Transmission Dynamics of Lassa fever with Variability in Infectiousness and Awareness Levels

Richard Jenije[1]; Emeke O. Aghanenu[2]; Enoriuwa N. Jimade[3]

1. Department of Mathematics, College of Education, Mosogar, Delta State, Nigeria
2. Department of Mathematics, Delta State University, Abraka, Nigeria.
3. Department of Mathematical Sciences, National Open University of Nigeria, Abuja.

Abstract

Classical mathematical models with enhanced flexibility have been used extensively to simulate and analyse the course and effect of intervention programmes on the dynamics of several infectious diseases. Lassa fever is one of such diseases whose outbreak is often witnessed in West Africa. This work presents a mathematical model that investigates the impact of awareness levels of susceptible individuals as well as the diagnosis and treatment of both symptomatic and asymptomatic individuals on the transmission dynamics of Lassa fever in a population. The model developed in this paper divided the host population into two: the human host population and the non-human primates (animal reservoirs). The total human host population was further sub-divided into eight human compartments according to the prevailing level of awareness, diagnostic status and the resulting treatment action plan. Our analysis showed that the model has a disease-free equilibrium (DFE), which is locally asymptotically stable whenever the reproduction number is less than unity. Numerical simulations of the model, using relevant demographic data from Nigeria, revealed that increasing the fraction of susceptible individuals with reasonable awareness will help in reducing the cumulative number of new Lassa fever cases. The simulation also suggests that increasing the fraction of symptomatic individuals that are diagnosed, isolated and treated will result in the reduction of the number of individuals infected with the disease in the population. However, the impact of diagnosis will be more positively felt if there are robust treatment and isolation policies that will allow for increased treatment rates for diagnosed infections.

Keywords: Lassa fever, Dynamics, Awareness, Diagnosis, Symptomatic, Reproduction number.

1 Introduction

Lassa fever is an animal-borne or a zoonotic acute viral illness. According to the World Health Organization [1], it is a viral hemorrhagic fever that is transmitted to humans via contact with rodent urine or faeces. The virus (also referred to as Mastony Natalenis), affects the liver, nervous system, spleen and kidney [2]. Lassa fever is known to be endemic in sub-saharan African countries such as Nigeria, Benin, Ghana, Liberia, Mali, and Sierra Leone, amongst others [1,3]. Lassa fever illness usually lasts between 2 and 21 days in humans, with an incubation period ranging from 6 to 21 days before it becomes symptomatic with fever, general weakness and malaise. Death can occur within the first 14 days of onset in fatal cases. In Nigeria there were documented cases of Lassa fever in 2019, with 324 confirmed cases and 72 deaths, spread across many states [4].

Classical mathematical models have been adapted and used extensively to analyse and predict the course and effect of intervention programmes on the dynamics of several infectious diseases. A model to study the dynamics of COVID-19 in Ghana and to consider the impact of testing and quarantine of immigrants, contact tracing and isolation as measures in the mitigation of the spread of the disease was developed [5]. Also developed a mathematical Model for the dynamics and

DOI: https://doi.org/10.5281/zenodo.18495967

control of Malaria in Nigeria [6]. Another study[7] adapted a compartmentalized epidemiological model to explain the dynamical relationship between cybercrime, poverty and prostitution, while [8] investigated the relationship between model assumption violation and multi-collinearity, and used illustrations to show the role of variance inflation factor (VIF) in detecting model violations. The synthesis of traditional epidemiology with mathematical and computational modelling has been boosted as reflected in many Nigerian scientific contributions. From statistical theory and probability, to applied statistics, models have become invaluable in in explaining associated natural phenomena so as to optimize human efforts. For instance, in epidemiological studies, a numerical collocation model[9] was used to analyse an SEIR compartmental disease transmission model, while a lifetime probability distribution with established survival and hazard rate functions[10] was used to estimate recovery and mortality rates arising from the Covid-19 pandemic in Nigeria. In another study, a time series model was used to analyse infant mortality rates [11] in some regions of Nigeria. All these are instances of use of mathematical models in explaining population related issues, and this supports the assertion that in any attempt to explain the dynamics of an infectious disease, population distribution of the host community was an important denominator that should not be overlooked [12].

On Lassa fever, several studies have been conducted to investigate the transmission dynamics in human population. Among these is the SIS model developed to investigate the transmission of Lassa fever [13]. The study obtained the equilibrium states of the model and also examined the endemic and epidemic situations. In the same vein, [14] constructed a deterministic mathematical model for the transmission dynamics of Lassa fever with quarantine policy. This work partitioned the infectious human population compartment into two: the quarantine and the un-quarantine classes and considered the contributions of both to human-to-human transmission of the virus in a human host population. Also developed was a mathematical model for the transmission dynamics of Lassa fever with possible isolation of infectious humans as the control strategy of the spread of the disease among humans [15]. Also significant is the work of [16] who developed a mathematical model for the transmission dynamics of the Lassa fever infection by splitting the infectious human population into symptomatic and asymptomatic infective and with the assumption that animal reservoir do not recover once infected.

Following the outbreak of the disease in Nigeria in January, 2019, relevant agencies adopted the strategy of reliance on community engagement and promotion of hygienic conditions [4] for the prevention of Lassa fever. Ever since, these agencies have continued to advocate the need to enhance awareness for early detection and management of cases to reduce the case fatality rate of the disease. It is based on this advocacy that this paper is out to investigate the transmission dynamics of Lassa fever with variability of infectiousness and awareness levels, diagnosis and treatment plans.

2 Model Formulation

The model sub-divides the total human population denoted by N_H into eight (8) compartments, and also sub-divides the host population into two, which are, the human host population and the non-human primates (animal reservoirs). The total human host population $N_H(t)$ at time t, was divided into eight (8) human compartments; wholly susceptible (high risk group with low level of awareness), S_w, the susceptibles with high level of awareness (low risk group) S_H , the exposed class (E_H), infectious class ($\mathrm{I_H}$), diagnosed actively infected class (J_1), undiagnosed actively infected class (J_2), isolated class ($\mathrm{I_S}$) and the recovered class (R). Thus we have;

$$\mathbf{N_H(t) = S_w(t) + S_A(t) + E_H(t) + I_H(t) + J_1(t) + J_2(t) + I_S(t) + R(t)} \quad (1)$$

The non-human primate population $N_R(t)$ at time t, was further divided into susceptible (S_R) and infected (I_R) sub-populations, such that,

$$\mathbf{N_R(t) = S_R(t) + I_R(t)} \quad (2)$$

DOI: https://doi.org/10.5281/zenodo.18495967

2.1 Transmission by Human and Non-human Primates

Susceptible non-human primates (rodents) in S_R become exposed to lassa fever and move to the (I_R) class after getting into contact with an infected rodent at a rate λ_R, with

$$\boldsymbol{\lambda_R = \beta_R \frac{I_R}{N_R}} \qquad (3)$$

where β_R is the product of effective contact rate and probability of the non-human primate getting infected per contact.

