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MATHEMATICAL MODELLLING OF THE SPREAD AND TREATMEANT OF LASSA FEVER

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Abstract
In this work we formulated and analyzed a mathematical model of the spread and treatment of Lassa fever. The model is a system of first order Ordinary Differential Equations, in which the human population is divided into six mutually exclusive compartments namely; Susceptible Humans (S_H), Exposed humans(E_H) , Asymptomatic Infected humans (A_H), Symptomatic infected humans (I_H) , Treated humans (T_H) and Recovered humans (R_H). And the reservoir population is subdivided into two mutually exclusive compartments namely; susceptible reservoir (S_R) and Infected Reservoir (I_R). The equilibrium states of the model were obtained and their local stabilities were analyzed by using Jacobian matrix approach coupled with Routh-Hurwitz condition. We also analyzed the global stability of the disease-free-equilibrium using Castillo-Chavez, Feng and Huang approach. The result shows that the disease-free-equilibrium state is both locally and globally asymptotically stable since it satisfies the aforementioned criteria. The result of the numerical simulation shows that at high treatment rate, the number of recovered individuals increases and the virus can be eradicated completely.

Keywords: *Modelling, Exposed, Asymptomatic, Symptomatic, infected, Equilibrium, Stability, Basic reproduction Number, Numerical Simulation, Next-generation matrix.*

Introduction
Lassa fever is a viral infection belonging to arena-virus family (Centre for Disease Control and Prevention, 2013). It was first discovered in the town of Lassa in 1969 in Borno State, Nigeria in the Yedseran river valley near south end of Lake Chad (Frame et al, 1970). The Lassa virus is transmitted to humans through exposure to food or household items contaminated with rodent urine or faeces (

World Health Organization, 2000). The natural reservoir of the virus is the mastomyms rats which are common in endemic areas (Eze, 2010). Lassa fever is mostly common in West African countries such as Nigeria, Ghana, Guinea, Liberia, Mali, Sierra Leone, and, Benin (World Health organization, 2017). Person-to-Person transmission of Lassa virus also occurs through direct contact with the blood, urine, faeces, or other bodily secretions or fluids of an infected person (World health Organization, 2017). Nosocomial transmission may occur in hospital lacking adequate prevention and control measures (World Health Organization, 2017). Aerosol transmission of Lassa fever often occurs in the dry season because dust particles from dead rats carrying this virus are more mobile and making it easy to inhale. In some places, the rodents are eaten as delicacy, hence providing extra exposure to the infected rat blood, as well as allowing ingestion of potentially infectious meat (Eze et al, 2010).

In general, disease-induced death rate is 1% but it is approximately 15% among hospitalized patients (World Heaalth Organization, 2017). This virus attacks the liver, kidney, nervous system and spleen, causing them to bleed. The incubation period takes between 6-21 days for the symptoms of Lassa fever to be obvious (World Health Organization, 2000). 80 % of the cases are asymptomatic (Centre for disease control, 2013).The symptoms of Lassa fever include fever, facial swelling, muscle fatigue, vomiting, cough, meningitis, and hypertension (Omilabu *et al*, 2005). In some patients neurological problems such hearing loss may be transient or permanent and tremors have been described (Omilabu *et al*, 2005). People with highest chance of acquiring the infection are the people living in the rural areas where the Mastomys reside (Keelyside *et al*, 1983).

Nearly 500000 individuals are affected with about 5000-10,000 disease-induced death yearly (Ogbu *et al*, 2007) . As at March 2012, approximately 623 cases including 70 deaths were recorded from 19 states out of the 36 states in Nigeria with Edo and Taraba having the highest number of deaths.Lassa fever outbreak occurs regularly in West Africa with the most recent one in Nigeria (Amy, 2018). From 1 January 2018 through 18 March 2018, about 1495 suspected cases and 119 deaths was recorded in Nigeria from across 19 States of the country which include Anambra, Bauchi, Benue, Delta, Ebonyi, Edo,Ekiti, Taraba, Gombe, Imo, Kaduna, Kogi, Lagos, Nassarawa, Ondo, Osun, Plateau, Rivers and FCT Abuja (World Health

Organization, 2018). During this period, 376 cases were confirmed, 9 were classified probable, 1084 were reported negative and 26 were awaiting laboratory results (World Health Organization, 2018). Among the 376 confirmed and the 9 classified probable cases, 95 deaths were reported giving a disease-induced death rate of the confirmed and probable cases to be 24.7% (World Health Organization, 2018). There is currently no US approved vaccine for Lassa fever but it can be treated using Ribavirin which is effective if administered during the early stage of infectiousness (Omale *et al*, 2014).

Literature

Okuonghae et al., (2006) developed and analyzed an SIS model for the transmission of Lassa virus. They obtained the equilibrium states of their model and analyzed them for stability. They gave the conditions for the disease to be endemic and also calculated the reproductive number for their model. They concluded that the best strategies to stop the spread of the diseases are isolation policy and the control of rodents carrying the virus. But they didn't consider treatment and recovered classes.

Bawa *et al.,(2014)* formulaed a mathematical model which incorporated vital dynamics, standard incidence, disease induced death due to human infection, reservoirs R and aerosol (airborne) transmissions . Their analysis revealed that the disease can be control if the basic reproduction number R_0 is strictly less than unity. Their work didn't take into account treated and recovered humans.

