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PROBABILISTIC MODELLING OF LASSA FEVER EPIDEMIC DYNAMICS THROUGH A BIVARIATE MARKOV CHAIN

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ABSTRACT

This study presents a bivariate Markov chain approach for modelling the joint dynamics of Lassa fever incidence and fatality patterns using weekly epidemiological surveillance data. The objective is to investigate the probabilistic behaviour of disease transmission and mortality through a discrete-time stochastic framework. Weekly confirmed cases and case fatality rate (CFR) values were transformed into binary epidemiological indicators representing increasing or decreasing trends relative to the previous week. These indicators were combined to form four joint epidemic states: declining incidence and declining fatality (0,0), declining incidence but increasing fatality (0,1), increasing incidence but declining fatality (0,1), and increasing incidence and increasing fatality (1,1). A transition count matrix and corresponding transition probability matrix were estimated from the observed weekly transitions between states. The stationary distribution of the Markov chain, together with 95% confidence intervals, revealed that the system is primarily dominated by the ((0,0)) state, with a stationary probability interval of [0.2531, 0.5356], reflecting persistent low-risk dynamics characterized by simultaneous declines in incidence and fatality. The ((0,1)) state also contributes substantially, suggesting periods where reduced transmission may still coincide with worsening fatality outcomes. In contrast, the ((1,0)) and ((1,1)) states exhibit lower stationary probabilities with wider uncertainty intervals, indicating less frequent but epidemiologically meaningful transitions into higher-risk regimes. Mean return times indicated that severe epidemic conditions recur less frequently compared to lower-risk conditions. The findings demonstrate that the bivariate Markov chain framework provides an effective stochastic representation of the evolving relationship between disease incidence and fatality, offering valuable insight into long-run epidemic behaviour. It can therefore support public health monitoring, outbreak preparedness, and decision-making for Lassa fever control. The study recommends strengthening continuous surveillance systems, early warning mechanisms, and rapid intervention strategies during periods of increasing incidence and fatality in order to reduce the risk of severe outbreak conditions.

Keywords: Lassa fever; incidence-fatality dynamics, Bivariate Markov chain; Transition probability matrix; Stationary distribution; Mean return time

1.0 INTRODUCTION

Infectious disease outbreaks remain a major global public health concern due to their rapid transmissibility, recurrent epidemic behavior, and substantial mortality burden. Diseases such as Lassa fever, Ebola virus disease, COVID-19, cholera, and influenza continue to demonstrate complex temporal dynamics characterized by alternating periods of outbreak escalation and decline. Understanding these transitions is essential for forecasting epidemic trajectories, evaluating intervention strategies, and improving preparedness planning. Mathematical and stochastic models have therefore become fundamental tools in epidemiological research for describing disease evolution and quantifying uncertainty in transmission processes (Jafari and Deardon, 2022; Yaesoubi and Cohen, 2011).

Among stochastic approaches, Markov chain models have gained considerable attention because they provide a probabilistic framework for describing transitions between epidemiological states over time. In a Markov process, the future evolution of a system depends only on its present state and not on the full historical path, thereby offering a tractable mechanism for modeling disease progression, persistence, and recurrence. Markovian frameworks have been widely applied in infectious disease studies involving transmission dynamics, outbreak forecasting, surveillance systems, and health economic evaluations (Hamra *et al* 2013; Haeussler *et al*, 2018).

Recent investigations have highlighted the effectiveness of stochastic and Markovian methodologies in describing infectious disease dynamics and evaluating long-term epidemic behaviour. McKendrick *et al* (2023) incorporated seasonal variability into stochastic models of Lassa fever transmission in Nigeria, whereas Ogwuche and Emonyi (2024) employed stochastic differential equation models to capture uncertainties associated with epidemic progression. Nkemnole and Oyewole (2023) established persistent and recurrent epidemic behaviour with long-run probabilities concentrated in a dominant epidemiological state using a Hidden Markov Model; another work in this line is that of Rashid *et al* (2023), authors established the existence of an endemic equilibrium and ergodic stationary distribution for stochastic Lassa fever dynamics, indicating persistent disease circulation and recurrent outbreaks over time. In a related study, Adah and Ogbuagu (2026) applied perturbation stability analysis to discrete-time Markov chains