In the same vein, a susceptible human in the (S_H) class becomes exposed to lassa fever following effective contact with an infectious human or non-human primate at a rate λ_H with

$$\boldsymbol{\lambda_H = \beta_{RH}\frac{I_R}{N_R} + \beta_H \frac{(E + I + J_1 + J_2 + I_S)}{N_H}} \qquad (4)$$

where β_{RH} denotes the product of the effective contact rate and probability of the human being infected per contact with an infectious non-human primate (rodent), and β_H connotes the effective contact rate and the probability of human beings infected with lassa fever following effective contact with an infectious human per contact.

2.2.Model Equations

The wholly susceptible human population $\left(S_w(t)\right)$ is generated by the recruitment of individuals (assumed to have low level of awareness) into the population at a rate Λ_H. The population of individuals in the $S_w(t)$ compartment is reduced due to Lassa fever infection at the rate $(1-n)\lambda_H$ where n represents the fraction of susceptible individuals with high level of awareness. The population is further decreased by natural death at a rate μ_H, natural death occurs in all epidemiological compartments at this rate. Due to an education programme which creates a high level of awareness, a fraction of the wholly susceptible humans move to S_A (low risk) class at a rate $n\pi$, where π is the rate of awareness. Due to forgetfulness which is caused by lack of continuous exposure to the enlightenment program while the disease persist in the community, the wholly susceptible class $S_w(t)$ is increased at a rate σ. Thus we have,

$$\boldsymbol{\frac{dS_w}{d_t} = \Lambda_t + \sigma(1-P)S_A + \alpha_1 R - \left((1-n)\lambda_H + n\pi + \mu_H\right)S_w} \quad (5)$$

The susceptible humans with high level of awareness $\left(S_A(t)\right)$ is increased by those who are exposed to the enlightenment program at a rate π. It is further increased by those human who recover from the disease and loose their immunity at a rate α_2 . The $S_A(t)$ class is reduced by those who become effected with lassa fever at a rate $\tau\lambda_H$ where τ accounts for the effectiveness of the program. It is further reduced by those who loose awareness due to forgetfulness at a rate σ. This class is further decreased by natural death. Hence,

$$\boldsymbol{\frac{dS_A}{dt} = n\pi\overline{S_w} + \alpha_2 R_H - (\sigma + \tau\lambda_H + \mu_H)S_A} \qquad (6)$$

The exposed human class $\left(E_H(t)\right)$ is increased following infection of wholly susceptible humans and susceptible with high awareness level at rates $(1-n)\lambda_H$ and $\tau\lambda_H$ respective. This population is decreased by those who develop clinical symptoms (symptomatic patients) and move to the infectious class at a rate θ . The exposed human class is further reduced by natural death so that we have,

$$\boldsymbol{\frac{dE_H}{dt} = (1-n)\lambda_H S_w + \tau\lambda_H S_A - (\theta + \mu_H)E_H} \qquad (7)$$

The infectious class of infected individuals with Lassa fever is increased by those who progressed from the exposed and reduced by those who progress to the diagnosed active infectious class and undiagnosed active infectious class at the rate qk and $(1-q)k$ respectively, (where q represents the fraction of symptomatic individuals who progressed to the diagnosed and undiagnosed classes). The population is further reduced by natural mortality and disease-induced mortality at the rates μ_H and δ_1 respectively. Thus, we have:

$$\boldsymbol{\frac{dI_H}{dt} = \theta E_H - (k + \mu_H + \delta_1)I_H} \qquad (8)$$

DOI: https://doi.org/10.5281/zenodo.18495967

The population of the diagnosed actively infected class is increased by those who progressed from the infectious class $(I_H(t))$ and the undiagnosed actively infected class $(J_2(t))$ at the rates qk and Ɣ respectively (where Ɣ is the rate at which the undiagnosed actively infected individual progresses to the actively infected diagnosed class). This population is decreased by those who progress to the isolated class at the rate $\emptyset_1$, and the recovered class at the rate r_2. It is further decreased by natural death and disease-induced mortality at the rates μ_H and δ_2.

$$\frac{dJ_1}{dt} = qkI_H + \text{Ɣ}J_2 - (\emptyset_1 + r_2 + \mu_H + \delta_2)J_1 \qquad (9)$$

The population of the undiagnosed actively infected class $(J_2(t))$ is increased by those who progressed from the infectious class but diminished by the progression of these individuals to the diagnosed actively infected class, at the rate Ɣ, by natural death and disease-induced mortality, at the rates μ_H and δ_3. Thus we have,

$$\frac{dJ_2}{dt} = (1-q)kI_H - (\text{Ɣ} + r_3 + \mu_H + \delta_3)J_2 \qquad (10)$$

The population of the isolated individuals is increased by those who progressed from the $J_1(t)$ class at the rate $\emptyset_1$ but diminished by the progression of these individuals to the recovered class, at the rate r_1, by natural death and disease induced mortality, at the rate μ_H and δ_4. Thus we have

$$\frac{dI_s}{dt} = \emptyset_1 J_1 - (r_1 + \mu_H + \delta_4)I_s \qquad (11)$$

The population of the recovered individuals is increased by those who progressed from $J_1(t)$, $J_2(t)$ and $I_s(t)$ classes, at the rates r_2, r_3 and r_1 respectively. This population is decreased following the loss of temporary immunity and the progression to the $S_A(t)$ or $S_w(t)$ classes at the rates α_2 and α_1 respectively. The population is further decreased by natural death. Thus

$$\frac{dR_H}{dt} = r_1 I_s + r_2 J_1 + r_3 J_2 - (\alpha_1 + \alpha_2 + \mu_H)R_H \qquad (12)$$

The susceptible non-human primate population is generated by the recruitment of rodents into the S_R class at a constant rate Λ_R . This population is decreased following effective contact with infectious rodents at a rate λ_R. It is further decreased by natural death and death due to hunt by humans and other predators, at the rates μ_R and ε, respectively. Thus we have;

$$\frac{dS_R}{dt} = \Lambda_R - (\lambda_R + \mu_R + \varepsilon)S_R \qquad (13)$$

