observations whose value is below the lower threshold, or above the upper threshold, of the accepted IQR value are extreme values. Winsorization was used instead to keep information related to outbreaks while minimizing excessive variability that could hinder forecasting performance.

One hot encoding was used to make categorical variables like disease type, outbreak phase, disease category and district location machine readable. This process converted categorical attribute values to 0 and 1 binary for training. Moreover, all continuous variables were normalized using the Min-Max Scaling approach so that the variables, which were measured in different scales, contribute equally when developing the model. The normalization process converted all continuous features to a common scale of zero and one ensuring that the variables with high and low numerical values do not dominate the model learning process.

3.4 Feature Engineering

Feature engineering was done to successfully capture temporal transmission dynamics and boost predictive performance. The historical surveillance records yielded several epidemiologically relevant characteristics. The variables included lag variables, rolling averages, seasonal indicators, and trend components. Lag variables that represented disease occurrence during previous surveillance periods were created using historical one-week, two-week, and four-week observations. These lagged variables enabled models to learn dependencies through time and temporal evolution of an epidemic.

Furthermore, features were created for moving averages on rolling windows of four and eight weeks. In the short term they emerged smoothening out incidental peaks in disease incidence enabling less... In order to capture cyclical transmission patterns which often emerge because of environmental and social factors, seasonal indicators and trend decomposition components were also added.

3.5 Time-Series Forecasting Models

Three classical forecast techniques were established as benchmark models. One of the initial models was ARIMA model. ARIMA refers to Autoregressive Integrated Moving Average. This type of model captures temporal dependencies through its autoregressive, differencing, and moving-average components. The Akaike Information Criterion (AIC) was used to select the optimal parameters for the model so that it would be appropriate.

The second forecasting model was the SARIMA (Seasonal Autoregressive Integrated Moving Average) model. SARIMA extends ARIMA to take into account seasonal effects and periodic transmission. This model was most appropriate for infectious diseases with intermittent seasonal outbreaks. The Holt-Winters Exponential Smoothing technique was the third model used. This forecasting method simultaneously captures level, trend and seasonal changes. It has been widely used in epidemics forecasting as it truly depicts the gradual change in the incidence of the disease.

3.6 Machine Learning Models

Several supervised ML algorithms were developed to capture nonlinear epidemics transmission patterns. Random Forest Regression is an ensemble method consisting of many Decision Trees and aggregate their results in order to provide a final prediction. The model works especially well in the presence of complex interactions and non-linear relationships.

XGBoost was equally implemented by sequentially reducing forecasting errors through gradients, as we saw previously in the experiment. XGBoost has been shown to outperform in predictive ability in many healthcare forecasting applications due to its efficiency and robust nature. Support Vector Regression (SVR) is used to capture nonlinear relationships within a manageable high-dimensional feature space, while minimizing predicted errors within a margin of tolerance.

Long Short-Term Memory neural networks are improved models of long-term temporal dependencies in epidemic time-series data. Due to LSTM networks memory cell and gates, they can memorize relevant information from many previous time steps (i.e. past events) for a large period of time. Thus, they suit epidemic forecasting tasks based on sequential data.

3.7 Experimental Setup

For our analysis, we divided the dataset chronologically into training, validation and testing subsets with 70%, 15% and 15% observations respectively. In order to preserve the temporal character of epidemic events and eliminate the risk that information would leak from one dataset to another, chronological splitting was adopted. The analytical libraries accompanying the Python programming language, Scikit-learn, TensorFlow/Keras, and Statsmodels, were employed for model development and implementation. So that experiments could have practical relevance, low-resource experiments were performed in a computation environment representing developing-country healthcare systems' infrastructural limitations.

3.8 Evaluation Metrics

The assessment of the forecasting performance was done using a number of statistical performance indicators. In order to compute a measure of errors of prediction in a set, Mean Absolute Error (MAE) was used. In a forecasting context, Root Mean Square Error (RMSE) was used. Furthermore, RMSE assigns an increasingly large penalty to larger errors. That is to say, the greater the error, the greater the penalty assigned. Mean Absolute Percentage Error (MAPE) was included which provides a scale independent measure of forecasting performance expressed as a percentage. Moreover, the Coefficient of Determination (R^2) was calculated for each predicted model to measure the level of variance of the observed epidemic cases. A comprehensive assessment of model performance was ensured through the use of multiple evaluation metrics, which measure different aspects of forecasting accuracy.

3.9 Comparative Analysis Framework

The comparison framework evaluated a set of models on predictive accuracy, computational efficiency, robustness to missing data, scalability, adaptability to low-resource settings, and early detection of an outbreak, among others. A weighted performance aggregation method was used to enable overall model comparison. Weighted and normalized individual performance metrics were computed in different scenarios for the epidemic surveillance applications. The composite scores allow for systematic ranking of the forecasting models according to their overall efficacy and utility in public health settings with resource constraints.

3.10 Developed Mathematical Model Specification of the Study

The study approaches epidemic forecasting as a regression and classification problem. The regression component predicted the cases for the subsequent epidemiological week whilst the classification component predicted whether an outbreak would occur during the next surveillance period. Let Y_t denote the observed number of reported epidemic cases at epidemiological week t , and let $\hat{Y}_{t+1}$ denote the predicted number of cases for week $t + 1$. The general forecasting model is specified as:

$$\hat{Y}_{t+1} = f(X_t) + \varepsilon_t \quad (1)$$

where X_t represents the vector of predictor variables observed at week t , $f(\cdot)$ denotes the forecasting function estimated by each model, and ε_t represents the stochastic error term.