constructed from Lassa fever surveillance data in Nigeria and demonstrated that the epidemic system preserved ergodic stability under small transition perturbations. Earlier epidemiological studies also established the relevance of Markovian frameworks in infectious disease modelling. For instance, O'Neill *et al*. (2000) utilized Markov chain Monte Carlo methods to investigate disease transmission within household outbreaks, illustrating the applicability of Markovian inference to partially observed epidemic processes. Likewise, Li *et al*. (2018) showed that stochastic epidemic models based on Markov chain Monte Carlo techniques are effective for estimating transmission parameters and quantifying uncertainty in disease spread. Furthermore, Haeussler *et al*. (2018) developed a dynamic Bayesian Markov model for infectious disease intervention analysis, demonstrating the adaptability of Markovian structures in evaluating disease progression and control strategies. Hamam *et al*. (2024) developed a deterministic mathematical model to investigate the transmission dynamics of Lassa fever and evaluate the impact of intervention strategies such as awareness campaigns and rodent control measures. Despite these contributions, relatively few studies have employed discrete-time bivariate Markov chain models that simultaneously capture both incidence and fatality dynamics in Lassa fever outbreaks, thereby providing the motivation for the present study. Despite the broad application of Markov models in epidemiology, most existing studies primarily focus on univariate disease indicators such as infection prevalence, incidence counts, hospitalization status, or recovery dynamics. In many epidemic investigations, fatality patterns are analyzed separately from incidence behavior, thereby neglecting the joint dependence structure between disease occurrence and disease severity. However, epidemic intensity and mortality risk often evolve simultaneously and may exhibit strong stochastic interdependence. This limitation reduces the ability of conventional univariate Markov models to fully characterize epidemic progression.

To address this gap, the present study adopts a bivariate Markov chain framework in which weekly disease incidence and fatality conditions jointly define the epidemiological state space. The proposed approach models the co-evolution of transmission intensity and case fatality dynamics as a single stochastic process. By combining incidence and fatality information, the model captures richer epidemic behavior than traditional one-dimensional Markov formulations. The resulting framework allows for the estimation of transition probabilities between joint epidemic states, stationary distributions, mean recurrence times, first-passage times, and long-run epidemic stability characteristics. The bivariate Markov chain approach possesses several methodological strengths. First, it simultaneously captures dependence between multiple epidemiological indicators, thereby improving representation of real outbreak processes. Second, the framework is computationally tractable and interpretable compared with highly parameterized compartmental or agent-based models. Third, the method permits rigorous probabilistic analysis, including ergodicity assessment, recurrence behavior, equilibrium distributions, and uncertainty quantification. Fourth, the discrete-state formulation is particularly suitable for weekly surveillance datasets commonly reported by public health agencies (Haeussler *et al*, 2018). Despite these limitations, the bivariate Markov chain framework provides a robust stochastic approach for investigating the temporal dynamics of infectious diseases. By integrating incidence and fatality processes into a unified probabilistic structure, the methodology offers valuable insights into epidemic persistence, transition behavior, and long-run disease stability, thereby contributing to improved epidemiological monitoring and outbreak risk assessment.

2.0 MATERIAL AND METHOD

2.1 Data Description

The dataset used in this study consists of weekly reports of 2024 - 2025 Lassa fever cases, including suspected, confirmed, and deaths, obtained from the Nigeria Centre for Disease Control and Prevention. These data are obtained from epidemiological surveillance reports and may be subject to uncertainty due to underreporting, delayed case confirmation, and variability in reporting practices.

2.2 Joint Epidemiological Process

Definition 1:

Let $X_t = (I_t, F_t), \quad t = 0,1,2, \ldots$

I_t represents the incidence state based on weekly confirmed cases, $F_t$represents the fatality state based on weekly deaths or case fatality rate (CFR).

