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An epidemic model for control and possible elimination of Lassa fever

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Abstract. Lassa fever is a deadly viral disease whose incubation period ranges from six to twenty-one days and about eighty percent of Lassa virus infection is asymptomatic. A deterministic model was formulated to quantify the transmission dynamics of the disease under isolation and treatment of the isolated asymptomatic and symptomatic humans for effective management and possible elimination of the disease. The solutions of the model were shown to be positive and bounded. Equilibrium analysis was conducted and both the disease-free and the endemic equilibria were derived. The threshold quantity for disease elimination , R_0 , was also obtained and used to derive conditions for the existence of stability of the eqilibria. The quantity was also employed to examine the sensitivity of the model parameters to disease propagation and reduction. The theoretical analysis was then complemented with the quantitative analysis by adopting a set of realistic values for the model parameters in order to show the effect of isolation and treatment on the spread and fatality of Lassa fever. Results from the quantitative study showed that death and infection from Lassa fever fell continuously as more and more exposed individuals were detected and isolated for treatment. The study therefore suggested that any measure taken to eradicate or curtail Lassa fever spread should include detection and isolation of the exposed humans for prompt treatments.

Keywords. Isolation, incubation period, asymptomatic, symptomatic, equilibria

1 Introduction

Lassa fever came into existence in 1969 when it erupted in the midst of health workers at a particular missionary hospital in Lassa town, Borno State of Nigeria, and the contributory agent, Lassa virus, was detached from the body fluid of the affected health workers [7]. Laura Wine, one of the first infected nurses at Lassa missionary hospital, was the first victim of the disease. Today, Lassa fever is a confirmed widespread zoonotic infection in West Africa, with a staggering 100 000 - 300 000 cases yearly, and nearly 5 000 deaths [38]. Since the first occurrence in Lassa town in 1969, Lassa fever has been occurring from time to time in Nigeria. In 2016, case fatality from Lassa fever stood at 61% with 108 deaths from 176 reported cases [28]. Also, within the

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first twelve weeks in 2017, 2018 and 2019, case fatalities from Lassa fever were 47%, 26% and 21% respectively [20, 4]. By May 2018, the reported cases of Lassa fever rose to 1 914 across 21 States of Nigeria with case fatality rate of 25.5% [16]. Apart from Nigeria, Lassa fever is a major health issue in Guinea, Sierra Leone and Liberia. The disease has also been reported in Senegal, Ghana, Burkina faso, Mali, Benin and Cote d'Ivoire [28, 6].

The agent of Lassa fever is a small rat, the Multimammate rodent that belongs to the genus *Mastomys natelensis* [7]. An infected rat remains carrier of the infection for life and does not manifest any clinical signs but spread the virus in the human and animal populations via saliva, urine, faeces, respiratory secretions and blood spillage [28]. The virus can also be contracted through inhalation of aerosol and exposure to contaminated medical tools [25]. Human-to-human spread of the virus occurs through exposure to the secretions of the infectious individuals including semen during sexual intercourse [29]. Almost eighty percent of individuals who contract Lassa fever virus are asymptomatic while the symptoms and signs of the disease take a week or three weeks to develop [4]. The symptoms begin with body ache, fever, tiredness, headache and sore throat, back, chest and abdominal pains, diarrhea, nausea and vomiting [40]. At the advanced stage, an infected individual manifests disorientation, seizures, tremor, shock and coma [21]. In grave cases, facial swelling, bleeding from the virginal, nose, mouth as well as low blood pressure manifest [35]. Severe cases are often accompanied with death within fourteen days even though, one out of five infections brings about a fatal case [39]. Besides, up to fifteen to twenty percent hospitalisation due to Lassa fever results in death as a result of failure of multiple organs like kidney, liver and spleen [34].

Lassa fever preventions require sophisticated food storage methods, rats control strategies such as cleanliness, good waste disposal system, traps and other attempts that can limit contact with rodents [24]. Isolation of infectious individuals is an ideal method of preventing human-to-human transmission of Lassa virus [1]. Isolation has been a popular method of checking transmission of contagious diseases (e.g. leprosy) since time immemorial [22]. At present, no vaccine protects against the infection of Lassa virus [3]. In case of nonexistence or inadequate access to medical interventions like treatment and vaccine, isolation is one of the major options to decrease the spread of transmittable diseases [9]. Infections can take two forms in epidemiological study. It can be asymptomatic or symptomatic [10]. It is asymptomatic if the symptoms of the disease are yet to be manifested in the infected individuals. At this stage, the infected individual may be infectious as in the case of measles or may not be infectious as in the case of Lassa fever [11, 36]. Infection is symptomatic if the symptoms of the disease have been fully developed in the infected individuals. At this stage, the infected individual is fully infectious [13]. Since Lassa fever does not spread from asymptomatic humans [36], mortality from the disease can be averted and the spread of the virus can be curtailed if the infection is detected at the asymptomatic stage and the infected individuals are promptly isolated for treatments.

Mathematical epidemiology offers theoretical framework for the study of disease transmission mechanisms and proposes possible intervention strategies. Mathematical study of the transmission dynamics of Lassa fever has received considerable attentions of researchers and a good number of models has been developed to study the disease over the years. A model was developed in [18] to examine the effect of non-drug compliance on the transmission dynamics of Lassa fever. It was discovered that non-drug compliance triggered reappearance of signs and symptoms after some time. The researcher therefore concluded that all hands must be on desk to encourage drug compliance in order to prevent reemergence of Lassa fever. [7] proposed a model for Lassa fever and performed the sensitivity analysis of the model parameters. Results from their analysis showed that the most sensitive parameter to Lassa fever spread was contact rate between susceptible humans and infectious rodents. A robust model of Lassa fever was developed in [35] and

the authors conducted the sensitivity analysis of the model parameters. Birth rate of rodents was discovered the most sensitive parameter to animal-to-human spread of the disease while hunting/predation rate was established the most sensitive to the reproductive ratio of rodents. The researchers therefore advocated for the control of the two parameters in an attempt to destroy Lassa fever reservoirs.

A mathematical model was designed in [27] to investigate the implication of separation and treatment of infectious individuals on the dynamics of Lassa fever. The authors estimated some important parameters like the reproduction number which they used to predict possible eradication of Lassa fever in Nigeria with time. [28] designed a Lassa fever model incorporating variable human and animal population to study possible prevention and control of Lassa fever. The results of the study suggested hygienic environment, early treatment and rodents control measures as the best methods against the transmission of Lassa fever. The result of the model developed in [29] to study the dynamics of Lassa fever with control strategies advocated for the awareness of the disease in both non-affected and the affected regions to bring people to the knowledge of Lassa fever prevention, symptoms and treatment. In their study, [3] designed a model for the control of dynamical spread of Lassa fever. Their findings showed that Lassa virus transmission and spread in human population was shaped by the population of rodents. They therefore called for the control of rodent population in a bid to eradicate Lassa fever.

[31] formulated a model and derived a threshold quantity for the transmission and control of Lassa fever virus. They focused on human-to-human transmission of the virus in terms of sexual relations and animal-to-human transmission in terms of contact with the infected rodents. The result of their analysis showed that reduction in human-to-human transmission is a function condom efficacy and condom usage compliance while reduction in animal-to-human transmission is a function of the rate of usage of rodenticide. [2] also developed a model for Lassa fever with isolation of infectious humans as a main target for disease control. They conducted theoretical and numerical studies of the model and discovered that isolation of infectious individuals and treatment of the isolated infectious humans yielded a better result in combating the spread of Lassa fever.

