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Research Article

Statistical Inference of Lassa Fever Transmission Dynamics from Routine Surveillance Data

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ABSTRACT

Lassa fever, a zoonotic viral disease endemic in Nigeria, periodically erupts, causing considerable morbidity and mortality. To estimate the dynamics of its transmission and aid in its control, we require an understanding of the underlying dynamics. Yet, in most cases, the missing information pertains to the hidden reservoir dynamics. Accordingly, we applied the stochastic renewal equation model parameterized for the number of confirmed cases and deaths in Nigeria during weeks 1 through 48 of the year 2025 to investigate the dynamics of its transmission over time. Our model also incorporates seasonality through a periodically forced reproduction number and overdispersion in observation through an overdispersed count process. Through the use of a biologically motivated delay linking incidence and mortality rates, we can reconstruct both from a single surveillance effort. Our fit does exhibit strong seasonality in transmission, with a baseline reproduction number of 1.06 and frequent crossings of the epidemic threshold. In our stochastic simulations, there is a great deal of short-term variability even in the baseline scenario. In our scenario analyses, a reduction in transmission of 20-40% can lead to a significantly decreased total number of cases. This study shows that incidence-based renewal models have proved to be a very valuable method for the investigation of endemic zoonotic diseases such as Lassa fever.

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1. INTRODUCTION

Lassa fever, also referred to as Lassa hemorrhagic fever, is an acute viral illness characterized by hemorrhagy, which is caused by infection with the Lassa virus, an Old World arenavirus that is indigenous to several West African countries where there is a significant rate of morbidity and mortality each year (McCormick & Fisher-Hoch, 1987; Frame et al., 1970; Richmond & Baglole, 2003; World Health Organization, 2017). It has been estimated that Lassa virus infection results in the infection of hundreds of thousands of persons each year in the region, with thousands of recorded deaths annually, and Case Fatality Ratios among hospitalized cases estimated to range between 15% and 30% in the region (McCormick & Fisher-Hoch, 1987; World Health Organization, 2017). It has been established that the country most significantly impacted by Lassa fever is Nigeria, with frequent outbreaks exhibiting significant seasonality. The disease has a zoonotic nature, with the main reservoir being the multimammate rat (Mastomys natalensis).

Infection in human populations occurs via contact with rodent excreta infecting food, surfaces within houses, and the environment, as opposed to human-to-human infections, which may occur through direct contact with body fluids, especially in domestic and healthcare facilities, thus making healthcare a major risk (Fisher-Hoch, 2000; Fichet-Calvet & Rogers, 2014; Lecompte et al., 2006; Olayemi et al., 2016). The geographic and seasonally varying patterns exhibited by Lassa Fever are influenced by rodent ecology and environmental and human behaviors, resulting in annual peaks especially during the dry seasons within specific regions (Gibb et al., 2017; Monath, 1974; Musa et al., 2019). Knowledge of the mechanisms by which the transmission of the disease occurs is paramount in the design and prioritization of control strategies. This is especially the case for control strategies that involve control of the viral reservoir through handling the environment in which the rodents live, early detection of cases, isolating infected individuals to prevent the spread of the infection through contact, and infection control practices in health-care settings.

The theoretical techniques used to investigate the epidemiology of different diseases including Lassa fever range from deterministic compartmental models to control theory and network models. Deterministic compartmental models, commonly SIR, SEIR, with optional inclusion of a rodent reservoir, have formed a backbone of models of various studies, past and recent, for modeling and analyzing the spread of Lassa fever infection. These models are useful to understand at a model level how the process of infection occurs and which parameters can possibly be used to reduce the spread, though these models require a large number of hidden parameters (for instance, the size of rodent populations, infection contact rates, and duration of latency periods). More recent developments have added either optimal control to these models or considered delays to investigate when and with which type of delay, infection reporting or, for example, treatment can influence outcomes.