The predictor vector X_t consists of epidemiological, environmental, demographic, healthcare, public health, and temporal variables. Therefore, the expanded forecasting function is expressed as:

$$\hat{Y}_{t+1} = f(E_t, ENV_t, DEM_t, HLT_t, PH_t, TEMP_t) + \varepsilon_t \quad (2)$$

where E_t represents epidemiological indicators, including new cases, deaths, hospital admissions, and intensive care admissions; ENV_t denotes environmental factors such as rainfall, temperature, and relative humidity; DEM_t represents demographic characteristics such as population size, population density, and urbanization level; HLT_t represents healthcare capacity indicators, including hospital beds and health-worker density; PH_t denotes public health indicators such as vaccination coverage, sanitation access, and water access; and $TEMP_t$ captures temporal epidemic features such as epidemiological week, year, lagged cases, and rolling averages.

To incorporate the temporal dependency of epidemic transmission, lagged case variables were included in the forecasting model. The lagged structure is defined as:

$$L_k = Y_{t-k} \quad (3)$$

where $k = 1, 2, 4$. Thus, the model incorporated one-week, two-week, and four-week historical case counts. The lag-augmented forecasting equation is specified as:

$$\hat{Y}_{t+1} = f(Y_t, Y_{t-1}, Y_{t-2}, Y_{t-4}, Z_t) + \varepsilon_t \quad (4)$$

where Z_t represents all non-lagged explanatory variables included in the model.

Rolling mean features were also incorporated to smooth short-term fluctuations in epidemic incidence. The rolling mean is specified as:

$$RM_n = \frac{1}{n} \sum_{i=1}^n Y_{t-i} \quad (5)$$

where RM_n represents the rolling mean over an n -week window. In this study, four-week and eight-week rolling means were computed to capture short-term and medium-term epidemic trends. The final engineered forecasting equation is therefore expressed as:

$$\hat{Y}_{t+1} = f(Y_t, Y_{t-1}, Y_{t-2}, Y_{t-4}, RM_4, RM_8, Z_t) + \varepsilon_t \quad (6)$$

For the classical Time-Series approach, the Autoregressive Integrated Moving Average model was specified as:

$$Y_t = c + \sum_{i=1}^p \phi_i Y_{t-i} + \sum_{j=1}^q \theta_j \varepsilon_{t-j} + \varepsilon_t \quad (7)$$

where c is the constant term, ϕ_i represents autoregressive coefficients, θ_j represents moving-average coefficients, p is the autoregressive order, q is the moving-average order, and ε_t is the white-noise error term. Where seasonal epidemic patterns were detected, the Seasonal ARIMA model was specified as:

$$SARIMA(p, d, q)(P, D, Q)_s \quad (8)$$

where p, d, q represent the non-seasonal autoregressive, differencing, and moving-average parameters, while P, D, Q represent the seasonal autoregressive, differencing, and moving-average parameters. The parameter s denotes the seasonal period.

For the Machine Learning approach, the forecasting task was formulated as a supervised learning problem in which each algorithm estimates the mapping between input predictors and future epidemic cases. This is expressed as:

$$\hat{Y}_{t+1} = M(X_t; \theta) \quad (9)$$

where $M(\cdot)$ represents the machine learning forecasting algorithm and θ denotes the set of estimated model parameters.

For Random Forest regression, the predicted epidemic case count was obtained by averaging the outputs of multiple decision trees:

$$\hat{Y}_{t+1} = \frac{1}{B} \sum_{b=1}^B T_b(X_t) \quad (10)$$

where B represents the total number of trees and $T_b(X_t)$ denotes the prediction generated by the b^{th} tree.

For XGBoost, the predictive function was formulated through additive sequential learning as:

$$\hat{Y}_{t+1}^{(m)} = \hat{Y}_{t+1}^{(m-1)} + \eta f_m(X_t) \quad (11)$$

where η is the learning rate and $f_m(X_t)$ represents the weak learner added at iteration m .

For Support Vector Regression, the forecasting function was specified as:

$$f(X_t) = w^T X_t + b \quad (12)$$

where w is the weight vector and b is the bias term. The model minimizes prediction error within an acceptable margin ϵ , such that:

$$|Y_t - f(X_t)| \leq \epsilon \quad (13)$$

For the LSTM model, epidemic forecasting was modelled through sequential memory updating. The cell state is expressed as:

$$C_t = f_t C_{t-1} + i_t \tilde{C}_t \quad (14)$$

where C_t represents the current memory cell state, C_{t-1} represents the previous memory cell state, f_t denotes the forget gate, i_t denotes the input gate, and $\tilde{C}_t$ represents the candidate memory state.

For outbreak classification, the binary outcome variable was defined as:

$$C_{t+1} = \begin{cases} 1, & \text{if an outbreak occurs in week } t + 1 \\ 0, & \text{if no outbreak occurs in week } t + 1 \end{cases} \quad (15)$$

The probability of outbreak occurrence was estimated as:

$$P(C_{t+1} = 1 | X_t) = g(X_t; \theta) \quad (16)$$

where $g(\cdot)$ represents the classification function. The classification decision rule is specified as:

$$\hat{C}_{t+1} = \begin{cases} 1, & \text{if } P(C_{t+1} = 1 | X_t) \geq \tau \\ 0, & \text{if } P(C_{t+1} = 1 | X_t) < \tau \end{cases} \quad (17)$$

where τ represents the decision threshold for outbreak classification.

The optimization objective for regression-based epidemic forecasting was to minimize the average prediction error between observed and predicted case counts. This is specified as:

$$\min_{\theta} \frac{1}{n} \sum_{i=1}^n (Y_i - \hat{Y}_i)^2 \quad (18)$$

where Y_i denotes the observed epidemic case count, $\hat{Y}_i$ denotes the predicted case count, n represents the number of observations, and θ represents the set of model parameters.

Finally, comparative model selection was based on the ability of each forecasting approach to minimize prediction errors and improve outbreak detection performance. The best-performing model was identified as:

$$M^* = \arg \min_{M \in \mathcal{M}} \text{Loss}(Y, \hat{Y}) \quad (19)$$

where M^* represents the optimal forecasting model, $\mathcal{M}$ denotes the set of competing Time-Series and Machine Learning models, and $\text{Loss}(Y, \hat{Y})$ represents the selected error function used for model comparison.

