Stabiizing The Steady State Solution of Lasser Fever: Problems and Prospect

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ABSTRACT: The study of mathematical modeling of the stability analysis of Lassa fever was examined. A mathematical model for the spread and control of Lassa fever was formulated and analyzed. The model incorporates a control parameter, the use of condom to control human to human transmission through sexual contact with opposite sex. The disease free and endemic equilibrium states were analyzed.

KEYWORDS: Mathematical model, Ordinary differential equations, Stability, Laser Fever.

1. INTRODUCTION

Mathematical representation of disease parameters is a data reliant process and this prediction is often based on the implementation of mathematical models. The important feature is bridging the gap between mathematics (models) and the real world (data). In these models, the important features are theoretically developed but applied to real life scenarios represented by a given data. Such data may contain the signature of social effect, hence a comprehensive understanding of the phenomenon of disease involves a variety of mathematically tools, from model creation to the determination of solution to differential equation and to statistical analysis.

Lassa virus is a member of the Arenaviridae, a family of single-stranded RNA virus. This virus is an old world arenavirus which is enveloped, single-stranded and bi-segmented RNA. The natural reservoir of Lassa virus is multimammate Rat species known as mastomys natalensis which breed frequently and are distributed widely throughout West, Central and East Africa. They are the common rodents in Africa and they are found predominantly in rural areas and dwelling more often than surrounding country side. Member of this genus are infected persistently and shed the virus in their excrete and other bodily fluid throughout life. Sulaiman *et al*. (2018) investigated the transmission dynamics of the Lassa fever infection model with conclusion that the reproduction numbers in the humans are most sensitive to the transmission rates, recovery rates and the natural mortality rates of the humans, while the reproduction number in the rodents is most sensitive to the transmission rate, hunting/predation rate and the natural mortality rate of the rodents. The qualitative analysis of the study revealed that the disease becomes endemic in the rodents population and also do not die out of the human population over time without controlling the growth of the rodents population, preventing animal-humans transmissions and improvement on the recovery rates of humans.

Onuorah *et al*. (2016) studied the basic reproductive number for the spread and control of Lassa fever. In this research work, a mathematical model was developed and analyzed to study the transmission and control of Lassa fever. The model incorporate two control parameters, the use of rodenticide and condom. The disease free equilibrium points of the model were obtained and analyzed. They obtained an important threshold parameter called the basic reproductive number R_0, as it was known that when $R_0 <1$ the disease dies out and when $R_0 >1$ the disease persists in the population.

Lanlege *et al*. (2018) studied measuring the spread and control of Lassa fever using the basic reproduction number R_0. In this study, a mathematical model for the spread and control of Lassa fever was presented showing that the most effective strategy to curb the disease is the usage of condom. It was evaluated that as the compliance to the use of condom as a control measure increase, the reproduction number R_0 decreases to less than one ($R_0 < 1$) which means that the disease is under control within the country and when the control measure is at lower rate or moderate rate then R_0, hence the disease is not under control within the country.

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A mathematical model of the transmission dynamics of Lassa fever with separation of infected individual and treatment as control measures was studied by Nwasuka *et al.* (2019). The model assumes susceptible humans acquired the infection through interaction with the infected rodent populations. It was found that treatment is only given to separate human population. A threshold parameter called the effective reproduction number R_{eff} was obtained. The disease free equilibrium state was obtained and analyzed before the reproduction number was obtained. If $R_{eff} < 1$ the disease-free equilibrium exists and it is locally and globally asymptotically stable, implying that Lassa fever can be controlled and eradicated within the population in a finite time and if the

$R_{eff} > 1$, the disease invade and become endemic in the population.

A study by Eraikhueman *et al.* (2017) considered Lassa fever and its control measures. In their study, a mathematical model was used to investigate the dynamics of spread of Lassa fever in human population. The contributions from regular contact with the species of rodents that carry the virus that cause Lassa fever and infections, contract with persons suffering from the disease was examined to be significant in the spread of the disease. The paper gathered among several intervention measures, control of the rodents carrying the virus, isolation policy for persons infected with the virus and introducing vaccines to the human population are some of the best strategies against the spread of the disease.

Obabiyi *et al.* (2017) discussed a mathematical model for Lassa fever transmission dynamics with variable human and reservoir population. Their study highlighted a compartmental modeling approach for two different populations: human and rodent with rigorous analysis. The analytical results showed the spread of Lassa fever can be effectively controlled in the population if the associated intervention strategies can make R_0 less than 1 $(R_0 < 1)$. But if $R_0 > 1$ the disease will persist in the population. The results of simulations reveal that increase in recovery rate contributes to decrease in the number of exposed and infectious human in the population and increase in the number of recovered human. The study concluded that early diagnostic of infected humans, maintaining hygienic environment, use of new needle when taking injection and interim control of the rodent carrying the virus are the best strategies against the spread of the disease.

Akinwande *et al.* (2018) investigated a mathematical model for Lassa fever and sensitivity analysis. In this study, a mathematical model of five compartments was formulated. The disease free equilibrium point of the model was performed and the local and global stability was obtained and analyzed based on the reproduction number. The sensitivity analysis shows that the most sensitive parameters to the basic reproduction number R_0 are the contact rate β

Faniran (2017) investigated a mathematical modeling of Lassa fever dynamics with non-drug compliance rate. The model incorporate a non-drug compliance rate in the parameters for the human population. The basic reproduction number was derived and so also was the stability of the disease-free and endemic equilibrium points analyzed. It was established that the disease-free equilibrium is globally asymptotically stable when the reproduction, $R_0 < 1$ and the disease always dies out. Also, the disease-free equilibrium point becomes unstable when $R_0 > 1$, hence endemic equilibrium point is globally asymptotically stable.

Sensitivity analysis of Lassa fever model by Onuorah *et al.* (2016), an extension of the proposed model by Onuorah and Akinwande was formulated by incorporating the sensitivity analysis. Sensitivity tells us how important each parameter is to disease transmission. Key to analysis was the reproduction number. Reasonable sets of values for the parameter in the model were compiled and sensitivity analysis around the baseline parameter value were computed, which shows that the most sensitive parameter to R_0 is human birth rate, followed by condom efficacy and compliance. Obasi *et al.* estimated the basic reproduction of Lassa fever epidemics and its relationship with inter-epidemic period. (2019). In this work, a realistic mathematical model that incorporate all the known transmission routes into Lassa fever epidemiology was presented. The basic reproduction number for the model R_0, was derived and the inter-epidemic period of infection disease was examined. From the result, it can be said that the inter-epidemic period is useful to estimate the effect of intervention on Lassa fever incidence quantitatively. The paper highlighted the relationship between the Lassa fever basic reproduction and inter-epidemic period of infection disease. Therefore, any policy or measures taken to reduce the basic reproduction number will definitely make the disease to take a very long time to re-occur.