Compartmental and branching process models have been employed to address the stochasticity associated with the dynamics of the population and the external environment, which would be particularly important in scenarios involving small numbers of cases generated by animal-to-human transmission events. These models can inform about the probability of extinction and super spreading events but are computationally intensive. Network models and agent models allow for the inclusion of heterogeneous contacts, geographical distributions, and behavioral responses and have been used to examine targeted interventions and healthcare associated cases (Eubank et al., 2004). For Lassa fever, such models can account for household aggregation, hospital wards, or community contacts. They generally require a high level of detail regarding contacts and movements that are often not recorded in endemic countries (Ajelli et al., 2016; Lo Iacono et al., 2015).

A further, more recently developed class of models is the incidence-based/renewal-equation models, which assume that new cases at time point depend on past incidence through a generation interval distribution and a time-varying reproductive number Rt (Fraser, 2007; Wallinga & Teunis, 2004). These renewal models work directly with the observed time series of incidences, thus not incorporating unobserved states like the susceptibles/exposed populations directly into the models. Nonetheless, these models were extensively used for real-time estimation of Rt values and forecasting, especially within influenza, Ebola, measles, as well as SARS-CoV-2 outbreaks (Abbott et al., 2020; Chowell et al., 2015; Cori et al., 2013; Garske et al., 2009; Park et al., 2020; Thompson et al., 2019).

Formulations of renewal models are related to compartmental models and obtained as a reduced model form of a general mechanistic system under certain assumptions (Champredon & Dushoff, 2018; Diekmann, Heesterbeek, & Britton, 2013). By conditioning on a specified distribution of generation intervals, renewal models are used to resolve the issue of imperfect identification, which would otherwise appear when trying to estimate intensity and stage-change process parameters jointly from incidence reports alone (Champredon & Dushoff, 2018; Fraser, 2007). The reduced form makes renewal models very useful for routine data analysis with a focus on distinguishing changes in transmissibility over time,

which may include seasonal forcing, from those in reporting or detection practices (Cori et al., 2013; Thompson et al., 2019).

Despite extensive work with compartmental, stochastic, and optimal control models for Lassa fever, the use of renewal or generation-interval approaches is still limited, particularly in integrating incidence and mortality time series data while accounting for seasonality and overdispersion. Given the endemic and zoonotic traits of Lassa fever in Nigeria, as well as the availability of routine weekly monitoring data, renewal models offer a natural and data-driven framework for inferring transmission dynamics that does not include explicit modelling of unknown reservoir processes. To our knowledge, this is the first study to use a stochastic renewal framework with seasonal forcing to examine routinely reported Lassa disease incidence and mortality data in Nigeria. This method permits direct inference of time-varying transmission dynamics while accounting for reporting variability and biologically plausible delays. Specifically, this study aims to: estimate the seasonal pattern in the time-varying reproduction number using surveillance data, establish a biologically grounded link between incidence and mortality through delay distributions, and to evaluate the impact of transmission reduction scenarios.

2. METHODOLOGY

2.1. Model Formulation

Let C_t be the number of newly confirmed Lassa fever cases reported in epidemiological week t, where 107 t = 1, 2, . . . , 48. Transmission is thought to occur by a mix of zoonotic overflow from infected rodents and 108 secondary human-to-human transmission. Rather than explicitly modeling these transmission routes, the 109 combined effect is summarized using a time-varying reproduction number Rt, which represents the average number of secondary confirmed cases generated by a typical confirmed case at time t under the current ecological, behavioral, and public-health conditions. According to the renewal formula, the anticipated number of newly confirmed cases in week t is provided by

$$\mathbb{E}[C_t] \;=\; R_t \sum_{s=1}^{t-1} C_{t-s}\, w_s, \tag{1}$$

where w_s represents the generation interval distribution, which is defined as the likelihood that a secondary case is confirmed weeks after the primary case. The series $\{w_s\}_{s\geq 1}$ has $w_s \geq 0$ and $\sum_{s=1}^{\infty} w_s = 1$. In this study, ws is calculated by discretizing a continuous generation-interval distribution based on published epidemiological estimates for Lassa fever, and it is considered as fixed to assure transmission parameter identification.

