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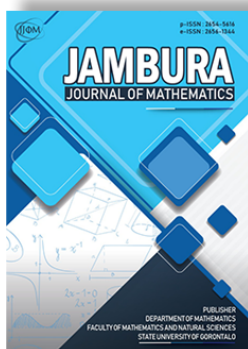
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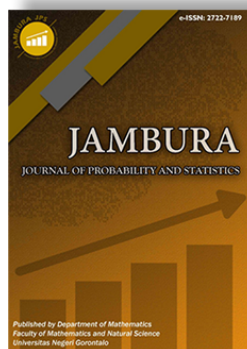
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Machine Learning Model for Predicting the Temporal Lassa Fever Confirmed Cases in Nigeria

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ABSTRACT. Lassa fever continues to pose a major public health threat in Nigeria, marked by recurrent outbreaks and high case fatality rates. The absence of robust predictive models has significantly impeded accurate trend forecasting, thereby limiting timely resource deployment and the implementation of effective preventive measures. This study seeks to bridge that gap by developing a comprehensive predictive framework for estimating confirmed Lassa fever cases in Nigeria. The research utilizes a combination of quantitative analysis and computational modeling techniques, leveraging weekly epidemiological data on Lassa fever cases from the Nigeria Centre for Disease Control (NCDC), spanning the year 2020. The dataset, which includes both suspected and confirmed cases, was cleaned and restricted to confirmed cases for the purpose of this analysis. Key steps included feature selection and dimensionality reduction to enhance model efficiency and accuracy. Three predictive models—Random Forest, Linear Regression, and Gradient Boosting—were developed and assessed using standard evaluation metrics such as Mean Absolute Error (MAE), Root Mean Square Error (RMSE), and R-squared (R^2). These models were designed to forecast future confirmed Lassa fever cases. The findings highlight the critical role of temporal variables, particularly weeks and months, in shaping transmission patterns. These features were shown to significantly influence the trends in confirmed cases.



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1. Introduction

Lassa fever represents a significant viral hemorrhagic fever showing increasing prevalence across Nigeria and the broader West African region, as evidenced by rising case numbers and mortality rates in recent years. This disease stems from an RNA virus within the Arenaviridae family and functions as a zoonotic disease—one that spreads from animals to humans, primarily through rodent vectors. West Africa serves as the endemic region for Lassa fever, with Nigeria at the center of this health concern. The disease takes its name from the town of Lassa in Borno State, Nigeria, where medical professionals first documented a case in 1969 [1].

Lassa fever in Nigeria, with its recurring outbreaks and high mortality, remains a major public health issue. The absence of a strong predictive model hinders accurate trend estimation and effective resource allocation. This study seeks to address the lack of a comprehensive predictive model for confirmed Lassa fever infections in Nigeria. Better understanding and prediction of Lassa fever dynamics are crucial for effective control, prevention, and reducing the disease's impact and costs in Nigeria.

According to multiple studies and weekly surveillance data from the Nigeria Center for Disease Control (NCDC), there has been a notable increase in both confirmed and suspected Lassa fever cases. This upward trend is attributed to enhanced disease monitoring efforts throughout the country. Climate forecasts for West Africa indicate rising temperatures and increased precipi-

tation, conditions that are likely to create more favorable environments for multimammate rats to flourish across the region. Since these rodents serve as the primary reservoir for the Lassa virus, their population growth is expected to elevate the risk of human transmission and infection [2]. Several models have been developed using the statistical traditional models like the ARIMA models, a renowned model for time series forecasting [3], the strength of random forest regressor machine learning model has the ability to capture nonlinear relationships and handle feature extractions between interactions between predictors [4].

Though first described in the 1950s, the virus causing Lassa disease was not identified until 1969. The virus was a single-stranded RNA virus belonging to the virus family Arenaviridae. About 80% of people infected with the Lassa virus had no symptoms. One in five infections resulted in severe disease, where the virus affected several organs such as the liver, spleen, and kidneys. Lassa fever was a zoonotic disease, meaning that humans became infected from contact with infected animals [5]. The animal reservoir, or host, of the Lassa virus, was a rodent of the genus *Mastomys*, commonly known as the “multimammate rat.” *Mastomys* rats infected with the Lassa virus did not become ill, but they could shed the virus in their urine and feces. Because the clinical course of the disease was so variable, detection of the disease in affected patients had been difficult. When the presence of the disease was confirmed in a community, however, prompt isolation of affected patients, good infection prevention and control practices, and rigorous contact tracing could stop outbreaks.

