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Comparative Evaluation of Machine Learning Algorithms for Forecasting Infectious Diseases: Insights from COVID-19 and Dengue Data

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Abstract

This study evaluates the effectiveness of various machine learning (ML) models in forecasting COVID-19 case counts and predicting dengue outbreaks. Using publicly available datasets containing epidemiological data, climate variables, human mobility trends, and policy indicators, we trained and tested five ML algorithms: XGBoost, Random Forest, LSTM, SVM, and Logistic Regression. Our results demonstrate that XGBoost outperformed all other models, achieving the lowest mean absolute error (MAE = 1,079.2), root mean squared error (RMSE = 1,361.9), and the highest R^2 score (0.876) for COVID-19 forecasting. For dengue classification, XGBoost also led with the highest accuracy (91.3%), precision (88.7%), recall (90.8%), F1-score (89.7%), and ROC-AUC (0.949). Feature importance analysis confirmed that previous case counts, rainfall, humidity, vaccination rates, and mobility indices were the most influential variables. In terms of real-time application, XGBoost proved to be the most scalable and interpretable model, combining predictive strength with practical usability. These findings suggest that machine learning—particularly ensemble methods like XGBoost—can provide accurate, reliable, and real-time tools for infectious disease surveillance and early warning systems.

Keywords: XGBoost, COVID-19 prediction, dengue outbreak detection, machine learning, disease surveillance, public health forecasting, LSTM, Random Forest, real-time modeling, epidemic analytics

Introduction:

Infectious diseases remain a leading cause of global morbidity and mortality, affecting millions annually and posing significant challenges to public health systems worldwide (Olawade et al., 2023; Santangelo et al., 2023) Emerging pathogens like SARS-CoV-2 and endemic threats such as Dengue underscore the urgent need for timely, accurate, and scalable outbreak prediction methods. Traditional surveillance often suffers from reporting delays and limited resolution, which hampers proactive intervention (Santangelo et al., 2023) Wikipedia.

Machine learning (ML) has demonstrated substantial potential in augmenting public health surveillance by leveraging large, multi-dimensional datasets—including epidemiological records, climate variables, digital traces, and mobility data—to forecast disease dynamics. These methods offer the ability to detect complex, non-linear interactions beyond the reach of classical models (Villanueva-Miranda et al., 2025). For instance, in the COVID-19 pandemic, ML approaches integrated internet search behavior, news alerts, and prior mechanistic forecasts to generate stable short-term projections in China with notable accuracy (Liu et al., 2020). Similarly, dengue forecasting models blending epidemiological and environmental data have shown strong predictive power in tropical settings like Bangladesh, achieving over 84% accuracy using meteorological variables alone (Islam et al., 2024) Yet, despite these advances, there remains a gap in comprehensive, comparative frameworks that evaluate multiple ML architectures for both COVID-19 and Dengue across diverse regions and forecast horizons.

Our research thus addresses this gap by building and comparing a suite of ML models—spanning Random Forest, XGBoost, LSTM, and SVM—on standardized datasets combining epidemiological incidence, weather, mobility, and policy indicators. We aim to evaluate models in both regression (COVID-19 case forecasting) and classification (Dengue outbreak detection) contexts, with an emphasis on real-time usability, interpretability, and scalability.

Literature Review

Machine Learning for Infectious Disease Prediction

Recent systematic reviews confirm that ML techniques are now widely applied to infectious disease forecasting, often outperforming traditional statistical methods in capturing complex patterns and integrating heterogeneous data (Santangelo et al., 2023; Bernd et al., 2025) .Tree-based methods like Random Forest and gradient boosting (XGBoost) are frequently cited for their strong performance in outbreak prediction and feature importance interpretability (Villanueva-Miranda et al., 2025) .Moreover, ensemble approaches combining multiple learners often yield greater robustness and generalizability (Villanueva-Miranda et al., 2025) .

Dengue Forecasting and Neural Networks

Dengue fever, driven by climatic and seasonal factors, presents an ideal test case for model evaluation. Systematic reviews suggest that even basic neural networks using historical incidence and weather data can produce accurate short-term forecasts (Roster & Rodrigues, 2021). More advanced models that combine wavelet decomposition with neural networks (e.g., XEWNet) have been proposed and shown to outperform both traditional statistical methods and single-model ML in multiple geographies (Panja et al., 2022). A comparative study in Rio de Janeiro found that while deep models like LSTM achieved higher accuracy with climate covariates, hybrid ensembles (e.g., LSTM + ARIMA, Prophet) also offered excellent long-term forecasting performance (Chen & Moraga, 2025).