Akinade *et al.* (2020) studied sensitivity and stability analysis of a Lassa fever disease model with control strategies. The research brought into limelight three control strategies which include; early diagnosis of the the infected human before onset of noticeable symptoms resulting in the treatment of the human-carriers, vaccination of the susceptible humans and the use of rodenticide on the vector populations as effective means of limiting the spread of Lassa fever disease within an endemic population. An increase in the value of these three controls, yields a rapid and continuous decrease in the members of the carrier human, infected human and vector populations and eventually in the eradication of the disease from an endemic population. In this work, the recovered population experiences a continuous increase and no decrease in its size suggesting that these controls are very efficacious in

controlling the disease. The basic reproduction number was obtained, so also was the disease-free equilibrium analyzed for stability. The sensitivity analysis results show the sensitiveness of each model parameter to the transmission of the disease and it was obtained that the rate at which the susceptible human population contracts the infection via contact with human-carrier is the most sensitive parameter to the spread of the disease.

Sensitivity analysis of multiple control intervention measures of Lassa fever disease model by Onah *et al.* (2019) was developed that incorporates the basic and important dynamics of Lassa fever disease transmission under the assumption of a homogeneously mixed population. The study extended the model by introducing various control intervention measures, like external protection, isolation, treatment and rodent control. Sensitivity analysis was carried out to investigate the impact of the control parameters on the persistence or eradication of Lassa fever disease.

2. MODEL FORMULATION

For the sake of clarity in this chapter, we assume a homogeneous mixing of the human and vector population such that there are equal chances of transmitting the virus when there is contact between susceptible human and active vector. Thus the total human population at time t denoted by $N_H(t)$ is sub-divided into four (4) and they are; susceptible male $S_M(t)$, infected male $I_M(t)$, susceptible female $S_F(t)$, infected female $I_F(t)$ Hence:

$$N_H(t) = S_M(t) + I_M(t) + S_F(t) + I_F(t)$$

Similarly, the total vector population at timet, denoted by $N_V(t)$ is sub-divided into dormant vector $D_V(t)$ and active vector $A_V(t)$, such that

$$N_V(t) = D_V(t) + A_V(t)$$

The schematic diagram of the model is shown in fig 3.1.

The dashed line from infected male I_M to susceptible female S_F shows that the infected male infects the susceptible female. This could be as a result of sexual interaction between the infected male and susceptible female.

The line from infected female I_F to susceptible male S_M shows that the infected female infects the susceptible male. This also could be as a result of sexual interaction between the infected female and susceptible male.

The dashed line also from active vector A_V (carrier vector) to the susceptible male population S_M shows the transfer of the virus from infected rodent to susceptible male. When susceptible male is exposed to the droppings of infected mastomy rats, they become infected.

The dashed line from active vector A_V (carrier vector) to the susceptible female population S_F shows the transfer of the virus from infected rodent to susceptible female. That is, susceptible female become infected with Lassa fever virus from exposure to the droppings of infected mastomy rats.

The susceptible male population $S_M(t)$ is generated through male birth at the rate $\beta_H \theta N_H$ where $0 < \theta < 1$.

The dormant vector D_V population is generated through natural birth rate by active vector A_V denoted by $\beta_R N_V$ and is reduced by progression to active vector (A_V) population due to maturity at the rate σ, natural death at the rate μ_2 and death due to application of pesticide at the rate δ_2 Males who recovered from the infection at the rate γ is at the other hand reduced by natural death at the rate μ_1, interaction with infected female I_F and active vector A_V, which results to the force of infection.

$$\text{i. e;} \frac{(C_2\alpha_1(1-\varepsilon\tau)I_F + \alpha_3 A_V)S_M}{N_H}, \text{ where}$$

C_2 is the average sexual partners acquired by susceptible male S_M

α_1 is the probability of transmission of infection resulting from sexual interaction between infected infected female and susceptible male.

The factor $(1 - \varepsilon\tau)$ is the effect of condom usage by susceptible male S_M.

α_3 is the probability of transmission of infection when there is interaction between Active Vector and Susceptible male.

The infected male population $I_M(t)$ is generated by sexual interaction with infected female $I_F(t)$ and interaction with Active Vector $A_V(t)$ i.e

$$\frac{(C_2\alpha_1(1-\varepsilon\tau)I_F + \alpha_3 A_V)S_M}{N_H}.$$

It is decreased by natural death at the rate μ_1, death due to infection at the rate δ_1 and recovery of infected male I_M as a result of treatment at the rate γ. The Susceptible female $S_F(t)$ population is generated through female birth at the rate $\beta_H(1 - \theta)N_H$ where

$0 < \theta < 1$. It is increased by recovered infected female at the rate γ. It is on the other hand reduced by natural death at the rate μ_1 and interaction with infected male I_M and Active Vector A_V which results to the force of infection $\frac{(C_1\alpha_2(1-\varepsilon\tau)I_M + \alpha_4 A_V)S_F}{N_H}$ where C_1 is the average sexual partners acquired by susceptible females.

α_2 is the probability of transmission of infection when there is interaction between infected male I_M and Susceptible female.

The factor $(1 - \tau\varepsilon)$ is the effect of condom usage by Susceptible female.

α_4 is the probability of transmission of infection when there is interaction between Active Vector and Susceptible female.

The infected female $I_F(t)$ population is generated by sexual interaction with infected male I_M and interaction with Active Vector A_V i.e

$\frac{(C_1\alpha_2(1-\varepsilon\tau)I_M+\alpha_4 A_V)S_F}{N_H}$. It is decreased by natural death at the rate μ_1, death due to infection at the rate δ_1 and recovery of infected female I_F as a result of treatment at the rate γ.
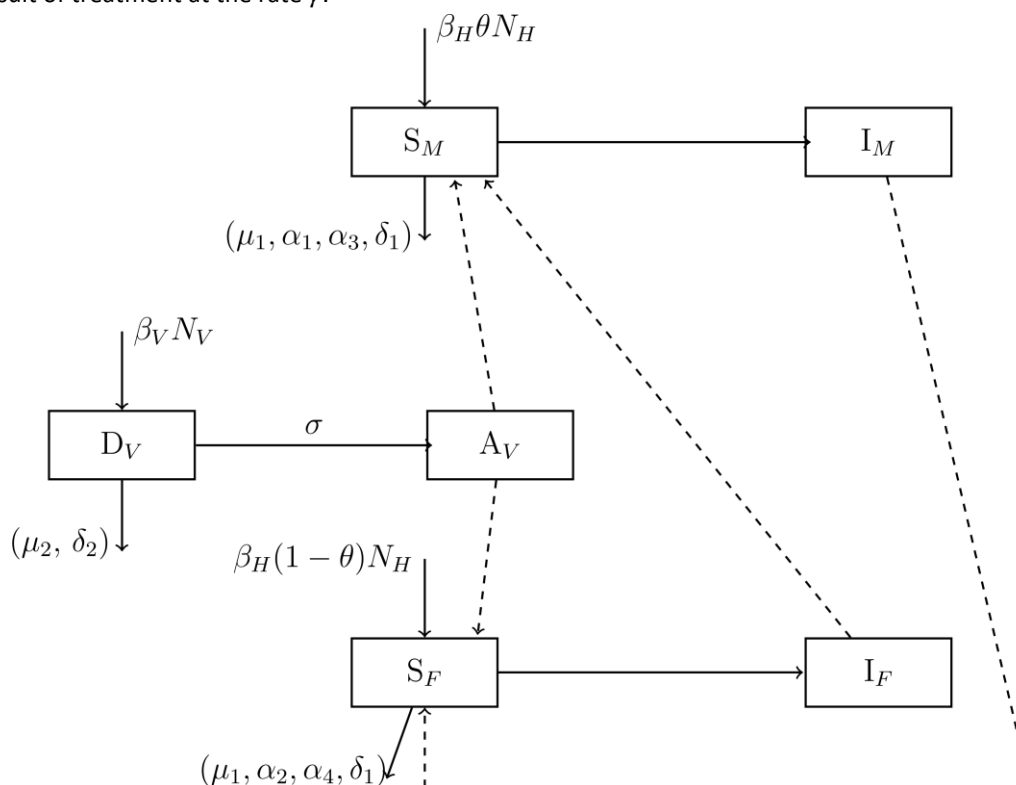
Figure3. 1: Schematic Diagram of the Mathematical model for the Lassa Fever Transmission.