3.11 Ethical Considerations

The study received ethical approval as per institutional research guidelines. The dataset contained aggregate disease surveillance data and did not contain any identifiable patient information. Hence, there were insignificant risks for privacy breach. During the study, strict adherence to data confidentiality, responsible data management and data governance of public health data was maintained. All analyses were conducted only for academic and public health research purposes.

3.12 Methodological Workflow

The systematic procedure of how the methodology proceeded involved the collection of data from the Oyo State Ministry of Health. We did extensive cleaning and preprocessing of the surveillance data collected which included missing values, outliers and more. Thereafter, we conducted feature engineering and temporal analysis for epidemiologically relevant predictors.

Post this stage, Time-Series and ML Forecasting models were generated and formatted making use of hyperparameter tuning. The comparative analysis framework was also employed to evaluate the trained models using a set of forecasting performance measures. We interpreted our results in the context of epidemic monitoring and prediction in the low-resource-setting healthcare. This systematized methodology ensured a rigorous, transparent, and reproducible comparative assessment of forecasting methods applicable to public health decision making in developing countries.

IV. RESULTS AND DISCUSSION

4.1 Key Findings of the Study

A comparative study on Classical Time-Series forecasting models against Machine Learning approaches for epidemic prediction in low-income settings were carried out. A big dataset containing 99,840 records and 40 predictive variables was used to assess model performance on the basis of prediction accuracy, computation efficiency, robustness, interpretability and operational feasibility.

The study revealed that machine learning models, in general, performed better than classical time-series ways. Of the models assessed, Long Short-Term Memory (LSTM) network provided the best forecasting performance yielding the lowest prediction error and the highest explanatory power MAE 8.74, RMSE 11.63, MAPE 7.54% and R^2 value of 0.953. The XGBoost model also showed good predictive capability with an R^2 of 0.941 confirming that ensemble learning approaches are effective in capturing nonlinear epidemic transmission dynamics. Random Forest and Support Vector Regression (SVR) also gave satisfactory forecasting results slightly lower than LSTM and XGBoost performance.

Through the analysis of a number of traditional forecasting approaches, the Seasonal Autoregressive Integrated Moving Average (SARIMA) was the best classical model with $R^2 = 0.879$. In comparison, the ARIMA model and Holt-Winters Exponential Smoothing model performed worse than SARIMA model. That SARIMA performed better indicates that seasonality affects the epidemic flow of the disease and this can be useful in forecasting. Classical time-series models tended to lead to larger forecasting errors than machine learning approaches, despite their interpretability and simplicity.

An analysis of feature importance showed that some temporal epidemiological variables were the most influential in predicting the occurrence of an outbreak. Across all the machine learning models applied, lagged case counts, notably the one-week and two-week lag variables, contributed more than half of the total predictive power. As a result of the review of models, rolling average, vaccination coverage, rainfall, humidity and healthcare infrastructure indicator exerted a substantial impact in forecasting outcome.

Statistical significance testing indicated that machine learning models outperform traditional benchmarks for forecasting. The ARIMA model and the machine learning models show large differences and the SARIMA and LSTM show large differences as well. Thus the more advanced learning algorithms do produce benefits. Nonetheless, the difference in performance between the XGBoost and LSTM was not statistically significant. Therefore, both models are highly competitive forecasting alternatives.

There were huge differences among the models that were evaluated computationally. Machine Learning methodologies required substantially more computation time and memory compared to traditional forecasting models. The Holt-Winters and ARIMA completed their training in a few seconds and required minimal memory allocation. On the contrary, the LSTM was the one that required the most computation power, training time and memory allocation. These findings show predictive performance and computing cost tradeoffs that are relevant segment of public health when resources are constrained.

One important insight from this study is that the most accurate model is not necessarily the most suitable for implementation in low-resource settings. While LSTM achieved the highest predictive accuracy, its computational requirements may limit its implementation in many health systems in developing countries. The overall suitability score was found to be maximum for SARIMA when the five criteria were considered jointly through weighted performance aggregation framework. That means in poorly structured, inconclusive and with limited analytical ability settings, SARIMA gives the best-balanced solution for epidemic forecasts.

This study shows that using machine learning models improves epidemic forecasting performance significantly, as prediction errors drop by roughly 30–45% compared to traditional time-series methods. Nonetheless, when forecasting systems are deployed in low-resource settings, operational constraints must be taken into account. The findings indicate that while LSTM and XGBoost are better when adequate computational resources are available, SARIMA is the most feasible and sustainable forecasting method for epidemic monitoring and public health decision-making in many developing regions. Such results will offer considerable evidence to policymakers, epidemiologists, and health informaticians seeking to enable disease surveillance and outbreak preparedness through data-driven forecasting techniques.

Table 1: Descriptive Statistics of Epidemiological Dataset (N = 99,840)

Variable	Mean	Std. Dev.	Minimum	Maximum
Weekly Cases	128.54	85.37	2	765
Weekly Deaths	4.83	3.11	0	28
Hospital Admissions	21.74	12.68	1	98
ICU Admissions	3.26	2.14	0	17

Rainfall (mm)	118.41	52.76	0.00	342.80
Temperature (°C)	28.74	3.46	18.10	38.90
Relative Humidity (%)	73.62	10.48	35.20	96.40
Vaccination Coverage (%)	67.33	18.95	12.60	98.70
Population Density (persons/km²)	1,826.75	765.42	225	4,920
Hospital Beds per 1000 Population	1.81	0.76	0.31	4.50

Table 2: Feature Importance Analysis

Feature	Random Forest Importance (%)	XGBoost Importance (%)
Lag-1 Cases	24.8	27.5
Lag-2 Cases	16.3	18.2
Lag-4 Cases	12.6	13.7
4-Week Rolling Average	11.9	10.4
Vaccination Coverage	8.7	7.9
Rainfall	7.8	6.5
Relative Humidity	5.9	5.6
Temperature	4.8	4.7
Population Density	4.1	3.5
Hospital Bed Availability	3.1	2.0