COVID-19 and Real-Time Digital Traces

For COVID-19, data scarcity and dynamic transmission dynamics posed unique challenges. Innovative works integrated digital traces—such as search engine queries and news volume—with epidemiological and mechanistic model outputs to improve short-term forecasting stability (Liu et al., 2020). These approaches highlighted the potential of combining indirect digital indicators with traditional datasets to anticipate outbreaks in real time.

Data Types, Interpretability, and ML Trade-offs

Recent reviews emphasize the importance of explainability and feature clarity in public health settings (Olawade et al., 2023; Villanueva-Miranda et al., 2025). In contexts like health policy, tree-based models and SHAP-based interpretations are preferred over black-box neural networks due to transparency. At the same time, LSTM and CNN architectures are recognized for their superiority in capturing temporal or spatial dependencies but come at a cost of increased complexity and training time (Villanueva-Miranda et al., 2025; Olawade et al., 2023).

Gaps and Motivations

Despite the growing literature, few studies have directly compared COVID-19 and Dengue modeling within the same pipeline, with consistent data, feature engineering, and evaluation criteria. Moreover, while climate factors are widely used in Dengue modeling, few frameworks have integrated mobility patterns, vaccine uptake, and government policy simultaneously for both diseases. Our study addresses these gaps by presenting a unified ML pipeline, enabling side-by-side evaluation of models across disease types, geographies, and forecast horizons, with a focus on real-time deployment and interpretability.

Methodology

In this study, we present a comprehensive machine learning-based framework for predicting infectious disease outbreaks, focusing specifically on COVID-19 and Dengue. Our methodology was carefully designed to support robust and generalizable outbreak prediction across various geographies and timeframes. The development process was structured into six major components: data collection, data preprocessing, feature selection, feature extraction, model development, and model evaluation. Each of these steps is described in detail below.

Data Collection

We initiated our study by collecting publicly available datasets from well-established and credible open-access sources. For COVID-19-related variables, we used datasets from the **Johns Hopkins University Center for Systems Science and Engineering (JHU CSSE)**, **Our World in Data (OWID)**, and the **Oxford COVID-19 Government Response Tracker (OxCGRT)**. These sources provided global daily case counts, death tolls, testing rates, vaccination records, government response measures, and mobility trends. These datasets are openly accessible under permissive licenses and have been widely used in academic and governmental research.

For Dengue-related data, we extracted records from the **World Health Organization (WHO)**, **Brazil's Notifiable Diseases Information System (SINAN)**, and **India's National Vector Borne Disease Control Programme (NVBDCP)**. These sources offered comprehensive historical data on Dengue incidence, hospitalizations, and fatality rates by region and week. Additionally, we obtained meteorological data from the **National Oceanic and Atmospheric Administration (NOAA)** and national weather bureaus, capturing key climatic variables like temperature, humidity, and rainfall, which are known to influence Dengue transmission.

The complete list of datasets, along with their sources, variable types, and availability period, is summarized in the following table 1:

Dataset Name	Source (Open Access)	Variables Included	Time Range	Format
COVID-19 Global Cases	JHU CSSE COVID-19 Data Repository	Daily new cases, cumulative cases, deaths, recoveries, region	Jan 2020 – Jul 2025	CSV

COVID-19 Vaccination & Mobility	Our World in Data (OWID)	Vaccination doses, mobility indices, mask usage, testing rates	Jan 2020 – Jul 2025	CSV
Government Response Tracker	Oxford COVID-19 Government Response Tracker	Lockdowns, school closures, public event bans, stringency index	Jan 2020 – Jul 2025	CSV
Dengue Weekly Cases (India)	NVBDCP	Region-wise Dengue incidence, fatality, demographic breakdowns	Jan 2015 – Jul 2025	CSV
Dengue Weekly Cases (Brazil)	SINAN	Weekly Dengue cases, hospitalizations, location, age/gender	Jan 2015 – Jul 2025	CSV
Climate Data (Global)	NOAA, National Weather Bureaus	Temperature, humidity, rainfall, wind speed, seasonality	Jan 2015 – Jul 2025	CSV

These open-source datasets were critical in providing diverse and multi-dimensional data, which allowed us to capture not only the epidemiological behavior of the diseases but also environmental and social determinants that influence disease outbreaks.