3. MODEL ASSUMPTIONS

We assumed that:

1. New births are Susceptible
2. Virus does not kill the reservoir host. I.e. their death can be natural or accidental.
3. Vector class is divided into two; Active Vector A_V and Dormant Vector D_V

4. MODEL EQUATIONS

Considering the above assumptions, definition of variables and parameters and relationship between the variables and parameters described in the schematic diagram, we developed six (6) ordinary differential equations for the causes, spread and control of Lassa fever in a population. The differential equations are given as the following;

$$\frac{dS_M}{dT} = \beta H\theta N_H + \gamma I_M - \frac{(C_2\alpha_1(1-\varepsilon\tau)I_F+\alpha_3 A_V)S_M}{N_H} - \mu_1 S_M. \tag{3.1}$$

$$\frac{dI_M}{dT} = \frac{(C_2\alpha_1(1-\varepsilon\tau)I_F+\alpha_3 A_V)S_M}{N_H} - (\mu_1 + \delta_1 + \gamma)I_M . \tag{3.2}$$

$$\frac{dS_F}{dT} = \beta H(1-\theta)N_H + \gamma I_F - \frac{(C_1\alpha_2(1-\varepsilon\tau)I_M+\alpha_4 A_V)S_F}{N_H} - \mu_1 S_F \tag{3.3}$$

$$\frac{dI_F}{dT} = \frac{(C_1\alpha_2(1-\epsilon\tau)I_M+\alpha_4 A_V)S_F}{N_H} - (\mu_1 + \delta_1 + \gamma)I_F \tag{3.4}$$

$$\frac{dD_V}{dT} = \beta_V N_V - (\sigma + \mu_2 + \delta_2)D_V \tag{3.5}$$

$$\frac{dA_V}{dT} = \sigma D_V - (\mu_2 + \delta_2)A_V \qquad\qquad (3.6)$$

Where

$S_M(t)$	Number of susceptible male at time **t**
$I_M(t)$	Number of Infected male at time **t**
$S_F(t)$	Number of susceptible female at time **t**
$I_F(t)$	Number of Infected female at time **t**
$D_V(t)$	Number of dormant vector at time **t**
$A_V(t)$	Number of active vector at time **t**
β_H	The natural birth rate of Human population
β_V	The natural birth rate of Vectors
θ	The proportion of Human birth that is male ($0 < \theta < 1$)
α_1	The probability of transmission of infection resulting from sexual interaction between infected female and susceptible male
α_2	The probability of transmission of infection resulting from sexual interaction between infected male and susceptible female
α_3	The probability of transmission of infection resulting from interaction between active vectors and susceptible male
α_4	The probability of transmission of infection resulting from interaction between active vectors and susceptible female
c_1	Average number of male partners acquired by a susceptible female
c_2	Average number of male partners acquired by a susceptible male
μ_1	Natural death rate of Human population
μ_2	Natural death rate of vector population
σ	Progression rate from dormant to active vector
δ_1	Death rate of Human population due to infection
δ_2	Death rate of vector population due to application of pesticide
γ	Recovery rate of infected Human
ε	Efficacy of condom
τ	Compliance of condom usage

From the above model equations, by adding equations (1)--(4) we can derive the rate of change of the total Human population. Thus;

$$\beta_H\theta N_H + \gamma I_M - \frac{(C_2\alpha_1(1-\varepsilon\tau)I_F + \alpha_3 A_V)S_M}{N_H} - \mu_1 S_M + \frac{(C_2\alpha_1(1-\varepsilon\tau)I_F + \alpha_3 A_V)S_M}{N_H} - (\mu_1 + \delta_1 + \gamma)I_M + \beta_H(1-\theta)N_H + \gamma I_F$$

$$-\frac{(C_1\alpha_2(1-\varepsilon\tau)I_M + \alpha_4 A_V)S_F}{N_H} - \mu_1 S_F + \frac{(C_1\alpha_2(1-\varepsilon\tau)I_M + \alpha_4 AV)S_F}{N_H} - (\mu_1 + \delta_1 + \gamma)I_F$$

$$= \beta_H\theta N_H + \gamma I_M - \mu_1 S_M - (\mu_1 + \delta_1 + \gamma)I_M + \beta_H(1-\theta)N_H + \gamma I_F - \mu_1 S_F - (\mu_1 + \delta_1 + \gamma)I_F$$

$$= \beta H\theta N_H + \gamma I_M - \mu_1 S_M - (\mu_1 + \delta_1)I_M - \gamma I_M + \beta_H(1-\theta)N_H + \gamma I_F - \mu_1 S_F - (\mu_1 + \delta_1)I_F - \gamma I_F$$

$$= \beta_H\theta N_H - \mu_1 S_M - (\mu_1 + \delta_1)I_M + \beta_H(1-\theta)N_H - \mu_1 S_F - (\mu_1 + \delta_1)I_F \qquad = \beta_H\theta N_H - \mu_1 S_M - \mu_1 I_M -$$

$$\delta_1 I_M + \beta_H N_H - \beta_H\theta N_H - \mu_1 S_F - \mu_1 I_F - \delta_1 I_F \qquad = \beta_H N_H - \mu_1 S_M - \mu_1 I_M - \mu_1 S_F - \mu_1 I_F - \delta_1 I_M - \delta_1 I_F$$

$$=\beta_H N_H - \mu_1(S_M + I_M + S_F + I_F) - \delta_1(I_M + I_F)$$

Recall that

$$N_H = S_M + I_M + S_F + I_F$$

Hence;

$$\beta_H N_H - \mu_1 N_H - \delta_1(I_M + I_F)$$

Hence, the rate of change of the total human population is

$$\frac{dN_H}{dT} = \beta_H N_H - \mu_1 N_H - \delta_1(I_M + I_F) \qquad (3.7)$$

Also by adding equations (5)−(6) , we can derive the rate of change of the total vector population. Thus;

$$= \beta_V N_V - (\sigma + \mu_2 + \delta_2)D_V + \sigma D_V - (\mu_2 + \delta_2)A_V$$
$$= \beta_V N_V - \sigma D_V - \mu_2 D_V - \delta_2 D_V + \sigma D_V - \mu_2 A_V - \delta_2 A_V$$
$$= \beta_V N_V - \mu_2 D_V - \delta_2 D_V - \mu_2 A_V - \delta_2 A_V$$
$$= \beta_V N_V - D_V(\mu_2 + \delta_2) - A_V(\mu_2 + \delta_2)$$
$$= \beta_V N_V - (\mu_2 + \delta_2)(D_V + A_V)$$