Lassa fever dynamics is shaped by a number of factors such as latency, re-infection and isolation. Latency stage is omitted in some of the existing Lassa fever models despite the incubation period of between one week to three weeks for Lassa fever [22, 17, 29, 31, 18, 19, 3]. Also, while antibody to Lassa virus exists in recoverd individuals, it does not deactivate the virus in usual neutralisation experiment [33]. Therefore, a recovered individual can be re-infected with Lassa virus but models in [22, 17, 19, 7, 28, 2] exclude possible re-infection. Again, isolation is key to preventing Lassa fever spread but is not considered in [17, 31, 19, 35]. The model in [17] even incorporated vaccination which confers immunity on the susceptible individuals despite the fact that no vaccine guarantees protection against Lassa fever virus at the moment [24]. Also, the models in [4], [5] considered Lassa fever transmission from exposed individuals but there is no clinical evidence to back the spread of Lassa fever from an asymptomatic individual [36]. None of the exiting models support the spread of Lassa virus from an asymptomatic individual. Another crucial aspect of Lassa fever dynamics that has not been taken into consideration is the detection and isolation of the exposed individuals for effective treatments. Since the disease does not spread at the asymptomatic stage [36], there is tendency to delay or eliminate its outbreaks if appropriate methods are designed to identify and isolate asymptomatic humans for effective treatments. The present study therefore aims to bridge the gaps in the existing Lassa fever models by taking care of latency, re-infection, isolation and treatment, both at the asymptomatic and symptomatic stages of infection for effective management and possible elimination of the disease.

2 Materials and Methods

A seven deterministic compartmental model was considered with the notations $S_h(t), E_h(t), I_h(t), I_{sh}(t), R_h(t), S_r(t)$ and $I_r(t)$ to give an insight into the transmission dynamics of Lassa fever. $N(t)$ is the entire population at time t which is partitioned into two sub-populations $N_h(t)$ and $N_r(t)$: human and rodent populations respectively; that are in turn sub-categorised into classes $S_h(t), E_h(t), I_h(t), I_{sh}(t), R_h(t), S_r(t)$ and $I_r(t)$ denoting susceptible human population at time t, exposed human population at time t, infected human population at time t, isolated human population at time t, recovered human population at time t, susceptible rodent population at time t and infected rodent population at time t respectively such that

$$N_h(t) = S_h(t) + E_h(t) + I_h(t) + I_{sh}(t) + R_h(t),$$

and

$$N_r(t) = S_r(t) + I_r(t).$$

The transmission diagram of the dynamics is illustrated in Figure 1.

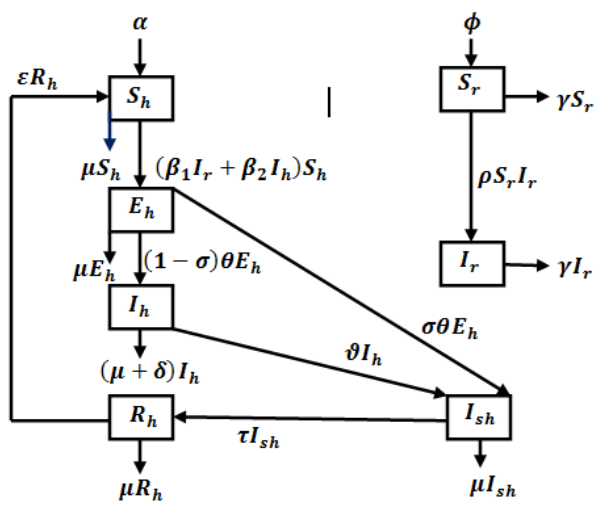

Figure 1: Transmission diagram of the model

The population of the susceptible human is risen when the individuals are recruited into it either by immigration or bith at the rate α. It also increases by ε, the waning rate of immunity after recovery. The compartment decreases by β_1 and β_2 which are the contact rates with the infectious animals and man respectively and by μ, which is the natural mortality rate. Thus;

$$\frac{dS_h}{dt} = \alpha + \varepsilon R_h - (\beta_1 I_r + \beta_2 I_h)S_h - \mu S_h.$$

The exposed human compartment is generated when there is an effective contact between the susceptible individuals, the infectious rodents and the infectious humans. While σ is the proportion of the exposed human who are identified through the measure which has been put in

place to track the potential Lassa fever cases, $(1-\sigma)$ is the remaining proportion of the exposed individuals who will progress to the infectious class at the expiration of the latency. Hence, the exposed human compartment is reduced by $\sigma\theta$ and $(1-\sigma)\theta$ respectively where both the identified exposed and the unidentified exposed humans progress to the isolated human and the infectious human compartments respectively at the same rate θ. The exposed human compartment is also reduced by μ, the natural mortality rate. Thus;

$$\frac{dE_h}{dt} = (\beta_1 I_r + \beta_2 I_h)S_h - \sigma\theta E_h - (1-\sigma)\theta E_h - \mu E_h.$$

The infected human population is generated at the expiration of the latency at rate $(1-\sigma)\theta$ where $(1-\sigma)$ is the proportion of the individuals who could not be identified during their latency stage. The compartment is however reduced by ϑ, δ and μ, the isolation of the infectives, disease-induced and natural mortality rates respectively. Thus;

$$\frac{dI_h}{dt} = (1-\sigma)\theta E_h - \vartheta I_h - (\mu+\delta)I_h.$$

The isolated human compartment I_{sh} is produced when some of the exposed and the infectious humans move into it at the rates θ and ϑ respectively. It is however decreased by τ and μ, the rates of successful treatment and natural mortality respectively. Thus;

$$\frac{I_{sh}}{dt} = \sigma\theta E_h + \vartheta I_h - \tau I_{sh} - \mu I_{sh}.$$

The recovered human compartment is produced through successful treatment of the isolated individuals at rate τ. It is however reduced by the natural mortality rate μ and the waning rate of immunity ε. Thus;

$$\frac{dR_h}{dt} = \tau I_{sh} - \varepsilon R_h - \mu R_h.$$

The compartment for the susceptible animals (S_r) is produced at the rate ϕ but reduces through ρ and γ, the effective contact rate with the infected animals and the natural mortality rate respectively. Thus;

$$\frac{dS_r}{dt} = \phi - \rho S_r I_r - \gamma S_r.$$

The compartment for the infected animals grows through the effective contact between the susceptible and the infected animals at the rate ρ but reduces by γ, the natural mortality rate. Thus;

$$\frac{dI_r}{dt} = \rho S_r I_r - \gamma I_r.$$

It is assumed that while natural mortality occurs for all the human compartments at the same rate μ, natural mortality occurs for all the animal compartments at the same rate γ. Bringing the above assumptions, formulations and flow diagram together, the following system of equations are derived.

$$\frac{dS_h}{dt} = \alpha + \varepsilon R_h - (\beta_1 I_r + \beta_2 I_h)S_h - \mu S_h, \tag{2.1}$$

$$\frac{dE_h}{dt} = (\beta_1 I_r + \beta_2 I_h)S_h - \sigma\theta E_h - (1-\sigma)\theta E_h - \mu E_h, \tag{2.2}$$

$$\frac{dI_h}{dt} = (1-\sigma)\theta E_h - \vartheta I_h - (\mu+\delta)I_h, \tag{2.3}$$

$$\frac{I_{sh}}{dt} = \sigma\theta E_h + \vartheta I_h - \tau I_{sh} - \mu I_{sh}, \tag{2.4}$$

$$\frac{dR_h}{dt} = \tau I_{sh} - \varepsilon R_h - \mu R_h, \tag{2.5}$$

$$\frac{dS_r}{dt} = \phi - \rho S_r I_r - \gamma S_r, \tag{2.6}$$

$$\frac{dI_r}{dt} = \rho S_r I_r - \gamma I_r. \tag{2.7}$$

Parameter descriptions are stated in Table 1 for ease of reference.