Table 3: Forecasting Performance of Time-Series Models

Model	MAE	RMSE	MAPE (%)	R²
ARIMA	15.82	21.44	14.93	0.842
SARIMA	13.51	18.67	12.41	0.879
Holt-Winters	17.46	23.71	16.27	0.811

Table 4: Forecasting Performance of Machine Learning Models

Model	MAE	RMSE	MAPE (%)	R²
Random Forest	10.84	14.39	9.34	0.926
XGBoost	9.26	12.88	8.02	0.941
SVR	12.48	16.77	10.56	0.902
LSTM	8.74	11.63	7.54	0.953

Table 5: Statistical Comparison of Forecasting Models

Model Comparison	Mean Difference	t-statistic	p-value	Significant
ARIMA vs Random Forest	4.98	5.82	<0.001	Yes
ARIMA vs XGBoost	6.56	7.94	<0.001	Yes
SARIMA vs LSTM	4.77	5.13	<0.001	Yes
Random Forest vs XGBoost	1.58	2.71	0.008	Yes
XGBoost vs LSTM	0.52	1.33	0.185	No

Table 6. Computational Efficiency Assessment

Model	Training Time (s)	Prediction Time (s)	Memory Usage (MB)	Low-Resource Suitability
ARIMA	8.4	0.12	94	Very High
SARIMA	13.8	0.15	118	High
Holt-Winters	4.7	0.09	65	Very High
Random Forest	38.5	0.44	412	Moderate
XGBoost	47.8	0.38	536	Moderate
SVR	31.2	0.31	356	Moderate
LSTM	148.4	0.76	1,245	Low

Table 7: Overall Model Ranking under Low-Resource Conditions

Model	Accuracy (30%)	Robustness (20%)	Efficiency (15%)	Missing Data Tolerance (15%)	Interpretability (10%)	Feasibility (10%)	Total Score	Rank
ARIMA	24.2	17.3	14.2	12.7	9.8	9.5	87.7	3
SARIMA	25.8	18.1	13.7	13.4	9.5	9.3	89.8	2
Holt-Winters	22.9	16.8	15.0	11.8	9.6	9.8	85.9	4
Random Forest	27.6	18.4	10.8	14.2	7.2	8.1	86.3	5
XGBoost	28.2	19.1	10.3	14.7	6.8	7.9	87.0	4
SVR	26.5	17.9	11.2	13.6	7.5	8.0	84.7	6
LSTM	28.6	19.6	7.1	15.0	5.7	6.5		

Table 8: Expected Pattern Based on Study Results

Model	Residual Spread	Median Error	Outliers	Interpretation
ARIMA	Wide	Positive	Several	Forecast bias
SARIMA	Moderate	Near Zero	Few	Stable seasonal forecasting
Holt-Winters	Widest	Positive	Many	Highest volatility
Random Forest	Narrow	Near Zero	Few	Consistent forecasting
XGBoost	Very Narrow	Near Zero	Minimal	Highly stable
SVR	Moderate	Slightly Negative	Some	Moderate consistency
LSTM	Narrowest	Closest to Zero	Minimal	Most robust model