Recall that $N_V = D_V + A_V$

Hence; $= \beta_V N_V - (\mu_2 + \delta_2)N_V$

Therefore the rate of change of the total vector population is

$$\frac{dN_V}{dT} = \beta_V N_V - (\mu_2 + \delta_2)N_V \qquad (3.8)$$

5. EQUILIBRIUM STATE

Using the dictionary definition of equilibrium, we know it to be a state of balance. But with respect to this chapter, we will narrow down the definition as, at equilibrium state, the rate of change must be equal to zero (0). i.e.

$$\frac{dS_M}{dT} = \frac{dI_M}{dT} = \frac{dS_F}{dT} = \frac{dI_F}{dT} = \frac{dD_V}{dT} = \frac{dA_V}{dT} = 0$$

We let;

$$(S_M, I_M, S_F, I_F, D_V, A_V) = (X, Y, Z, U, V, W)$$

6. DISEASE-FREE EQUILIBRIUM STATE

From the name, we derive the definition. It is a state in which a disease does not exist. So from this we have that the classes where the disease does not exist equals zero (0) i.e. at the disease-free equilibrium state;

$$I_M = I_F = D_V = A_V = 0 \qquad (3.9)$$

Substitute equation (3.9) into equation (3.1)

$$\beta_H \theta N_H + \gamma I_M - \frac{(C_2 \alpha_1(1 - \varepsilon\tau)I_F + \alpha_3 A_V)S_M}{N_H} - \mu_1 S_M = 0$$

$$\beta H \theta N_H + \gamma(0) - \frac{(C_2 \alpha_1(1 - \varepsilon\tau)(0) + \alpha_3(0))S_M}{N_H} - \mu_1 S_M = 0$$

$$\beta_H \theta N_H - \mu_1 S_M = 0 \Rightarrow \mu_1 S_M = \beta_H \theta N_H$$

Making S_M subject formulae

$$S_M = \frac{\beta_H \theta N_H}{\mu_1} \qquad (3.10)$$

Also substituting equation (3.9) into equation (3.3)

$$\frac{dS_F}{dT} = \beta_H(1 - \theta)N_H + \gamma I_F - \frac{(C_1 \alpha_2(1 - \varepsilon\tau)I_M + \alpha_4 A_V)S_F}{N_H} - \mu_1 S_F$$

$$\beta_H(1 - \theta)N_H + \gamma I_F - \frac{(C_1 \alpha_2(1 - \varepsilon\tau)I_M + \alpha_4 A_V)S_F}{N_H} - \mu_1 S_F = 0$$

$$\beta H(1 - \theta)N_H + \gamma(0) - \frac{(C_1 \alpha_2(1 - \varepsilon\tau)(0) + \alpha_4(0))S_F}{N_H} - \mu_1 S_F = 0$$

$$\beta H(1 - \theta)N_H - \mu_1 S_F = 0 \Rightarrow \mu_1 S_F = \beta_H(1 - \theta)N_H$$

$$S_F = \frac{\beta_H(1-\theta)N_H}{\mu_1} \qquad (3.11)$$

Where

$$(S_M, I_M, S_F, I_F, D_V, A_V) = (X, Y, Z, U, V, W)$$

Hence the disease free equilibrium (DFE) state is

$$E_0 = (X, Y, Z, U, V, W) = \left[\frac{\beta_H \theta N_H}{\mu_1}, 0, \frac{\beta_H H(1-\theta)N_H}{\mu_1}, 0, 0, 0\right] \qquad (3.12)$$

7. ENDEMIC EQUILIBRIUM STATE

In the endemic state, the disease exists for every class in the population. That is the endemic equilibrium state is the state where the disease cannot be totally eradicated but remains in the population. Hence;

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$$I_M = I_F = D_V = A_V \neq 0$$

To obtain the number of susceptible male S_M at the endemic equilibrium state, we solve equation (3.2)

$$\frac{dI_M}{dT} = \frac{(C_2\alpha_1(1-\varepsilon\tau)I_F + \alpha_3 A_V)S_M}{N_H} - (\mu_1 + \delta_1 + \gamma)I_M$$

$$0 = \frac{(C_2\alpha_1(1-\varepsilon\tau)I_F + \alpha_3 A_V)S_M}{N_H} - (\mu_1 + \delta_1 + \gamma)I_M$$

$$\frac{(C_2\alpha_1(1-\varepsilon\tau)I_F + \alpha_3 A_V)S_M}{N_H} = (\mu_1 + \delta_1 + \gamma)I_M$$

$$S_M = \frac{N_H(\mu_1+\delta_1+\gamma)I_M}{(C_2\alpha_1(1-\varepsilon\tau)I_F+\alpha_3 A_V)} = \frac{N_H(\mu_1+\delta_1+\gamma)I_M}{C_2\alpha_1(1-\varepsilon\tau)I_F+\alpha_3 A_V} \qquad (3.13)$$

To obtain the number of infected male I_M at the endemic equilibrium state, we solve equation (1)

$$\frac{dS_M}{dT} = \beta H\theta N_H + \gamma I_M - \frac{(C_2\alpha_1(1-\varepsilon\tau)I_F + \alpha_3 A_V)S_M}{N_H} - \mu_1 S_M.$$

$$0 = \beta_H\theta N_H + \gamma I_M - \frac{(C_2\alpha_1(1-\varepsilon\tau)I_F + \alpha_3 A_V)S_M}{N_H} - \mu_1 S_M.$$

$$S_M\left[\frac{C_2\alpha_1(1-\varepsilon\tau)I_F + \alpha_3 A_V}{N_H} + \mu_1\right] = \beta_H\theta N_H + \gamma I_M$$

$$S_M\left[\frac{C_2\alpha_1(1-\varepsilon\tau)I_F + \alpha_3 A_V + N_H\mu_1}{N_H}\right] = \beta_H\theta N_H + \gamma I_M$$

Multiply both side by $\frac{N_H}{C_2\alpha_1(1-\varepsilon\tau)I_F+\alpha_3 A_V+N_H\mu_1}$

$$S_M = \frac{N_H(\beta_H\theta N_H+\gamma I_M)}{C_2\alpha_1(1-\varepsilon\tau)I_F+\alpha_3 A_V+N_H\mu_1} \qquad (3.14)$$