Table 1: Description for model parameters

Parameters	Descriptions
α	recruitment rate for humans
ε	waning rate of immunity
β_1	contact rate with infectious animals for susceptible humans
β_2	contact rate with infectious humans for susceptible humans
μ	natural mortality rate for humans
σ	proportion of humans identified and isolated at the exposed stage
θ	progression rate from the exposed stage
ϑ	rate of isolation of infectious humans
δ	mortality rate due to Lassa fever for humans
τ	successful treatment rate
ϕ	recruitment rate for animals
ρ	contact rate between susceptible and infectious animals
γ	natural mortality rate for animals

The variables and parameters for the model are nonnegative for $t \geq 0$ in the region Ω, where $\Omega = \Omega_h \times \Omega_r = \left\{S_h, E_h, I_h, R_h, I_{sh}, S_r, I_r \in \Re_+^7\right\}$. Since the model variables and parameters are nonnegative, we can show that the solutions for the model are bounded and positive in Ω. The total changes in human population with time is

$$\begin{aligned}
\frac{dN_h}{dt} &= \alpha - \mu(S_h + E_h + I_h + R_h + I_{sh}) - \delta I_h \\
&= \alpha - \mu N_h - \delta I_h \Rightarrow \\
\frac{dN_h}{dt} &\leq \alpha - \mu N_h \Rightarrow \\
\frac{dN_h}{(\alpha - \mu N_h)} &\leq dt \Rightarrow \\
\ln(\alpha - \mu N_h) &\geq t + m \Rightarrow \\
\alpha - \mu N_h &\geq pe^{-\mu t},
\end{aligned}$$

when $t = 0$ then

$$\alpha - \mu N_h(t) \geq (\alpha - \mu N_{h0})e^{-\mu t} \Rightarrow N_h(t) \leq \frac{\alpha}{\mu} - \left(\frac{\alpha - \mu N_{h0}}{\mu}\right) e^{-\mu t}.$$

As $t \to \infty$ then $N_h(t) \leq \frac{\alpha}{\mu}$. Hence, the bounded region for the solution of $N_h(t)$ exists in

$$\Omega_h = \left\{ (S_h, E_h, I_h, R_h, I_{sh}) \in \Re_+^5; N_h(t) \leq \frac{\alpha}{\mu} \right\}.$$

For animals, the addition of the rodent population is given as

$$\frac{dN_r}{dt} \leq \phi - \gamma N_r \Rightarrow N_r(t) \leq \frac{\phi}{\gamma}[1 - ke^{-\gamma t}].$$

As $t \to \infty$ then $N_r(t) \leq \frac{\phi}{\gamma}$. Hence, the bounded region for the solution of $N_r(t)$ exists in

$$\Omega_r = \left\{ (S_r, I_r) \in \Re_+^2; N_r(t) \leq \frac{\phi}{\gamma} \right\}.$$

Therefore, the set of all feasible solutions for the Lassa fever model is bounded within $\Omega = \Omega_h \times \Omega_r = \left\{ S_h, E_h, I_h, R_h, I_{sh}, S_r, I_r \in \Re_+^7; N_h(t) \leq \frac{\alpha}{\mu}; N_r(t) \leq \frac{\phi}{\gamma} \right\}$. Since the system considers human and animal populations, the initial conditions for the variables are necessarily positive and the solutions to the model ought to be nonnegative as well for $t \geq 0$. We therefore verify the positivity of the model solutions.
From (2.1),

$$\begin{aligned}
\frac{dS_h}{dt} &= \alpha + \varepsilon R_h - (\beta_1 I_r + \beta_2 I_h) S_h - \mu S_h, \\
&\geq -(\beta_1 I_r + \beta_2 I_h + \mu) S_h, \\
\Rightarrow \int \frac{dS_h}{S_h} &\geq -\int (\beta_1 I_r + \beta_2 I_h) dt - \int \mu dt, \\
\ln S_h(t) &\geq -\int (\beta_1 I_r + \beta_2 I_h) dt - \mu t + c, \\
S_h(t) &\geq e^{-\int (\beta_1 I_r + \beta_2 I_h) dt} \times e^{-\mu t} \times e^c, \\
&\geq W(e^{-[\int (\beta_1 I_r + \beta_2 I_h) dt + \mu t]}),
\end{aligned}$$

when $t = 0$, $S_h(0) \geq W$.

$$\therefore S_h(t) \geq S_h(0)(e^{-\int (\beta_1 I_r + \beta_2 I_h) dt + \mu t}) \geq 0.$$

Also from (2),

$$\begin{aligned}
\frac{dE_h}{dt} &= (\beta_1 I_r + \beta_2 I_h) S_h - \theta E_h - \mu E_h, \\
&\geq -(\mu + \theta) E_h, \\
\Rightarrow \int \frac{dE_h}{E_h} &\geq -\int (\mu + \theta) dt, \\
\ln E_h(t) &\geq -(\mu + \theta) t + c, \\
E_h(t) &\geq e^{-(\mu+\theta)t + c}, \\
&\geq X e^{-(\mu+\theta)t},
\end{aligned}$$

when $t = 0$, $E_h(0) \geq X$.

$$\therefore E_h(t) \geq E_h(0) e^{-(\mu+\theta)t} \geq 0.$$

Following the same process, we can show that the solutions for other equations are nonnegative for $t \geq 0$.

3 Model Analysis

3.1 Equilibria

The system allows a zero equilibrium $\mathcal{E}_\circ = (S_h^\circ, E_h^\circ, I_h^\circ, R_h^\circ, I_{sh}^\circ, S_r^\circ, I_r^\circ) = \left(\frac{\alpha}{\mu}, 0, 0, 0, 0, \frac{\phi}{\gamma}, 0\right)$ and a nonzero equilibrium $\mathcal{E}_* = (S_{h*}, E_{h*}, I_{h*}, R_{h*}, I_{sh*}, S_{r*}, I_{r*})$ with coordinates

$$
\begin{aligned}
S_{h*} &= \left[\frac{\beta_1\gamma}{\rho}\left(\frac{\rho\phi}{\gamma^2}-1\right)+\frac{\beta_2(1-\sigma)\theta}{(\mu+\vartheta+\delta)}E_h+\mu\right]\left\{\alpha+\frac{\varepsilon\tau[\sigma\theta(\mu+\vartheta+\delta)+\vartheta(1-\sigma)\theta]}{(\mu+\varepsilon)(\mu+\tau)(\mu+\vartheta+\delta)}E_h\right\},\\
E_{h*} &= \frac{\beta_1\alpha\gamma}{\mu\rho}\left(\frac{\rho\phi}{\gamma^2}-1\right)\Big/\left(\frac{\beta_2(1-\sigma)\alpha\theta}{\mu(\mu+\theta)(\mu+\vartheta+\delta)}-1\right),\\
I_{h*} &= \frac{(1-\sigma)\theta}{(\mu+\vartheta+\delta)}E_{h*},\\
R_{h*} &= \frac{\tau[\sigma\theta(\mu+\vartheta+\delta)+\vartheta(1-\sigma)\theta]}{(\mu+\varepsilon)(\mu+\tau)(\mu+\vartheta+\delta)}E_{h*},\\
I_{sh*} &= \frac{\sigma\theta(\mu+\vartheta+\delta)+\vartheta(1-\sigma)\theta}{(\mu+\tau)(\mu+\vartheta+\delta)}E_{h*},\\
S_{r*} &= \frac{\gamma}{\rho},\\
I_{r*} &= \frac{\phi}{\gamma}-\frac{\gamma}{\rho}.
\end{aligned}
\tag{3.1}
$$