Mohammed *et al.*, (2014) carried out sensitivity analysis on a Lassa fever deterministic mathematical model. This was done to ascertain the most sensitive parameters in the model and they discovered that the most sensitive parameters are; the human immigration, human recovery rate and then person to person contact rate. They concluded that control strategies should be focused on human immigration, effective drugs for treatment and education to reduce person to person contact. But their work didn't include treatment class

James *et al.*, (2015) formulated an SIR model of Lassa Fever disease dynamics. The disease free equilibrium and the endemic equilibrium states were calculated and analyzed for stability. The result of their analysis show that the disease free equilibrium will be stable any time the birth rate of the human population is smaller than the death rate and also when the birth rate of the mastomys-natalensis is smaller than the whole population. In their work, they didn't consider the rodents population.

Onuorah *et al.*, (2016) formulated a sex-structured mathematical model which subdivided the human population into males and females, and the animal reservoirs into active and inactive reservoirs. They considered sexual transmission of the virus among sexually active humans as one of the means of transmitting the virus in humans. Sensitivity analysis on the parameters of their model showed that, the basic reproduction number is most sensitive to parameters representing human birth, condom efficacy and compliance rates.

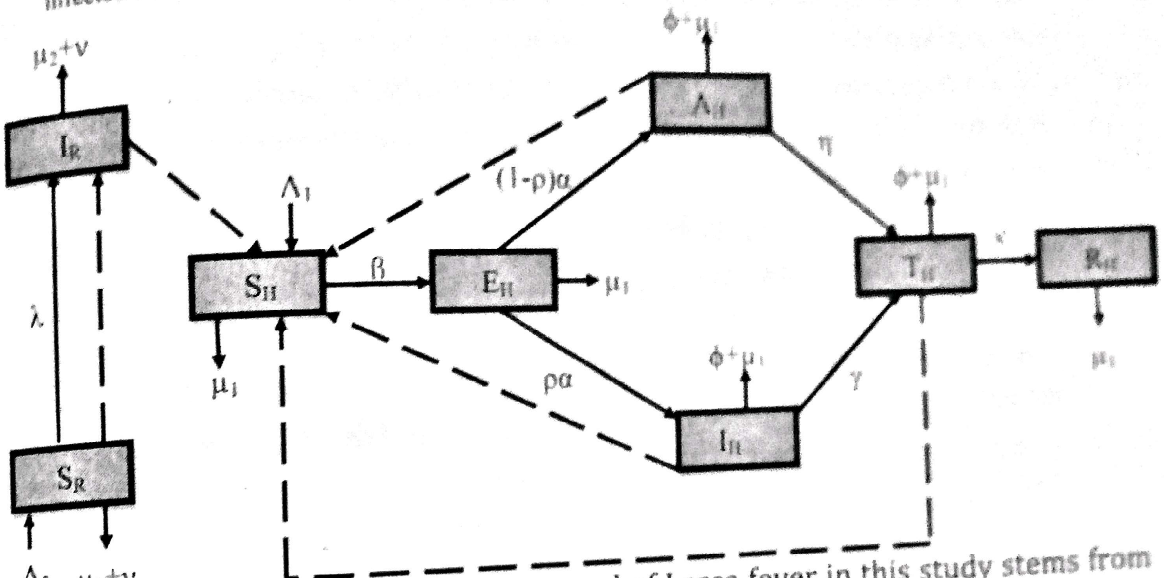
Akanni *et al.*, (2018) ran sensitivity analysis of the dynamical transmission of Lassa fever virus. This was done to discover the most sensitive parameters on the transmission of the disease. Their findings indicated that the most sensitive parameter is the progression rate to active Lassa fever (γ), followed by the force of infection of the susceptible individuals with the infected individuals (λ). They also discovered that the least sensitive parameter is the treatment rate of infective class (θ).they concluded that the parameters (γ) and (λ) that have great sensitivity to the transmission of Lassa fever be put in check. But they didn't consider asymptomatic infected compartment.

Suleiman et al., (2018) formulated a mathematical model for the transmission dynamics of the Lassa fever virus infection by splitting the infectious human population into symptomatic and asymptomatic infectious and also assumed that the rodents do not recover from the infection. They obtained the equilibrium states and analyzed them for stability. The also obtained the basic reproduction number of the humans' population and carried out sensitivity analysis on the basic reproduction number of which they ascertained that are most sensitive to the transmission rates, recovery rates and the natural mortality rates of the humans.

Therefore, in this work, we formulated a mathematical model for the transmission of Lassa virus by considering both humans and rodents populations. We also take into account the exposed class which account for incubation process; we subdivided the infectious class into asymptomatic and symptomatic infectious compartments and also considered the treatment compartment since the only way to recover from Lassa fever is through medical care.

Model Formulation

infected reservoirs (I_R).



Formulation of the model for the spread of Lassa fever in this study stems from the ideas of the models reviewed in chapter two. This model takes into account salient aspects of the transmission dynamics of Lassa fever. We analyze and investigate the effect of treatment on the Lassa fever transmission dynamics. The model subdivides the human population into six (6) mutually exclusive compartments, which are; susceptible humans (S_H), exposed humans (E_H), asymptomatic infected humans (A_H) , symptomatic infected humans (I_H), Treated humans (T_H) and recovered humans (R_H). Similarly, the reservoir population is subdivided into two (2) mutually exclusive compartments, which are; susceptible reservoirs (S_R) and

Figure 3.1; Schematic diagram of the model equation

Interaction - - - - -➔ ⟶ Flow

Model Assumptions

The population of the susceptible human (S_H) increases through the recruitment of individuals into the population by birth or immigration at a constant rate Λ_1. The population decreases as susceptible human move to the Exposed compartment (E_H) through interaction between the susceptible humans (S_H) with infected reservoirs (I_R), asymptomatic infected humans, symptomatic infected human and humans undergoing treatment at the rate β , and also through natural death of human at a rate μ_1. Infection rate is reduced due to treatment at the rate δ, where $\delta \epsilon [0, 1]$.