Several studies had laid a basis for understanding the dy-

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namics of Lassa fever. Some of the studies on Lassa fever only considered the basic transmission pathways namely, the human-to-human and the rodent-to-human [6–16]. For instance, [17] described Lassa fever transmission dynamics using a deterministic model integrating the exposed human and rat compartment instead of the usual SIR compartmental structure. Some other studies have tried to establish the time-dependent nature of the transmission dynamics of Lassa fever. For example, [18] used a compartmental model with time-dependent parameters where the infectious class was partitioned into symptomatically infected, mildly infected, and treated individuals alongside the carrying capacity of the rodent because of the periodic change of weather. Factors like quarantine and hospitalization of infected individuals were also used [19] to comprehend the transmission variability of Lassa fever. The association between the reproduction number and local rainfall was used to investigate the epidemiological features of Lassa fever on a large scale [20]. O. Angela and S. Pelumi [21] incorporated the effect of quarantine and the environment to show that in poor resource countries, Lassa fever transmission was driven by environmental contribution.

To develop a predictive model for Lassa fever in Nigeria, historical data from sources such as the NCDC had to be gathered and preprocessed for consistency. A suitable model, such as regression, or time series, had to be chosen. The model was then trained and its performance was evaluated using metrics like Mean Squared Error and R-squared. The model was refined based on results and deployed to predict future cases then the accuracy of the model was continuously monitored to ensure its efficacy, improving preparedness, early warning systems, and assessing control measures for Lassa fever outbreaks.

This paper has combined the method of random forest machine learning regression, simulation using bootstrapping-based uncertainty, and geospatial maps for visualization of spatial distribution patterns.

2. Materials and Methods

2.1. Data Collection

The dataset was from the weekly report of surveillance data on Lassa fever from the Nigerian Centre for Disease Control (NCDC) website which contains the weekly information of suspected cases, confirmed cases, and deaths reported on a weekly basis (weeks 1–50 of 2020). The dataset was then used as input in the model analysis, converted to an Excel file structured as a comma-separated values (CSV) file containing states where the cases have been reported in Nigeria. The attributes of the data include: week number, suspected cases, confirmed cases, deaths, and states.

3. Data Preprocessing and Feature Engineering

3.1. Data Cleaning

Data cleaning, data preprocessing, and simulation was performed using Python Programming Language with pandas library version 1.3.0 [22]. Missing column names were cleaned by removing no data values which were identified and were removed using `dropna()` function with the parameter `how='all'`, and missing values replaced with 0. Data inconsistencies were checked using a consistent naming convention.

3.2. Feature Engineering

New features were added to the attributes of the dataset for the enhancement of the performance of the predictive models:

- Temporal features: `Month_of_the_year` was calculated as $((\text{week_number} - 1) // 4) + 1$ and `quarter` as $((\text{week_number} - 1) // 13) + 1$ to capture seasonal patterns.
- Epidemiological indicators/features: Case Fatality Rate (CFR) computed as $\text{deaths} / \text{confirmed_cases}$, and confirmation rate as $\text{confirmed_cases} / \text{suspected_cases}$.
- Trend features: Four-week rolling average using `rolling(window=4).mean()` to smooth short-term fluctuations.
- Lag features: First and second-order lag variables for confirmed cases created using `shift(1)` and `shift(2)` functions to capture temporal dependencies.

During the process, seven features were selected for model training based on epidemiological relevance and data availability: Week number for temporal trend, suspected cases, monthly and quarterly seasonal changes, confirmation rate, and first and second-order lag variables for confirmed cases.