The infectious non-human primates are increased by those who progress from the susceptible population at the rate λ_R . The population is decreased by natural death and death due to hunt by humans and other predators, at the rates μ_R and ε. Hence

$$\frac{dI_R}{dt} = \lambda_R S_R - (\mu_R + \varepsilon)I_R \qquad (14)$$

Based on the assumptions that led to the formulation of the model, the model for the transmission dynamics of Lassa fever with diagnosis and awareness is given by the following systems of nonlinear ordinary differential equations. Table 1 describes the associated state variables and parameters in the model while figure 1 gives the flow diagram of model (15)).

$$\begin{aligned}
\frac{dS_w}{dt} &= \Lambda_H + \sigma(1-P)S_A + \alpha_1 R - \big((1-n)\lambda_H + n\pi + \mu_H\big)S_w \\
\frac{dS_H}{dt} &= n\pi S_w + \alpha_2 R_H - (\sigma + \tau\lambda_H + \mu_H)S_A \\
\frac{dE_H}{dt} &= (1-n)\lambda_H S_w + \tau\lambda_H S_A - (\theta + \mu_H)E_H \\
\frac{dI_H}{dt} &= \theta E_H - (k + \mu_n + \delta_1)I_H \\
\frac{dJ_1}{dt} &= qkI_H + \text{Ɣ}J_2 - (\emptyset_1 + r_2 + \mu_H + \delta_2)J_1 \qquad (15) \\
\frac{dJ_2}{dt} &= (1-q)kI_H - (\text{Ɣ} + r_3 + \mu_n + \delta_3)J_2 \\
\frac{dI_s}{dt} &= \emptyset_1 J_1 - (r_1 + \mu_n + \delta_4)I_s \\
\frac{dR_H}{dt} &= r_1 I_s + r_2 J_1 + r_3 J_2 - (\alpha_1 + \alpha_2 + \mu_H)R_H
\end{aligned}$$

DOI: https://doi.org/10.5281/zenodo.18495967

$$\frac{\mathbf{dS_R}}{\mathbf{dt}} = \Lambda_R - (\lambda_R + \mu_R + \varepsilon)S_R$$

$$\frac{\mathbf{dI_R}}{\mathbf{dt}} = \lambda_R S_R - (\mu_R + \varepsilon)I_R$$

All parameters and state variables for model (15) are assumed to be non-negative to be consistent with human and animal populations.

3 Variables, Parameter Values and Flow Diagram of the Model

The state variables, parameters and their adopted values, and the state diagram of the model are as presented in Table 1 and Figure 1, respectively.

Table 1: Variables and adopted parameter values of the model

Variables	Interpretation	Values / References
β_H	Rate of infection	0.05 [17]
N	Fraction of individuals with awareness	0.6 (assumed)
π	Rate of awareness	3 (assumed)
P	Fraction of individuals infected	0.2 (assumed)
σ	Loss of awareness due to forgetfulness	0.1 (assumed)
τ	Effectiveness of awareness program	0.5 (assumed)
α_1	Loss of immunity to S_A	0.03 (assumed)
α_2	Loss of immunity to S_W	0.02 (assumed)
Q	Fraction of individuals diagnosed	0.85 (assumed)
K	Rate of diagnosis	0.9 [18]
$\emptyset_1$	Rate of isolation	0.6 [17]
r_1	Recovery rate of isolated individuals	0.7 [17]
r_2	Recovery rate of diagnosed individuals	0.7 [18]
r_3	Recovery rate of undiagnosed individuals	0.25 [18]
μ_H	Death rate	0.02041 [19]
ɣ	Rate of isolation of undiagnosed cases	0.3 [18]
^	Recruitment rate of individuals	4098510 (assumed)
δ_i (i = 1, 2, 3, 4,)	Death rates in $I_H(t)$, $J_1(t)$, $J_2(t)$, $I_S(t)$, respectively	0.022, 0.021, 0.012, 0.014 (assumed)

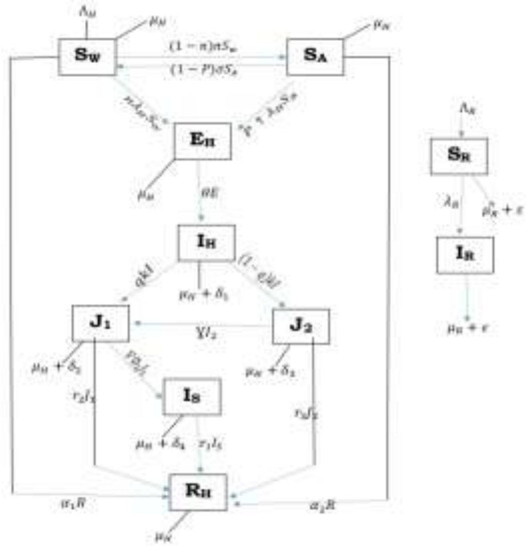


Figure 1: Flow diagram of model (15)

3 Model Analysis

3.1 Feasibility Region

Lemma 2.1

The feasible region

$$\Omega = \begin{cases} (S_W, S_A, E_H, I_H, J_1, J_2, I_s, R_H) \epsilon \mathbb{R}_+^8 : N_H \leq \dfrac{\Lambda_H}{\mu_H + n\pi} \\ (S_R, I_R)\ \epsilon \mathbb{R}_+^2 : N_R \leq \dfrac{\Lambda_R}{\mu_R + \varepsilon} \end{cases}$$

is positively invariant and attracts all positive solutions of the model (15).