The population of the exposed humans compartment (E_H) decreases due to natural death at the rate μ_1 and also due to movement to infected classes after incubation period at the rate α. A Proportion of α move to the symptomatic infected compartment (I_H) at the rate $\rho\alpha$, while the remaining of the proportion move to the asymptomatic infected compartment (A_H) at the rate $(1)-\rho\alpha$, where $\rho \epsilon [0,1]$. The population of the asymptomatic infected compartment decreases due to treatment at the rate η, also due to disease-induced death at the rate (ϕ), and also due to natural death at the rate(μ_1).

The population of the symptomatic infected compartment decreases due to treatment at the rate γ, also due to disease-induced death at the rate (ϕ), and also due to natural death at the rate (μ_1).

The population of the treatment compartment decreases due to recovery at the rate κ, also due to diseaseinduced death at the rate (ϕ), and also due to natural death at the rate (μ_1).

The population of the recovered compartment decreases due to natural death at the rate (μ_1).

The population of the susceptible reservoir (S_R) increases through the recruitment of reservoir into the population by birth or immigration at a constant rate $\wedge_2$. The population decreases as susceptible reservoir move to the infected reservoirs compartment (I_R) through interaction between the susceptible reservoirs (S_R) with infected reservoirs (I_R) at the rate λ, due to hunting at the rate ν, and due to natural death at the rate μ_2.

The population of the infected reservoirs decreases due to hunting at the rate ν, and due to natural death at the rate μ_2.

Model Equations

$$\frac{dS_H}{dt} = \Lambda_1 - \beta(I_R + I_H + A_H + \delta T_H)S_H - \mu_1 S_H \quad (1)$$

$$\frac{dE_H}{dt} = \beta(I_R + I_H + A_H + \delta T_H)S_H - (\alpha + \mu_1)E_H \quad (2)$$

$$\frac{dA_H}{dt} = (1-\rho)\alpha E_H - (\eta + \phi + \mu_1)A_H \quad (3)$$

$$\frac{dI_H}{dt} = \rho\alpha E_H - (\gamma + \phi + \mu_1)I_H \quad (4)$$

$$\frac{dT_H}{dt} = \gamma I_H + \eta A_H - (\kappa + \phi + \mu_1)T_H \quad (5)$$

$$\frac{dR_H}{dt} = \kappa T_H - \mu_1 R_H \quad (6)$$

$$\frac{dS_R}{dt} = \Lambda_2 - \lambda S_R I_R - (\nu + \mu_2)S_R \quad (7)$$

$$\frac{dI_R}{dt} = \lambda S_R I_R - (\nu + \mu_2)I_R \quad (8)$$

MODEL VARIABLES AND PARAMETERS

Table 1; Model Variables

Variable	Description
S_H	Susceptible human at time t
E_H	Exposed humans at time t
A_H	Asymptomatic infected humans at time t
IH	Symptomatic infected human at time t
T_H	Treated humans at time t
R_H	Recovered humans at time t
S_R	Susceptible reservoir at time t
IR	Infected reservoir at time t

Table 2: Model Parameters

Parameter	Description
Λ_1	Recruitment rate into susceptible human population
Λ_2	Recruitment rate into susceptible rodent population
μ_1	Natural death rate of human population
μ_2	Natural death rate of rodent population
β	Transmission rate in the susceptible human population
λ	Transmission rate in the susceptible rodent population
δ	Reduction rate in transmission due to treatment in human population
α	Progression from of exposed class to infectious class
ρ	Proportion of exposed individuals that progresses to symptomatic infectious class
$(1-\rho)$	Proportion of exposed individuals that progress to asymptomatic class
ϕ	Death rate due to Lassa virus in human population
η	Treatment rate of asymptomatic infected individuals
γ	Treatment rate of symptomatic infected individuals
κ	Recovery rate due to treatment
ν	Rate at which rodents are hunted

Dynamics of Model Properties

In this section, we start the analysis of the model by showing that all feasible solutions of the model system are positive invariant in a proper subset of D.

The total human population is $N_H = S_H, E_H + A_H + I_H + T_H + R_H$ (9)

And the total reservoir population is $N_R = S_R + I_R$ (10)

Where,

$$\frac{dN_H}{dt} = \frac{dS_H}{dt} + \frac{dE_H}{dt} + \frac{dA_H}{dt} + \frac{dI_H}{dt} + \frac{dT_H}{dt} + \frac{dR_H}{dt}$$

$$\frac{dN_H}{dt} \leq \wedge_1 - \mu_1 N_H \quad (11)$$

Similarly,

$$\frac{dN_R}{dt} = \frac{dS_R}{dt} + \frac{dI_R}{dt}$$

$$\frac{dN_R}{dt} = \wedge_2 - (\nu + \mu_2) N_R \quad (12)$$

The positive invariant region can be established by using the following theorem.

Theorem 1

The solutions of the system of equations (1) through (8) are feasible for $t > 0$ if they enter the invariant region D.