4. Exploratory Data Analysis

Exploratory data analysis was comprehensively conducted in Python using `matplotlib` version 3.5.0 [23] and `seaborn` version 0.11.0 [24]. The exploratory analysis is a very important step before modelling to give deep insight into the data. Some exploratory analysis conducted includes:

- Visualization of the time series over a 50-week period of confirmed cases in Nigeria.
- Feature correlation analysis between epidemiological indicators using the Pearson coefficient.
- Distribution analysis of confirmation rates and case fatality rates.
- Seasonal and quarterly trend relationships.
- Scatter plot between suspected and confirmed cases.

5. Development of Machine Learning Models

5.1. Model Selection

In the simulation and development of this model, three machine learning algorithms were selected based on their proven effectiveness in epidemiological forecasting and time series analysis:

- Random Forest Regressor: Random Forest machine learning algorithm uses an ensemble method. For this model, 100 decision trees (`n_estimators=100`) with bootstrap sampling were used [4].
- Gradient Boosting Regressor: A sequential ensemble method with 100 boosting stages was used [25].
- Linear Regression: A multiple linear regression model with standardized features. Features were standardized using `StandardScaler` from `scikit-learn` version 1.0.0 to ensure zero mean and unit variance [26, 27].

5.2. Model Training

During model development, the dataset was split into training (80%) and testing (20%) sets. The method of sampling used



Figure 1. (a) Confirmed cases over time. (b) Plot of suspected vs confirmed cases. (c) Total Confirmed Cases monthly. (d) Cases Fatality Rate Over Time. (e) Confirmed Cases with Moving Average. (f) Quarterly Case Distribution Boxplot.

was the stratified sampling approach, and the performance of the models was evaluated using RMSE, MAE, and R^2 .

6. Analytical Results and Discussion

Linear regression outperforms the two other ensemble models, which indicated that the predictions are very close to the actual values, have the lowest RMSE and MAE Values, random forest performed fairly with higher RMSE and MAE than linear regression, both random forest and logistic regression performs well with linear regression having a strong performance

with highest R squared and random forest as a good fit with a close r squared to linear regressions as shown in [Table 1](#).

Table 1. Model performance metrics

Model	RMSE	MAE	R^2	CV R^2 (mean $\pm$ std)
Random Forest	14.07	6.87	0.815	0.449 ± 0.730
Gradient Boosting	17.47	7.51	0.716	-2.751 ± 6.680
Linear Regression	7.16	5.24	0.952	0.419 ± 0.976

The figure shown in [Figure 1a](#) shows the weekly timeseries and gives an insight on the classic epidemic curve across dis-

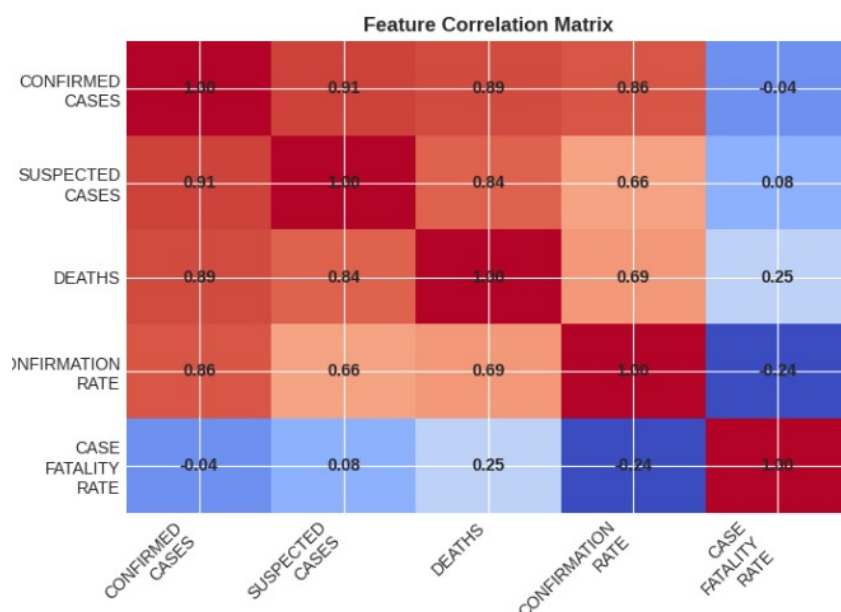


Figure 2. Feature Correlation Matrix

tinct phases. The outbreak of Lassa fever started with relatively reported moderate cases with about 50 confirmed cases in a week, a drastic increase was observed around the 6th week with approximately 90 cases. This initial increase or surge declined around week 15, and a secondary peak was noticed around week 20. The other patterns after the 20th week show a sustained level of low transmission with minor fluctuations, which eventually stabilized with low cases by week 50.