Proof

Adding up equations (5) to (12) of model (15) gives

$$\frac{\mathbf{dN_H}}{\mathbf{dt}} = \Lambda_H - (\mu_H + n\pi)N_H - (\delta_1 I_H + \delta_2 J_1 + \delta_3 J_2 + \delta_4 I_s) \qquad (16)$$

Similarly adding up equations (13) and (14) of model (15) gives

$$\frac{\mathbf{dN_R}}{\mathbf{dt}} = \Lambda_R - (\mu_R + \varepsilon)N_R$$

Now, since

$$\frac{\mathbf{dN_H}}{\mathbf{dt}} \leq \Lambda_H - (\mu_H + n\pi)N_H$$

$$\frac{\mathbf{dN_R}}{\mathbf{dt}} \leq \Lambda_R - (\mu_R + \varepsilon)N_R$$

DOI: https://doi.org/10.5281/zenodo.18495967

ISSN NO-2584-2706

Then, by standard comparison theorem [20], we have

$$\begin{cases} N_H(t) = N_H(0)e^{-(\mu_h+n\pi)t} + \frac{\Lambda_H}{\mu_H+n\pi}\left(1-e^{-(\mu_H+n\pi)t}\right) \\ N_R(t) = N_R(0)e^{-(\mu_R+\varepsilon)t} + \frac{\Lambda_R}{\mu_R+\varepsilon}\left(1-e^{-(\mu_R+\varepsilon)t}\right) \end{cases} \quad (17)$$

where $N_H(0)$ and $N_R(0)$ are the initial populations of humans and the animal reservoirs respectively.
Thus

$0 \le N_H \le \frac{\Lambda_H}{\mu_H+n\pi}$ and $0 \le N_R \le \frac{\Lambda_R}{\mu_R+\varepsilon}$ $as\ t \to \infty$

This shows that $\frac{\Lambda_H}{\mu_H+n\pi}$ and $\frac{\Lambda_R}{\mu_R+\varepsilon}$ are the upper bounds for the human population $N_H(t)$ and the animal population $N_R(t)$ respectively, as long as $N_H(0) \le \frac{\Lambda_H}{\mu_H+n\pi}$ and $N_R(0) \le \frac{\Lambda_R}{\mu_R+\varepsilon}$. Hence, the feasible region is positively invariant. Furthermore, if $N_H(0) > \frac{\Lambda_H}{\mu_H+n\pi}$ and $N_R(0) > \frac{\Lambda_R}{\mu_R+\varepsilon}$, then the feasible solution enters the region Ω in finite time t or $N_H(t) \to \frac{\Lambda_H}{\mu_H+n\pi}$ and $N_R(t) \to \frac{\Lambda_R}{\mu_R+\varepsilon}$ asymptotically as $t \to \infty$. Hence, the region Ω attracts all solution in $\mathbb{R}_+^8$ and $\mathbb{R}_+^2$.
Since the feasible region is positively invariant, it is enough to investigate the dynamics of the flow generated by model (15) in Ω. Hence, the model (15) is mathematically and epidemiologically well posed.

3.2Local stability of Disease-free Equilibrium

Model (15) has a disease-free equilibrium (DFE) obtained by setting the right hand sides of the equations of model (15) to zero and solving for the state variables with no infections, given by

$$\xi_0 = (S_W^*, S_A^*, E_H^*, I_H^*, J_1^*, J_2^*, I_s^*, R_H^*, S_R^*, I_R^*)$$

$$= \left[\frac{\Lambda_H}{\mu_H}\frac{(\sigma+\mu_H)}{(\sigma+n\pi+\mu_H)}, \frac{\Lambda_H}{\mu_H}\left(\frac{n\pi}{\sigma+n\pi+\mu_H}\right), 0,0,0,0,0,0, \frac{\Lambda_R}{\mu_R+\varepsilon}, 0\right] \quad (18)$$

Clearly, the susceptible human classes, at the DFE, depend on a factor of the asymptotic population size, $\frac{\Lambda_H}{\mu_H}$

The local stability of model (15) ξ_0 can be established with the next generation operator method [21, 22]. Using the notations in [22], it follows that matrices F and V for the new infectious terms and the remaining transition terms respectively are given by:

$$F = \begin{bmatrix} \beta_R & 0 & 0 & 0 & 0 & 0 \\ \frac{(1-n)\beta_R\Lambda_H(\mu_R+\varepsilon)}{\Lambda_R(\mu_H+\Lambda\pi)} & 0 & (1-n)\frac{\beta_H S_w^*}{N_H^*} & (1-n)\frac{\beta_H S_w^*}{N_H^*} & (1-n)\frac{\beta_H S_w^*}{N_H^*} & (1-\Lambda)\frac{\beta_H S_w^*}{N_H^*} \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix}$$

$$V = \begin{bmatrix} \mu_R+\varepsilon & 0 & 0 & 0 & 0 & 0 \\ 0 & \mu_n+\theta & 0 & 0 & 0 & 0 \\ 0 & -\theta & H_1 & 0 & 0 & 0 \\ 0 & 0 & -qk & H_2 & -ɣ & 0 \\ 0 & 0 & -k(rq) & 0 & H_3 & 0 \\ 0 & 0 & 0 & \emptyset_1 & \emptyset_2 & H_4 \end{bmatrix}$$

where
$H_1 = k + \mu_h + \delta_1$ $\quad H_2 = \emptyset_1 + r_2 + \mu_h + \delta_2$

$H_3 = \emptyset_2 + ɣ + r_3 + \mu_h + \delta_3$ $\quad H_4 = r_1 + \mu_h + \delta_4$

Thus, the basic reproduction numbers for the model is given as:

$$R_{ON} = \frac{\beta_R}{\mu_R+\varepsilon} \quad (19)$$

and

$$R_{OH} = \frac{\beta_H(1-n)(\sigma+\mu_H)[H_2H_3 + qkH_3 + ɣk(1-q)]}{H_1H_2H_3\,(\sigma+n\pi+\mu_H)} \quad (20)$$

which are both obtained from $P(FV^{-1})$ with P being the spectral radius of the matrix FV^{-1}.
The following result follows from theorem of [22].

Lemma 3.2
The disease-free equilibrium ξ_0 is locally asymptotically stable whenever
$R_{OH} < 1$ and $R_{ON} < 1$ and unstable otherwise.
The threshold quantity, R_{OH}, measures the average number of new infections generated by a single infected individual in the susceptible population with already existing controls such as

DOI: https://doi.org/10.5281/zenodo.18495967

ISSN NO-2584-2706

treatment ([22, 23]. The epidemiological implication of lemma 2.2 is that Lassa fever can be effectively eliminated from the community (when $R_{OH} < 1$ and $R_{ON} < 1$) if the initial sizes of the subpopulations of the model (15) are in the basin of attraction of the DFE (ξ_0) – in the presence of control strategies including effective awareness program, diagnosis, isolation, effective cost factor and treatment. Hence, a small influx of individuals with Lassa fever into the community will not generate large Lassa fever outbreak in the community, and the disease will eventually die out in time.

3.3 Analysis of Reproduction Number (R_{OH}) under Control

Using the threshold quantity, R_{OH}, in (20), we wish to investigate the effect of diagnosis of infected individuals as well as the effect of isolation of infectious individuals on the dynamics of the disease in the population, and thus glean effective control strategies involving parameters that characterize these effects. We also wish to investigate the effect of diagnosis of Lassa fever awareness, isolation and treatments as well as a combination of some of these factors on the dynamics of Lassa fever in the population.