3.2 Reproduction Number

The average number of secondary infections to be produced when a single infectious individual gets into the susceptible population is governed by a threshold quantity known as the reproduction number, $\mathcal{R}_\circ$. If $\mathcal{R}_\circ > 1$, the infectious individual will infect at least one person and the disease will spread in the population. On the other hand, if $\mathcal{R}_\circ < 1$, the infectious individual will fail to infect a single person and the disease will die out or fail to spread. Because infection can spread from both infectious humans and animals, $\mathcal{R}_\circ$ in the present analysis is made up of two parts as in other Lassa fever models [30]. It is made up of $\mathcal{R}_{\circ h}$ and $\mathcal{R}_{\circ a}$, the infection transmission potentials from human and animal respectively which are derived following the approach in [37] outlined as follows

$$
\mathcal{F} = \begin{pmatrix}(\beta_1 I_r + \beta_2 I_h)S_h\\ 0\\ \rho S_r I_r\end{pmatrix}; \quad \mathcal{V} = \begin{pmatrix}(\theta+\mu)E_h\\ -(1-\sigma)\theta E_h + (\mu+\vartheta+\delta)I_h\\ \gamma I_r\end{pmatrix}, \tag{3.2}
$$

$$
\Rightarrow F = \begin{pmatrix}0 & \beta_2 S_h & \beta_1 S_h\\ 0 & 0 & 0\\ 0 & 0 & \rho S_r\end{pmatrix}; \quad V = \begin{pmatrix}\frac{1}{(\mu+\theta)} & 0 & 0\\ \frac{(1-\sigma)\theta}{(\mu+\theta)(\mu+\vartheta+\delta)} & \frac{1}{(\mu+\vartheta+\delta)} & 0\\ 0 & 0 & \frac{1}{\gamma}\end{pmatrix}, \tag{3.3}
$$

$$FV^{-1} = \begin{pmatrix} \dfrac{\alpha\beta_2(1-\sigma)\theta}{\mu(\mu+\theta)(\mu+\vartheta+\delta)} & \dfrac{\alpha\beta_2}{\mu(\mu+\vartheta+\delta)} & 0 \\ 0 & 0 & 0 \\ 0 & 0 & \dfrac{\rho\phi}{\gamma^2} \end{pmatrix}. \tag{3.4}$$

$$\therefore \mathcal{R}_\circ = max.(\mathcal{R}_{\circ h}, \mathcal{R}_{\circ a}) = max.\left(\frac{\alpha\theta\beta_2(1-\sigma)}{\mu(\mu+\theta)(\mu+\vartheta+\delta)}, \frac{\rho\phi}{\gamma^2}\right). \tag{3.5}$$

Keeping other parameters constant in (3.5) but increasing isolation parameter for asymptomatic humans σ as well as isolation parameter for infectious humans ϑ while recruitment rate for animals ϕ is reduced will ultimately reduce $\mathcal{R}_\circ$ and Lassa fever may fail to spread in the population under the condition. Expressing the endemic equilibrium $\mathcal{E}_*$ in (3.1) in terms of $\mathcal{R}_\circ$ (*i.e.*, $\mathcal{R}_{\circ h}, \mathcal{R}_{\circ a}$) then

$$\begin{aligned}
S_{h*} &= \left[\frac{\beta_1\gamma}{\rho}(\mathcal{R}_{\circ a}-1) + \frac{\beta_2(1-\sigma)\theta}{(\mu+\vartheta+\delta)} \times \left[\frac{\beta_1\alpha\gamma}{\mu\rho}(\mathcal{R}_{\circ a}-1)\Big/(\mathcal{R}_{\circ h}-1)\right] + \mu\right] \\
&\quad \times \left\{\alpha + \frac{\varepsilon\tau[\sigma\theta(\mu+\vartheta+\delta)+\vartheta(1-\sigma)\theta]}{(\mu+\varepsilon)(\mu+\tau)(\mu+\vartheta+\delta)} \times \left[\frac{\beta_1\alpha\gamma}{\mu\rho}(\mathcal{R}_{\circ a}-1)\Big/(\mathcal{R}_{\circ h}-1)\right]\right\}, \\
E_{h*} &= \frac{\beta_1\alpha\gamma}{\mu\rho}(\mathcal{R}_{\circ a}-1)\Big/(\mathcal{R}_{\circ h}-1), \\
I_{h*} &= \frac{(1-\sigma)\theta}{(\mu+\vartheta+\delta)} \times \left[\frac{\beta_1\alpha\gamma}{\mu\rho}(\mathcal{R}_{\circ a}-1)\Big/(\mathcal{R}_{\circ h}-1)\right], \\
R_{h*} &= \frac{\tau[\sigma\theta(\mu+\vartheta+\delta)+\vartheta(1-\sigma)\theta]}{(\mu+\varepsilon)(\mu+\tau)(\mu+\vartheta+\delta)} \times \left[\frac{\beta_1\alpha\gamma}{\mu\rho}(\mathcal{R}_{\circ a}-1)\Big/(\mathcal{R}_{\circ h}-1)\right], \\
I_{sh*} &= \frac{\sigma\theta(\mu+\vartheta+\delta)+\vartheta(1-\sigma)\theta}{(\mu+\tau)(\mu+\vartheta+\delta)} \times \left[\frac{\beta_1\alpha\gamma}{\mu\rho}(\mathcal{R}_{\circ a}-1)\Big/(\mathcal{R}_{\circ h}-1)\right], \\
S_{r*} &= \frac{\gamma}{\rho}, \\
I_{r*} &= \frac{\gamma}{\rho}(\mathcal{R}_{\circ a}-1).
\end{aligned} \tag{3.6}$$

Since the existence of nonzero equilibrium $\mathcal{E}_*$ depends on the positivity of each point in $\mathcal{E}_*$, it is therefore shown in (3.6) that $\mathcal{E}_*$ exists if and only if $\mathcal{R}_\circ > 1$ i.e., $\mathcal{R}_{\circ a} > 1$ and $\mathcal{R}_{\circ h} > 1$. One or more of the points may be negative if $\mathcal{R}_{\circ a}$ or $\mathcal{R}_{\circ h}$ or both $\mathcal{R}_{\circ a}$ and $\mathcal{R}_{\circ h}$ are less than one.

3.3 Local and global stability of zero equilibrium, $\mathcal{E}_\circ$

The local and global stability of the zero equilibrium, $\mathcal{E}_\circ$ is a function of $\mathcal{R}_{\circ a}$ and $\mathcal{R}_{\circ h}$. Both are stable if $\mathcal{R}_{\circ a} < 1$ and $\mathcal{R}_{\circ h} < 1$ but they are unstable if either $\mathcal{R}_{\circ a}$ or $\mathcal{R}_{\circ h}$ exceeds one or both $\mathcal{R}_{\circ a}$ and $\mathcal{R}_{\circ h}$ exceed one.

Theorem 3.1. *The disease-free equilibrium $\mathcal{E}_\circ$ is locally and globally stable if $\mathcal{R}_{\circ a} < 1$ and $\mathcal{R}_{\circ h} < 1$.*

Proof. To verify the local stability of the zero equilibrium, $\mathcal{E}_\circ$, we compute the Jacobian matrix

of the system as follows

$$J = \begin{pmatrix} -(\mu+\beta_1 I_r+\beta_2 I_h) & 0 & -\beta_2 S_h & \varepsilon & 0 & 0 & -\beta_1 S_h \\ (\beta_1 I_r+\beta_2 I_h) & -(\mu+\theta) & \beta_2 S_h & 0 & 0 & 0 & \beta_1 S_h \\ 0 & (1-\sigma)\theta & -(\mu+\vartheta+\delta) & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & -(\mu+\varepsilon) & \tau & 0 & 0 \\ 0 & \sigma\theta & \vartheta & 0 & -(\mu+\tau) & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & -\rho I_r-\gamma & -\rho S_r \\ 0 & 0 & 0 & 0 & 0 & \rho I_r & \rho S_r-\gamma \end{pmatrix}. \tag{3.7}$$

Evaluating J at the zero equilibrium $\mathcal{E}_\circ$ then (3.7) becomes

$$J(\mathcal{E}_\circ) = \begin{pmatrix} -\mu & 0 & -\frac{\alpha\beta_2}{\mu} & \varepsilon & 0 & 0 & -\frac{\alpha\beta_1}{\mu} \\ 0 & -(\mu+\theta) & \frac{\alpha\beta_2}{\mu} & 0 & 0 & 0 & \frac{\alpha\beta_1}{\mu} \\ 0 & (1-\sigma)\theta & -(\mu+\vartheta+\delta) & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & -(\mu+\varepsilon) & \tau & 0 & 0 \\ 0 & \sigma\theta & \vartheta & 0 & -(\mu+\tau) & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & -\gamma & -\frac{\rho\phi}{\gamma} \\ 0 & 0 & 0 & 0 & 0 & 0 & \frac{\rho\phi}{\gamma}-\gamma \end{pmatrix}. \tag{3.8}$$