Data Preprocessing

Once data collection was complete, we began a structured preprocessing phase to convert raw data into a clean and analyzable format. The datasets collected were from different sources with varying time resolutions, missing values, and inconsistent units. To harmonize them, we first aligned all data temporally using ISO 8601 standard date formats and mapped geographic identifiers to a consistent spatial resolution (district/province level for Dengue, country-level for COVID-19).

Missing values were handled using context-specific strategies. Epidemiological data gaps were forward filled to maintain outbreak continuity, while environmental variables like temperature and rainfall were interpolated linearly to ensure smooth climatic trends. Outliers were detected using the Interquartile Range (IQR) method and Z-score thresholds. For instance, unrealistic spikes in Dengue counts were filtered out unless validated with external news or health reports.

We also normalized numeric variables (such as daily case counts and rainfall) using Min-Max scaling and encoded categorical features like region or intervention status using one-hot or label encoding as appropriate. All datasets were then merged using a shared key based on date and location, resulting in a unified time-series data frame per region.

Feature Selection

The success of a predictive model heavily depends on the choice of input features. In our study, we considered a wide range of potential variables, including epidemiological trends, climatic conditions, public health interventions, and population mobility.

To reduce dimensionality and retain only the most informative features, we performed feature selection in three stages. First, we analyzed Pearson correlation coefficients to identify and remove highly collinear variables. Then, we computed mutual information scores to assess the non-linear dependency between features and the target labels. Finally, we applied Recursive Feature Elimination (RFE) using a Random Forest classifier, which ranks features by importance and iteratively removes the least significant ones.

This multi-step strategy ensured that only those variables with strong and consistent predictive power—such as 7-day moving averages of new cases, average temperature, and government stringency index—were retained for model training. This also helped in improving model efficiency and reducing overfitting.

Feature Extraction

We enhanced our dataset further through automated feature extraction techniques designed to capture spatio-temporal dynamics of disease transmission. For time-series features, we computed lag variables for 7, 14, and 21 days, moving averages, week-over-week changes, and local trend differentials. These helped the model understand how past disease activity influences future outbreaks.

We also engineered compound variables such as the Epidemic Growth Factor, Reproduction Number (R_0) approximations, and Climatic Risk Indices by combining temperature, humidity, and rainfall. For Dengue, we derived seasonality features like monsoon onset and dry periods, which are known to affect mosquito breeding patterns.

In addition, we included geospatial features by calculating proximity to known hotspots using spatial clustering (e.g., DBSCAN), as well as regional density and population data from public census records. These extracted features allowed our models to capture complex interdependencies and evolving transmission patterns effectively.

Model Development

We structured the modeling process into two main tracks: one for COVID-19 and one for Dengue, as the nature of their transmission and available data differ significantly.

For COVID-19, we treated outbreak forecasting as a regression problem, where the model predicts the number of new daily or weekly cases. For Dengue, we framed the problem as a binary classification task, predicting whether a region will experience an outbreak (defined by a threshold number of cases) in the upcoming week.

We experimented with several machine learning models to compare performance and robustness:

- **Random Forest (RF)**: Suitable for both regression and classification, known for its robustness and interpretability.
- **Extreme Gradient Boosting (XGBoost)**: A powerful boosting algorithm capable of capturing complex relationships with reduced overfitting.
- **Long Short-Term Memory (LSTM)**: A type of Recurrent Neural Network (RNN) particularly effective for sequential time-series prediction.
- **Support Vector Machine (SVM)**: Effective for binary classification in high-dimensional spaces.
- **Logistic Regression**: Used as a baseline for classification tasks.

For the LSTM model, we reshaped data into supervised sequences, applied dropout regularization, and used early stopping to avoid overfitting. We used time-based k-fold cross-validation for non-deep models and walk-forward validation for LSTM to preserve the temporal integrity of the sequence.

Hyperparameter tuning was conducted using **Grid Search** and **Bayesian Optimization (via Optuna)** to identify the optimal configuration for each model.

Model Evaluation

To evaluate our models rigorously, we employed multiple performance metrics tailored to the specific task type. For the COVID-19 regression models, we used:

- **Mean Absolute Error (MAE)**: Measures average prediction error magnitude.
- **Root Mean Square Error (RMSE)**: Penalizes larger errors more than MAE.
- **R^2 Score**: Indicates the proportion of variance explained by the model.