To account for systematic temporal variation in transmission strength, the reproduction number is permitted to change over time using a seasonal forcing formulation:

$$R_t = R_0\, exp\left(\epsilon\, cos\left(\frac{2\pi t}{52} + \phi\right)\right), \tag{2}$$

In this specific model, R_0 is given as the reproduction ratio, and epsilon denotes how prominently the seasonality is expressed. Additionally, φ identifies exactly when the period with the greatest transmission occurs. Indeed, this model reflects accurately the seasonality exhibited by Lassa fever in Nigeria, which is influenced by changes in rodent populations, weather conditions, and human behaviors. The weekly number of cases comes with some noise due to the reporting, demographic randomness and unobserved heterogeneities. To introduce more variability than that assumed by a Poisson model, the number of cases confirmed in week t is assumed to be drawn from a negative binomial distribution:

$$C_t \backsim NegBin(\mu_t, k\,), \tag{3}$$

where $\mu_t \;= \mathbb{E}[C_t]$μt is defined by (1) and k > 0 is an over dispersion parameter. Smaller values of k correspond to greater variability in reported incidence, while the limiting case k → ∞ recovers a Poisson observation model under this parameterization, $Var(C_t) \;=\; \mu_t + \mu_t^2/k$.

Deaths among the confirmed cases can be measured using a distribution of delays from the time of confirmed cases to the time of death. D_t can be used to denote the number of deaths recorded among confirmed cases within epidemiological week t. The average number of deaths would be:

$$\mathbb{E}[D_t] \;=\; \pi \sum_{s=1}^{t-1} C_{t-s} g_s, \tag{4}$$

where π is the case fatality ratio among confirmed cases and g_s is the discretized probability distribution describing the delay from confirmation to death. The delay distribution $\{g_s\}$ satisfies $g_s \geq 0$ and $\sum_{s=1}^{\infty} g_s = 1$ and is fixed a priori based on clinical and epidemiological evidence. Observed deaths are assumed to follow a Poisson distribution with mean $\mathbb{E}[D_t]$.

To capture the early phases of an outbreak, an initialize the stochastic process based on the real number of confirmed cases observed at the beginning is analysed. By this, the issue of the issue of setting initial values for unseen model states is avoided. In particular, no assumptions on the initial number of the susceptible population or the prevalence in the human or rodent populations at the outset of the observation process. The model is thus basic yet adaptable, directly integrating routinely observed incidence and death statistics to transmission dynamics and allowing for inference on time-varying transmissibility from surveillance alone.

2.2. Data Description

The data for weekly surveillance cases for epidemiological weeks 1 through 48 in the year 2025 was extracted from the Nigeria Centre for Disease Control and Prevention situation reports. The data is based on the numbers of suspected cases notified on a weekly basis and is further categorized based on the number of confirmed cases as well as deaths due to those cases, aggregated data will be utilised. This dataset includes the number of suspected Lassa fever cases, confirmed Lassa fever cases, and deaths among confirmed Lassa fever cases, all of which are submitted on a weekly basis to the NCDC. These numbers are estimates of new (incident) cases in each epidemiological week, rather than cumulative totals. Cases that are defined as confirmed are those that are suspected and have been laboratory confirmed (by PCR, antigen, or serology), which serves as the best indicator of transmission dynamics as they are considered the most reliable proxy. Suspected cases, on the other hand, are considered unreliable and are therefore not employed in model estimation.

Weekly confirmed case numbers were determined by comparing the cumulative confirmed case totals given in subsequent NCDC status reports, ensuring that the study is based on event rather than cumulative data. Let Ct represent the number of newly confirmed Lassa fever cases reported per epidemiological week t, where t= 1, 2, . . . , 48. The weekly confirmed case counts are the major input for the transmission model. Deaths among confirmed cases are recorded separately and designated by D_t, which represents the number of confirmed-case deaths reported during week t. Table 1 below, a summary of situations related to Lassa Fever from week to week in 2025 is presented. During epidemiological weeks 1-48, there were 1036 reported cases, with an average of at least 22 cases per week. The number of cases per week varied, with a median of 10 and an evident surge to 251 in week 4. However, the fatalities in confirmed cases numbered 187, giving an average of about 4 fatalities per week. Even the fatality rate per week had variations and peaked at 13 in weeks 22 and 32. The identifiable pattern in both confirmed cases and fatalities shows that the spread of Lassa fever alone does not follow a stationarity process; thus, the transmission model should incorporate the change in time.