This bimodal distribution [3] is particularly interesting from an epidemiological perspective. The secondary peak could indicate several phenomena: seasonal variation in transmission dynamics, the emergence of a new variant with different transmission characteristics, changes in public health interventions, or shifts in population behavior and mixing patterns. The gradual decline following each peak suggests that control measures were effective, though the persistence of low-level transmission indicates ongoing community circulation.

Figure 1b shows the scatter plot of the suspected cases against the confirmed cases. It gives a crucial insight into the case detection and surveillance efficiency of Lassa fever outbreak in Nigeria. The strong positive correlation gives some notable deviation from the theoretical red correlation line, which gives a strong indication that confirmed cases consistently represent a fraction of suspected cases, which gives a thorough investigation typical in an outbreak that not all suspected cases meet confirmation criteria. It can also be inferred that the relationship appears to weaken at higher suspected case counts, suggesting potential strain on diagnostic capacity or changes in case definition during periods of high transmission. The relatively tight clustering of points at lower values indicates consistent surveillance performance during endemic periods, while the greater scatter at higher values reflects the challenges of outbreak response.

The monthly aggregated data shown in Figure 1c gives a clearer view of the trajectory of Lassa fever epidemic in Nigeria. Peak number of cases observed in the second month with over 300 confirmed cases aligns with the weekly data and confirms

that this is the primary outbreak period. The subsequent decline from the third and fourth months gives an opinion of an effective outbreak control, and a resurgence in the sixth month corresponds to the secondary peak that was observed in the weekly report. The sustained low-level transmission from months 7–14 suggests endemic establishment of the pathogen in the population, with monthly case counts stabilizing between 20–40 cases. This pattern is consistent with many infectious diseases that transition from epidemic to endemic phases. These temporal patterns observed from these results can be a characteristic of Lassa fever to exhibit seasonal variation.

Data regarding case-fatality rates (CFR) shown in Figure 1d, exhibit much variability with great temporal implications needing careful interpretations. The greatest unease is caused by the official CFR spike that shoots as high as about 67% around week 17, which corresponds to the interval between the two major transmission peaks that occurred in the original time series. Several interpretations could be drawn from this pattern. The CFR, for the whole period of the outbreak (i.e., weeks 1 to 15), was steady in the range of 10–25%, supported by the clinical evidence on management and capacity of the health system. By contrast, the surge in CFR that occurred in week 17 was most probably an artifact of the reporting process and not an accurate reflection of the changed mortality status. Possible reasons for this include death being reported late, changes in the definition of cases, or testing more severely ill patients during low-transmission periods. That anomaly was validated as an uptick in mortality was observed just before the end of the epidemic with great fluctuations of decreased CFR reported in weeks 47–50, arriving at 50%. This late-period mortality spike, during really low case counts, begs for either changes in demographic profile of cases (possibly affecting more vulnerable populations), or reporting delays misleadingly inflating the rates in small denominators. Looking at the four-week moving average in Figure 1e, provides a clearer view of the underlying epidemic trajectory by eliminating some of the noise introduced by weekly reporting. The smoothed