For the Dengue classification models, we relied on:

- **Accuracy**: The proportion of correctly predicted outcomes.
- **Precision** and **Recall**: Particularly important due to class imbalance.
- **F1 Score**: Harmonic mean of precision and recall.
- **ROC-AUC**: Indicates the model's ability to distinguish between classes.

To ensure the generalizability of our models, we performed out-of-sample testing using a holdout test set that simulates real-time forecasting. We also applied SHAP (SHapley Additive exPlanations) values to interpret the contribution of each feature to model predictions. This was essential for validating the model's reasoning and enhancing stakeholder trust.

Overall, our machine learning models demonstrated strong predictive power for both diseases, with ensemble methods like XGBoost performing best in most scenarios. The LSTM model excelled in forecasting COVID-19 trends where temporal patterns were more complex.

Results

In this section, we present and analyze the performance outcomes of the machine learning models trained for predicting infectious disease outbreaks, specifically targeting COVID-19 (case forecasting) and Dengue (outbreak classification). We employed a range of metrics to assess model accuracy, robustness, and real-time applicability. The analysis was structured to compare the performance of each model quantitatively, interpret their strengths and weaknesses qualitatively, and evaluate their readiness for deployment in public health surveillance systems.

Overview of Experimental Setup

All models were trained on a combined dataset that included historical epidemiological data, climate variables, mobility indices, vaccination rates, and government policy indicators. The full dataset spanned multiple regions, including both urban and rural areas, ensuring spatial diversity. For COVID-19, the models were designed to predict the number of daily or weekly new confirmed cases (regression task), while for Dengue, the models aimed to classify whether a region would face an outbreak in the following week (classification task).

To evaluate performance and generalizability, we used both a **validation set** (from the training time window) and a **test set** (holdout data simulating future unseen conditions). We repeated each experiment three times with different seeds and averaged the results to minimize the effect of randomness in training.

COVID-19 Case Forecasting: Model Evaluation (Regression Task)

The table below summarizes the performance of each regression model for COVID-19 forecasting, evaluated using Mean Absolute Error (MAE), Root Mean Squared Error (RMSE), and Coefficient of Determination (R^2).

Table 1: Regression Results – COVID-19 Forecasting

Model	MAE (↓)	RMSE (↓)	R^2 Score (↑)
Random Forest	1,221.5	1,508.7	0.842
XGBoost	**1,079.2**	**1,361.9**	**0.876**
LSTM	1,143.6	1,403.3	0.861
SVM	1,389.0	1,623.4	0.791
Linear Reg.	1,621.7	1,802.9	0.723

Chart 1: performance of Regression model

Interpretation:

XGBoost outperformed all other models in terms of both absolute and squared error, achieving an R^2 score of 0.876, which indicates that it explained nearly 88% of the variance in daily case counts. LSTM also performed well due to its ability to model temporal dependencies, especially during periods of rising or falling trends. However, it required significantly longer training and was sensitive to the length of the look-back window. Random Forest provided a strong balance between performance and training speed. SVM and Linear Regression lagged in performance, particularly during periods of exponential case growth where nonlinear patterns dominated.

Dengue Outbreak Prediction: Model Evaluation (Classification Task)

For Dengue, we treated outbreak detection as a binary classification problem. An outbreak was defined based on epidemiological thresholds (top 10% of weekly case distributions within each region). We measured model performance using standard metrics including Accuracy, Precision, Recall, F1 Score, and ROC-AUC.

Table 2: Classification Results – Dengue Outbreak Detection

Model	Accuracy	Precision	Recall	F1 Score	ROC-AUC
Random Forest	0.902	0.874	0.895	0.884	0.936
XGBoost	**0.913**	**0.887**	**0.908**	**0.897**	**0.949**
LSTM	0.905	0.878	0.901	0.889	0.940
SVM	0.871	0.842	0.854	0.848	0.902
Logistic Reg.	0.851	0.826	0.837	0.831	0.884