Proof

Let $D = (S_H, E_H, A_H, I_H, T_H, R_H, S_R, I_R) \in R^8_+$

Be any solution of the system of equations (1) to (8) with positive initial conditions $N_H(0)=N_{H0}$ and $N_R(0)=N_{R0}$

From equations (11) and (12), using standard comparison theorem as in (Lakshmickantham *et al*, 1999)

We have $0 \leq N_H \leq \frac{\Lambda_1}{\mu_1}$ and $0 \leq N_R \leq \frac{\Lambda_2}{(\nu + \mu_2)}$ $t \to \infty$, which implies that $\frac{\Lambda_1}{\mu_1}$ and $\frac{\Lambda_2}{(\nu + \mu_2)}$ are the carrying capacity as well as the upper bound for the human and the reservoir population respectively. Hence the region model equation (1) through (8) has feasible solution that enters the

$D=\left\{(S_H,E_H,A_H,I_H,T_H,R_H,S_R,I_R)\in R^8+:S_H,E_H,A_H,I_H,T_H,R_H,S_R,I_R\geq 0;\wedge_H\leq\frac{\wedge_1}{\mu_1},\wedge_R\leq\frac{\wedge_2}{(v+\mu_2)}\right\}$ which is positive invariant set.Therefore, according to (Hethcote, 1978), the model equations (1) through (6) are well posed mathematically and epidemiologically.

Disease-Free-Equilibrium State

At equilibrium, the derivative of the state variables with respect to time is zero

i.e $\frac{dS_H}{dt}=\frac{dE_H}{dt}=\frac{dA_H}{dt}=\frac{dI_H}{dt}=\frac{dT_H}{dt}=\frac{dR_H}{dt}=\frac{dS_R}{dt}=\frac{dI_R}{dt}=0$

Solving equations (1) through (8) simulteneously at equilibrium, we obtain the disease free equilibrium state as

$$U_0=[S_H,E_H,A_H,I_H,T_H,R_H,S_R,I_R]=\left[\frac{\wedge_1}{\mu_1},0,0,0,0,0,\frac{\wedge_2}{v+\mu_2},0\right] \qquad (13)$$

Local Stability Analysis of the Disease-Free Equilibrium State (DFE)

In analyze the stability of the disease-free equilibrium, we obtain the jacobian matrix of the model equations (1) through (8) and the basic reproduction number for both the humans and the reservoir populations. The Jacobean matrix

$$J(U_0)=\begin{bmatrix}-\mu_1 & 0 & -p & -p & -\delta p & 0 & 0 & -p\\ 0 & -q & p & p & \delta p & 0 & 0 & p\\ 0 & (1-\rho)\alpha & -r & 0 & 0 & 0 & 0 & 0\\ 0 & \rho\alpha & 0 & -s & 0 & 0 & 0 & 0\\ 0 & 0 & \eta & \gamma & -u & 0 & 0 & 0\\ 0 & 0 & 0 & 0 & \kappa & -\mu_1 & 0 & 0\\ 0 & 0 & 0 & 0 & 0 & 0 & -x & \frac{-\lambda\wedge_2}{v+\mu_2}\\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & y\end{bmatrix} \qquad (14)$$

of the system of equations at disease-free equilibrium state gives:

Where,

$$\left[\begin{array}{l} p=\frac{\beta\wedge_1}{\mu_1}, q=(\alpha+\mu_1), r=(\eta+\phi+\mu_1), s=(\gamma+\phi+\mu_1),\\ u=(\kappa+\phi+\mu_1), x=(v+\mu_2), y=\frac{\lambda\wedge_2}{v+\mu_2}-v+\mu_2\end{array}\right] \qquad (15)$$

Basic Reproduction Number

The basic reproductive number, R_0, is defined as the number of secondary infections that an infective individual produces over the duration of the infectious period in an entirely susceptible population. The basic reproduction number is a threshold number that if it is less than unity, that is if $R_0 \pi 1$, then the disease-free-

equilibrium (DFE) is locally asymptotically stable. And if it is greater than unity, that is if $R_0 > 1$ then the disease free equilibrium is unstable. In this study, we employ the next generation matrix approach as described by (Driessche and Watmough, 2002) to obtain the Basic Reproductive Number. We take the basic reproduction number as the spectral radius of the product of the two matrices. F and V^{-1} that is, $R_0 = \rho(FV^{-1})$
The model has four infected classes for the human population; hence we have the next generation matrices F and V for new infection terms and transmission terms respectively as

