MATHEMATICAL MODEL INCORPORATING SCREENING OF IMMIGRANTS AS A CONTROL AGAINST THE SPREAD OF EBOLA

BY

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ABSTRACT

Ebola Disease Outbreak (EVD) is an acute and often fatal disease in humans and non-human primates (monkeys, gorillas and chimpanzees). The disease is caused by infection with a virus of the family of Filoviridae, genus Ebolavirus. It's case fatality ratio ranges from 25%-90% in humans. The number of travel-related cases in the absence of screening exponentially increases with every successive outbreak.The objective of this study is to develop a mathematical model incorporating screening of immigrants as a control against the spread of Ebola. To achieve the objective of this study, a deterministic non-linear mathematical model for the transmission dynamics of Ebola incorporating screening is developed and analyzed. The analysis shows that the disease free equilibrium of the model may not be globally asymptotically stable whenever R_0 is less than unity. The Ger Sgorin disc argument is used to show that the model has a unique, locally asymptotically stable Endemic Equilibrium (EE). This means that given a small perturbation near the EE, the system returns to EE. We present numerical simulation results in which we observe a significant decrease in the number of Ebola infectives as a result of screening. Hence, we can conclude that screening of immigrants should be considered alongside other control and treatment measures for the effective management and control of Ebola.

This EVD outbreak, believed to have started in Guinea in March 2014 spread to Nigeria through an airline passenger, who arrived from Liberia. It also spread to Senegal by a student from Guinea, who arrived by land transportation [9, 17]. The outbreak eventually spread to other regions outside Africa. For instance, some Ebola-infected patients were flown to the US, France, Germany, Norway, Spain and the UK [4, 17] for health-care delivery. The US diagnosed its first imported travel-related Ebola case in September 2014 (by a person who had travelled to Dallas, Texas, from Liberia). The imported case, who later died of the disease on 8 October 2014, resulted in the infection of two health-care workers who cared for the deceased patient [12]. One of the cases flown to Spain also led to an infection of healthcare workers [4]. A total of 17,942 cases, with 6,388 deaths were reported to WHO as of December 2014.

With this threat of international spread of such a highly infectious disease, compounded by symptom overlap with common illnesses such as malaria, typhoid and flu, screening of immigrants for EVD is imperative if its spread is to be kept under check.

Chapter 1

INTRODUCTION

1.1 BACKGROUND OF THE STUDY

EVD formerly known as hemorrhagic fever(Ebola HF)is a severe, often fatal disease in humans and non-human primates (monkeys, gorillas and chimpanzees)that has appeared sporadically since its initial recognition in 1976. The disease is caused by infection with a virus of the family of Filoviridae, genus Ebolavirus. It has a case fatality ratio ranging from 25%-90% in humans. Individuals become symptomatic after an average incubation period ranging from 2-21 days and infectiousness is increased during the later stages of the disease. EVD transmission during the incubation period is very unlikely and occurs via direct contact with blood, secretions, and/or other body fluids of dead or living infected persons.

The onset of the disease is abrupt and is characterized by sudden onset of fever, headache, intense weakness, joint and muscle aches, sore throat followed by diarrhea, vomiting and impaired kidney and liver function. A rash, red eyes, hiccups and internal and external bleeding may be seen in some patients. Currently there is no cure for Ebola. However the search for an effective Ebola virus vaccine is on-going with interim results showing 100% efficacy in individuals [14].

EVD transmission occur in the general community, in hospital settings and during

funeral rites, yet there is increasing risk of international spread due to air travel and human mobility.

There have been four major known outbreaks of EVD since the disease first appeared in 1976 in Zaire, now the Democratic Republic of Congo. However, the largest, and most devastating, outbreak of EVD is the 2014 epidemic in three West African countries (Guinea, Liberia and Sierra Leone). The populations of Guinea, Liberia and Sierra Leone are highly interconnected, with much cross border traffic at the epicentre and relatively easy connections by road between rural towns and villages and between densely populated national capitals. The large intermixing populations favoured the spread of the infection.