Table 1. Descriptive summary statistics of weekly confirmed Lassa fever cases and deaths in Nigeria, epidemiological weeks 1-48, 2025

Statistic	Confirmed cases (Ct)	Confirmed deaths (Dt)
Total	1036	187
Mean per week	21.6	3.90
Median per week	10	6
Minimum	1	1
Maximum	251	13
Week(s) of maximum	4	22,32

Weekly confirmed case counts were obtained by differencing cumulative confirmed case totals reported in successive NCDC situation reports

Figure 1 illustrates the weekly trend in confirmed Lassa fever cases in Nigeria during epidemiological weeks 1-48, 2025. From the graph, the fluctuations in the number of cases are evident. Figure 2 also illustrates the change over time for the confirmed cases of Lassa fever patients. From the two epidemic curves, the variation in the rates over time indicates the reasons why the reproduction number is time-varying. For each analysis, incidence data for each week is used, so that it conforms to the rhythm of reports, avoiding any inconsistencies that might arise from a week of missing data. No week is estimated for missing data, and each entry is taken as it is reported in the NCDC reports.

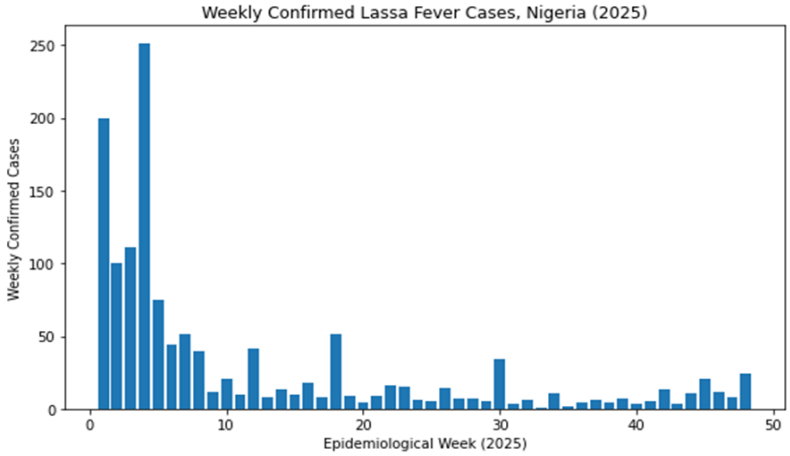

Figure 1. Weekly confirmed Lassa fever cases in Nigeria, epidemiological weeks 1-48, 2025.

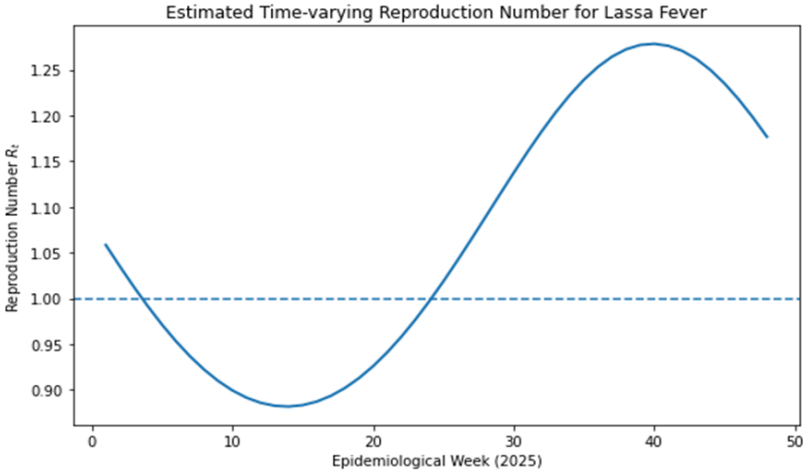

Figure 2. Estimated time-varying reproduction number R_t for Lassa fever in Nigeria, epidemiological weeks 1-48, 2025. The dashed horizontal line indicates the epidemic threshold (R_t = 1).