$$F = [illegible] \quad (16)$$

$$V = [illegible] \quad (17)$$

From (16) and (17), we have

$$FV^{-1} = [illegible] \quad 18$$

The characteristics equation gives

$$\begin{vmatrix} \dfrac{\beta\wedge_1(1-\rho)\alpha}{\mu_1(\alpha+\mu_1)(\eta+\phi+\mu_1)} + \dfrac{\beta\wedge_1\rho\alpha}{\mu_1(\alpha+\mu_1)(\gamma+\phi+\mu_1)} + \dfrac{\beta\wedge_1\delta\alpha\begin{pmatrix}\eta(1-\rho)\\(\gamma+\phi+\mu_1)\\+\gamma\rho(\eta+\phi+\mu_1)\end{pmatrix}}{\begin{pmatrix}\mu_1(\alpha+\mu_1)(\eta+\phi+\mu_1)\\(\gamma+\phi+\mu_1)(\kappa+\phi+\mu_1)\end{pmatrix}} - \omega & \left(\dfrac{\beta\wedge_1}{\mu_1(\eta+\phi+\mu_1)} + \dfrac{\beta\wedge_1\delta\eta}{\mu_1(\eta+\phi+\mu_1)(\kappa+\phi+\mu_1)}\right) & \left(\dfrac{\beta\wedge_1}{\mu_1(\gamma+\phi+\mu_1)} + \dfrac{\beta\wedge_1\delta\gamma}{\mu_1(\gamma+\phi+\mu_1)(\kappa+\phi+\mu_1)}\right) & \dfrac{\beta\wedge_1\delta}{\mu_1(\kappa+\phi+\mu_1)} \\ 0 & -\omega & 0 & 0 \\ 0 & 0 & -\omega & 0 \\ 0 & 0 & 0 & -\omega \end{vmatrix} \quad 19$$

From (19), we have

$$\begin{bmatrix} \dfrac{\beta\wedge_1(1-\rho)\alpha}{\mu_1(\alpha+\mu_1)(\eta+\phi+\mu_1)} + \dfrac{\beta\wedge_1\rho\alpha}{\mu_1(\alpha+\mu_1)(\gamma+\phi+\mu_1)} + \dfrac{\beta\wedge_1\delta\alpha\begin{pmatrix}\eta(1-\rho)\\(\gamma+\phi+\mu_1)\\+\gamma\rho(\eta+\phi+\mu_1)\end{pmatrix}}{\begin{pmatrix}\mu_1(\alpha+\mu_1)(\eta+\phi+\mu_1)\\(\gamma+\phi+\mu_1)(\kappa+\phi+\mu_1)\end{pmatrix}} \\ 0 \\ 0 \\ 0 \end{bmatrix} \quad (20)$$

Therefore,

$$R_{0H} = \frac{\beta\wedge_1(1-\rho)\alpha}{\mu_1(\alpha+\mu_1)(\eta+\phi+\mu_1)} + \frac{\beta\wedge_1\rho\alpha}{\mu_1(\alpha+\mu_1)(\gamma+\phi+\mu_1)} + \frac{\beta\wedge_1\delta\alpha\begin{pmatrix}\eta(1-\rho)\\(\gamma+\phi+\mu_1)\\+\gamma\rho(\eta+\phi+\mu_1)\end{pmatrix}}{\begin{pmatrix}\mu_1(\alpha+\mu_1)(\eta+\phi+\mu_1)\\(\gamma+\phi+\mu_1)(\kappa+\phi+\mu_1)\end{pmatrix}} \quad (21)$$

And for the reservoir population, our model has one infected class; hence we have the next generation matrices F and V for new infection terms and transmission terms respectively as

$$F = \left[\frac{\lambda\wedge_2}{v+\mu_2}\right], \quad V = v + \mu_2 \quad (22)$$

Therefore,

$$R_{0R} = \frac{\lambda\wedge_2}{(v+\mu_2)^2} \quad (23)$$

Theorem 2 The disease-free equilibrium is locally asymptotically stable if $R0 < 1$, and unstable if $R0 > 1$ with $R_0 = \max\{R_{0,s}, R_{0,h}\}$

Proof

At disease-free equilibrium, the characteristic equation gives

The characteristic equation is

$$|J-\omega I| = \begin{vmatrix} -\mu_1-\omega & 0 & -\rho & -\rho & -\delta\rho & 0 & 0 & -\rho \\ 0 & -q-\omega & \rho & \rho & \delta\rho & 0 & 0 & \rho \\ 0 & (1-\rho)\alpha & -r-\omega & 0 & 0 & 0 & 0 & 0 \\ 0 & \rho\alpha & 0 & -s-\omega & 0 & 0 & 0 & 0 \\ 0 & 0 & \eta & \gamma & -u-\omega & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \kappa & -\mu_1-\omega & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & -x-\omega & -\frac{\lambda\Lambda_2}{v+\mu_2} \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & y-\omega \end{vmatrix} = 0 \qquad (24)$$

We obtain the eigenvalues

$(\omega_1 = -\mu_1$ or $\omega_2 = -q = -(\alpha+\mu_1)$ or $\omega_3 = -r = -(\eta+\phi+\mu_1)$ or $\omega_4 = -s = -(\gamma+\phi+\mu_1)$ or

$\omega_5 = -u = -(\kappa+\phi+\mu_1)$ or $\omega_6 = -\mu_1$ or $\omega_7 = -x = -(v+\mu_2)$ or $\omega_8 = y = \frac{\lambda\Lambda_2}{v+\mu_2} - (v+\mu_2)$

$\omega_1, \omega_2, \omega_3, \omega_4, \omega_5, \omega_6, \omega_7 < 0$ and $\omega_8 < 0$ if and only if $\frac{\lambda\Lambda_2}{(v+\mu_2)} < (v+\mu_2)$ and

$\omega_8 > 0$ if and only if $\frac{\lambda\Lambda_2}{(v+\mu_2)} > (v+\mu_2)$. Hence the Disease-Free equilibriums is stable if $\frac{\lambda\Lambda_2}{(v+\mu_2)} < (v+\mu_2)$

and unstable otherwise.