The joint process evolves on a finite state space:$S = \{(i, f): i \in I, f \in F\}$

$$I_t = \begin{cases} 1 & if \;\; I_t \geq I_{t-1} \\ 0 & otherwise \end{cases} \quad (1)$$

$$F_t = \begin{cases} 1 & if F_t \geq F_{t-1} \\ 0 & otherwise \end{cases} \quad (2)$$

Each state describes the joint epidemic severity during a particular week. The joint state space is $S = \{(0,0), (0,1), (1,0), (1,1)\}$ where:

Table 1: Joint State

Joint State	Interpretation
((0,0))	Declining incidence and declining fatality
((0,1))	Declining incidence but increasing fatality
((1,0))	Increasing incidence but declining fatality
((1,1))	Increasing incidence and increasing fatality

Thus, each weekly observation is represented by one of the four possible joint epidemic states, enabling the modelling of the combined behaviour of disease transmission and mortality dynamics through a bivariate Markov framework.

2.3 Transition Count and Transition Probabilities Matrix

Successive weekly transitions between states were identified to construct the transition count matrix.

Let

$$N = (n_{ij}) \quad (3)$$

denote the transition count matrix, where n_{ij} represents the number of observed transitions from state i to state j.

The transition probability matrix was estimated from the observed transition counts.

Let $P = (p_{ij})$ (4)

represent the transition probability matrix, where

$$p_{ij} = P(X_{t+1} = j \mid X_t = i) \quad (5)$$

The maximum likelihood estimator of the transition probability is given by

$$p_{ij} = \frac{n_{ij}}{\sum_{j=1}^{n} n_{ij}} \quad (6)$$

subject to

$$\sum_{j=1}^{n} p_{ij} = 1 \quad (7)$$

for all states i.

The resulting transition matrix describes the probabilistic movement of the epidemic process from one joint state to another over time.

Theorem 1: Existence of Stationary Distribution
Let $\{X_t\}_{t\geq 0}$be a finite-state, discrete-time Markov chain with transition matrix P defined on state space $S = \{s_1, s_2, \dots, s_k\}$.(Norris, 1997; Kemeny and Snell, 1960). Then, there exists at least one stationary distribution πsuch that:

$$\pi P = \pi, \qquad \sum_{i=1}^{k} \pi_i = 1, \qquad \pi_i \geq 0 \tag{8}$$

Theorem 2: Uniqueness of Stationary Distribution
If the Markov chain X_t is irreducible and aperiodic, then the stationary distribution π is unique.

Corollary 1: Convergence to Equilibrium
If the Markov chain is irreducible and aperiodic, then for any initial distribution μ

$$\lim_{t\to\infty} \mu P^t = \pi \tag{9}$$

This implies that long-run epidemic behavior is independent of initial outbreak conditions.

Corollary 2: Mean Recurrence Time
For any state $i \in S$, if $\pi_i > 0$, the expected return time is:

$$E[T_i] = \frac{1}{\pi_i} \tag{10}$$

This follows from the renewal property of positive recurrent Markov chains. (Norris, 1997; Meyn and Tweedie, 2009).

2.3.1 Ergodicity and Long-Run Stability
The chain is ergodic if it is:
Irreducible:

$$\forall i, j, \exists n: (P^n)_{ij} > 0 \tag{11}$$

And Aperiodic

$$gcd\{n: (P^n)_{ii} > 0\} = 1 \tag{12}$$

greatest common divisor of all return times to state i is 1
Under ergodicity:

$$\lim_{t\to\infty} P^t = 1\pi \tag{13}$$

2.4 Stationary Distribution
To investigate the long-run behaviour of the epidemic process, the stationary distribution of the Markov chain was computed.
Let

$$\pi = (\pi_1, \pi_2, \pi_3, \pi_4) \tag{14}$$

denote the stationary probability vector satisfying

$$\pi P = \pi$$

with the normalization condition

$$\sum_{i=1}^{4} \pi_i = 1$$

The stationary distribution provides the long-run proportion of time the epidemic process spends in each epidemiological state.
The mean recurrence time for each state was estimated to determine the expected number of weeks until the process revisits a particular epidemic state.
For an irreducible Markov chain, the mean return time to state i is defined in Section 2.3
This measure provides insight into the recurrence frequency of various epidemic conditions.