2.3. Parameter Estimation and Inference

Parameters for the models are estimated using data on reported cases and deaths due to Lassa fever for weeks 1 to 48 in 2025, which are reported by the Nigeria Center for Disease Control. The method for estimation is based on likelihood and takes into account the variability in reported values. Let $\theta = (R_0, \epsilon, \phi, \kappa, \pi)$ represent the vector of parameters to be evaluated. To prevent identifiability difficulties, the generation interval distribution $\{w_s\}$ and confirmation-to-death delay distribution $\{g_s\}$ are determined a priori based on independent epidemiological evidence and not considered as free parameters. Given the renewal equation (1), the expected number of confirmed cases in epidemiological week t is

$$\mu_t(\theta) \;=\; R_t(\theta) \sum_{s=1}^{t-1} C_{t-s}\, w_s,$$

where $R_t(\theta)$ is defined by (2). Conditional on μ_t, the likelihood contribution of the observed number of confirmed cases C_t is given by the negative binomial probability mass function

$$\mathcal{L}_C(C_t \mid \theta) \;= Pr(C_t \mid \mu_t(\theta), \kappa).$$

Similarly, the expected number of deaths in week t is

$$\lambda_t(\theta) \;=\; \pi \sum_{s=1}^{t-1} C_{t-s}\, g_s,$$

and the likelihood contribution of the observed deaths D_t is given by

$$\mathcal{L}_C(C_t \mid \theta) \;= Pr\big(D_t \mid \lambda_t(\theta)\big)\,,$$

where a Poisson observation model is assumed.

Given the model parameters and assuming conditional independence of weekly observations, the joint 158 log-likelihood function can be written as

$$\ell(\theta) = \sum_{t=1}^{48}[\log \mathcal{L}_C(C_t \mid \theta) + \log \mathcal{L}_D(D_t \mid \theta)].$$

Parameter estimates are obtained by maximizing $\ell(\theta)$ numerically subject to the constraints $R_0 > 0$,$\epsilon \geq 0$, $0 \leq \phi < 2\pi, \kappa > 0,\ and\ 0 \leq \pi \leq 1$.

Uncertainty in the parameter values is modeled using likelihood-based confidence intervals, which are obtained from the profile likelihood. For each parameter, we re-optimize the remaining parameters while setting the parameter of interest to a series of values, and then construct the confidence intervals based on the likelihood ratio statistics. This procedure is not based on asymptotic normality and can handle moderately long time series. On the other hand, bayesian inference can also be carried out with prior distributions assigned to parameters in θ.

In this case, weakly informative priors are used to keep parameters within epidemiologically sensible bounds, while letting the data steer the inference. Posterior samples are drawn with Markov chain Monte Carlo methods and uncertainty is summarized with credible intervals. The time-varying reproduction number, R_t, is constructed directly from the estimated parameters via the relationship in equation (2). Parameter uncertainty is propagated through into R_t by calculating R_t over the complete distribution of estimated parameters. This produces week-by-week estimates of transmission intensity and it is straightforward to identify points at which transmission was above or below the epidemic threshold. It links all estimated quantities in a coherent way to what is observed from surveillance data, and the framework propagates uncertainty consistently from the data via the methods to the epidemiological measures of interest.

Table 2. Estimated transmission and mortality parameters for Lassa fever in Nigeria, epidemiological weeks1-48, 2025

Parameter	Estimate	Description
R_o	1.062	Baseline reproduction number
ϵ	0.186	Amplitude of seasonal forcing
ϕ(rad)	1.467	Seasonal phase shift
k	1.785	Overdispersion parameter
π	0.237	Case fatality ratio

3. RESULTS AND DISCUSSION

In order to give an indication of how things might look in the near term, forward stochastic simulations were made for cases and deaths due to the Lassa fever infection, using the already fitted renewal model. These types of runs are not intended to be precise forecasts but rather an indication of possible futures and 181 how much the variability is contributed from the randomness associated with the transmission process. Figure 3 illustrates the simulation results for forward projections of cases for the Lassa fever illness that occurred after epidemiological week 48.The actual numbers recorded at that point are represented by black markers, and the solid line shows the path followed by the median value for the respective predictions.