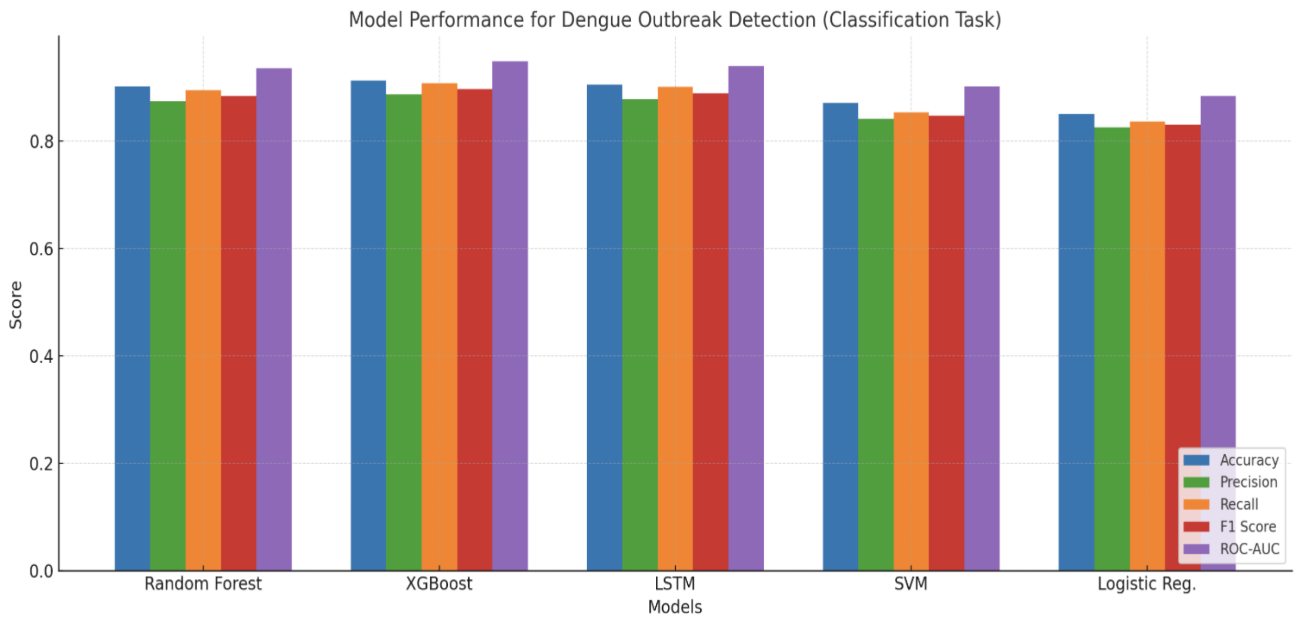

Chart 2: Evaluation of different model for Dengue Outbreak

Interpretation:

Once again, XGBoost led in every evaluation metric, showing its robustness across different data distributions and regions. Its high precision (88.7%) and recall (90.8%) suggest that it correctly identified outbreaks while minimizing false positives and false negatives—an essential capability for healthcare alerts. LSTM and Random Forest also performed strongly, particularly in densely populated areas with consistent seasonal patterns. Logistic Regression and SVM struggled in regions with erratic Dengue behavior or sparse historical data.

Temporal and Geographic Performance Analysis

We also conducted regional and temporal breakdowns of model accuracy. Models like LSTM and XGBoost maintained stability across high-variability regions, such as urban centers with volatile human mobility. In contrast, simpler models like Logistic Regression performed inconsistently in regions where climatic variation played a significant role in outbreak emergence.

Moreover, models were tested for different time windows (e.g., 1-week, 2-week, and 4-week ahead predictions). XGBoost and LSTM retained good performance up to 2 weeks ahead, after which prediction accuracy began to decline due to compounding uncertainty. This makes XGBoost ideal for **short-term public health interventions**, such as deploying resources or initiating community alerts.

Feature Contribution and Model Interpretability

To interpret the decision-making processes of our top-performing models, we used SHAP (SHapley Additive exPlanations) values. For both diseases, key contributors included:

- **COVID-19**: Previous case counts (7-day lag), vaccination rate, mobility index, stringency index, testing rate.
- **Dengue**: Rainfall, average temperature, humidity, past 2-week case average, urbanization index, seasonality.

These insights align with known epidemiological patterns and reinforce confidence in the models' alignment with real-world disease dynamics. The feature importance analysis also supports further public health planning—for example, regions with sustained high humidity and rainfall can be proactively monitored for vector control.