2.5 Expected Duration in Each State
Let $\{X_t\}_{t>0}$be a discrete-time Markov chain on a finite state space S with transition matrix $P = [p_{ij}]$ The expected duration (sojourn time) in state $i \in S$ is the expected number of consecutive time steps the process remains in state i before transitioning to a different state. Since the probability of staying in state i is $p_{ii}$and the probability of leaving is $1 - p_{ii}$, the sojourn time follows a geometric distribution with parameter $1 - p_{ii}$. Therefore, the expected duration is given by:

$$E[T_i] = \sum_{k=1}^{\infty} k(p_{ii})^{k-1}(1 - p_{ii}) \tag{15}$$

Using the standard result:

$$\sum_{k=1}^{\infty} k(p_{ii})^{k-1} = \frac{1}{(1-r)^2}, \quad |r| < 1 \tag{16}$$

Let $r = p_{ii}$ then:

$$E[T_i] = (1 - p_{ii})\frac{1}{(1-p_{ii})^2} \tag{17}$$

$$E[T_i] = \frac{1}{(1-p_{ii})}$$

This expression shows that states with high self-transition probabilities ($p_{ii} \approx 1$) correspond to longer persistence, while low self-transition probabilities imply rapid transitions and short expected durations. In epidemiological terms, this provides a direct measure of how stable each disease state is over time.

2.6 Uncertainty Quantification (Bootstrap Approach)
Bootstrap resampling is used to estimate the variability of transition probabilities:

$$P^{(b)} \sim Resample(X_1, \dots, X_1), \quad b = 1,2, \dots, B$$

For each bootstrap sample b, a transition matrix $P^{(b)} = p_{ij}^{(b)}$is estimated. The bootstrap mean of each transition probability is:

$$\bar{p}_{ij} = \frac{1}{B}\sum_{b=1}^{B} p_{ij}^{(b)} \tag{19}$$

B is the total number of bootstrap replications.
Standard error:

$$SE_{(p_{ij})} = \sqrt{\frac{1}{B-1}\sum_{b=1}^{B}(p_{ij}^{(b)} - \bar{p}_{ij})^2} \tag{20}$$

This measure quantifies the sampling variability of the estimated transition structure and provides a basis for constructing confidence intervals and assessing the robustness of the Markov model. In epidemiological applications, it is particularly useful for evaluating the stability of inferred disease transmission dynamics under data uncertainty (Efron, 1979; Efron and Tibshirani, 1993).

2.7 First-Passage Times Between Epidemic and Non-Epidemic States
Assume the four joint states are ordered as

$$S = \{(0,0), (0,1), (1,0), (1,1)\}$$

where:

- State 0: non-epidemic incidence and non-fatal state
- State 1: non-epidemic incidence and fatal state
- State 2: epidemic incidence and non-fatal state
- State 3: epidemic incidence and fatal state

Define:
Non-epidemic states: $N = \{0,1\}$ and Epidemic states: $E = \{2,3\}$

The first-passage time measures the expected number of weeks required to move from one class to another. For a Markov chain with transition matrix P, partition the matrix as

$$P = \begin{pmatrix} Q & R \\ 0 & 1 \end{pmatrix}$$

where Q contains transitions among transient states.
The fundamental matrix is

$$F = (I - Q)^{-1} \quad (21)$$

and the expected first-passage time vector is

$$t = F1 \quad (22)$$

where 1 is a vector of ones.
Expected number of weeks before the system first enters an epidemic regime starting from a non-epidemic state. Expected number of weeks required for epidemic conditions to return to non-epidemic conditions.
Large first-passage times imply persistent epidemic phases, stronger temporal dependence, and slower recovery dynamics.
Small first-passage times imply rapid switching between outbreak and non-outbreak regimes.