Global Stability of the Disease-Free Equilibrium State

Theorem 3: (Castillo-Chavez, Feng and Huang Theorem)
Consider epidemiological models written in the form

$$\left.\begin{aligned} \frac{dx}{dt} &= f(x,E,I) \\ \frac{dE}{dt} &= g(x,E,I) \\ \frac{dI}{dt} &= h(x,E,I) \end{aligned}\right\} \qquad (25)$$

Where $x\epsilon R^r$, $E\epsilon R^s$, $I\epsilon R^n$, r, s, n ≥ 0. The components of x represent the classes of susceptible, recovered and other non-infected classes. The components of E represent exposed and latent classes and the components I represent infected and infectious classes.
Let equation (25) be written in the form

Where $x\epsilon R^m$ denotes uninfected classes and $I\epsilon R^n$ denotes infected classes including latent and exposed, and infectious classes.
Then;
The disease-free-equilibrium state $U_0(x^*,0)$ is globally asymptotically stable provided $R_0<1$ and the following two conditions (H1) and (H2) are satisfied.

(H1) For $\frac{dx}{dt} = F(x,0), x^*$ is globally asymptotically stable

(H2) $G(x,I) = AI - \overline{G}(x,I), \overline{G}(x,I) \geq 0$ for $(x,I)\epsilon D$

Where $A=G(x^*,0)$ is an M-matrix(the off diagonal elements are nonnegative) and D is the region where the model makes biological sense.

Proof

in this study, the global stability of the disease-free-equilibrium is established using the two conditions (H1) and (H2) as stated in (Castillo-Chavez et al, 2001) must be satisfied for $R_0<1$.
For the first condition, We write our equations of the model (1) through (8) in the form

$$\frac{dX}{dt} = F(X,Y) \qquad (27)$$

$$\frac{dY}{dt} = G(X,Y); G(X,0) = 0 \qquad (28)$$

Where $X = (S_H, R_H, S_R)$ and $Y = (E_H, A_H, I_H, T_H, I_R)$

With the elements $X \epsilon R^3$ representing the uninfected compartments and the elements $Y \epsilon R^5$ representing infected compartments. From (25), we have

$$\frac{dX}{dt} = F(X,0) = \begin{bmatrix} \wedge_1 - \mu_1 S_H \\ 0 \\ \wedge_2 - (v + \mu_2) S_R \end{bmatrix} \qquad (29)$$

From equation (29), we have

$$\frac{dS_H}{dt} = \wedge_1 - \mu_1 S_H \qquad (30)$$

Equation (30) can be written as

$$\frac{dS_H}{dt} + \mu_1 S_H = \wedge_1 \qquad (31)$$

(32)

The integrating factor (IF) of (31) is $e^{\mu_1 t}$

Muliplying both sides of equation (31) by (32) gives

$$e^{\mu_1 t}\frac{dS_H}{dt} + \mu_1 e^{\mu_1 t} S_H = \wedge_1 e^{\mu_1 t} \qquad (33)$$

Equation (33) can be written as

$$\frac{d}{dt}(S_H e^{\mu_1 t}) = \wedge_1 e^{\mu_1 t} \qquad (34)$$

Integrating both sides gives

$$S_H e^{\mu_1 t} = \wedge_1 \int_0^t e^{\mu_1 \tau} d\tau + c \qquad (35)$$

$$S_H e^{\mu_1 t} = \frac{\wedge_1}{\mu_1} e^{\mu_1 t} + c \qquad (36)$$

$$\Rightarrow S_H(t) = \frac{\wedge_1}{\mu_1} + c e^{-\mu_1 t}$$

From equation (36), for $S_H(0)=S_{H0}$, we have

$$c = S_{H0} - \frac{\wedge_1}{\mu_1} \qquad (37)$$

Substituting equation (37) into (36) gives

$$S_H(t) = \frac{\Lambda_1}{\mu_1}\left(1-e^{-\mu_1 t}\right) + S_{H0}e^{-\mu_1 t}$$

$$\text{As } t \to \infty,\ S_H(t) \to \frac{\Lambda_1}{\mu_1} \quad (38)$$

Similarly, from equation (29), we have

$$\frac{dS_R}{dt} = \Lambda_2 - (\nu + \mu_2)S_R \quad (39)$$

Equation (39) can be written as

$$\frac{dS_R}{dt} + (\nu + \mu_2)S_R = \Lambda_2 \quad (40)$$

The integrating factor of (40) is $e^{(\nu+\mu_2)t}$ (41)

Multiplying both sides of equation (40) by (41) gives

$$e^{(\nu+\mu_2)t}\frac{dS_R}{dt} + (\nu + \mu_2)e^{(\nu+\mu_2)t}S_R = \Lambda_2 e^{(\nu+\mu_2)t} \quad (42)$$

Equation (42) can be written as

$$\frac{d}{dt}\left(S_R e^{(\nu+\mu_2)t}\right) = \Lambda_2 e^{(\nu+\mu_2)t} \quad (43)$$

Integrating both sides gives

$$\frac{d}{dt}\left(S_R e^{(\nu+\mu_2)t}\right) = \Lambda_2 \int_0^t e^{(\nu+\mu_2)t} d\tau + k$$

$$\left(S_R e^{(\nu+\mu_2)t}\right) = \frac{\Lambda_2}{(\nu+\mu_2)} e^{(\nu+\mu_2)t} + k \quad (44)$$