It can be seen from (20), that as As $k \to \infty$,

$$\lim_{q\to 1} R_{OH} = \frac{\beta_H(1-n)(\sigma+\mu_h)}{(\emptyset_2 + ɣ + r_3 + \mu_h + \delta_3)(\sigma + n\pi + \mu_h)} \quad (21)$$

and

$$\lim_{q\to 1} R_{OH} = \frac{\beta_H(1-n)(\sigma+\mu_h)}{(\sigma + n\pi + \mu_h)} \quad (22)$$

As $k \to \infty$, $\emptyset_1 \to \infty$.

The limit in (21) implies that a control programme for Lassa fever that focuses on correct diagnosis of a large fraction of new infections ($q \to 1$) at a rate ($k \to \infty$) can lead to effective control of lassa fever provided it results in making the right-hand side of (21) less than unity. Similarly, the limit in (22) implies that a control programme for Lassa fever that combines correct diagnosis of a large fraction of new infections ($q \to 1$) at a rate ($k \to \infty$) which results in the isolation of the diagnosed infectious at a rate ($\emptyset \to \infty$) can lead to effective control of Lassa fever provided it results in making the right-hand side of (22) less than unity.

Also, from (21), we can also see that as $q \to 1,\ k \to \infty,\ \pi \to \infty,\ \emptyset_1 \to \infty$ and $\sigma \to 0$, then $\lim_{n\to 1} R_{OH} = 0$ (23)

The limit in (23) implies that a Lassa fever control programme that focuses on effective combination of effective awareness programme of a large fraction of susceptible, diagnosis of a large fraction of new latent infections, isolation of diagnosed latently infectives and a high treatment rate of diagnosed latently infected (that is, $n \to 1, \pi \to \infty, q \to 1, k \to \infty, \emptyset_1 \to \infty, \sigma \to 0$) can lead to the effective control of lassa fever since the result in (23) is less than unity.

Further sensitivity analysis on some key parameters associated with awareness programme, diagnosis and isolation of diagnosed active Lassa fever cases $(n, \pi, q, k, \emptyset, \sigma, r)$ in the model (20) are carried out by computing the partial derivatives of R_{OH} with respect to these parameters.

The partial derivative of R_{OH} with respect to the fraction of susceptibles who are exposed to the awareness programme as well as the rate of awareness yields

$$\frac{\partial R_{OH}}{\partial n} = \frac{-H_1H_2H_3\beta_H(\sigma+\mu_h)(\sigma+\pi+\mu_h)[H_2H_3 + qkH_3 + ɣk(1-q)]}{H_1H_2H_3(\sigma+n\pi+\mu_h)^2} \quad (24)$$

and

$$\frac{\partial R_{OH}}{\partial \pi} = \frac{-nH_1\,H_2\,H_3\beta_H(1-n)(\sigma+\mu_h)[H_2H_3 + qkH_3 + ɣk(1-q)]}{H_1H_2H_3(\sigma+n\pi+\mu_h)^2} \quad (25)$$

Clearly, it follows that $\frac{\partial R_{OH}}{\partial n} < 0$ and $\frac{\partial R_{OH}}{\partial \pi} < 0$ unconditionally. Hence, increasing the fraction of susceptibles exposed to the awareness programme at a high rate will have a positive impact in reducing the risk of Lassa fever infection in a population, regardless of the values of other parameters in the expression for R_{OH}.

Similarly, considering the rate of change of (20) with respect to loss of awareness, we have

DOI: https://doi.org/10.5281/zenodo.18495967

$$\frac{\partial R_{OH}}{\partial \sigma} = \frac{H_1 H_2 H_3 \beta_H (1-n) n\pi [H_2 H_3 + qkH_3 + \text{Ɣ} k(1-q)]}{H_1 H_2 H_3 (\sigma + n\pi + \mu_h)^2} \quad (26)$$

It follows that R_{OH} is an increasing function of σ (rate of loss of awareness). This result implies that a loss of awareness over time by susceptible individuals who previously had a high level of awareness (due to forgetfulness) would increase the number of individuals who become susceptible to Lassa fever infection in the population. The above results are summarized below.

Lemma 3.3

A high awareness rate of a large fraction of susceptibles will have a positive impact on the burden of lassa fever in a population by reducing the incidence of the disease in a population. The result is reversed for the rate of loss of awareness by susceptibles.

This result highlights the need for sustaining awareness programmes for Lassa fever so that forgetfulness could be minimized and the power of the knowledge of Lassa fever could help in reducing the likelihood of new Lassa fever infections in the population.

Considering the partial derivative of R_{OH} with respect to the fraction of diagnosed infectives with Lassa fever (q), we have

$$\frac{\partial R_{OH}}{\partial q} = \frac{\beta_H (1-n)(\sigma + \mu_h)[H_3(H_2 + k) - \text{Ɣ} k]}{H_1 H_2 H_3 (\sigma + n\pi + \mu_h)} \quad (27)$$

It follows from (27) that $\frac{\partial R_{OH}}{\partial q} < 0$ if

$$\text{Ɣ} > \text{Ɣ}^* = \frac{H_3(H_2+k)}{k} \quad \text{or} \quad H_3 < H_3^* = \frac{\text{Ɣ} k}{H_2 + k} \quad (28)$$

Equation (28) implies that the diagnosis of a fraction of infectives will have a positive impact in reducing the burden of Lassa fever in the population only if $\text{Ɣ} > \text{Ɣ}^*$ $(or\ H_3 < H_3^*)$. Such control strategy will fail to reduce the burden of the disease if $\text{Ɣ} = \text{Ɣ}^*$ $(or\ H_3 = H_3^*)$, and will have a detrimental impact in the impact in the population if $\text{Ɣ} < \text{Ɣ}^*$ $(H_3 > H_3^*)$, since this will increase the reproduction number R_{OH}. The results are summarized below;

Lemma 3.4

The diagnosis of a fraction of Lassa fever infectives will have a positive impact in reducing the incidence of the disease in the community only if $\text{Ɣ} > \text{Ɣ}^*$ $(or\ H_3 < H_3^*)$, no impact if $\text{Ɣ} > \text{Ɣ}^*$ $(or\ H_3 = H_3^*)$, and a detrimental impact if $\text{Ɣ} < \text{Ɣ}^*$ $(or\ H_3 > H_3^*)$.