2.8 Model Assumptions

The bivariate Markov chain model is based on the following assumptions:

1. The epidemic process satisfies the Markov property, whereby the future state depends only on the current state.
2. Transition probabilities remain constant over time.
3. The state space is finite and discrete.
4. Weekly observations are independent conditional on the present state.
5. All states communicate within the chain, ensuring recurrence and existence of a stationary distribution.

3.0 RESULTS AND DISCUSSION

The estimated transition dynamics, stationary behavior, and uncertainty measures of the bivariate Lassa fever Markov chain model are presented and discussed in this section, with a focus on the stability of the joint epidemiological states and long-term epidemic characteristics.

Transition Count Matrix

Let the states be ordered as: $[(\mathbf{0},\mathbf{0}), (\mathbf{0},\mathbf{1}), (\mathbf{1},\mathbf{0}), (\mathbf{1},\mathbf{1})]$
Then the transition count matrix is

$$N = \begin{bmatrix} 17 & 21 & 2 & 0 \\ 21 & 6 & 4 & 1 \\ 1 & 4 & 7 & 6 \\ 2 & 1 & 4 & 5 \end{bmatrix}$$

where each entry n_{ij} represents the number of transitions from state i to state j.

Transition Probability Matrix

The transition probability matrix is obtained using

$$p_{ij} = \frac{n_{ij}}{\sum_j n_{ij}}$$

Thus,

$$P = \begin{bmatrix} 0.425 & 0.525 & 0.050 & 0.000 \\ 0.656 & 0.188 & 0.125 & 0.031 \\ 0.056 & 0.222 & 0.389 & 0.333 \\ 0.167 & 0.083 & 0.333 & 0.417 \end{bmatrix}$$

The transition probability matrix indicates a stochastic and dynamically evolving Lassa fever epidemiological system with notable persistence within both low-risk and high-risk states. The diagonal elements show moderate to high probabilities of remaining in the same state, particularly in the low incidence–low fatality (0.425) and high incidence–high fatality (0.4167) regimes, suggesting relative stability in both non-epidemic and severe Lassa fever outbreak conditions. In contrast, the low incidence–high fatality state exhibits weak persistence (0.1875), indicating that it is largely transient and quickly transitions back to lower-risk or alternative states, consistent with unstable mortality fluctuations often observed in Lassa fever surveillance data. Off-diagonal entries further reveal asymmetric transition behaviour, where progression from low-risk to higher-risk epidemic states occurs gradually, while recovery transitions are more dispersed across multiple states rather than concentrated in a single return path. Notably, high incidence Lassa fever states demonstrate a tendency to persist or escalate, particularly from high incidence–low fatality to high incidence–high fatality (0.3333), reflecting potential epidemic intensification and sustained transmission pressure. However, the absence of absorbing states implies that the Lassa fever system remains ergodic, with continuous switching between epidemic and non-epidemic regimes over time, highlighting both the persistence and reversibility of Lassa fever dynamics within the studied population. From a Markovian perspective, the absence of absorbing states confirms that the process is irreducible and ergodic, implying long-run probabilistic movement across all epidemiological states. This interpretation is theoretically supported by Kemeny and Snell (1960), Norris (1997), and Meyn and Tweedie (2009), who established that finite stochastic systems without absorbing states exhibit recurrent long-run behaviour and converge toward a stationary distribution.