Substituting equation (3.13) into (3.14)

$$\frac{N_H(\mu_1+\delta_1+\gamma)I_M}{C_2\alpha_1(1-\varepsilon\tau)I_F+\alpha_3 A_V} = \frac{N_H(\beta_H\theta N_H+\gamma I_M)}{C_2\alpha_1(1-\xi j\tau)I_F+\alpha_3 A_V+N_H\mu_1}$$

$$\frac{(\mu_1+\delta_1+\gamma)I_M}{C_2\alpha_1(1-\varepsilon\tau)I_F+\alpha_3 A_V} = \frac{(\beta_H\theta N_H+\gamma I_M)}{C_2\alpha_1(1-\varepsilon\tau)I_F+\alpha_3 A_V+N_H\mu_1}$$

Let $C_2\alpha_1(1-\varepsilon\tau) = P$ and $(\mu_1+\delta_1+\gamma) = A$

Thus;

$$\frac{AI_M}{PI_F + \alpha_3 A_V} = \frac{\beta_H\theta N_H + \gamma I_M}{PI_F + \alpha_3 A_V + N_H + \mu_1}$$

$$AI_M(PI_F + \alpha_3 A_V + N_H\mu_1) = (PI_F + \alpha_3 A_V)(\beta_H\theta N_H + \gamma I_M)$$

$$AI_M PI_F + AI_M\alpha_3 A_V + AI_M N_H\mu_1 = PI_F\beta_H\theta N_H + PI_F\gamma I_M + \alpha_3 A_{VH}\beta_H\theta N_H + \alpha_3 A_V\gamma I_M$$

Collect like terms

$$AI_M PI_F + AI_M\alpha_3 A_V + AI_M N_H\mu_1 - PI_F\gamma I_M - \alpha_3 A_V\gamma I_M = PI_F\beta H\theta N_H + \alpha_3 A_V\beta_H\theta N_H$$

$$I_M(PAI_F + A\alpha_3 A_V + AN_H\mu_1 - PI_F\gamma - \alpha_3 A_V\gamma) = PI_F\beta_H\theta N_H + \alpha_3 A_V\beta_H\theta N_H$$

$$I_M = \frac{PI_F\beta H\theta N_H + \alpha_3 A_V\beta_H\theta N_H}{PAI_F + A\alpha_3 A_V + AN_H\mu_1 - PI_F\gamma - \alpha_3 A_V\gamma}$$

Thus

$$I_M = \frac{\beta_H\theta N_H[C_2\alpha_1(1-\in\tau)I_F+\alpha_3 A_V]}{(\mu_1+\delta_1+\gamma)[C_2\alpha_1(1-\varepsilon\tau)I_F+\alpha_3 A_V+N_H\mu_1]-C_2\alpha_1(1-\varepsilon\tau)I_F\gamma-\alpha_3 A_V\gamma} \qquad (3.15)$$

To solve for the number of susceptible female S_F at the endemic equilibrium state, we solve equation (4)

$$\frac{dI_F}{dT} = \frac{(C_1\alpha_2(1-\varepsilon\tau)I_M + \alpha_4 A_V)S_F}{N_H} - (\mu_1 + \delta_1 + \gamma)I_F$$

$$0 = \frac{(C_1\alpha_2(1-\varepsilon\tau)I_M + \alpha_4 A_V)S_F}{N_H} - (\mu_1 + \delta_1 + \gamma)I_F$$

$$\frac{(C_1\alpha_2(1-\varepsilon\tau)I_M + \alpha_4 A_V)S_F}{N_H} = (\mu_1 + \delta_1 + \gamma)I_F$$

$$S_F = \frac{N_H(\mu_1+\delta_1+\gamma)I_F}{C_1\alpha_2(1-\varepsilon\tau)I_M+\alpha_4 A_V} \qquad (3.16)$$

To solve for the number of infected female I_F at the endemic equilibrium state, we solve

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Equation (3.3)

$$\frac{dS_F}{dT} = \beta_H(1-\theta)N_H + \gamma I_F - \frac{(C_1\alpha_2(1-\xi j\tau)I_M + \alpha_4 A_V)S_F}{N_H} - \mu_1 S_F$$

$$0 = \beta_H(1-\theta)N_H + \gamma I_F - \frac{(C_1\alpha_2(1-\in\tau)I_M + \alpha_4 A_V)S_F}{N_H} - \mu_1 S_F$$

$$S_F\left[\frac{C_1\alpha_2(1-\varepsilon\tau)I_M + \alpha_4 A_V}{N_H} + \mu_1\right] = \beta_H(1-\theta)N_H + \gamma I_F$$

$$S_F = \frac{N_H[\beta_H(1-\theta)N_H + \gamma I_F]}{C_1\alpha_2(1-\varepsilon\tau)I_M + \alpha_4 A_V + N_H\mu_1} \tag{3.17}$$

Substituting equation (3.16) into (3.17)

$$\frac{N_H(\mu_1 + \delta_1 + \gamma)I_F}{C_1\alpha_2(1-\varepsilon\tau)I_M + \alpha_4 A_V} = \frac{N_H[\beta_H(1-\theta)N_H + \gamma I_F]}{C_1\alpha_2(1-\varepsilon\tau)I_M + \alpha_4 A_V + N_H\mu_1}$$

$$\frac{(\mu_1 + \delta_1 + \gamma)I_F}{C_1\alpha_2(1-\xi j\tau)I_M + \alpha_4 A_V} = \frac{[\beta_H(1-\theta)N_H + \gamma I_F]}{C_1\alpha_2(1-\xi j\tau)I_M + \alpha_4 A_V + N_H\mu_1}$$

Let $C_2\alpha_2(1-\varepsilon\tau) = q$ and let $(\mu_1 + \delta_1 + \gamma) = A$

Thus

$$\frac{AI_F}{qI_M + \alpha_4 A_V} = \frac{\beta_H(1-\theta)N_H + \gamma I_F}{qI_M + \alpha_4 A_V + N_H\mu_1}$$

$$AI_F(qI_M + \alpha_4 A_V + N_H\mu_1) = (qI_M + \alpha_4 A_{VH})(\beta_H(1-\theta)N_H + \gamma I_F)$$

$$AI_F(qI_M + \alpha_4 A_V + N_H\mu_1) = qI_M\beta_H(1-\theta)N_H + qI_M\gamma I_F + \alpha_4 A_V\beta_H(1-\theta)N_H + \alpha_4 A_V\gamma I_F$$

$$AI_F(qI_M + \alpha_4 A_V + N_H\mu_1) = \beta_H(1-\theta)N_H(qI_M + \alpha_4 A_V) + I_F(qI_M\gamma + \alpha_4 A_V\gamma)$$

Collect like terms

$$I_F(qI_M + \alpha_4 A_V + N_H\mu_1)A - I_F(qI_M\gamma + \alpha_4 A_V\gamma) = \beta_H(1-\theta)N_H(qI_M + \alpha_4 A_V)$$

$$I_F[(qI_M + \alpha_4 A_V + N_H\mu_1)A - (qI_M\gamma + \alpha_4 A_V\gamma)] = \beta_H(1-\theta)N_H(qI_M + \alpha_4 A_V)$$

$$I_F = \frac{\beta_H(1-\theta)N_H(qI_M + \alpha_4 A_V)}{(qI_M + \alpha_4 A_V + N_H\mu_1)A - (qI_M\gamma + \alpha_4 A_V\gamma)}$$