Five of the eigenvalues of $J(\mathcal{E}_\circ)$ are $\lambda_1 = -\mu, \lambda_2 = \gamma(\mathcal{R}_{\circ a}-1), \lambda_3 = -\gamma, \lambda_4 = -(\mu+\tau)$ and $\lambda_5 = -(\mu+\varepsilon)$. The remaining elements of $J(\mathcal{E}_\circ)$ are contained in submatrix B given as

$$B = \begin{pmatrix} -(\mu+\theta) & \frac{\alpha\beta_2}{\mu} \\ (1-\sigma)\theta & -(\mu+\vartheta+\delta) \end{pmatrix}. \tag{3.9}$$

Following Gershgorin's circle theorem [8, 32], the following inequalities are satisfied by matrix B

$$\begin{aligned} (\mu+\theta) &> \frac{\alpha\beta_2}{\mu}, \\ (\mu+\vartheta+\delta) &> (1-\sigma)\theta \end{aligned}. \tag{3.10}$$

Combining the inequalities in (3.10),

$$1 > \frac{\alpha\beta_2(1-\sigma)\theta}{\mu(\mu+\theta)(\mu+\vartheta+\delta)}.$$

$$\Rightarrow \mathcal{R}_{\circ h} < 1. \tag{3.11}$$

The DFE is locally stable if all the eigenvalues of $J(\mathcal{E}_\circ)$ in (3.8) are negative. Considering λ_2, it is observed that the local stability of DFE is ensured only if $\mathcal{R}_{\circ a} < 1$ and $\mathcal{R}_{\circ h} < 1$.
To verify the global stability of DFE, the approach in [14] is adopted. With the approach, the model is partitioned into

$$\begin{aligned} \dot{\mathbf{x}} &= F(\mathbf{x}, \mathbf{I}), \\ \dot{\mathbf{I}} &= G(\mathbf{x}, \mathbf{I}), \\ G(\mathbf{x}, \mathbf{0}) &= 0, \end{aligned} \tag{3.12}$$

where $\mathbf{x} \in \Re^3$ denotes the uninfected components of the model, $\mathbf{I} \in \Re^4$ denotes the infected components of the model and $\mathbf{E}_\circ=(x^*,0)$ denotes the DFE of the model. $\mathbf{x} \in \Re^3$ implies $\mathbf{x} = (S_h, R_h, S_r)^T$ while $\mathbf{I} \in \Re^4$ implies $\mathbf{I} = (E_h, I_h, I_{sh}, I_r)^T$. The conditions $(H1)$ and $(H2)$ in [14] must be satisfied by the system (3.12) to ensure global stability of the model's DFE. The conditions $(H1)$ and $(H2)$ in [14] are stated as follows
$(H1)$ For $\dot{\mathbf{x}} = F(\mathbf{x}, \mathbf{0})$, $\mathbf{x}^*$ is g.a.s.
$(H2)$ $\hat{G}(\mathbf{x}, \mathbf{I})$=$\mathbf{AI} - G(\mathbf{x}, \mathbf{I})$, $\hat{G}(\mathbf{x}, \mathbf{I}) \geq 0$ for $\hat{G}(\mathbf{x}, \mathbf{I}) \in \Omega$.
$F(\mathbf{x}, \mathbf{0})$ is a 2×1 column matrix which is derived by evaluating the uninfectious and the infectious compartments of the model with the values of the models' variables at DFE. In $(H2)$, $\mathbf{A}$=$D_I G(\mathbf{x}^*, \mathbf{0})$ is an M-matrix (the off diagonal elements of A are nonnegative) and Ω is the medel's region of feasibility. If the system (3.12) meets the two conditions, then $\mathcal{R}_{\circ a}$ and $\mathcal{R}_{\circ h}$ are less than unity and the DFE of the model is globally asymptotically stable. We verify the two conditions as follows

$$
\begin{aligned}
F(\mathbf{x}, \mathbf{0}) &= \begin{pmatrix} \alpha + \phi - \mu S_h^\circ - \gamma S_r^\circ \\ 0 \end{pmatrix}, \\
\hat{G}(\mathbf{x}, \mathbf{I}) &= \mathbf{AI} - G(\mathbf{x}, \mathbf{I}) \\
&= \begin{pmatrix} -(\mu+\theta) & \beta_2 S_h^\circ & 0 & \beta_1 S_h^\circ \\ (1-\sigma)\theta & -(\mu+\vartheta+\delta) & 0 & 0 \\ \sigma\theta & \vartheta & -(\mu+\tau) & 0 \\ 0 & 0 & 0 & \rho S_r^\circ - \gamma \end{pmatrix} \begin{pmatrix} E_h \\ I_h \\ I_{sh} \\ I_r \end{pmatrix} \\
&\quad - \begin{pmatrix} -(\mu+\theta)E_h & \beta_2 I_h S_h & 0 & \beta_1 I_r S_h \\ (1-\sigma)\theta E_h & -(\mu+\vartheta+\delta)I_h & 0 & 0 \\ \sigma\theta E_h & \vartheta I_h & -(\mu+\tau)I_{sh} & 0 \\ 0 & 0 & 0 & (\rho S_r^\circ - \gamma) I_r \end{pmatrix} \\
\Rightarrow \hat{G}(\mathbf{x}, \mathbf{I}) &= \begin{pmatrix} \hat{G}_1(\mathbf{x}, \mathbf{I}) \\ \hat{G}_2(\mathbf{x}, \mathbf{I}) \\ \hat{G}_3(\mathbf{x}, \mathbf{I}) \\ \hat{G}_4(\mathbf{x}, \mathbf{I}) \end{pmatrix} = \begin{pmatrix} \beta_2 I_h (S_h^\circ - S_h) + \beta_1 I_r (S_h^\circ - S_h) \\ 0 \\ 0 \\ \rho(S_r^\circ - S_r) \end{pmatrix}.
\end{aligned}
\tag{3.13}
$$

It is observed from (3.13) that $\hat{G}(\mathbf{x}, \mathbf{I}) \geq 0$ since $S_h^\circ \geq S_h$ and $S_r^\circ \geq S_r$. Hence, the conditions $(H1)$ and $(H2)$ in [14] are satisfied and the DFE $\mathcal{E}_0$ is globally asymptotically stable if $\mathcal{R}_{\circ a} < 1$ and $\mathcal{R}_{\circ h} < 1$. □

3.4 Local and global stability of nonzero equilibrium, $\mathcal{E}_*$

As in zero equilibrium, $\mathcal{E}_\circ$, the stability of nonzero equilibrium $\mathcal{E}_*$ also depends on the values of $\mathcal{R}_{\circ a}$ and $\mathcal{R}_{\circ h}$. However, unlike in $\mathcal{E}_\circ$, $\mathcal{E}_*$ is stable locally and globally if $\mathcal{R}_{\circ a} > 1$ and $\mathcal{R}_{\circ h} > 1$ while it is unstable if $\mathcal{R}_{\circ a} < 1$ and $\mathcal{R}_{\circ h} < 1$.

Theorem 3.2. *The endemic equilibrium $\mathcal{E}_*$ exists and is locally and globally asymptotically stable if $\mathcal{R}_{\circ a} > 1$ and $\mathcal{R}_{\circ h} > 1$ otherwise $\mathcal{E}_*$ is locally and globally unstable (i.e., if $\mathcal{R}_{\circ a} < 1$ and $\mathcal{R}_{\circ h} < 1$).*

Proof. To investigate the local stability of the nonzero equilibrium, $\mathcal{E}_*$, the center manifold theory [15] is employed. $\beta_2 = \beta_2^*$ is considered as the bifurcation parameter at the bifurcation point

$\mathcal{R}_{\circ h} = 1$. Computing the Jacobian matrix of the system at the DFE $\mathcal{E}_0$ with $\beta_2 = \beta_2^*$ then

$$J^* = J(\mathcal{E}_0)|_{\beta_2=\beta_2^*} = \begin{pmatrix} -\mu & 0 & -\frac{\alpha\beta_2^*}{\mu} & \varepsilon & 0 & 0 & -\frac{\alpha\beta_1}{\mu} \\ 0 & -(\mu+\theta) & \frac{\alpha\beta_2^*}{\mu} & 0 & 0 & 0 & \frac{\alpha\beta_1}{\mu} \\ 0 & (1-\sigma)\theta & -(\mu+\vartheta+\delta) & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & -(\mu+\varepsilon) & \tau & 0 & 0 \\ 0 & \sigma\theta & \vartheta & 0 & -(\mu+\tau) & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & -\gamma & -\frac{\rho\phi}{\gamma} \\ 0 & 0 & 0 & 0 & 0 & 0 & \frac{\rho\phi}{\gamma} - \gamma \end{pmatrix}. \tag{3.14}$$