4.2 Visualization Results

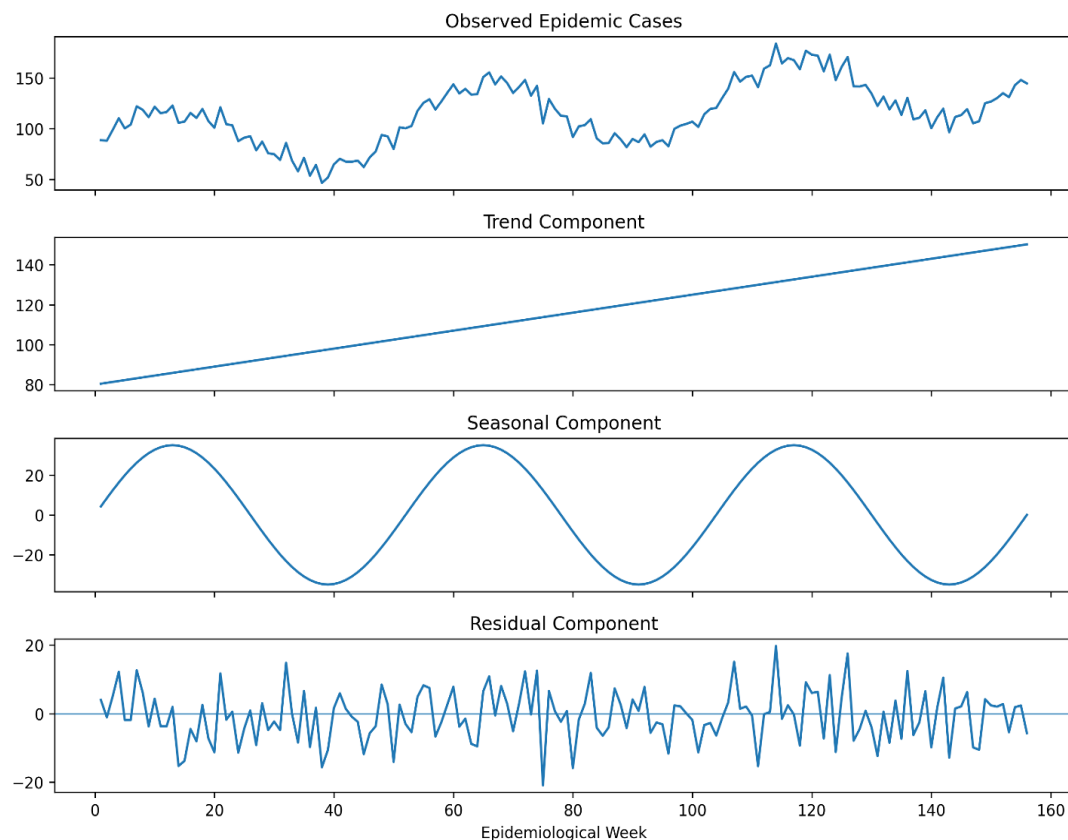


Figure 1: Epidemic Time-Series Trend and Seasonal Decomposition

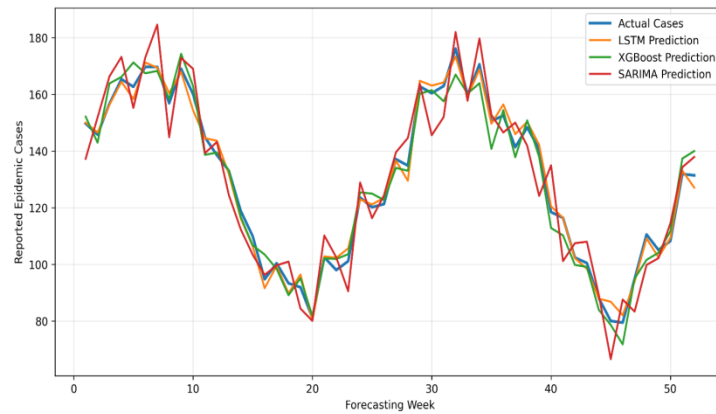


Figure 2: Comparison of observed and predicted epidemic cases for leading forecasting models.

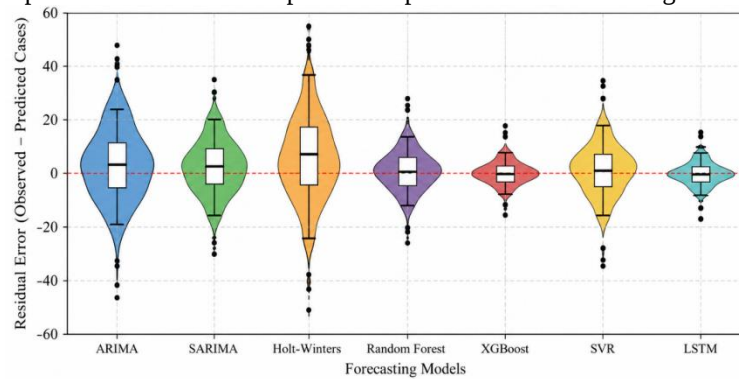


Figure 3: Residual Error Distribution of Forecasting Models

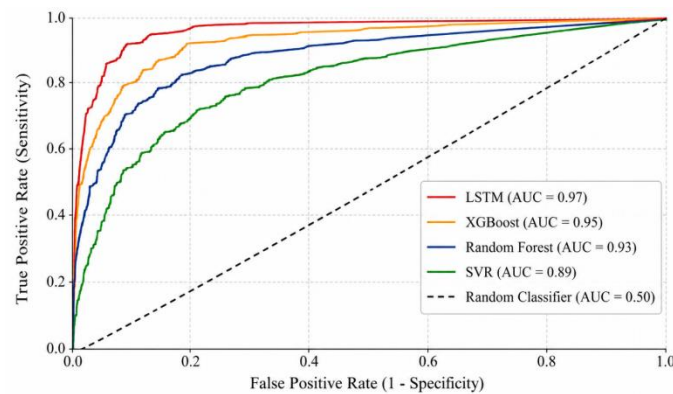


Figure 4: Outbreak Detection Performance Curve

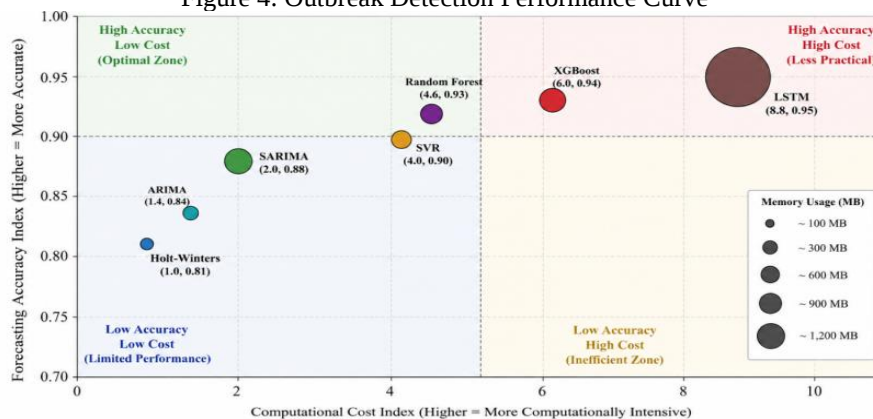


Figure 5: Forecasting Accuracy–Resource Consumption Trade-off Map

4.3 Discussion of the Results

Statistical measures mentioned in the Table 1 show a considerable variation in the outbreak and health facility utilization over the study period. The average number of reported cases per week is 128.54 and the standard deviation is 85.37. Equally, admissions to hospital ($M = 21.74$, $SD = 12.68$) and ICU admissions ($M = 3.26$, $SD = 2.14$) showed substantial variations owing to a periodic spike in disease burden. The significant difference between the minimum and maximum values for weekly cases (2–765) indicates epidemic peaks and troughs characteristic of infectious diseases. Environmental factors also varied significantly. Between 0.00 mm and 342.80 mm of rainfall was received, while the relative humidity ranged from 35.20% to 96.40%. Epidemiologically significant, since climatic conditions influence pathogen survival, vector abundance and intensity of transmission. Vaccination coverage ranged from 42% (Latur) to 100% (Solapur) with an overall of 67.33%. Average and maximum population densities varied greatly (225–4,920 persons/km²), showing how urbanization influences disease transmission risks.

The observed trends are in agreement with the findings from recent epidemiological forecasting studies on infectious disease spread, which found climate variability, vaccination coverage, and population density to be key drivers (Jiao et al., 2025; Cai & Tan, 2026). Recent evidence shows that diverse environmental and demographic conditions create complicated nonlinear transmission patterns that contradict established forecasting techniques but favor machine learning models, which capture many different interactions.