Thus

$$I_F = \frac{\beta_H(1-\theta)N_H(C_1\alpha_2(1-\varepsilon\tau)I_M + \alpha_4 A_V)}{[C_1\alpha_2(1-\varepsilon\tau)I_M + \alpha_4 A_V + N_H\mu_1](\mu_1 + \delta_1 + \gamma) - (C_1\alpha_2(1-\varepsilon\tau)I_M\gamma + \alpha_4 A_V\gamma)} \tag{3.18}$$

Similarly for the vector population, we solve equation (5) and (6)

From equation (5)

$$\frac{dD_V}{dT} = \beta_V N_V - (\sigma + \mu_2 + \delta_2)D_V$$

$$0 = \beta_V N_V - (\sigma + \mu_2 + \&)D_V$$

$$(\sigma + \mu_2 + \&)D_V = \beta_V N_V$$

$$D_V = \frac{\beta_V N_V}{\sigma + \mu_2 + \delta_2} \tag{3.19}$$

Also from equation (6)

$$\frac{dA_V}{dT} = \sigma D_V - (\mu_2 + \&)A_V$$

$$0 = \sigma D_V - (\mu_2 + \delta_2)A_V$$

$$\sigma D_V = (\mu_2 + \delta_2)A_V$$

$$A_V = \frac{\sigma D_V}{\mu_2 + \delta_2} \tag{3.20}$$

So the endemic equilibrium state is given by

$$E^0 = (X, Y, Z, U, V, W) = \frac{N_H(\mu_1 + \delta_1 + \gamma)I_M}{C_2\alpha_1(1-\varepsilon\tau)I_F + \alpha_3 A_V}, \tag{3.21}$$

$$\frac{\beta_H\theta N_H[C_2\alpha_1(1-\varepsilon\tau)I_F + \alpha_3 A_V]}{(\mu_1 + \delta_1 + \gamma)[C_2\alpha_1(1-\varepsilon\tau)I_F + \alpha_3 A_V + N_H\mu_1] - C_2\alpha_1(1-\varepsilon\tau)I_F\gamma - \alpha_3 A_V\gamma}, \tag{3.22}$$

$$\frac{N_H(\mu_1 + \delta_1 + \gamma)I_F}{C_1\alpha_2(1-\varepsilon\tau)I_M + \alpha_4 A_V}, \tag{3.23}$$

$$\frac{\beta_H(1-\theta)N_H(C_1\alpha_2(1-\varepsilon\tau)I_M + \alpha_4 A_V)}{[C_1\alpha_2(1-\varepsilon\tau)I_M + \alpha_4 A_V + N_H\mu_1](\mu_1 + \delta_1 + \gamma) - (C_1\alpha_2(1-\varepsilon\tau)I_M\gamma + \alpha_4 A_V\gamma)}, \tag{3.24}$$

$$\frac{\beta_V N_V}{\sigma + \mu_2 + \delta_2}, \tag{3.25}$$

$$\frac{\sigma D_V}{\mu_2 + \delta_2} \tag{3.26}$$

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STABILITY ANALYSIS FOR THE EQUILIBRIUM STATE

We refer to an equilibrium as being stable if the real parts of the eigenvalues of the Jacobian at the equilibrium are negative. An equilibrium is unstable if at least one of the eigenvalues of the Jacobian at that point is positive. In other to obtain the Eigenvalues to check for the stability of the system, we carryout standard linearization of the system by letting the functions F_1, F_2, F_3, F_4, F_5, F_6 to represent equations $(1) - (6)$ respectively as follows

$$F_1 = \beta_H \theta N_H + \gamma I_M - \frac{(C_2 \alpha_1 (1 - \varepsilon\tau) I_F + \alpha_3 A_V) S_M}{N_H} - \mu_1 S_M \qquad (3.27)$$

$$F_2 = \frac{(C_2 \alpha_1 (1 - \varepsilon\tau) I_F + \alpha_3 A_V) S_M}{N_H} - (\mu_1 + \delta_1 + \gamma) I_M \qquad (3.28)$$

$$F_3 = \beta_H (1 - \theta) N_H + \gamma I_F - \frac{(C_1 \alpha_2 (1 - \varepsilon\tau) I_M + \alpha_4 A_V) S_F}{N_H} - \mu_1 S_F \qquad (3.29)$$

$$F_4 = \frac{(C_1 \alpha_2 (1 - \varepsilon\tau) I_M + \alpha_4 A_V) S_F}{N_H} - (\mu_1 + \delta_1 + \gamma) I_F \qquad (3.30)$$

$$F_5 = \beta_V N_V - (\sigma + \mu_2 + \delta_2) D_V \qquad (3.31)$$

$$F_6 = \sigma D_V - (\mu_2 + \delta_2) A_V \qquad (3.32)$$

We differentiate equations $(3.27) - (3.32)$ partially with respect to S_M, I_M, S_F, I_F, D_V and A_V and also putting it in mind that at disease free equilibrium,

$$I_M = I_F = D_V = A_V = 0$$

Hence;

$$J_{11} = \frac{\partial F_1}{\partial S_M} = -\frac{(C_2 \alpha_1 (1 - \varepsilon\tau) I_F + \alpha_3 A_V)}{N_H} - \mu_1 \qquad\qquad J_{21} = \frac{\partial F_2}{\partial S_M} = \frac{(C_2 \alpha_1 (1 - \varepsilon\tau) I_F + \alpha_3 A_V)}{N_H}$$

$$J_{11}(I_F = 0, A_V = 0) = \frac{\partial F_1}{\partial S_M} = -\mu_1 \qquad\qquad J_{21}(I_F = 0, A_V = 0) = \frac{\partial F_2}{\partial S_M} = 0$$

$$J_{31} = \frac{\partial F_3}{\partial S_M} = 0 \qquad J_{41} = \frac{\partial F_4}{\partial S_M} = 0 \qquad\qquad J_{51} = \frac{\partial F_5}{\partial S_M} = 0 \qquad J_{61} = \frac{\partial F_6}{\partial S_M} = 0$$

$$J_{12} = \frac{\partial F_1}{\partial I_M} = \gamma \qquad\qquad\qquad J_{22} = \frac{\partial F_2}{\partial I_M} = -(\mu_1 + \delta_1 + \gamma) = -A_1$$

$$J_{32} = \frac{\partial F_3}{\partial I_M} = -\frac{C_1 \alpha_2 (1 - \varepsilon\tau) S_F}{N_H} = -\frac{qZ}{N_H} \qquad J_{42} = \frac{\partial F_4}{\partial I_M} = \frac{C_2 \alpha_2 (1 - \varepsilon\tau) S_F}{N_H} = \frac{qZ}{N_H}$$