The right eigen vector corresponding to $J^* = J(\mathcal{E}_0)|_{\beta_2=\beta_2^*}$ is computed as

$$\begin{aligned} w_1 &= \frac{1}{\mu}\left\{\frac{\varepsilon\tau}{(\mu+\tau)(\mu+\varepsilon)}\left(\sigma\theta + \frac{\vartheta(1-\sigma)\theta}{(\mu+\vartheta+\delta)}\right) - (\mu+\theta)\right\} w_2, \\ w_2 &= w_2 > 0, \\ w_3 &= \frac{(1-\sigma)\theta}{(\mu+\vartheta+\delta)} w_2 > 0, \\ w_4 &= \frac{\tau}{(\mu+\tau)(\mu+\varepsilon)}\left(\sigma\theta + \frac{\vartheta(1-\sigma)\theta}{(\mu+\vartheta+\delta)}\right) w_2 > 0, \\ w_5 &= \frac{1}{(\mu+\tau)}\left(\sigma\theta + \frac{\vartheta(1-\sigma)\theta}{(\mu+\vartheta+\delta)}\right) w_2 > 0, \\ w_6 &= \frac{\mu\rho\phi}{\alpha\beta_1\gamma^2}\left[\frac{\alpha\beta_2^*(1-\sigma)\theta}{\mu(\mu+\vartheta+\delta)} - (\mu+\theta)\right] w_2, \\ w_7 &= \frac{\mu}{\alpha\beta_1}\left[(\mu+\theta) - \frac{\alpha\beta_2^*(1-\sigma)\theta}{\mu(\mu+\vartheta+\delta)}\right] w_2. \end{aligned} \tag{3.15}$$

Also, the left eigen vector corresponding to $J^* = J(\mathcal{E}_0)|_{\beta_2=\beta_2^*}$ which satisfies the condition $\mathbf{v}.\mathbf{w} = \mathbf{1}$ is derived as $v_1 = v_3 = v_4 = v_5 = v_6 = v_7 = 0$ but $v_2 = v_2 > 0$. The bifurcation coefficients of a and b are then computed following [Theorem 4.1, [15]] as

$$\begin{aligned} a &= 2v_2w_1w_3\beta_2^* + 2v_2w_1w_7\beta_1 \\ &= \frac{2v_2}{\mu}\left\{\frac{\varepsilon\tau}{(\mu+\tau)(\mu+\varepsilon)}\left(\sigma\theta + \frac{\vartheta(1-\sigma)\theta}{(\mu+\vartheta+\delta)}\right) - (\mu+\theta)\right\} \\ &\times \left[\frac{(1-\sigma)\theta\beta_2^*}{(\mu+\vartheta+\delta)} + \frac{\mu}{\alpha\beta_1}\left((\mu+\theta) - \frac{(1-\sigma)\alpha\theta\beta_2^*}{\mu(\mu+\vartheta+\delta)}\right)\right] w_2^2, \\ b &= \frac{\alpha}{\mu} v_2 w_2 > 0. \end{aligned} \tag{3.16}$$

Following [Theorem 4.1, [15]], b is always positive as shown in (3.16). The nonzero equilibrium is therefore locally asymptotically stable if $a < 0$ while it is unstable if $a > 0$. A close observation of the value of a in (3.16) reveals the effect of detecting and isolating asymptomatic humans for treatment on the stability of nonzero equilibrium. if the rate of detecting and isolating asymptomatic humans for treatment is maximal (i.e., if $\sigma \to 1$), a may be positive and the endemic equilibrium becomes unstable (i.e., $\mathcal{R}_{\circ a} < 1$ and $\mathcal{R}_{\circ h} < 1$). The instability of

nonzero equilibrium implies stability of zero equilibrium. The spread of Lassa fever from infectious humans to susceptible humans (β_2^*) could be largely neutralised with $\sigma \to 1$ as indicated in (3.16).

Having derived the sufficient conditions for the existence of local stability of nonzero equilibrium, we proceeded to establish the necessary and sufficient conditions for the existence of global stability of the endemic equilibrium following the popular Lyapunov function employed in [9]. Consider a nonlinear Lyapunov function

$$\begin{aligned}\mathcal{L}(S_{h*}, E_{h*}, I_{h*}, R_{h*}, I_{sh*}, S_{r*}, I_{r*}) = &\left(S_h - S_{h*} - S_{h*}\ln\frac{S_{h*}}{S_h}\right) + \left(E_h - E_{h*} - E_{h*}\ln\frac{E_{h*}}{E_h}\right)\\ &+ \left(I_h - I_{h*} - I_{h*}\ln\frac{I_{h*}}{I_h}\right) + \left(R_h - R_{h*} - R_{h*}\ln\frac{R_{h*}}{R_h}\right)\\ &+ \left(I_{sh} - I_{sh*} - I_{sh*}\ln\frac{I_{sh*}}{I_{sh}}\right) + \left(S_r - S_{r*} - S_{r*}\ln\frac{S_{r*}}{S_r}\right)\\ &+ \left(I_r - I_{r*} - I_{r*}\ln\frac{I_{r*}}{I_r}\right).\end{aligned}$$

The disease-endemic equilibrium is globally asymptotically stable and both $\mathcal{R}_{\circ a}$ and $\mathcal{R}_{\circ h}$ are greater than one if $\dot{\mathcal{L}} < 0$ is established. The time derivative of $\mathcal{L}$ (i.e., $\dot{\mathcal{L}}$) is given thus

$$\begin{aligned}\dot{\mathcal{L}} = &\left(1 - \frac{S_{h*}}{S_h}\right)\frac{dS_h}{dt} + \left(1 - \frac{E_{h*}}{E_h}\right)\frac{dE_h}{dt} + \left(1 - \frac{I_{h*}}{I_h}\right)\frac{dI_h}{dt}\\ &+ \left(1 - \frac{R_{h*}}{R_h}\right)\frac{dR_h}{dt} + \left(1 - \frac{I_{sh*}}{I_{sh}}\right)\frac{dI_{sh}}{dt} + \left(1 - \frac{S_{r*}}{S_r}\right)\frac{dS_r}{dt}\\ &+ \left(1 - \frac{I_{r*}}{I_r}\right)\frac{dI_r}{dt}.\end{aligned} \tag{3.17}$$

After a few algebraic processes, $\dot{\mathcal{L}}$ reduces to

$$\dot{\mathcal{L}} = A_1 + A_2, \tag{3.18}$$

where

$$\begin{aligned}A_1 = &(\alpha + \varepsilon R_h)\left(1 - \frac{S_{h*}}{S_h}\right) + (\beta_1 I_r S_h + \beta_2 I_h S_h)\left(1 - \frac{E_{h*}}{E_h}\right)\\ &+ (1-\sigma)\theta E_h\left(1 - \frac{I_{h*}}{I_h}\right) + \tau I_{sh}\left(1 - \frac{R_{h*}}{R_h}\right)\\ &+ (\sigma\theta E_h + \vartheta I_h)\left(1 - \frac{I_{sh*}}{I_{sh}}\right) + \phi\left(1 - \frac{S_{r*}}{S_r}\right)\\ &+ \rho I_r S_r\left(1 - \frac{I_{r*}}{I_r}\right)\end{aligned}$$

and,

$$A_2 = (\beta_1 I_r + \beta_2 I_h + \mu)S_{h*}\left(1 - \frac{S_h}{S_{h*}}\right) + (\mu + \theta)E_{h*}\left(1 - \frac{E_h}{E_{h*}}\right)$$
$$+ (\mu + \vartheta + \delta)I_{h*}\left(1 - \frac{I_h}{I_{h*}}\right) + (\mu + \varepsilon)R_{h*}\left(1 - \frac{R_h}{R_{h*}}\right)$$
$$+ (\mu + \tau)I_{sh*}\left(1 - \frac{I_{sh}}{I_{sh*}}\right) + (\rho I_r + \gamma)S_{r*}\left(1 - \frac{S_r}{S_{r*}}\right)$$
$$+ \gamma I_{r*}\left(1 - \frac{I_r}{I_{r*}}\right).$$