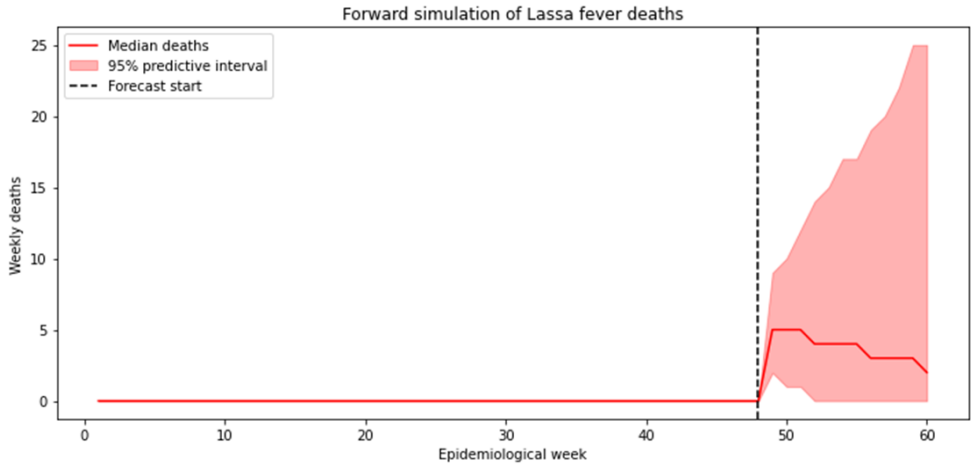

Figure 3. Forward projection of weekly Lassa fever deaths. Black dots indicate the reported deaths up to epidemiological week 48. The solid line represents the median projected deaths, while the shaded region indicates the 95% predictive interval. The vertical dashed line marks the start of the projection.

The shaded area depicts prediction uncertainties due to stochastic variability rather than parameter value uncertainties. The vertical dashed line indicates where the transition is made from actual observation to projections. Corresponding forward projections for weekly Lassa fever fatalities are presented in Figure 4. The deaths were generated conditionally on lagged case counts to preserve the relationship between infections and deaths epidemiologically plausible. Like the case forecasts, the median of the simulated deaths and the associated uncertainty bands provide a reasonable short term portrait of mortality dynamics under the baseline transmission scenario. To investigate how reducing transmission would affect the outcome, we performed counterfactual scenarios where transmission was reduced by 20% and 40% from epidemiological week 48 onwards. Figure 5 shows how the median weekly case trajectories under these counterfactuals compare to the baseline transmission scenario. The lower the transmission, the fewer projected cases, and the larger the reduction, the more pronounced the suppression of the intensity of the epidemic.

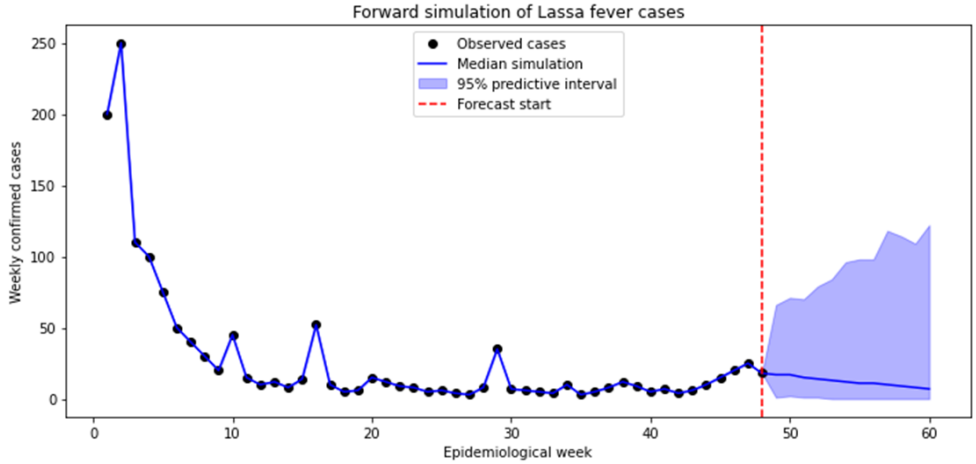

Figure 4. Forward projection of weekly confirmed Lassa fever cases. Black dots indicate the observed cases up to epidemiological week 48. The solid line represents the median projected cases, while the shaded region indicates the 95% predictive interval. The vertical dashed line marks the start of the projection.