$$J_{52} = \frac{\partial F_5}{\partial I_M} = 0 \qquad\qquad J_{62} = \frac{\partial F_6}{\partial I_M} = 0$$

$$J_{13} = \frac{\partial F_1}{\partial S_F} = 0 \qquad\qquad J_{23} = \frac{\partial F_2}{\partial S_F} = 0$$

$$J_{33} = \frac{\partial F_3}{\partial S_F} = -\frac{(C_2 \alpha_1 (1 - \varepsilon\tau) I_M + \alpha_4 A_V)}{N_H} - \mu_1 \qquad\qquad J_{43} = \frac{\partial F_4}{\partial S_F} = \frac{(C_2 \alpha_1 (1 - \varepsilon\tau) I_M + \alpha_4 A_V)}{N_H}$$

$$J_{33}(I_M = 0, A_V = 0) = \frac{\partial F_3}{\partial S_F} = -\mu_1 \qquad\qquad J_{43}(I_M = 0, A_V = 0) = \frac{\partial F_4}{\partial S_F} = 0$$

$$J_{53} = \frac{\partial F_5}{\partial S_F} = 0 \qquad J_{63} = \frac{\partial F_6}{\partial S_F} = 0$$

$$J_{14} = \frac{\partial F_1}{\partial I_F} = -\frac{C_2 \alpha_1 (1 - \varepsilon\tau) S_M}{N_H} = -\frac{pX}{N_H} \qquad\qquad J_{24} = \frac{\partial F_2}{\partial I_F} = \frac{C_2 \alpha_1 (1 - \varepsilon\tau) S_M}{N_H} = \frac{pX}{N_H}$$

$$J_{34} = \frac{\partial F_3}{\partial I_F} = \gamma \qquad\qquad\qquad J_{44} = \frac{\partial F_4}{\partial I_F} = -(\mu_1 + \delta_1 + \gamma) = -A_1$$

$$J_{54} = \frac{\partial F_5}{\partial I_F} = 0 \qquad\qquad\qquad J_{64} = \frac{\partial F_6}{\partial I_F} = 0$$

$$J_{15} = \frac{\partial F_1}{\partial D_V} = 0 \qquad\qquad J_{25} = \frac{\partial F_2}{\partial D_V} = 0 \qquad J_{35} = \frac{\partial F_3}{\partial D_V} = 0$$

$$J_{45} = \frac{\partial F_4}{\partial D_V} = 0 \qquad\qquad J_{55} = \frac{\partial F_5}{\partial D_V} = -(\sigma + \mu_2 + \delta_2) = -A_2 \qquad J_{65} = \frac{\partial F_6}{\partial D_V} = \sigma$$

$$J_{16} = \frac{\partial F_1}{\partial A_V} = \frac{-\alpha_3 S_M}{N_H} = \frac{-\alpha_3 X}{N_H} \qquad J_{26} = \frac{\partial F_2}{\partial A_V} = \frac{\alpha_3 S_M}{N_H} = \frac{\alpha_3 X}{N_H}$$

$$J_{36} = \frac{\partial F_3}{\partial A_V} = \frac{-\alpha_4 S_F}{N_H} = \frac{-\alpha_4 Z}{N_H} \qquad J_{46} = \frac{\partial F_4}{\partial A_V} = \frac{\alpha_4 S_F}{N_H} = \frac{\alpha_4 Z}{N_H} \qquad J_{56} = \frac{\partial F_5}{\partial A_V} = 0$$

$$J_{66} = \frac{\partial F_6}{\partial A_V} = -(\mu_2 + \delta_2)$$

$$\text{Where } (X, Y, Z, U, V, W) = (S_M, I_M, S_F, I_F, D_V, A_V)$$

$$p = C_2 \alpha_1 (1 - \varepsilon\tau) \qquad q = C_1 \alpha_2 (1 - \varepsilon\tau)$$

$$A_1 = (\mu_1 + \delta_1 + \gamma) \qquad A_2 = (\sigma + \mu_2 + \delta_2)$$

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At the DFE, the Jacobian matrix is;

$$J_{E_0} = \begin{bmatrix} -\mu_1 & \gamma & 0 & -\frac{px}{N_H} & 0 & -\frac{\alpha_3 x}{N_H} \\ 0 & -A_1 & 0 & \frac{px}{N_H} & 0 & \frac{\alpha_3 x}{N_H} \\ 0 & -\frac{qz}{N_H} & -\mu_1 & \gamma & 0 & -\frac{\alpha_4 z}{N_H} \\ 0 & \frac{qz}{N_H} & 0 & -A_1 & 0 & \frac{\alpha_4 z}{N_H} \\ 0 & 0 & 0 & 0 & -A_2 & 0 \\ 0 & 0 & 0 & 0 & \sigma & -(\mu_2 + \delta_2) \end{bmatrix} \quad (3.33)$$

We transform (3.33) represented above to an upper triangular matrix using elementary row reduction method to have

$$R_3 \to R_3 + R_4 = \begin{bmatrix} -\mu_1 & \gamma & 0 & -\frac{px}{N_H} & 0 & -\frac{\alpha_3 x}{N_H} \\ 0 & -A_1 & 0 & \frac{px}{N_H} & 0 & \frac{\alpha_3 x}{N_H} \\ 0 & -\frac{qz}{N_H} & -\mu_1 & \gamma & 0 & -\frac{\alpha_4 z}{N_H} \\ 0 & \frac{qz}{N_H} & 0 & -A_1 & 0 & \frac{\alpha_4 z}{N_H} \\ 0 & 0 & 0 & 0 & -A_2 & 0 \\ 0 & 0 & 0 & 0 & \sigma & -(\mu_2 + \delta_2) \end{bmatrix} \quad (3.34)$$

$$R_4 \to A_1 R_4 + \frac{qz}{N_H} R_2 = \begin{bmatrix} -\mu_1 & \gamma & 0 & -\frac{px}{N_H} & 0 & -\frac{\alpha_3 x}{N_H} \\ 0 & -A_1 & 0 & \frac{px}{N_H} & 0 & \frac{\alpha_3 x}{N_H} \\ 0 & 0 & -\mu_1 & \gamma - A_1 & 0 & 0 \\ 0 & \frac{qz}{N_H} & 0 & -A_1 & 0 & \frac{\alpha_4 z}{N_H} \\ 0 & 0 & 0 & 0 & -A_2 & 0 \\ 0 & 0 & 0 & 0 & \sigma & -(\mu_2 + \delta_2) \end{bmatrix} \quad (3.35)$$

$$R_4 \to \frac{1}{A_1} R_4 = \begin{bmatrix} -\mu_1 & \gamma & 0 & -\frac{px}{N_H} & 0 & -\frac{\alpha_3 x}{N_H} \\ 0 & -A_1 & 0 & \frac{px}{N_H} & 0 & \frac{\alpha_3 x}{N_H} \\ 0 & 0 & -\mu_1 & \gamma - A_1 & 0 & 0 \\ 0 & 0 & 0 & -A_1^2 + \frac{qzpx}{(N_H)^2} & 0 & \frac{A_1 \alpha_4 z}{N_H} + \frac{qz\alpha_3 x}{(N_H)^2} \\ 0 & 0 & 0 & 0 & -A_2 & 0 \\ 0 & 0 & 0 & 0 & \sigma & -(\mu_2 + \delta_2) \end{bmatrix} \quad (3.36)$$