It is estabilised that $A_1 > 0$ and $A_2 < 0$ because $S_{h*} < S_h, E_{h*} < E_h, I_{h*} < I_h, R_{h*} < R_h, I_{sh*} < I_{sh}, S_{r*} < S_r$ and $I_{r*} < I_r$. Therefore, $\dot{\mathcal{L}} < 0$ if $A_1 < A_2$ and by LaSalle's invariance principle [23], the nonzero equilibrium $\mathcal{E}_*$ is globally asymptomatically stable if $A_1 < A_2$. Since the disease-endemic equilibrium $\mathcal{E}_*$ is globally asymptomatically stable only if $\mathcal{R}_{\circ a} > 1$ and $\mathcal{R}_{\circ h} > 1$ therefore, the condition $A_1 < A_2$ is fulfilled if and only if the requirements $\mathcal{R}_{\circ a} > 1$ and $\mathcal{R}_{\circ h} > 1$ are met. □

3.5 Sensitivity analysis

The primary objective of sensitivity analysis is to evaluate how model results change as the model's parameters are changed. Knowing the relative importance of the various elements involved for the transmission and occurrence of an infectious disease like Lassa fever is crucial for determining the best way to diminish or eradicate it and minimize its mortality. A parameter is said to be sensitive if a little change in its value results in a significant change in how the differential equations are solved. To study a change in the model's solution with regard to a certain parameter, the derivative of the solution for the parameter is utilized [12]. We compute the sensitivity indices of the key parameters following the normalised forward sensitivity index approach [9] thus

$$\begin{aligned}
\Gamma_{\alpha}^{\mathcal{R}_{\circ h}} &= \frac{\beta_2\theta(1-\sigma)}{\mu(\mu+\theta)(\mu+\vartheta+\delta)} \times \frac{\alpha}{\mathcal{R}_{\circ h}},\\
\Gamma_{\sigma}^{\mathcal{R}_{\circ h}} &= -\frac{\sigma}{(1-\sigma)},\\
\Gamma_{\vartheta}^{\mathcal{R}_{\circ h}} &= -\frac{\vartheta}{(\mu+\vartheta+\delta)},\\
\Gamma_{\phi}^{\mathcal{R}_{\circ a}} &= \frac{\rho}{\gamma^2} \times \frac{\phi}{\mathcal{R}_{\circ a}}.
\end{aligned} \tag{3.19}$$

4 Numerical Simulations and Discussion of Results

Numerical simulations are conducted to visualise the disease dynamics in both human and animal populations. The parameter values which are peculiar to Nigeria are adopted to perform the simulations. Lassa fever originates from Nigeria. Besides, Nigeria remains one of the countries that experience frequent Lassa fever occurence and reoccurence till date. The values for the parameters are displayed in Table 2.

Table 2: Parameter values employed for simulations

Parameters	Values	Source
α	0.188	Estimated
ε	0.0085	[26]
β_1	0.5	-
β_2	0.2	-
μ	0.018	Estimated
σ	0.2	-
θ	0.2	-
ϑ	0.75	-
δ	0.0171	[26]
τ	0.030	[26]
ϕ	0.085	-
ρ	0.25	-
γ	0.000167	-

The fertility and life expectancy rates for Nigeria in 2019 were 5.32 births per woman and 54.69 years respectively. α and μ are therefore computed in Table 2 by finding the reciprocals of 5.32 and 54.69 respectively. From Table 3, the numerical values for the sensitivity indices of the key parameters are obtained after evaluating each quantity in (3.19) using the values in Table 2.

Table 3: Indices of sensitivity for key parameters in relation to $\mathcal{R}_{\circ h}$ and $\mathcal{R}_{\circ a}$

Parameters	Signs	Sensitivity indices
α	+	1
σ	-	0.25
ϑ	-	0.96
ϕ	+	1

As claimed in (3.5) and following [30], the reproduction number $\mathcal{R}_\circ$ for the model is measured in terms of $\mathcal{R}_{\circ h}$ and $\mathcal{R}_{\circ a}$, the transmission potential of Lassa fever from human and animal respectively. Table 3 indicates that when the corresponding parameters are increased, the values for the reproduction number $\mathcal{R}_\circ$ in terms of $\mathcal{R}_{\circ h}$ and $\mathcal{R}_{\circ a}$ decrease and vice versa according to the sensitivity indices for parameters with negative signs. Recruitment rates for humans and animals are more sensitive to disease propagation given the sensitivity index of $+1$ for each parameter. The disease tends to spread faster in crowded living areas and with large population of animals. The sensitivity indices for human and animal recruitment rates α and ϕ therefore support uncongested living conditions and animal predation as appropriate methods of preventing Lassa fever outbreaks. Overcrowded living areas are conducive for animal breedings therefore, any efforts to reduce overcrowding has a direct impact on animal population and Lassa fever outbreaks. The isolation parameters, σ and ϑ, are also sensitive to $\mathcal{R}_\circ$ with the isolation of the infectious humans for treatment ϑ producing the higher sensitivity. The high sensitivity index

for ϑ indicates that isolation and the effective treatments of the isolated infectious humans are important if Lassa fever epidemic is to be brought under instant control. As regards the isolation of the asymptomatic humans σ which is central to the present analysis and which makes the analysis different from the existing ones in the literature, the sensitivity index for σ indicates that Lassa fever outbreaks could be delayed or even be prevented in human populations if appropriate methods are designed to isolate individuals who are asymptomatic to Lassa fever for immediate treatments.

Since the main focus is to examine the proportion of individuals needed to be isolated for treatments at the asymptomatic stage of Lassa fever infection to delay or eliminate Lassa fever, the impact of σ on the disease dynamics is investigated by examining the changes in the reproduction number $\mathcal{R}_\circ$ in terms of $\mathcal{R}_{\circ h}$ due to changes in σ for $\sigma = 0.1, 0.2, 0.3, 0.4, 0.5, 0.6$ and 0.8, where $\sigma = 0.1$ implies that 10% of the asymptomatic humans are needed to be isolated for treatments to delay or combart Lassa fever spread. The other values of σ follow the same analogy. Table 4 displays the values of $\mathcal{R}_{\circ h}$ for various values of σ.

Table 4: Changes in σ and the corresponding changes in $\mathcal{R}_{\circ h}$

Changes in σ	Corresponding changes in $\mathcal{R}_{\circ h}$
0.1	2.20
0.2	1.95
0.3	1.71
0.4	1.46
0.5	1.22
0.6	0.98
0.8	0.49

Table 4 shows that some $\mathcal{R}_{\circ h}$ values are smaller than 1, which suggests that if we have those levels of σ, Lassa fever outbreaks may be delayed or completely eliminated. Apart from isolation parameters σ and ϑ as well as recruitments parameters α and ϕ, the effective contact rates, between susceptible and infectious humans β_2 as well as between susceptible and infectious animals ρ, are crucial to Lassa fever propagation based on the analytical values of $\mathcal{R}_\circ$ in terms of $\mathcal{R}_{\circ h}$ and $\mathcal{R}_{\circ a}$. However, the two disease spreading parameters, β_2 and ρ, can be limited by σ and by ϕ. Effective means of identifying and isolating asymptomatic humans for prompt treatments σ can limit β_2 while effective control of animal population ϕ can limit ρ. Given the sensitivity indices of σ, ϑ and ϕ, Figures 2, 3, 4 and 5 show the effects of isolation of both asymptomatic and symptomatic humans as well as changes in animal recruitment on the populations of infectious and recovered humans as well as susceptible and infected animals.