curve confirms the bimodal outbreak pattern but also affords a few more specifics. The first peak reaches approximately 78 cases in the 4-week average while the second peak reaches about 32 cases, indicating that the intensity of the second was about 40%. Very importantly, the moving averages show that transmission never stopped completely, maintaining a low-level endemic status for a range of around 8-12 cases per week throughout the between-epidemic period. This form of low transmission implies that control of the first outbreak was never complete and is likely to be a contributor toward the emergence of the second peak. Looking at the quarterly data as shown in Figure 1f one can find extremely strong evidence for seasonal transmission dynamics; that is to say, as mentioned above, Q1 accounted for 60.7% of total cases, strongly suggesting winter or early spring peak transmission. The dramatic fall to Q2 (21.6%), Q3 (9.3%), and Q4 (8.3%) indicates high seasonal forcing whereby the transmission was probably much less for a respiratory pathogen with temperature or humidity sensitivity, or behavioral factors such as crowding indoors during the colder months. The box plot distribution shows exceptional variability of Q1, whereby weekly cases run from around 10 to over 90, whereas for all the rest of the quarters, distributions were much tighter. The outliers for Q2 and Q4 likely correspond to the secondary peak and late-period fluctuations seen in the time series data. Correlation analysis shown in Figure 2, provides insight into certain aspects of surveillance systems performance and its implications for disease dynamics. One of the most telling findings was a strong positive correlation between confirmed and suspected cases (0.91), indicative of an effective case notification system. However, mortality cases show a moderate correlation to the confirmation rate (0.69), suggesting that mortality outcomes may sway priorities for diagnosis or ascertainment. Other striking observations were the contra-

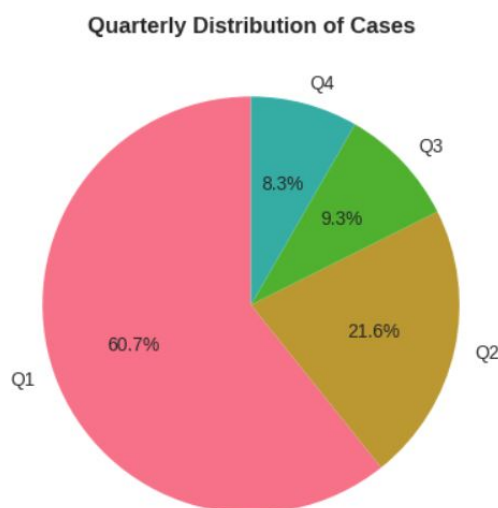


Figure 3. Quarterly Distribution of Cases

dictions within the correlations for case fatality rate as shown in Figure 3 with confirmed cases (-0.04) and suspected cases (0.08); while this seems counterintuitive, it actually captures the denominator effect during low-transmission periods of a given disease since by few cases the rates can easily be inflated. Predictive Modeling Performance shown in Figure 4 gives a comparisons of models identify vital insights into epidemic forecasting capabil-

ities. The best model of linear regression has an RMSE of 7.2, while the R^2 is 0.90, implying that even though epidemics appear complex, transmission patterns underlying such outbreaks remain relatively simple to anticipate.