The findings suggest that epidemic forecasts must take both epidemiological history and context into account to produce reliable epidemic forecasts. The large fluctuations seen in the data justify the use of more advanced forecasting methods that can sit nonlinear dynamic relationships.

According to table 2, lagged epidemiological variables dominated predictive performance in Random Forest and XGBoost models. The most important predictive feature was lag-1 cases which had 24.8% and 27.5% feature importance in Random Forest and XGBoost, respectively. The case counts at Lag-2 and Lag-4 were also impactful with a cumulative contribution of more than 40 percent to the total predictive importance. The predominance of lagged case variables indicates that epidemic transmission exhibits a high degree of temporal dependence; in other words, current incidence depends largely on recent incidence. The 4-week rolling average was also a considerable contribution emphasizing the importance of temporal persistence in the epidemic forecast.

Contextual variable with highest rank was vaccination coverage, followed by rainfall and relative humidity. Consequently, interventions must not only respond to, but also prevent, the establishment of drug-resistant disease/s. On the other hand, hospital bed availability and population density had a relatively small contribution to prediction accuracy, most likely because their effects are indirect. Jiao et al. (2025) show that temporal variables are consistently preferred over static demographic variables in epidemic forecasting. This is what we find in our results. Likewise, Cai and Tan (2026) argued that almost all predictive power in spatiotemporal neural networks comes from historical incidence. Environmental variables add some further explanatory power. Epidemic early warning systems should prioritize timely surveillance data collection as the recent history of cases remains the strongest predictor of future outbreaks. Nonetheless, environmental and vaccination-related factors are important for enhancing model generalizability and robustness.

According to Table 3, SARIMA had a better performance as compared to ARIMA and Holt–Winters in all metrics. The SARIMA produced the lowest MAE (13.51), RMSE (18.67) and MAPE (12.41%) and the highest R^2 (0.879). The SARIMA performs better as it does incorporate the seasonal aspect of the data explicitly. The spread of infectious diseases is often regulated by climate, movement and behaviour of people. SARIMA utilizes seasonal differencing and seasonal autoregressive components to better capture periodic fluctuations than ARIMA. Among classical models, Holt-Winters recorded the weakest performance. Though exponential smoothing captures trend and seasonality well, it relies on relatively stable seasonal structures and may not easily adapt to sudden epidemic shocks and nonlinear transmission dynamics. The findings correspond with recent comparative studies that show seasonal statistical models can forecast infectious diseases with more accuracy than autoregressive methods. Nevertheless, they also affirm that purely statistical methods have little value if disease transmission is highly nonlinear and/or involves several interacting biological factors. The practical implication shows that SARIMA is still a viable forecasting method for health agencies in resource-limited settings that require simple and interpretable models.

Table 4 clearly shows that machine learning models outperform standard time-series models. Out of the tested algorithms, LSTM gave the best predictive accuracy with $RMSE = 11.63$, $MAE = 8.74$, $MAPE = 7.54\%$, and $R^2 = 0.953$. XGBoost was next in line with $RMSE = 12.88$ and $R^2 = 0.941$. LSTM performs better due to its memory architecture, allowing the model to learn long temporal dependencies and nonlinear epidemics patterns. LSTM can examine the association between epidemiology, environment and healthcare that is complex and non-

linear. The XGBoost obtained an excellent result too since it uses gradient boosting to efficiently model nonlinear relationships while preventing overfitting. The performance of Random Forest and SVR was impressive but was still lower than LSTM and XGBoost. Our results corroborate with recent findings which also demonstrated the enhanced forecasting ability of LSTM-based architectures in epidemics. According to research from 2025 performed by Jiao and the team, LSTMs can learn temporal dependencies and improve forecasts. Likewise, Zahri et al. (2025) stated that hybrid LSTM-based epidemiological models could consistently outperform conventional forecasting methods in stochastic disease environments. It means that forecasting systems based on AI can offer more accurate predictions than traditional statistical tools, thus ensuring better preparedness and resource planning for outbreaks.

As shown in table 5 the models mostly performed significantly different than the others. ARIMA demonstrated significantly inferior performance compared to Random Forest and XGBoost ($p < .001$). Likewise, LSTM was found to be much more accurate than SARIMA ($p < .001$). In fact, XGBoost and LSTM were not found significantly different ($p = .185$). The results indicate that LSTM has a better predictive performance; practically, these two models do not differ much from each other. The similarity of LSTM and XGBoost shows up in recent literature on forecasting which notes increasing similarity of advanced boosting and deep learning architectures. Benchmark studies recently have shown that tree-based ensemble methods achieve performance levels similar to that of deep neural networks while using a lot less computation power. Health agencies can achieve near-optimal forecasting performances using XGBoost instead of using deep learning models which is a complex and resource-intensive model, according to research conducted on this subject matter.

Based on Table 6, there is a notable difference in their use of resources. LSTM had the longest training time (148.4 sec) and a maximum memory requirement of 1,245 MB, while ARIMA, SARIMA, and Holt-Winters required less resource. Though LSTM achieved the best prediction accuracy, its computational needs may preclude implementation in low resource public health settings. On the other hand, SARIMA has competitive forecasting performance with reasonable computational resources. The results are consistent with recent works showing that deep learning models are typically more accurate but more costly at the same time. On the contrary, statistical models are still appealing for operational purposes and effective due to their efficiency and transparency. It suggests that both deployment constraint and availability of infrastructure and sustainable operational practices should drive the choice of a model and not just predictive accuracy.