Stationary Distribution

$$\pi = (0.4130 \quad 0.3212 \quad 0.1582 \quad 0.1076)$$

The stationary distribution represents the long-run equilibrium behaviour of the Lassa fever joint epidemiological system, indicating the proportion of time the process is expected to spend in each state as the number of transitions becomes large. The results show that the system spends the highest proportion of time in the first state (0.4130), suggesting that the most stable condition of the Lassa fever dynamics corresponds to a low-risk epidemiological regime. The second state also has a relatively substantial equilibrium probability (0.3212), implying frequent transitions into moderate epidemiological activity. In contrast, the third and fourth states, which represent more severe Lassa fever conditions involving increasing incidence and/or fatality, have lower stationary probabilities (0.1582 and 0.1076, respectively), indicating that high-risk outbreak conditions are less persistent in the long run but still recurrent. The stationary distribution obtained in this study agrees with the findings of Rashid *et al* (2023). It is also in line with the findings of Nkemnole and Oyewole (2023), who showed through a Hidden Markov Model that Lassa fever transmission in Nigeria exhibits persistent and recurrent epidemic behaviour with long-run probabilities concentrated in dominant epidemiological states. Similarly, the present study reveals that although lower-risk states dominate the long-run dynamics, there remains a non-negligible

probability of sustained epidemic conditions, confirming the endemic and cyclical nature of Lassa fever transmission

Table 2: Expected Duration in Each State

State	Expected Duration
((0,0))	1.74 weeks
((0,1))	1.23 weeks
((1,0))	1.64 weeks
((1,1))	1.72 weeks

The expected duration across all four joint epidemiological states indicates short persistence times ranging from 1.23 to 1.74 weeks, suggesting a highly dynamic system with frequent transitions between states. The non-epidemic state (0,0) has the longest duration (1.74 weeks), implying relatively greater stability compared to other states. In contrast, state (0,1) shows the shortest duration (1.23 weeks), indicating that this condition is the least stable and changes rapidly. The epidemic-related states (1,0) and (1,1) exhibit intermediate durations (1.64 and 1.72 weeks), reflecting moderate persistence once epidemic conditions occur. The results suggest weak state persistence and a rapidly mixing process with no long-term dominant state.

Table 3: Expected First-Passage Times Between Epidemic and Non-Epidemic States

Transition Type	State 1	State 2
Non-Epidemic to Epidemic	10.9044586	10.0382
Epidemic to Non-Epidemic	3.73584906	3.84906

An obvious imbalance in the dynamics of the system is revealed by the expected first-passage time results. Slower outbreak onset and moderate resistance to epidemic commencement are indicated by longer transitions (about ten-time steps) from non-epidemic to epidemic states. On the other hand, after an outbreak, recovery happens more quickly because transitions from epidemic to non-epidemic states happen more quickly (approximately 3.7-3.8-time steps). Weak heterogeneity between sub-states is suggested by the similarity of values within each category. The system generally has a slower epidemic start and a comparatively quick recovery point to transitory rather than chronic epidemic behavior.

4.0 CONCLUSION

This study developed a bivariate Markov chain model to examine the joint dynamics of Lassa fever incidence and fatality patterns using weekly epidemiological data. By transforming weekly confirmed cases and case fatality rate (CFR) into binary epidemiological states, the study successfully represented the outbreak process through four joint states describing increasing and decreasing epidemic conditions. The estimated transition probability matrix revealed that the epidemic process frequently alternates between states of declining incidence and varying fatality conditions, while simultaneous increases in incidence and fatality occurred less frequently. The stationary distribution further showed that the system spends a larger proportion of time in relatively stable or declining epidemic states, indicating moderate long-run epidemic stability. In addition, the mean return times demonstrated that severe outbreak conditions recur less often compared to lower-risk states. The findings confirm that the bivariate Markov chain framework provides an effective and interpretable stochastic approach for analysing the interaction between disease transmission and fatality behaviour. The model captures the temporal dependence between weekly epidemic conditions and offers valuable insight into long-term outbreak behaviour. Consequently, the approach can support epidemic surveillance, risk assessment, and public health decision-making for Lassa fever control and management. Future studies may extend the model by incorporating fuzzy transition probabilities, hidden Markov structures, climatic variables, or spatial information to better capture uncertainty and regional variations in Lassa fever transmission dynamics.

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