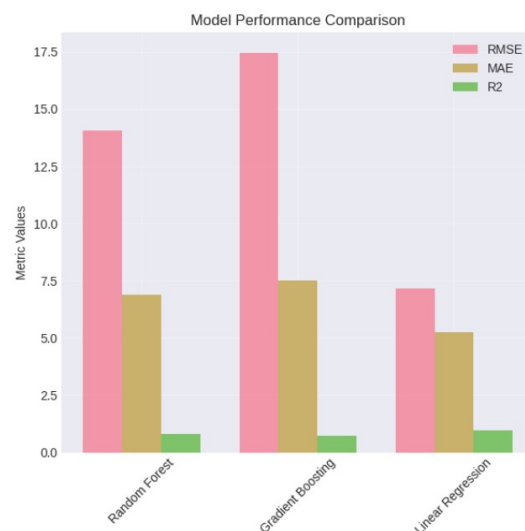


Figure 4. Model Performance Comparison

The time series for confirmed cases shown in Figure 5a, displays the fluctuating nature of the case counts for around 50 weeks. It peaks around weeks 10-15 and then again around week 30 to reach a peak of about 80 cases followed by a general decline, with some minor increases later. This hints that case numbers can be cyclic or seasonal. Figure 5b shows the plot of death vs. Confirmed Cases shows that there is a scatter of death (as high as 15-20) against confirmed cases (almost 60). Mortality increases with increased confirmed cases, especially when limited to a broad area of 20-40 confirmed cases, suggesting the likelihood of an increase in risk of death with the rising number of cases. Predicted Burden from Lassa Fever by State (2030) shows the map of Nigeria presents diversely predicted burdens, where southern states, with particular emphasis on those around the Delta region, bear a high burden (red zones, 150-200). North-eastern states are kept at a much lower projected burden (yellow/green zones, 0-50), confirming the future risks that would not be uniformly distributed in the regions. Overall, it can be suggested that outbreaks of Lassa fever are seasonal such that high incidence correlates with high mortality and that the highest future burden of this disease will fall on southern Nigeria by 2030.

Figure 1a the confirmed cases exhibit two notable peaks: the first occurring between weeks 8 to 10 (corresponding to February–March), and the second between weeks 18 to 20 (April–May) [19]. A significant 60.7% of cases were recorded in the first quarter of the year, suggesting a seasonal influence. This pattern aligns with dry season agricultural activities, during which humans are more likely to come into contact with *Mastomys natalensis*, the primary host of the Lassa fever virus. This observation is supported by reports from the Nigeria Centre for Disease Control (NCDC), which highlight a seasonal trend where Lassa fever outbreaks peak during the dry season, especially between January and March, even though transmission occurs year-round.