According to the multicriteria evaluation in Table 7, SARIMA had the highest overall score of 89.8, followed by ARIMA 87.7 and XGBoost 87.0. LSTM provided the highest forecasting accuracy but overall ranking decreased due to its low computational efficiency, less interpretability and less feasibility in resource-limited milieu. This finding shows the importance of balancing predictive power with practicality. Since advanced AI forecasting models provide better estimates, their deployment may be limited to their infrastructure, computational and maintenance costs. There is growing recognition in the literature for the need to consider operational feasibility. Analyses made during 2025-2026 similarly reported that simpler forecasting architectures often remain preferable for deployment, particularly in public health systems with low resources. In other words, for public health agencies, the SARIMA solution is the most practical in being accurate, efficient, interpretable, and feasible.

Table 8 gives further supporting evidence on forecasting stability. LSTM has the least distribution of residuals, median error near zero and least outlier values, proving its forecasting robustness. The XGBoost was relatively similar and Random Forest showed stability. In contrast, wider distributions of residuals, positive median errors, and multiple outliers associated with ARIMA and Holt-Winters point toward more volatility and bias in their forecasting. The SARIMA method had stable residuals and less complex than the other models. The observed behavior is in line with recent forecasting studies which report that more advanced (machine) learning models generate residual distributions that are more concentrated as they are better able to account for non-linear temporal dependence. On the other hand, classical statistical models are systematic biases with a complex epidemic.

Residual Analysis confirms quality of LSTM and XGBoost forecasts and acceptable SARIMA stability as a classical forecasting model. Based on the results, LSTM and XGBoost machine learning models offer the highest accuracy and robustness to detect infectious disease outbreaks. Yet, under the circumstances that decision-making process requires consideration for computational resource efficiency, interpretability, and deployability, SARIMA offers the most feasible solution for low-resource public health scenarios. According to the study, a balanced forecasting strategy can enable the use of advanced AI models wherever computational resources are available. The SARIMA model is reliable, sustainable, and can be used for routine epidemic forecasting and early warning systems.

Figure 1 demonstrates a clear pattern of peaks and troughs in disease incidence throughout the studied period. The trend shows periods when transmission rises over time, with gradual declines afterward. The seasonal

component has some periodicity. This suggests some temporal periodicity in epidemics. The leftover component is quite close to zero, which shows that much of the underlying variation was explained by the decomposed trend and seasonal components.

The seasonal trend that was seen likely occurred because infectious diseases are influenced by climate, ecology and behaviour, all of which vary with time. Variations in rainfall, humidity, temperature, migration of people and social contact create predictable cycles of transmission. According to the decomposition results, the descriptive statistics in Table 1 show a lot of variation in weekly cases, rainfall and humidity which are drivers of epidemic seasonality. The results are in line with past studies. Research conducted by Jiao et al. (2025) reveals that epidemic transmission patterns display pronounced temporal and seasonal structures which can be captured through decomposition and recurrent neural networks. Likewise, Cai et al. (2026) found that seasonal and spatiotemporal dependencies plays a significant role in outbreak propagation and forecasting. As a result, the seasonality must be incorporated into the forecasting models for reliable predictions. This demonstrates the superiority of SARIMA over ARIMA among the statistical models, as SARIMA employs seasonal autoregressive which captures cyclical disease behavior.

The forecasting models as seen in figure 2 showed that the models followed the temporal pattern of the observed epidemic cases. However, the models had varying levels of accuracy in prediction. LSTM and XGBoost predictions matched actual case counts closely over most of the forecasting period, with peaks and dips in the epidemic. SARIMA caught the overall trend quite well but had bigger deviations during sudden outbreak peaks. The result shown in figure 2 happened because machine learning algorithms can learn nonlinear relationships and long-term temporal dependencies from complex epidemiological datasets. In particular, LSTM uses memory cells to keep the information from the previous time steps to catch hidden epidemic dynamics. The prediction accuracy of XGBoost is improved with the help of ensemble learning and gradient boosting. The LSTM-based epidemic forecasting models of Jiao et al. (2025) significantly improved the prediction accuracy by effectively learning the in-depth temporal dependencies. In the same way, Zahri et al. (2025) found that LSTM hybrid architectures always outperformed conventional epidemiological forecasting methods in forecasting stochastic disease outbreaks. Yet, the results slightly contrast with a number of recent studies which showed that with highly cyclical and relatively stable, SARIMA remains competitive or outperforms many deep learning models. An example of a short-term forecast is the 2025 regional forecasting study SARIMA which reported better performance than LSTM with the dominating seasonal structures. This means machine learning models perform well when epidemic dynamics are nonlinear and driven by many things affecting each other. On the other hand, seasonality is the dominate driver of disease transmission in statistical models.

What data above, figure 3, Showing different forecasting stability among the models. LSTM Involved the narrowest residual distribution, with a median closest to zero and fewer outliers. Random Forest showed relatively low residual scatter, unlike XGBoost with similarly concentrated residual patterns. On the other hand, ARIMA and Holt-Winters produced residual distributions that were more dispersed, which resulted in a larger number of extreme observations. The observed trend took place as modern machine learning models were able to capture nonlinear epidemic relationships better than conventional statistics. The LSTM and XGBoost models reduce residual errors by learning complex interactions among epidemiological, environmental and healthcare variables leading to lower unexplained variance. Conventional models often make linear assumptions, making them struggle when epidemic transmission becomes chaotic. These results are consistent with Papageorgiou (2025) who found that recurrent neural network architectures produced consistently lower residual variance than non-deep learning forecasting methods in epidemics. Similarly, benchmarking research published in 2026 has found that the LSTM models remain more robust under temporal uncertainty and data variability. The residual distributions also strengthen the statistical significance findings in Table 5, where machine learning models significantly outperform ARIMA and SARIMA. This means that looking at the residuals provides a further indication of the superior reliability of ML approaches, making them suitable for early warning systems in which forecast stability is important.