The partial derivative of R_{OH} with respect to the rate of diagnosis of individuals infected with Lassa fever (k) as well as the rate of isolation of infectives $(\emptyset_1)$ gives

$$\frac{\partial R_{OH}}{\partial k} = \frac{H_2 H_3 \beta_H (1-n)(\sigma + \mu_h)[(\mu_h + \delta_1)(q_1 H_3 + \text{Ɣ}(1-q)) - H_2 H_3]}{H_1^2 H_2 H_3 (\sigma + n\pi + \mu_h)} \quad (29)$$

and

$$\frac{\partial R_{OH}}{\partial \emptyset} = \frac{-\beta_H (1-n)(\sigma+\mu_h)[k(qH_3 + \text{Ɣ}(1-q))]}{H_1 H_3 H_2^2 (\sigma + n\pi + \mu_h)} \quad (30)$$

Clearly, it follows from (29) that $\frac{\partial R_{OH}}{\partial k} < 0$ if

$$H_2 > H_2^* = \frac{(\mu_h + \delta_1)(qH_3 + \text{Ɣ}(1-q))}{H_3} \quad (31)$$

and also $\frac{\partial R_{OH}}{\partial \emptyset} < 0$ unconditionally.

The result from (29) and (31) is summarized below.

Lemma 3.5

A high rate of diagnosis of Lassa fever infectives will have:

i. a positive impact in reducing the incidence of the disease in the community if $H_2 > H_2^*$
ii. no impact in reducing the incidence of the disease in the community if $H_2 = H_2^*$ and
iii. a detrimental impact on the incidence of the disease if $H_2 < H_2^*$

This result highlights the need for early diagnosis of Lassa fever infectives so that these infectives can be isolated to prevent the further spread of the disease.

In the same vein, we summarize the result obtained from (30) below.

Lemma 3.6

A high rate of isolation of active Lassa fever infectives will have a positive impact in reducing the incidence of the disease in a population.

DOI: https://doi.org/10.5281/zenodo.18495967

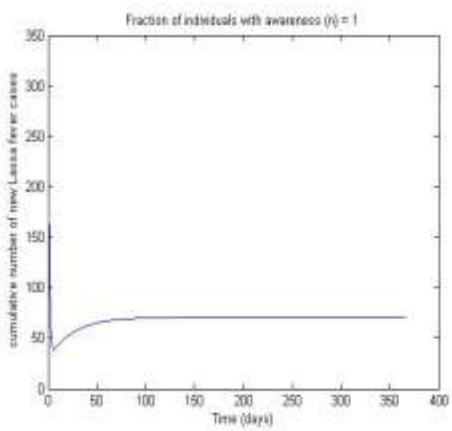
ISSN NO-2584-2706

This result gives credence to the fact that if individuals who are infected with Lassa fever are detected and isolated from other individuals, then the contact rate with non-infectives will be minimal and a reduced likelihood of human-to-human infection is attainable thereby reducing the incidence of the disease.

Considering the rate of change of R_{OH} with respect to the treatment rate of diagnosed actively infective (r_2) gives

$$\frac{\partial R_{OH}}{\partial r_2} = \frac{-\beta_H(1-n)(\sigma+\mu_h)[qkH_3 + \gamma k(1-q)]}{(k_1+\mu_h+d_1)(\emptyset_2+\gamma+r_3+\mu_h+\delta_3)(\sigma+n\pi+\mu_h)(\emptyset+r_2+\mu_n+\delta_2)} \quad (32)$$

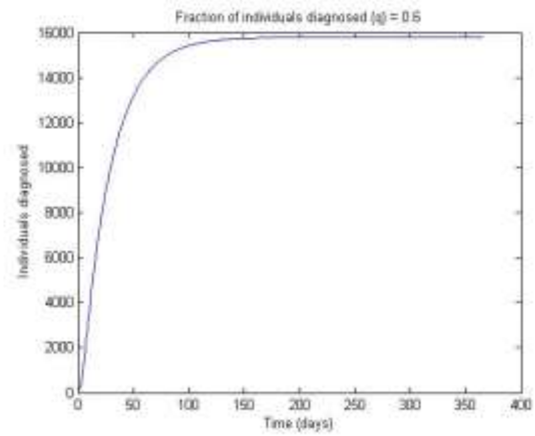
This result shows that $\frac{\partial R_{OH}}{\partial r_2} < 0$ unconditionally. Hence, treatment of diagnosed actively infective will go a long way in reducing the incidence of Lassa fever.

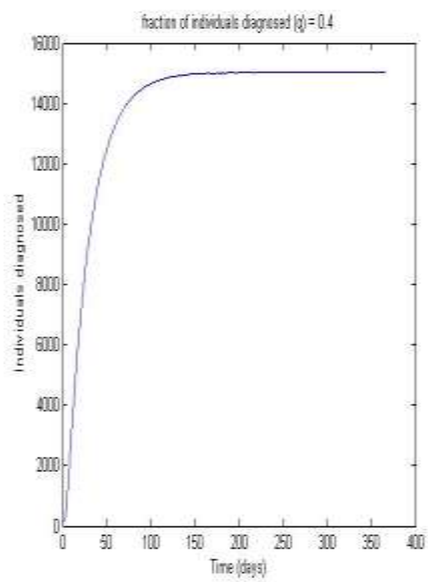


4 Numerical Simulations

The Lassa fever model (15) is numerically simulated to illustrate the effect of varying some key parameters related to awareness of susceptible individuals as well as diagnosis of symptomatic Lassa fever cases. The parameter value given in table (1) are used for the simulations, otherwise specific parameter values are stated in the caption of each figure. For the simulation in this section, demographic parameters relevant to Nigeria were chosen. The population of Nigeria in 2019 was estimated to be 200,808,917. Hence, it follows that at disease free equilibrium, $\frac{\Lambda_H}{\mu_H}$ = 200,808,917. The average mortality rate in Nigeria is μ_h = 0.02041 per year (UNAIDS, 2014)[19], so that the average recruitment rate is Λ_H = 4,098,510 per year. The total incidence of Lassa fever in Nigeria was estimated to be 327 in 2019 (WHO, 2019). These facts are employed to perform the numerical simulations presented in figures 2, 3 and 4. While Figure 2 shows the cumulative number of new Lassa fever cases with n = 0.4 and 1, Figure 3 shows the number of diagnosed individuals with varied q Figure 4: Number of infected individuals with varied k.