Equation (44) can be written as

$$S_R(t) = \frac{\Lambda_2}{(\nu+\mu_2)} + k e^{-(\nu+\mu_2)t} \quad (45)$$

From equation (45), for $S_R(0)=S_{R0}$, we have

$$k = S_{R0} - \frac{\Lambda_2}{\nu+\mu_2} \quad (46)$$

Substituting equation (46) into (45) gives

$$S_R(t) = \frac{\Lambda_2}{(\nu+\mu_2)}\left(1-e^{-(\nu+\mu_2)t}\right) + S_{R0}e^{-(\nu+\mu_2)t} \quad (47)$$

$$\text{As } t \to \infty,\ S_R(t) \to \frac{\Lambda_2}{(\nu+\mu_2)} \quad (48)$$

For the second condition (H2), $G(X,Y) = AI - \bar{G}(X,Y)$, we have

$$A = \begin{bmatrix} -(\alpha+\mu_1) & \beta & \beta & \beta\delta & \beta \\ (1-\rho)\alpha & -(\eta+\phi+\mu_1) & 0 & 0 & 0 \\ \rho\alpha & 0 & -(\gamma+\phi+\mu_1) & 0 & 0 \\ 0 & \eta & \gamma & -(\kappa+\phi+\mu_1) & 0 \\ 0 & 0 & 0 & 0 & \lambda-(\nu+\mu_2) \end{bmatrix} \quad (49)$$

$$\bar{G}(X,Y) = \begin{bmatrix} \beta(A_H + I_H + \delta T_H + I_R)(1-S_H) \\ 0 \\ 0 \\ 0 \\ \lambda I_R(1-S_R) \end{bmatrix} \quad (50)$$

Clearly, from equation (49), A is an M-matrix and from equation (50), $\bar{G}(X,Y) \geq 0$.

Hence $U_0(X^*,0) = \left[\frac{\Lambda_1}{\mu_1}, 0,0,0,0,0, \frac{\Lambda_2}{\nu+\mu_2}, 0\right]$ is globally asymptotically stable.

Numerical Simulations

In this section, we graphically simulate the dynamics of the model. Table 3; shows initial conditions for each plot and parameters values.

Parameters and State Variables	Value	Source
$S_H(0)$	10000	Assumed
$E_H(0)$	7000	Assumed
$A_H(0)$	5600	Calculated
$I_H(0)$	1400	Calculated
$T_H(0)$	6500	Assumed
$R_H(0)$	5500	Assumed
$S_R(0)$	3000	Assumed
$I_R(0)$	700	Assumed
$\wedge_1$	1200	Assumed
$\wedge_2$	400	Assumed
μ_1	0.02	CIA (2015)
μ_2	0.08	Assumed
β	0.02	Assumed
λ	0.03	Assumed
δ	0.2	Assumed
α	0.05	Assumed
ρ	0.2	WHO (2017)

ϕ	0.01	WHO (2017)
η	0.5	Assumed
γ	0.8	Assumed
κ	0.8	Assumed
ν	0.02	Assumed

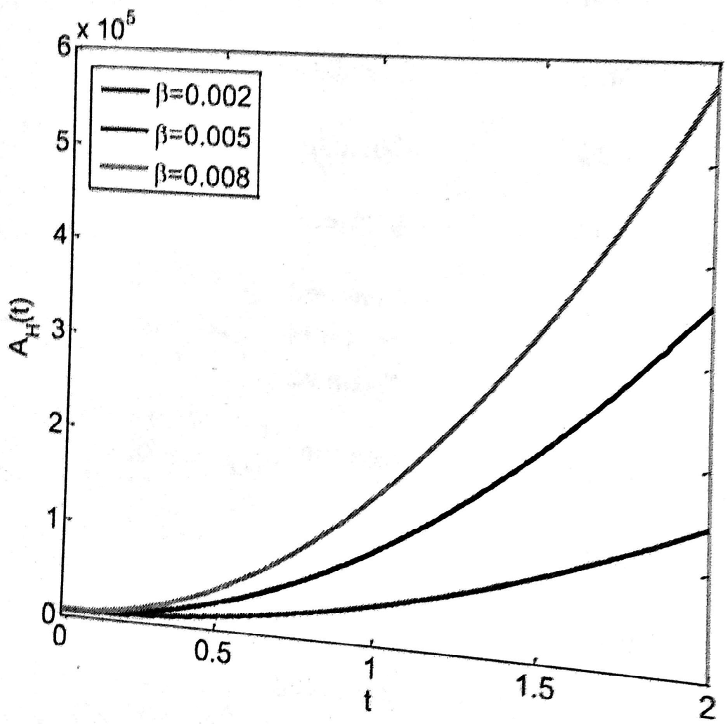


Figure 1: Graph of Asymptomatic infected individuals against time for different values of Infection rate

From figure 1, it is observed that the number of asymptomatic individuals increases with increase in infection rate β.