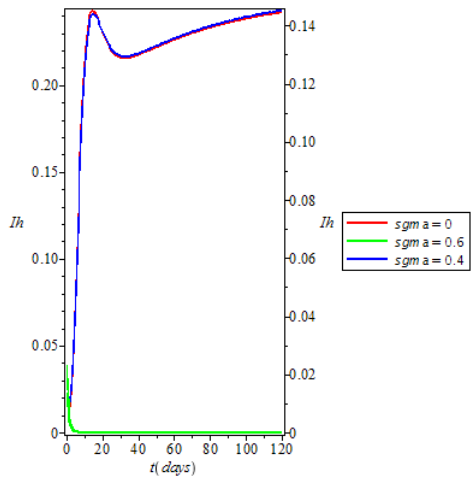

Figure 2: Effect of detecting and isolating asymptomatic humans on the population of infectious humans

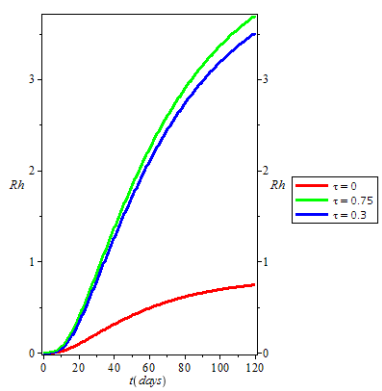

Figure 3: Effect of treatments on the population of recovered humans

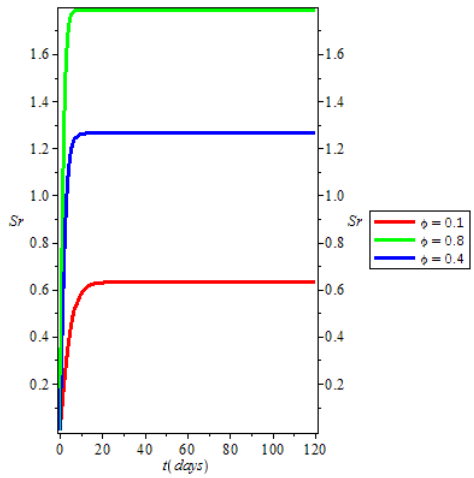

Figure 4: Effect of animal influx on the population of susceptible animals

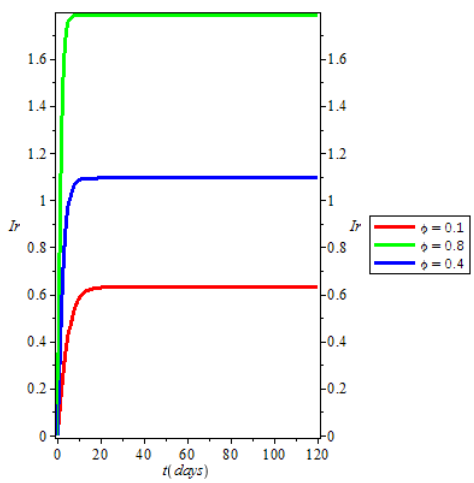

Figure 5: Effect of animal influx on the population of infectious animals

We consider the initial conditions that are proportional to the total populations of animals and humans. For the sake of illustrations, we choose $N_h = 2,567,369$ so that $I_h = 250000 \div 2567369 = 0.097, S_h = 0.903$ but $E_h = R_h = I_{sh} = 0$. For the population of animals, we assume that the population of humans is 1000 times the population of animals so that $I_r = 0.000097$ and $S_r = 0.000903$.

In Figure 2, it is observed that as σ increases in value, the population of humans who become fully infectious decreases. For example, when $\sigma = 0$, the plot for the infectious humans rises to almost 0.1 (i.e., about 257,732 individuals) after 20 days, and falls to about 0.085 after 30 days (i.e., about 219,072 individuals) before it rises again. Even when $\sigma = 0.4$, the behaviour of the curve is similar to when $\sigma = 0$. However, when $\sigma = 0.75$, the population of humans who become

fully infectious drops to about 0.03 after 10 days (i.e., about 77,320 individuals) and stabilises below 77,320 individuals after 20 days. The behaviours of the curves in Figure 2 are consistent with the values of $\mathcal{R}_{\circ h}$ for $\sigma = 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.8$ in Table 4. It shows that the values of $\mathcal{R}_{\circ h}$ corresponding to $\sigma = 0.1, 0.2, 0.3, 0.4, 0.5$ exceeds one while the values of $\mathcal{R}_{\circ h}$ for $\sigma = 0.6$ and above are less than one. It implies that for $\sigma \leq 0.5$, the disease converges to the EE but for $\sigma \geq 0.6$, the plots converge to DFE.

In Figure 3, the effect of treatments of the infectious humans is examined in terms of the population of humans who have been fully recovered from the disease. It is observed from Figure 3 that when treatment is not offered (i.e., when $\tau = 0$,) nobody recovered from the disease until after 10 days. Even the recovery remained at a low ebb after 120 days. However, with the improvement in the treatments of infectious humans (i.e., when $\tau = 0.3$ and more,) the population of individuals who recovered from the disease increases continuously. The behaviours of the curves in Figure 3 are in agreement with the sensitivity index of ϑ in Table 3 and confirm that isolation and the effective treatment of the isolated infectious humans tend to push Lassa fever epidemic towards DFE.

The impacts of recruitment rate on the dynamics of susceptible and infectious animals are shown in Figures 4 and 5. It is observed in Figures 4 and 5 that the populations of animals that are susceptible and infectious are fewer when it is difficult for animals to enter the population. When $\phi = 0.1$, the plots for susceptible and infectious animals rise to about 0.63 (i.e., about 730 and 79 susceptible and infectious animals respectively) after 10 days and remain steady for more than 120 days. However, as ϕ increases, the populations of susceptible and infectious animals also increase rapidly. For instance, when $\phi = 0.4$, the plots for susceptible and infectious animals rise to about 1.3 and 1.1 respectively (i.e., about 1, 507 susceptible animals and 138 infectious animals.) The behaviours of the curves in Figures 4 and 5 agree with the sensitivity index for ϕ in Table 3 and support uncongested living conditions as well as animal predation as basic strategies of ending Lassa fever.

5 Conclusion

This paper designed a mathematical model of Lassa fever to investigate the alternative ways of eradicating the disease in the endemic region. Because the disease does not spread from the asymptomatic humans and the fact that previous efforts have not been concentrated on the roles of asymptomatic in the dynamics of the disease, we incorporated isolation of the asymptomatic humans for prompt treatments in addition to the usual treatment of the infectious humans to examine the tendency of delaying or eradicating Lassa fever epidemic. The equilibria and reproductive ratio ($\mathcal{R}_{\circ}$) were derived. Stability analyses were performed for each equilibrium and the conditions for the existence of stable equilibria were established. Sensitivity analysis was also performed and the simulation was conducted to support the theoretical results. From the analysis of the parameters' sensitivity, α and ϕ were identified the most sensitive to Lassa fever propagation while treatment of the infectious humans ϑ was the most sensitive parameter to Lassa fever reduction.

The impact of identifying and isolating asymptomatic humans for prompt treatments on the possibility of delaying or eliminating Lassa virus was also assessed in terms of the results of sensitivity analysis and it was discovered that $\mathcal{R}_{\circ} \to 0$ as $\sigma \to 1$. It was particularly discovered that if the population of asymptomatic humans who were identified and isolated for prompt treatment was more than 50%, the Lassa virus would fail to spread or fade away in the human population. The effect of σ on the dynamics of Lassa fever as regards early detection and isolation

of asymptomatic humans for prompt treatments was captured in Figure 2. It was noticed that the population of infected humans converged to DFE after 15 days when $\sigma \geq 0.75$. This suggests that if efforts are implemented towards early detection and isolation of asymptomatic humans for prompt treatments by all tiers of government in Lassa fever endemic regions, then a remarkable reduction would be experienced in Lassa fever outbreak, resulting in a total elimination of Lassa fever in the endemic region and, by implication, throughout the world. A good example of such strategies is to encourage uncongested living conditions and to mandate periodic Lassa fever screening test in Lassa fever endemic regions.

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