This EVD outbreak, believed to have started in Guinea in March 2014 spread to Nigeria through an airline passenger, who arrived from Liberia. It also spread to Senegal by a student from Guinea, who arrived by land transportation [9, 17]. The outbreak eventually spread to other regions outside Africa. For instance, some Ebola-infected patients were flown to the US, France, Germany, Norway, Spain and the UK [4, 17] for health-care delivery. The US diagnosed its first imported travel-related Ebola case in September 2014 (by a person who had travelled to Dallas, Texas, from Liberia). The imported case, who later died of the disease on 8 October 2014, resulted in the infection of two health-care workers who cared for the deceased patient [12]. One of the cases flown to Spain also led to an infection of healthcare workers [4]. A total of 17,942 cases, with 6,388 deaths were reported to WHO as of December 2014.

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1.2 STATEMENT OF THE PROBLEM

The symptoms of Ebola are non-specific to the virus and are seen in other patients with diseases that occur more frequently like flu, malaria and typhoid. Despite applying a

package of interventions including contact tracing, there were more cases and deaths in the last outbreak in West Africa than all others combined. In the absence of screening of immigrants for EVD, the threat of international spread of this highly infectious and fatal disease is more real today than before as observed in the 2014 Ebola outbreak. Hence this study considers screening of immigrants as a control measure.

1.3 OBJECTIVE OF THE STUDY

1.3.1 MAIN OBJECTIVE

The broad objective of this study was to develop a mathematical model incorporating screening of immigrants as a control against the spread of Ebola.

1.3.2 SPECIFIC OBJECTIVES

The specific objectives of this research were:

(i) To formulate a mathematical model for EVD incorporating screening.

(ii)To perform stability analysis of the model formulated.

(iii) To determine the long term effect of screening of immigrants as a control strategy.

1.4 SIGNIFICANCE OF THE STUDY

International travel as witnessed in the last EVD outbreak greatly facilitates the spread of the disease. Therefore effective screening of immigrants is critical in the control of the spread of the infection. The results of this study underscore the significance of screening as a strategy for disease control to national governments, policy makers and health practitioners. The novelty of the mathematical results contribute to the body of knowledge and research in mathematics.

1.5 JUSTIFICATION OF THE STUDY

This study has been necessitated by the fact that Ebola is a highly infectious disease with a high mortality rate of between 25%-90%. A package of interventions has been applied since its first recognition in 1976 and yet there were more cases and deaths in the last outbreak than all others combined. Furthermore, Ebola has a symptom overlap with common diseases like flu, malaria and typhoid. It is therefore possible that in the absence of screening, its spread will continue to increase through human travel.

Chapter 2

LITERATURE REVIEW

2.1 BACKGROUND

Mathematical models are instrumental in providing guidance to the future projections of important public health crises such as the spread of infectious diseases, and in assessing what the potential impact interventions might have towards transmission control. Several mathematical models have been proposed to study Ebola outbreaks and possible interventions to control it's spread.

Using S-I-R(Susceptible, Infected, Recovered) and S-E-I-R(Susceptible, Exposed, Infected, Recovered) models, Jaime *et al* [3] simulated two outbreaks, in Yambuku 1976 and in Kikwit 1995, Zaire. The dynamics of this model were determined by the per-capita death rate of infected individuals and the per-capita effective contact rate of an individual contracting the disease. The basic reproductive number, R_0, determined the infectiousness of the disease. These models were to help health officials plan for the latter part of an outbreak by calculating the parameters from the data at the start of the epidemic. The number of deaths could be minimized by altering the environment i.e lowering the effective contact rate which could be accomplished by implementing quarantine.

Another study by Agusto *et al* [1], assessed the roles of traditional customs and public health-care systems on disease spread. They designed a model which incorporated the

effects of traditional belief system and customs along with disease transmission within health-care settings and by Ebola deceased individuals. A sensitivity analysis was performed to determine model parameters that most affect disease transmission. Numerical simulations were also performed and the parameters that drive disease transmission, with or without basic public health control measures determined. This study found that a significant reduction of new EVD cases can be achieved by increasing health-care workers' daily shifts from 8 hours' shift to 24 hours' shift, limiting hospital visitation to 1 hour and educating the populace to abandon detrimental traditional/cultural belief systems. In many African societies due to family attachments, people travel from far and wide to attend burials. Inappropriate handling of the dead may therefore be the origin of a spread facilitated by travelling.