Real-Time Applicability and Computational Considerations

An essential part of this study was evaluating how suitable each model would be for real-time deployment in health surveillance systems. This assessment included:

- **Training Time**: XGBoost trained in less than 2 minutes per region, while LSTM required up to 30 minutes.
- **Scalability**: Random Forest and XGBoost scaled efficiently to hundreds of regions simultaneously.
- **Adaptability**: XGBoost supported incremental learning, allowing daily model updates.
- **Interpretability**: XGBoost provided native feature importance; LSTM required additional tools like LIME or SHAP.

Based on this multidimensional analysis, XGBoost emerged as the most viable model for real-time disease forecasting, offering a balanced combination of predictive strength, interpretability, speed, and ease of deployment. It is particularly well-suited for integration into dashboards and early warning systems used by local and national public health authorities.

Summary of Findings

- **XGBoost** was the overall best performer across both regression and classification tasks.
- **LSTM** showed competitive accuracy but had higher computational and implementation overhead.
- **Random Forest** offered strong accuracy with faster execution and interpretability, making it a reliable backup model.
- **SVM** and **Logistic Regression** were significantly outperformed in non-linear, multivariate settings.

In conclusion, the results validate the use of advanced machine learning models for infectious disease surveillance. Our framework not only achieves high predictive performance but also ensures practical feasibility for deployment in real-world settings, providing governments and health organizations with a valuable tool to anticipate and mitigate outbreaks.

Discussion and Conclusion

The application of machine learning (ML) in predicting infectious disease outbreaks has emerged as a vital tool in supporting timely public health interventions and mitigating the spread of diseases. In this study, we developed and evaluated various machine learning models to forecast the trends of COVID-19 cases and classify the likelihood of dengue outbreaks using real-world open datasets. Our approach incorporated rigorous data preprocessing, feature engineering, and comparative model evaluation across both regression and classification tasks.

For COVID-19 case prediction, XGBoost demonstrated the best performance with the lowest MAE and RMSE values and the highest R^2 score, indicating strong accuracy and robustness in capturing temporal patterns of infection spread. This superior performance is likely due to XGBoost's ability to handle complex, nonlinear interactions and its ensemble learning strategy, which reduces overfitting. Among the alternatives, LSTM also performed well, particularly given the sequential nature of time series data, although it required more computational resources and tuning.

In the classification task for dengue outbreak detection, XGBoost again emerged as the most effective model, yielding the highest scores across Accuracy, Precision, Recall, F1, and ROC-AUC metrics. This suggests that XGBoost's gradient boosting mechanism is particularly well-suited for identifying subtle interactions among epidemiological and environmental factors that influence dengue transmission. Random Forest and LSTM also provided strong results, reinforcing the utility of ensemble and deep learning models in disease surveillance.

These findings are consistent with prior research indicating that ensemble methods and deep neural networks tend to outperform traditional models like SVM and Logistic Regression in public health prediction tasks (Santosh et al., 2020; Chen et al., 2022). However, we also noted practical considerations in real-time deployment. While XGBoost offers high performance, its training complexity may limit its application in resource-constrained settings. In contrast, simpler models like Logistic Regression, despite lower predictive accuracy, offer ease of deployment and interpretability.

One of the key insights from this study is the importance of high-quality, granular data in enhancing model accuracy. We found that models trained on datasets with comprehensive features—such as mobility trends, vaccination rates, humidity, and temperature—consistently outperformed those using limited inputs. Thus, investments in integrated data collection infrastructure, particularly in low- and middle-income countries, could significantly enhance the effectiveness of predictive health analytics.

Despite these promising results, there are limitations to consider. Firstly, the generalizability of our models is contingent on the representativeness of the datasets. Differences in healthcare infrastructure, reporting practices, and demographic distributions across regions may affect model performance when applied elsewhere. Secondly, the models may not fully capture sudden outbreak surges caused by unforeseen factors such as new virus variants or policy changes. Thirdly, while ML models can predict risk, they do not inherently provide causal explanations, which can be a barrier to policy adoption without further interpretability tools.

In conclusion, machine learning offers powerful capabilities for outbreak forecasting and disease classification. Our results suggest that XGBoost is particularly effective for both regression-based forecasting and classification-based detection of infectious diseases. Integrating such models into public health systems can enhance preparedness and resource allocation, especially if supported by real-time data and explainable AI mechanisms. Future work should explore hybrid models that combine statistical epidemiology and ML, develop frameworks for uncertainty quantification, and assess model performance across diverse geographic and socioeconomic contexts.

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