Figure 2: cumulative number of new Lassa fever cases with π = 0.4,1





DOI: https://doi.org/10.5281/zenodo.18495967

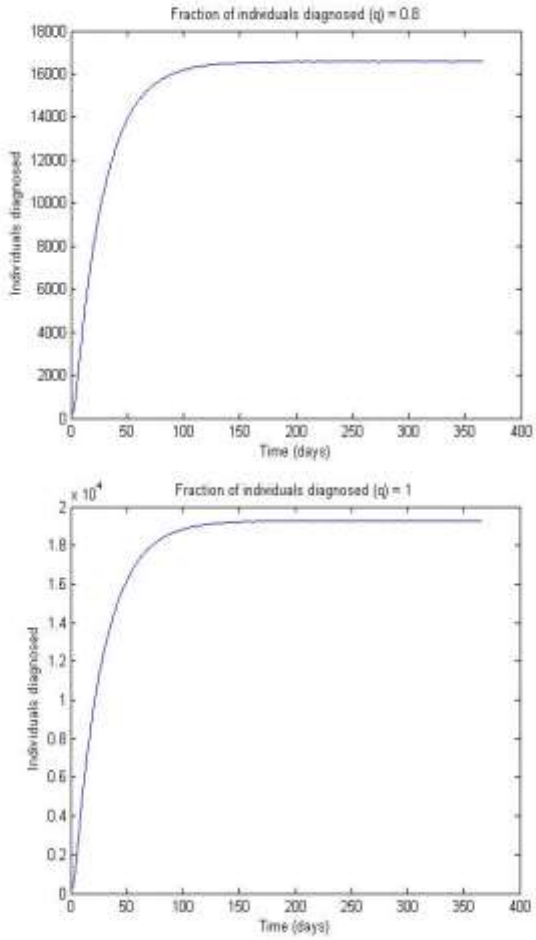
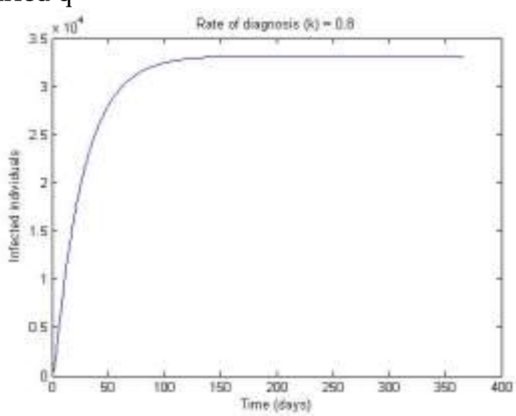


Figure 3: Number of diagnosed individuals with varied q



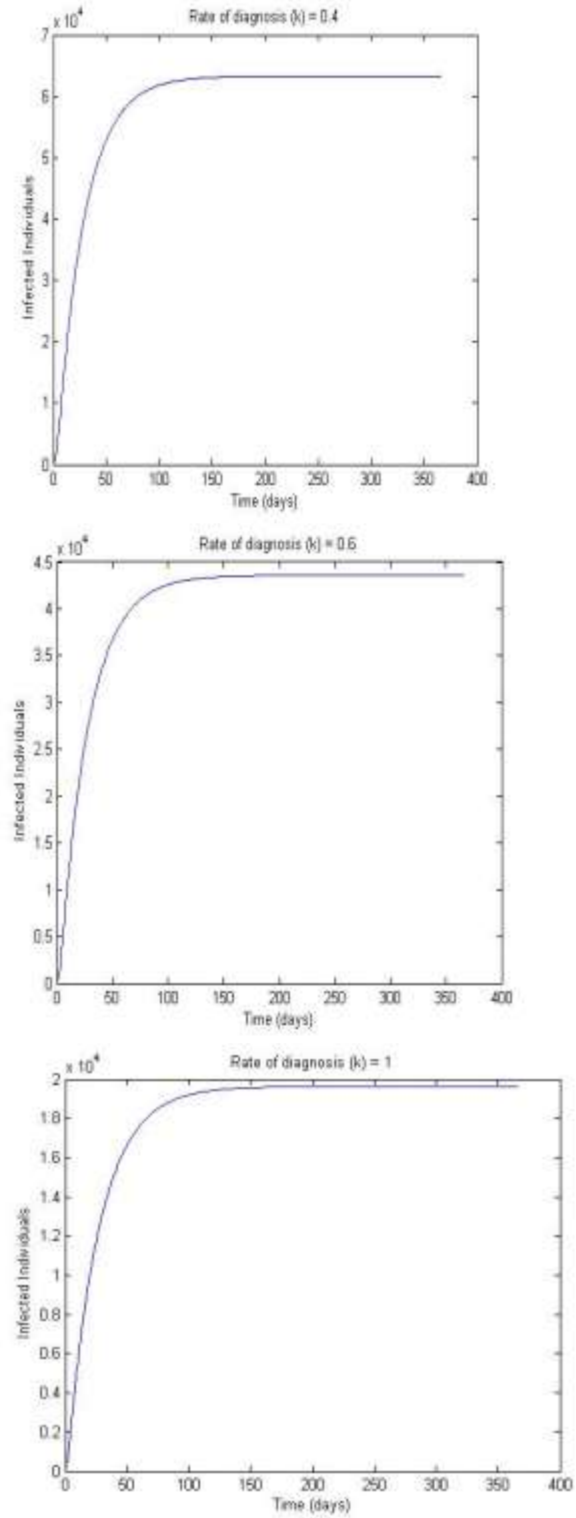


Figure 4: Number of infected individuals with varied k.

DOI: https://doi.org/10.5281/zenodo.18495967

5 Discussion

Considering figure 2, we have that the cumulative number of new Lassa fever cases significantly drops as the fraction of individuals with awareness approaches 1 (that is, $n \to 1$). This suggests that increasing the fraction of susceptibles with a significant level of awareness will have a positive effect in reducing the number of new Lassa fever cases over time. Figure 3 depicts the number of diagnosed individuals as we vary the fraction of individuals diagnosed (q) between 0.4 and 1. Thus, a valid reduction in the number of new Lassa fever cases and symptomatic cases can be achieved with a very high and early detection rate for symptomatic individuals. The plots in figure 4, reveal the number of infected individuals as we vary the rate of detection (diagnosis) of symptomatic individuals (k) between 0.4 and 1. The simulations shows that as more infected individuals are diagnosed, the fraction of infected individuals will be reduced as they will be isolated from the population and subjected to treatment. This implies that if the rate of detection continues to increase and as they are treated, the number of infectives will drastically decrease.