A model for the 2014 Ebola epidemic in Sierra Leone and Liberia was developed by Glenn *et al* [16]. The model describes the dynamic interactions of the susceptible and infected populations of these countries. The model incorporates the principle features of contact tracing, namely, the number of contacts per identified infectious case, the likelihood that a traced contact is infectious and the efficiency of the contact tracing process. The study shows that the most important elements for containment of the epidemic within a relatively short span are that:

(i) infectious case(independent of contact tracing) are efficiently reported and isolated with the average time between the appearance of symptoms and isolation being less than 3 days.

(ii) contact traced incubating infected cases are efficiently monitored, with isolation upon appearance of symptom (such that no new cases are caused by individuals)

However contact tracing is quite challenging especially with high mobility rates due to improved means of transport.

Stefano *et al*, [13] developed a model for Ebola virus transmission that integrates the movements of individuals, including patients not infected with EVD, seeking assistance

in health-care facilities, the movements of individuals taking care of patients infected with Ebola virus not admitted to hospital, and the attendance of funerals. The model was used to estimate Ebola virus transmission parameters and investigate the effectiveness of interventions such as availability of Ebola treatment units, safe burial procedures, and household protection kits. The model allowed for the assessment of these intervention options and the understanding of their role in the decrease in incidence. This model, however, is localized and did not consider mobility due to commuting patterns or other business travel which are likely to play an important part in EVD transmission.

In yet another research work by Gomes *et al*, [10] a mobility model integrating daily airline passenger traffic worldwide showing simulations of epidemic spread worldwide was developed. They provided a quantitative assessment of the international spread based on large-scale computer micro-simulations of the 2014 West African outbreak. This study modelled the short-term growth rate of the disease in the affected West African countries and estimated the basic reproductive number to be in the range 1.5-2.0. The estimates obtained from this model were used to generate the probability of international spread if the containment measures were not successful at curtailing the outbreak. Results indicated that if EVD outbreaks are not contained, the probability of international spread would increase consistently, especially if other countries are affected and not able to contain the epidemic.

The probability of any country to experience EVD case importation depends on the passenger flow from the areas affected by the outbreak, the case numbers and the duration of the incubation time. With this threat of international spread due to travel, screening of passengers for EVD is imperative if the spread is to be kept under check.

Chapter 3

METHODOLOGY

3.1 MODEL DECRIPTION AND FORMULATION

Mathematical models can project how infectious diseases progress to show the likely outcome of an epidemic and help inform public health interventions. Various mathematical models that analyze the dynamics of infectious human diseases have been formulated and analyzed. Many such models are based on systems of differential equations, see for instance [2].

To achieve the objective of this study we formulate a mathematical model based on a system of ordinary differential equations for the dynamics of Ebola virus disease incorporating screening. The model subdivides the human population into classes represented by the state variables Susceptible $S(t)$ (population capable of becoming infected), Exposed $E(t)$ (incubating infected), Infected $I(t)$ (infectious infected), Hospitalized $H(t)$ (hospitalized infectives) and Removed $R(t)$ (infectious cases who have recovered or died). The model is an S-E-I-R type where the Infected class is divided into those infected and not hospitalized and hospitalized infectives.

This model shall be based on the assumptions that:

(i) the infection term $\lambda = \theta I$ is of mass action form where θ is the effective contact rate.

Contacts are assumed to be proportional to the population density. Consequently,

the rate of transmission depends on the number of Susceptible individuals in the population rather than the proportion.

(ii) the Recovered individuals acquire temporary immunity. This is because evidence from previous Ebola outbreaks shows that people who survived the disease had antibodies to the virus that could still be detected 10 years after recovery [11].

Recruitment takes place at the constant rate Λ where a fraction $\sigma\lambda$ is into the Susceptible class whereas $(1-\sigma)\Lambda$ is the recruitment into the infected class. The parameter $0 \leq \rho \leq 1$ models the effectiveness of screening. When $\rho = 1$, there is no infected immigrants entering the population, in other words the screening is 100% efficient in terms of identifying infected individuals.

The other parameters of the model are given in the table 3.1 below.