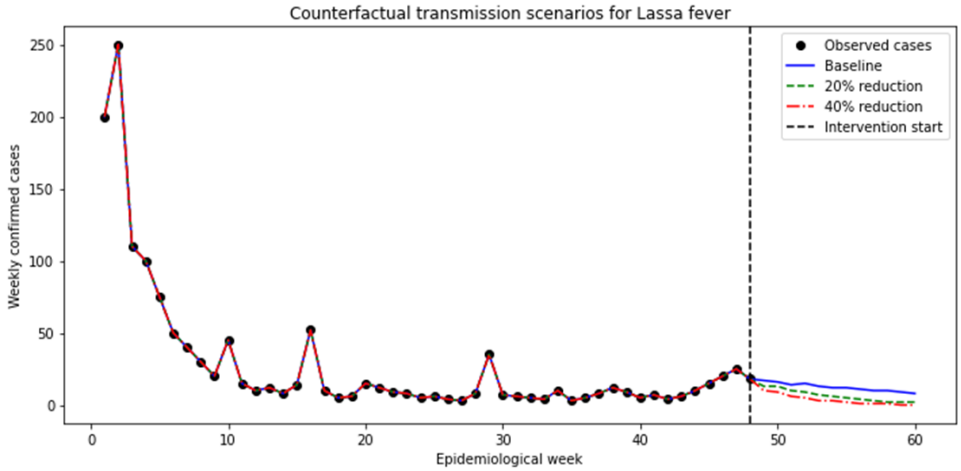

Figure 5. Counterfactual transmission scenarios for Lassa fever. The solid curves indicate the median of simulated cases on a weekly basis under baseline transmission and then 20% and 40% reduction in transmission intensity from epidemiological week 48 onwards. The black dots indicate the actual cases. The vertical dashed line indicates the start of the counterfactual intervention scenario.

Figure 6 diagrammatically illustrates how a reduction in the strength of transmission can progress in the case of an epidemic. These curves are not actual data; rather, they are fictional models that have been given arbitrary units. They are intended for illustrative purposes only. It is essential to note that the purpose of this graph is to allow the reader to visualize how the epidemic may be affected by the timing and magnitude of the intervention. Likewise, in Figure 7, a median outcome of cases averted over a 20% and 40% reduction scheme is plotted against the baseline. Notice that, after the intervention takes effect, the two lines differ, showing that a certain reduction in transmission can add up to a considerable level of averted cases. Together, these analyses demonstrate how forward simulation based on the fitted renewal model can be used to explore uncertainty in short-term epidemic dynamics and to evaluate

the potential benefits of transmission-reducing interventions under counterfactual scenarios. A forward stochastic simulations using the estimated renewal model parameters to explore possible near-term paths of Lassa fever incidence and mortality is conducted. We generated weekly confirmed cases via a negative binomial renewal process, simulating deaths in a manner dependent on lagged case data so as to maintain epidemiological consistency. These trajectories are meant to illustrate uncertainty surrounding future dynamics rather than providing exact forecasts.