5 Conclusion

This study has developed a deterministic model for investigating the effect of awareness level of susceptibles and diagnoses of symptomatic cases on the transmission dynamics of Lassa fever in a population. The model is shown to have a Disease-Free Equilibrium (DFE) that is locally asymptotically stable whenever the reproduction number is less than unity. Numerical simulation of the Lassa fever model (15), using relevant demographic data from Nigeria, reveals that the cumulative number of new cases is significantly reduced as we increase the fraction of susceptible individuals with awareness (n) as well as the rate of diagnosis (k) and the fraction of infected individuals who are diagnosed (q). This study has shown that with relatively high fraction of susceptibles with high awareness level and a high rate of diagnosis of infected individuals, it is possible to reduce the incidence of the disease in the population. However, the impact of diagnosis will be positively felt if there are robust treatment and isolation policies that will allow for high treatment rates for most Lassa fever infections diagnosed.

References

[1] World Health Organization, WHO (2017). Lassa Fever. WHO Factsheets. http://www.who.int/mediacentre/factsheets/fs179/en/. Retrieved on 14th august 2021.

[2] Akinpelu, F.O. & Akinwade, R. (2018). Mathematical Model for Lassa Fever and Sensitivity Analysis. Journal of Scientific and Engineering Research. 5(6), 1-9.

[3] World Health Organization, WHO (2018). Lassa Fever-Nigeria: Disease Outbreak News. WHO Factsheets. http://www.who.int/csr/don/23-march-2018-lassa-fever-nigeria/en. Retrieved on 19th November, 2022.

[4] World Health Organization, (2019). Lassa Fever in Nigeria: Emergencies preparedness, response. http://www.who.int/csr/don/14-february-2019-lassa-fever-nigeria/en. Retrieved on 13th October, 2022.

[5] Wiah, E. N., Danso – Addo E. & Bentil D. E. (2020) Modelling the Dynamics of COVID-19 Disease with Contact Tracing and Isolation in Ghana. Mathematical Modelling and Applications, 5(3), 146 – 155.

[6] Collins, O. C. & Duffy, K. J. (2022). A Mathematical Model for the dynamics and control of Malaria in Nigeria. Infectious Disease Modelling, 7. 728 – 741.

[7] Ohwojeheri, O. F., Igabari, J. N. & Tsetimi, J. (2025). Mathematical Modelling of Poverty, Cybercrime and Prostitution Dynamics in South-South Nigeria. Asian Journal of Pure and Applied Mathematics, 7(1),68-85. https://doi.org/10.56557/ajpam/2025/v7i11186

[8] Osemeke, R. F., Igabari, J. N. and Nwabenu, D. C. (2024). Model Violation and Multicolinearity: A preminary study. Journal of Mathematical Sciences and Computational Mathematics. ISSN 2644 – 3368 (online), 5(3), 233 – 250.

[9] Mamadu, E. J., Njoseh, I. N., Okposo, N. I., Ojarikre, H. I., Igabari, J. N., Ezimadu, P. E., Ossaiugboh, M. I. & Jonathan, A. M. (2020). Numerical Approximation of the SEIR Epidemic Model using Variational Iteration Orthogonal Collocation Method and Mamadu

DOI: https://doi.org/10.5281/zenodo.18495967

– Njoseh Polynomials. Preprints.org doi.org.10.20944/preprints/202009.0196.v1.

[10] Ehiwario, J. C., Igabari, J. N., & Ezimadu, P. E. (2023). Theory and Applications of the Alpha Power Type II Topp – Leone – Generated Family of Distributions. Reliability Theory and Applications, 18(3.74), 785 – 807.

[11] Onyemarin, N. N., Ojarikre H. I. and Igabari, J. N. (2023). An ARMA modelling approach on infant mortality rate in Nigeria. Nigerian Journal of Science and Environment, 21(1), 94 – 114.

[12] Igabari, J. N. (2017). The Population Question in Nigeria: Models and Reliable Projections. Asian Research Journal of Mathematics, 8(3), 1 – 10. DOI: 10.9734/ARJOM/2017/33989. www.sciencedomain.org

[13] Okuonghae, D.A. & Okuonghae, R. (2006). Mathematical Model for Lassa Fever. Journal of the Nigerian Association of Mathematical Physics, 10,457-464.

[14] Tolulope, O. J., Akinyemi, S. T. & Bamidele, O. (2015). Stability Analysis of Lassa Fever with Quarantine and Permanent Immunity. International Journal of Applied Science and Mathematical Theory, 1(8), 71-81.

[15] Adewale, S.O., Olopade, I. A., Ajao, S. O., Adeniran, G.A., & Oyedemi, O.T. (2016). Mathematical Analysis of Lassa Fever Model with Isolation. Asian Journal of Natural and Applied Science, 5(3), 47-57.

[16] Sulaiman, U. & Ibrahim, I. A. (2018). Modeling the Transmission Dynamics of Lassa Fever Infection. Mathematical Theory and Modelling. 8(5), 42-63.

[17] Onourah, M.O., Ojo, M.S., Usman, D.J., & Ademu, A. (2016). Basic Reproduction Number for the Spread and Control of Lassa Fever. International Journal of Mathematics Trends and Technology, 30(1), 1-7.

18] Obabiyi, O. S. & Akindele, A. O. (2017). Mathematical Model for Lassa Fever Transmission Dynamics with Variable Human and Animal Reservoir Population. International Journal of Differential Equations and Applications. 16(1), 67-91.

[19] UNAIDS (2014). United Nations Programme on HIV/AIDS (UNAIDS): Communication and global advocacy fact sheet.

[20] Lakshmikantham, V., Leela, S., & Martynyuk, A. A. (1991). Stability Analysis of Nonlinear Systems. SIAM Rev. 33(1), 152-154.

[21] Diekmann, O., Heestebeek, J. & Metz, J. (1990). On the definition and the computation of the basic reproduction ration R_0 in models for infectious diseases in heterogenous populations. Journal of Mathematical Biology. 28, 365 – 382.

[22] Van der Driessche, R., Watmough, J. (2002). Reproduction Number and Sub-threshold endemic equilibria for Compartmental models of disease transmission. Math. Biosci. 180, 29-48.

[23] Hethcote, H.W. (2000). The Mathematics of Infectious Disease. Soc. Ind. Appl. Rev., 42, 599-653.

DOI: https://doi.org/10.5281/zenodo.18495967