Table 3.1: Parameters in the model

Parameter	**Symbol**
Recruitment into susceptible	$\sigma\Lambda$
Natural death rate	μ
Average rate of infection	λ
Average incubation period	β
Rate of hospitalization	γ
Disease mortality	α
Disease mortality among the hospitalized	κ
Rate of recovery	η
Immigrant recruitment into the infected class	$(1-\sigma)\Lambda$
Effectiveness of screening	ρ

The flow chart diagram for the model is given in Figure 3.1 below:

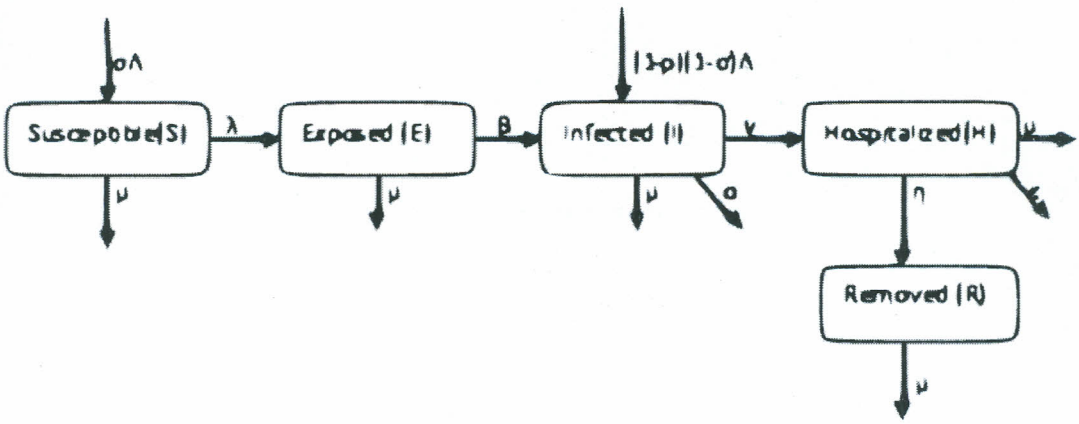

Figure 3.1: Mathematical model incorporating screening

From the above definition of parameters and state variables, the resulting system of non-linear ordinary differential equations for the dynamics of Ebola is given by

$$\begin{aligned}
\frac{dS}{dt} &= \sigma\Lambda - \theta IS - \mu S \\
\frac{dE}{dt} &= \theta IS - \beta E - \mu E \\
\frac{dI}{dt} &= \beta E + (1-\rho)(1-\sigma)\Lambda - (\mu + \gamma + \alpha)I \\
\frac{dH}{dt} &= \gamma I - (\eta + \mu + \kappa)H \\
\frac{dR}{dt} &= \eta H - \mu R
\end{aligned} \tag{3.1}$$

and $N(t)$, the total human population at time t is given by

$N(t) = S(t) + E(t) + I(t) + H(t) + R(t)$ and $N(t) = N(0)$, at $t = 0$

3.2 POSITIVITY AND BOUNDEDNESS OF SOLUTIONS

Model (3.1) describes human population and we therefore show that the associated state variables $S(t), E(t), I(t), H(t)$ and $R(t)$ are non-negative for all time t ≥ 0.

Taking the first equation of the model (3.1)

$$\begin{aligned}\frac{dS}{dt} &= \sigma\Lambda - \theta IS - \mu S \\ \frac{dS}{dt} &\geq -(\theta I + \mu)S\end{aligned}$$

Separating the variables,

$$\frac{dS}{S} \geq -(\theta I + \mu)dt \tag{3.2}$$

Integrating the differential inequality (3.2),

$$\begin{aligned}\int_{s_0}^{s} \frac{dS}{S} &\geq \int_{t0}^{t} -(\theta I + \mu)dt \\ \ln S|_{s_0}^{s} &\geq -(\theta I + \mu)|_{t_0}^{t}\end{aligned} \tag{3.3}$$

At $t = 0$, $S = S_0$

$$S(t) \geq S_0 \exp^{-(\theta I+\mu)(t-t_0)} \geq 0 \tag{3.4}$$

It can be shown in a similar manner that all the other solutions i.e $E(t), I(t), H(t), R(t)$ are non-negative for $t \geq 0$.