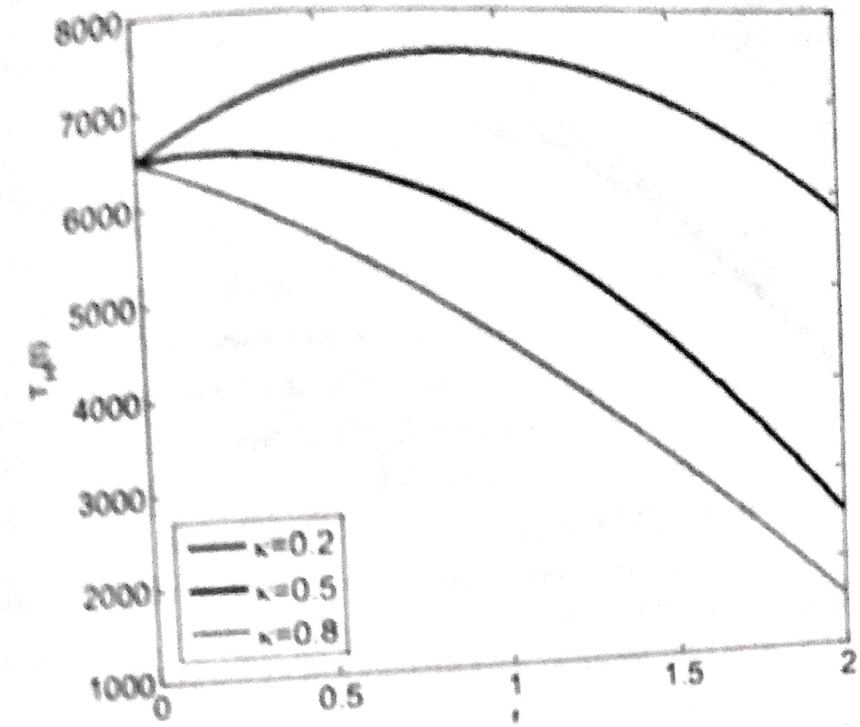


Figure 2: Graph of treated individuals against time for different values of recovery rate κ. From figure 2, it is observed that the number of treated individuals decreases as the recovery rate κ increases.

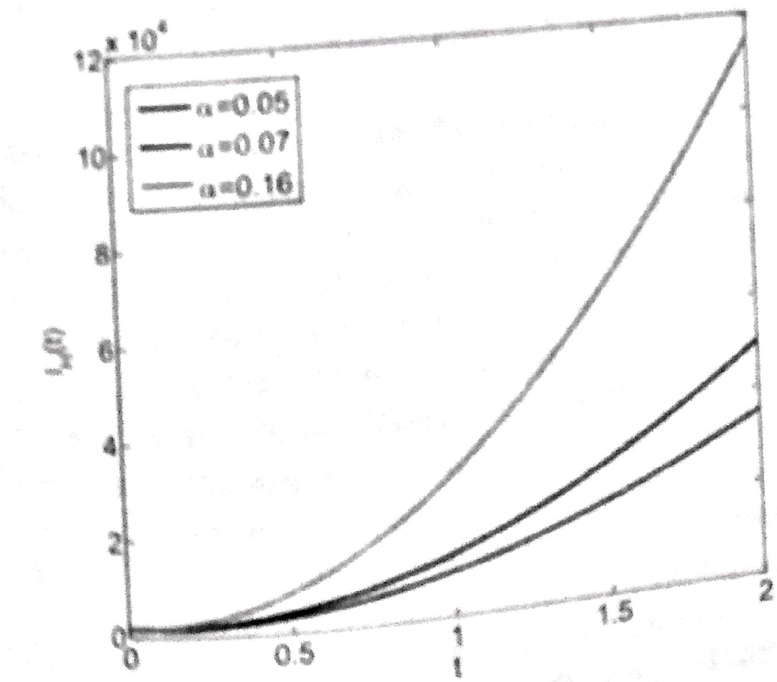


Figure 3: Graph of Symptomatic infected individuals against time for different values of disease-incubation rate α. It is observed from figure 3 that the number of symptomatic infected individuals increases as the diseaseincubation rate α increases.

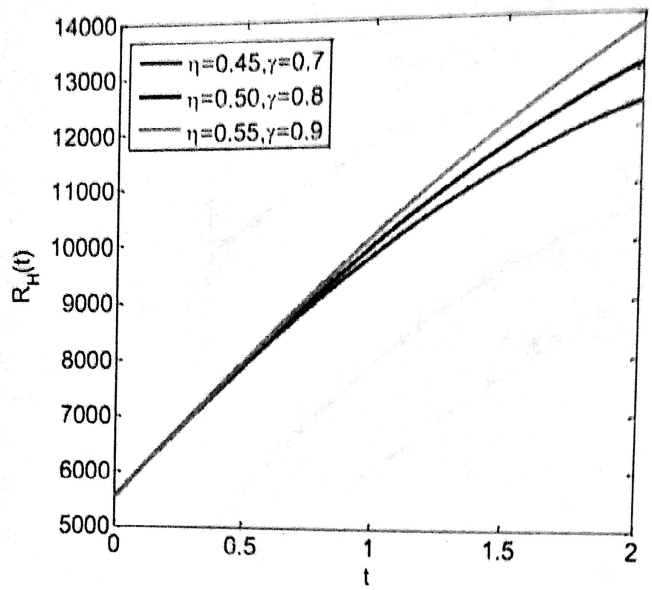


Figure 4: Graph of Recovered individuals against time for different values of treatment rates of asymptomatic and symptomatic infected individuals.

From Figure 4, it is observed that the number of recovered individuals increases as the treatment rates η and γ of asymptomatic and symptomatic individuals increase respectively.

Conclusion

In this study, we formulated a mathematical model for the spread and treatment of Lassa fever. We obtain the disease-free equilibrium and analyzed it for local and global stability. It was revealed that the disease-free equilibrium state is stable if $R_0<1$. The numerical simulation shows the dynamics of the population. It was observed from the simulation that at high treatment rate, the number of recovered individuals increases with time which indicate eventual dying out of the disease

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