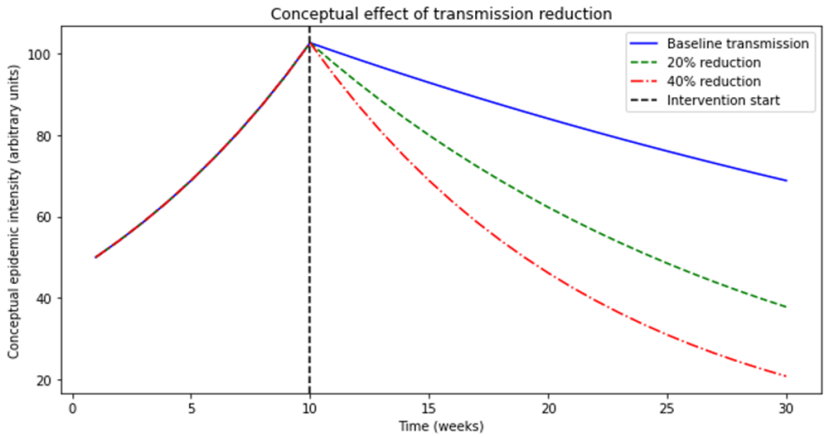

Figure 6. Conceptual illustration of the effect of transmission reduction on epidemic dynamics. The figure shows hypothetical epidemic intensity trajectories under baseline transmission and under 20% and 40% reductions in transmission intensity introduced at a specified intervention time (vertical dashed line). Curves are illustrative and expressed in arbitrary units, serving only to demonstrate qualitative epidemic behavior rather than data-driven predictions.

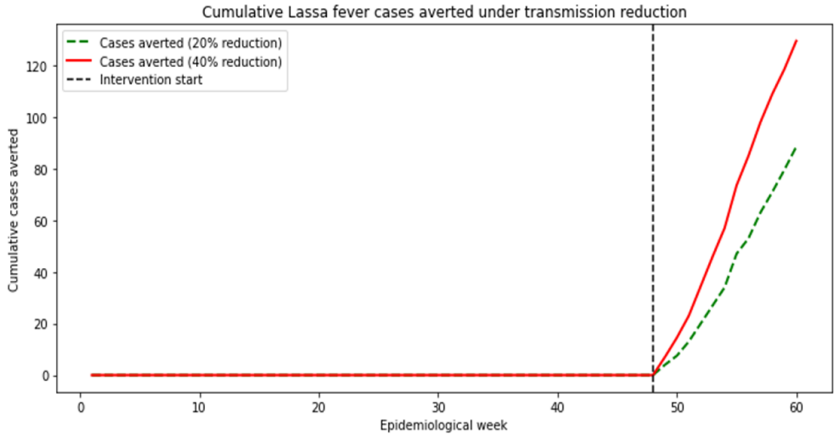

Figure 7. Number of Lassa fever cases averted under different counterfactual transmission reduction strategies. The curves show the median cumulative cases averted under 20% and 40% reductions in transmission compared with the baseline scenario. The vertical dashed line indicates the start of the intervention.

4. CONCLUSION

In this paper, the stochastic renewal equation modeling method is proposed for the Lassa fever dynamics in Nigeria. In this method, instead of the hidden compartmental states and the animal reservoir as in the compartmental model, the stochastic renewal equation modeling approach utilizes the directly observed weekly reported cases and death rates. These are the rates that are already being collected by the relevant authorities. The time series reproduction number indicates obvious seasonality patterns regarding transmission, with periods where the transmission rates are or approach the epidemic threshold. This fits the known ecological and behavioral patterns related to the transmission of Lassa fever and underlines the importance of considering seasonality for assessing the severity of transmission in the region. This approach also bridges the cases and the death toll by a biologically feasible pattern. By stochastic forward simulations, there are plausible scenarios of epidemic trajectory based on current transmission, with high degrees of uncertainty even in the presence of tightly constrained models of transmission. Transmission scenarios that are highly implausible in reducing transmission can show that even small reductions in transmission can lead to significant mitigation of disease impact, implying that there are benefits in reducing risk of exposure and in preventing human-to-human transmission. Overall, the research appears to indicate that the renewal models have the

benefit of being a clear, elegant, and efficient means for studying endemic zoonotic diseases, such as Lassa Fever, using renewal models. The model appears to have the advantage of monitoring the disease dynamics while testing scenarios related to intervention implemented in the populations under surveillance, with the possibility of improvements related to geographical factors, delays, and the effect of zoonosis.

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Not applicable.

CONFLICT OF INTEREST
The authors declare that they have no competing interests.

AUTHOR CONTRIBUTION
All authors contributed to the study conception, model development, data analysis, interpretation of results, and manuscript preparation. All authors read and approved the final manuscript.

DATA AVAILABILITY
All supporting data relevant to the results of this study are included in the article.

DECLARATION OF GENERATIVE AI
Not applicable.

ETHICS
Not applicable.

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