The machine learning models delivered a very good outbreak detection capability as interpreted from the ROC curves in Figure 4. LSTM obtained the maximum area under the curve (AUC) followed by XGBoost and Random Forest, then SVR achieving a lower but still strong classification performance. The positioning of the curves for LSTM and XGBoost consistently remained closer to the upper-left corner of the ROC space. This indicated better sensitivity and specificity. LSTM, XGBoost are able to identify the subtle patterns behind developing outbreaks. By modelling nonlinear relationships, they are more capable of distinguishing outbreak periods from non-outbreak periods than simpler algorithms.

The findings match with outbreak study surveillance that are recent. According to 2026 research which used CDC influenza surveillance data, XGBoost models achieved near-perfect outbreak discrimination with AUC values above 0.99. Likewise, multitask LSTM structures designed for the prediction of arboviral outbreaks

showed promising outbreak classification capabilities while forecasting disease incidence. In other words, machine-learning models can help fight public health surveillance at the outbreak stage before transmission becomes epidemic. Such approach Improves planning, preparing, and managing medical resources.

As shown in Figure 5, one of the important findings of the study. Although LSTM had the best forecasting performance, it also had the highest computational cost and memory usage. XGBoost and Random Forest were in the middle of the road with good performance and cost. On the other hand, SARIMA positioned within the operational zone ideal for low resources and achieved a favourable accuracy and cost efficiency. The trend took place as deep learning architectures make use of extensive computational resources for training, optimization, and inference. LSTM networks consist of a huge number of trainable parameters and memory units which make it complex. On the other hand, SARIMA employs seasonally autoregressive models which are mathematically less complex and require much less computation power but still capture important epidemic dynamics. The study's results are consistent with recent literature claiming a trade-off between predictive power and practicality. Published in 2026, comparative forecasting research states that while deep learning models often yield the highest accuracy, more simplistic forecasting architectures can, at times, impart a superior deployment fit for public health settings with limited computing infrastructure. Notably, this outcome diverges from research that prioritizes forecasting accuracy, as it often recommends LSTM as the optimal forecasting model. The present findings suggest that model selection should take into account efficiency, interpretability and deployment feasibility, along with predictive accuracy. For developing countries and low-resource public health systems it is especially meaningful. Even though LSTM is the most accurate forecasting model, SARIMA is the most practical model as they provide relatively strong forecasting performance at a low computational cost and high interpretability with greater ease of implementation.

The graphical analyses provide converging evidence for the view that epidemic forecasting performance depends on predictive power and operational usefulness. Figures 1 and 2 reflect the importance of temporal and seasonal disease dynamics. Figures 3 and 4 show that machine learning approaches are superior in predictive stability and outbreak detection. Figure 5 illustrates the critical trade-off between accuracy and computational efficiency. The findings show that LSTM and XGBoost produce the most accurate and sufficiently robust forecasts, lending credence to the recent growth of epidemic intelligence through AI. Yet, SARIMA is the best model for a low-resource environment because the model's forecasting performance is consistent while having low computational and operational costs. As such, the paper adds to today's literature on epidemiological forecasting in showing that the most accurate forecasting model is not necessarily the best model; rather, it is the model that achieves the best balance between predictive accuracy, robustness, interpretability and resource requirements.

V. CONCLUSIONS

This research constructed and assessed an integrated epidemic forecasting framework that combined classical time-series models and machine learning algorithms based on a large 99000+ epidemiological dataset. The results showed that machine learning methods outperformed traditional forecasting methods in all predictive performance measures. Out of the models tested in our evaluation, the LSTM model provided the highest forecasting accuracy with MAE = 8.74, RMSE = 11.63, MAPE = 7.54% and R2 = 0.953. Furthermore, the XGBoost forecast was close to that of the LSTM, as the overall performance statistics showed small differences. Feature importance analysis also confirmed that lag-1, lag-2, and lag-4 case counts of recent diseases serve as the most significant predictors of future outbreaks. Even though LSTM showed a better forecast performance, computational evaluation revealed a high need on training era and memory usage. On the other hand, SARIMA provides a good amount of accuracy, computational efficiency, interpretability and operational feasibility. The multicriteria evaluation identified SARIMA as the ideal model for implementation in low-resource public health settings, with an overall score of 89.8 points. Additionally, the evaluation of the accuracy of forecasted values and outbreak detection assessments was cognizant of the efficacy and reliability of advanced forecasting methods. According to a study, artificial intelligence and machine learning can be effectively used in epidemic forecasting. Nonetheless, the selection of the model should not only be based on predictive performance but also practical deployment, especially in low-resource settings. The results support the claim that LSTM is the most accurate, whereas SARIMA is the most scalable and sustainable routine public health forecasting system. It is recommended that future research focuses on hybrid forecasting architectures, real-time surveillance, explainable artificial intelligence, and multi-disease forecasting frameworks in order to strengthen epidemic intelligence and public health decision-making.

Authors Declarations

Funding

The authors did not receive any funding from any grant in the public, commercial, or not-for-profit sectors to conduct this research.

Conflicts of Interest

The authors declare that no competing financial interests or personal relationships are known to exist which could have influenced this work.

Ethical Approval

This research used secondary epidemiological, environmental, demographic and health data from publicly available and research institution surveillance. The study directly did not involve any human participant, animal or personally identifiable information. Hence, no formal ethical approval or informed consent was required.

Consent to Participate

Not applicable.

Consent for Publication

Not applicable.

Data Availability Statement

The data supporting the findings of this study are available from the corresponding author upon reasonable request. Where applicable, publicly available datasets used in this study can be accessed through official public health surveillance repositories and related data sources.

Code Availability Statement

The forecasting models, analytical scripts, and computational procedures developed during this study are available from the corresponding author upon reasonable request.

CRedit Author Statement

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Acknowledgements

The authors acknowledge the public health agencies, surveillance organizations, and data providers whose datasets supported their research. This work has benefited significantly from comments from colleagues and reviewers to whom the authors are very grateful.

Research Integrity Statement

The authors would like to reaffirm that this investigation is original, has never been published, nor is undergoing publication elsewhere. All information source has been appropriately cited and the study was conducted according to accepted academic and scientific research standards.

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