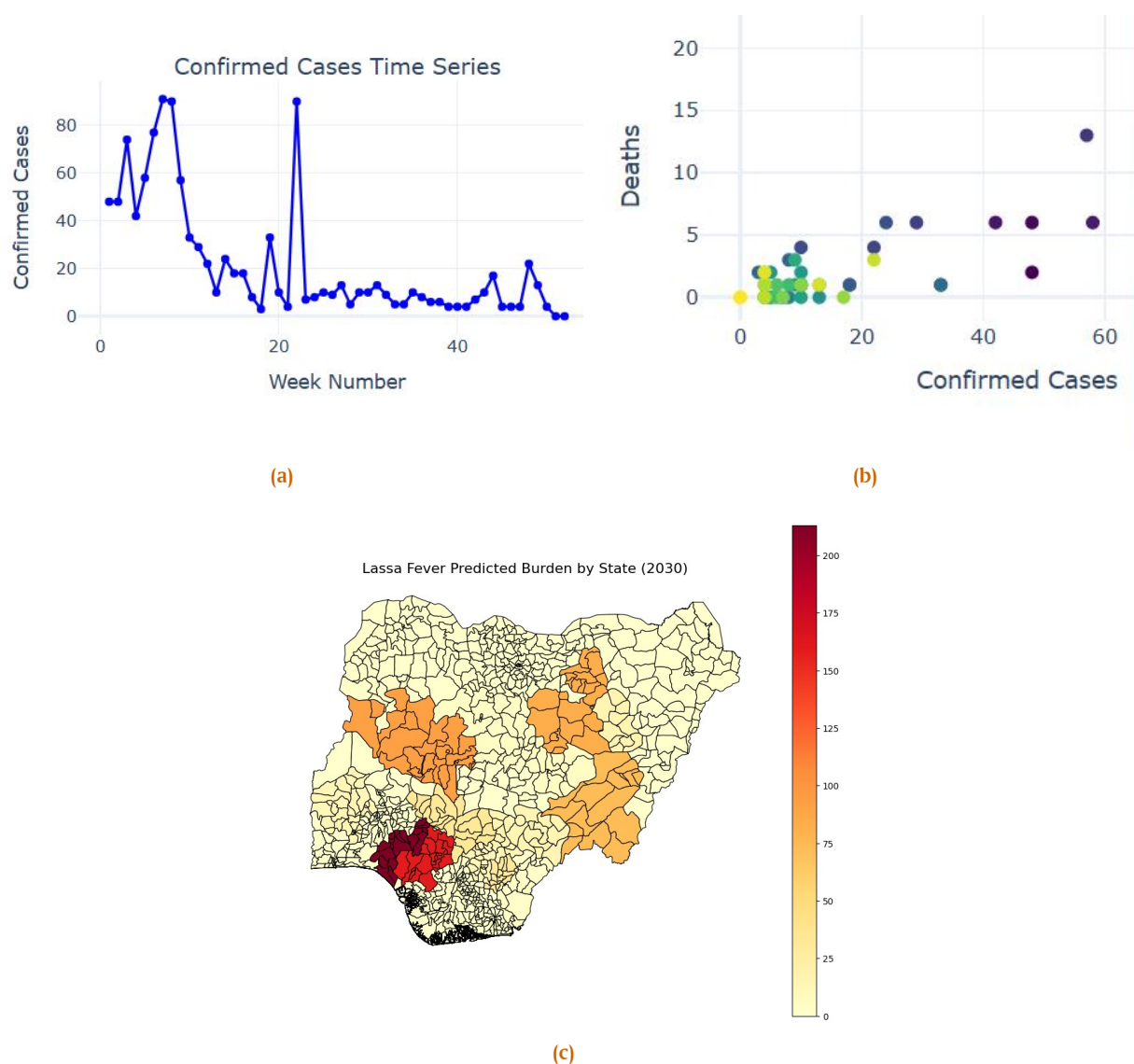


Figure 5. (a) Confirmed Cases over Time (Week Number). (b) Relationship with Confirmed Cases and Deaths. (c) Predicted Burden of Lassa Fever Confirmed Cases 2030.

The case fatality rate (CFR) among confirmed cases is alarmingly high. A total of 152 deaths have been recorded, translating to a CFR of 17%. The model also projects a potential rise in CFR for future outbreaks, indicating an increasing threat to public health. Analysis of the trend between suspected and confirmed cases reveals a confirmation rate consistently clustering between 5–15%, implying that a large proportion of suspected cases are not confirmed. This could be attributed to misidentification of non-cases or limited diagnostic capacity in many healthcare facilities. Weekly case distributions also show that most weeks recorded fewer than 1.5 confirmed cases, further emphasizing diagnostic or surveillance gaps. The correlation matrix demonstrates a strong positive correlation between suspected and confirmed cases, indicating that an increase in suspected cases generally leads to more confirmed cases. However, CFR showed weak correlations with other variables, suggesting that mortality is influenced by factors beyond the number of cases alone, such as healthcare access, comorbidities, or delays in treatment. This

finding has important public health implications, indicating that, particularly in resource-constrained settings that place premium on interpretability and computational efficiency, simpler statistical models may be more reliable than complex machine learning approaches. The integrated analysis identifies several crucial considerations for outbreak management. Sustained transmission suggests an ineffective elimination strategy, so the system would be wise to enhance surveillance and prevention. This extreme volatility in CFR illustrates just how urgent it is to put in place good surveillance for mortality and standardized reporting protocols in order to assess mortality properly. The strong seasonal pattern suggests that preparedness should take particular effort in the Q1 periods, with special attention to healthcare system capacity and targeted prevention campaigns. According to the correlation analysis, surveillance systems performed sufficiently during the early outbreak, but timely reporting of mortality may be further improved for CFR estimates during an active period of transmission. Most essentially, the successful working

of simple predictive models suggests the forecasting of outbreak trajectories based on simple epidemiological data needs cheering henceforth for preparing better response to outbreaks in settings with lesser analytical resources. Please reattempt all outputs.

7. Conclusion

A detailed analysis of Lassa fever confirmed cases in Nigeria has been conducted, accompanied by the development of predictive models using Random Forest, Gradient Boosting, and Linear Regression algorithms. The findings reveal a bimodal transmission pattern, with the first quarter of the year emerging as the primary peak, accounting for 60.7% of the total cases. The model outputs suggest a consistent pattern in confirmed case reporting, reflecting a relatively stable diagnostic system; however, the disparity between suspected and confirmed cases highlights limited laboratory capacity and weak healthcare infrastructure for effective testing. In this study, we applied a combination of ensemble learning techniques, including Random Forest and Gradient Boosting, alongside Linear Regression. While ensemble models such as Random Forest and Gradient Boosting offered robustness, each model displayed unique strengths and limitations in terms of predictive performance and generalizability.

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