$$R_6 \to A_2 R_6 + \sigma R_5 = \begin{bmatrix} -\mu_1 & \gamma & 0 & -\frac{px}{N_H} & 0 & -\frac{\alpha_3 x}{N_H} \\ 0 & -A_1 & 0 & \frac{px}{N_H} & 0 & \frac{\alpha_3 x}{N_H} \\ 0 & 0 & -\mu_1 & \gamma - A_1 & 0 & 0 \\ 0 & 0 & 0 & -A_1 + \frac{qzpx}{A_1(N_H)^2} & 0 & \frac{\alpha_4 z}{N_H} + \frac{qz\alpha_3 x}{A_1(N_H)^2} \\ 0 & 0 & 0 & 0 & -A_2 & 0 \\ 0 & 0 & 0 & 0 & \sigma & -(\mu_2 + \delta_2) \end{bmatrix} \quad (3.37)$$

$$\begin{bmatrix} -\mu_1 & \gamma & 0 & -\frac{px}{N_H} & 0 & -\frac{\alpha_3 x}{N_H} \\ 0 & -A_1 & 0 & \frac{px}{N_H} & 0 & \frac{\alpha_3 x}{N_H} \\ 0 & 0 & -\mu_1 & \gamma - A_1 & 0 & 0 \\ 0 & 0 & 0 & -A_1 + \frac{qzpx}{A_1(N_H)^2} & 0 & \frac{\alpha_4 z}{N_H} + \frac{qz\alpha_3 x}{A_1(N_H)^2} \\ 0 & 0 & 0 & 0 & -A_2 & 0 \\ 0 & 0 & 0 & 0 & 0 & -A_2(\mu_2 + \delta_2) \end{bmatrix} \quad (3.38)$$

Thus the characteristics equation of the upper triangular matrix (3.38) is given by $|J_{E_0} - \lambda I|$

$$J_{E_0} = \begin{bmatrix} -(\mu_1 + \lambda_1) & \gamma & 0 & -\frac{px}{N_H} & 0 & -\frac{\alpha_3 x}{N_H} \\ 0 & -(A_1 + \lambda_2) & 0 & \frac{px}{N_H} & 0 & \frac{\alpha_3 x}{N_H} \\ 0 & 0 & -(\mu_1 + \lambda_3) & \gamma - A_1 & 0 & 0 \\ 0 & 0 & 0 & -(A_1 - A_3 + \lambda_4) & 0 & A_4 \\ 0 & 0 & 0 & 0 & -(A_2 + \lambda_5) & 0 \\ 0 & 0 & 0 & 0 & 0 & -A_2(\mu_2 + \delta_2) - \lambda_6 \end{bmatrix}$$

$$(3.39)$$

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Equating the product of diagonal of an upper triangular Jacobian matrix to zero (0) gives the eigenvalues of the matrix. Therefore the eigenvalues are

$$-(\mu_1 + \lambda_1) = 0 \qquad\qquad -(A_1 + \lambda_2) = 0 \qquad\qquad -(\mu_1 + \lambda_3) = 0$$
$$\Rightarrow -\mu_1 - \lambda_1 = 0 \qquad\qquad -A_1 - \lambda_2 = 0 \qquad\qquad -\mu_1 - \lambda_3 = 0$$
$$\Rightarrow \lambda_1 = -\mu_1 \qquad\qquad \Rightarrow \lambda_2 = -A_1 \qquad\qquad \Rightarrow \lambda_3 = -\mu_1$$
$$-(A_1 - A_3 + \lambda_4) = 0 \qquad -(A_2 + \lambda_5) = 0 \qquad -A_2(\mu_2 + \delta_2) - \lambda_6 = 0$$
$$-(A_1 - A_3) - \lambda_4 = 0 \qquad\quad -A_2 - \lambda_5 = 0 \qquad\quad -A_2(\mu_2 + \delta_2) = \lambda_6$$
$$\Rightarrow \lambda_4 = -(A_1 - A_3) \qquad \Rightarrow \lambda_5 = -A_2 \qquad \Rightarrow \lambda_6 = -A_2(\mu_2 + \delta_2)$$

Where identity matrix (I) is

$$I = \begin{cases} 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 \end{cases}$$

Thus;

$$|\lambda I| = \begin{cases} \lambda_1 & 0 & 0 & 0 & 0 & 0 \\ 0 & \lambda_2 & 0 & 0 & 0 & 0 \\ 0 & 0 & \lambda_3 & 0 & 0 & 0 \\ 0 & 0 & 0 & \lambda_4 & 0 & 0 \\ 0 & 0 & 0 & 0 & \lambda_5 & 0 \\ 0 & 0 & 0 & 0 & 0 & \lambda_6 \end{cases}$$

$$A_1 = (\mu_1 + \delta_1 + \gamma) \qquad\qquad A_2 = (\sigma + \mu_2 + \delta_2)$$
$$A_3 = \frac{qZpX}{A_1(N_H)^2} \qquad\qquad A_4 = \frac{A_1\alpha_4 Z}{N_H} + \frac{qZ\alpha_3 X}{(N_H)^2}$$

Hence

$$\lambda_1 = -\mu_1 \qquad \lambda_2 = -(\mu_1 + \delta_1 + \gamma) \qquad \lambda_3 = -\mu_1$$
$$\lambda_4 = -\left[(\mu_1 + \delta_1 + \gamma) - \frac{qZpX}{(\mu_1 + \delta_1 + \gamma)(N_H)^2}\right] \qquad \lambda_5 = -(\sigma + \mu_2 + \delta_2)$$

$$\lambda_6 = -(\sigma + \mu_2 + \delta_2)(\mu_2 + \delta_2)$$

For stability of disease-free equilibrium Routh-Hurwitz criteria requires that all eigenvalues have negative real part. Since all the eigenvalues of (3.39) have negative real parts i.e. $\lambda_i < 0$ for

i = 1,2,3, . . . , 6 implies that the disease free equilibrium is stable. Thus the disease dies out in the long run and cannot invade the population.

If $R_e(\lambda) > 0$, the disease free equilibrium is unstable i.e. invasion is always possible and the infection will be able to spread in the population.

An endemic disease is a disease that is always present in a certain population or region. In DFE, we solve to know if the disease cannot invade a population or can but DEE, we already know that the disease have invaded the population and it is persistence. Once the disease invades the population, it becomes endemic.

CONCLUSION

The study analysed the spread and control and control of Lassa fever. Lassa fever is an acute viral haemorrhagic illness caused by Lassa virus. Noting that humans usually become infected with Lassa virus through exposure to food or household items contaminated with urine or feaces of infected Mastomys rats.

The stability analysis for disease free equilibrium of our model showed that the disease dies out in the long run and cannot invade the population.

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