To show that all feasible solutions are uniformly bounded, we sum up the five equations in the system (3.1) to get;

$$
\begin{aligned}
\frac{dN}{dt} &= \sigma\Lambda + (1-\rho)(1-\sigma)\Lambda - \alpha I - \kappa H - \mu(S+E+I+H+R)N \\
\frac{dN}{dt} &= \sigma\Lambda + (1-\rho)(1-\sigma)\Lambda - \alpha I - \kappa H - \mu N \\
\frac{dN}{dt} &\leq \sigma\Lambda - \mu N \\
\frac{dN}{dt} + \mu N &\leq \sigma\Lambda \\
N &\leq \frac{\sigma\Lambda}{\mu} + N(0)\exp^{-\mu t} \qquad (3.5)
\end{aligned}
$$

It follows that:

$$0 \leq N \leq \frac{\sigma\Lambda}{\mu} + N(0)\exp^{-\mu t} \qquad (3.6)$$

where N(0) represents the value of (3.5) evaluated at the initial values of the respective variables. Thus as $t \longrightarrow \infty$, we have;

$$0 \leq N \leq \frac{\sigma\Lambda}{\mu} \qquad (3.7)$$

Since the solutions are positive and bounded the model (3.1) is well-posed mathematically and epidemiologically and it is sufficient to consider its solutions.

Since the model (3.1) is non-linear it may not be possible to obtain closed form solutions. However we can still study the behaviour of the solutions near and away from the equilibrium points of the model. The two equilibrium points of interest are the Disease Free Equilibrium (D.F.E) and the Endemic Equilibrium (E.E).

3.3 DISEASE FREE EQUILIBRIUM POINT OF THE MODEL

Since the first three equations in model (3.1) do not contain terms of the state variables $H(t)$ and $R(t)$, we can analyze a reduced system given by

$$\begin{aligned}
\frac{dS}{dt} &= \sigma\Lambda - \theta IS - \mu S \\
\frac{dE}{dt} &= \theta IS - \beta E - \mu E \\
\frac{dI}{dt} &= \beta E + (1-\rho)(1-\sigma)\Lambda - (\mu+\gamma+\alpha)I
\end{aligned} \tag{3.8}$$

Disease Free Equilibrium (DFE) point of a model are its steady state solutions in the absence of infection (or disease). It's obtained by setting the right hand side of (3.8) to zero and solving for the state variables with $E(t) = I(t) = 0$.

$$\begin{aligned}
\frac{dS}{dt} &= \sigma\Lambda - \mu S = 0 \\
\sigma\Lambda &= \mu S \\
S &= \frac{\sigma\Lambda}{\mu}
\end{aligned}$$

For the system (3.8), the DFE is

$$(S^0, E^0, I^0) = (\frac{\sigma\Lambda}{\mu}, 0, 0) \tag{3.9}$$

3.3.1 THE STABILITY OF DFE

The dynamics of the system (3.8) is highly dependent on the basic reproduction number. The basic reproduction number denoted as R_0, is defined as the average number of secondary infections caused by a single infectious individual during their entire infectious life-time in a fully susceptible population [6].

We determine R_0 using the next generation operator approach by Van Den and Watmough [15] where R_0 is the spectral radius of the matrix FV^{-1} and F and V are next generation matrices.

The next generation matrix (operator) FV^{-1} is formed from matrices of the partial derivatives of $\mathscr{F}_i$ and $\mathscr{V}_i$ with respect to the infected classes computed at DFE.

The infected compartments of (3.8) are ($E(t)$ and $I(t)$). The right hand side of the infected compartments in equation (3.8) may be written as

$$\mathscr{F} - \mathscr{V}$$

where $\mathscr{F}$ is the matrix of infection while $\mathscr{V}$ is the matrix of transfer into and out of the two compartments. Thus,

$$\mathscr{F} = \begin{pmatrix} \theta IS \\ 0 \end{pmatrix}$$

$$\mathscr{V} = \begin{pmatrix} (\beta+\mu)E \\ -\beta E - (1-\rho)(1-\sigma)\Lambda + (\mu+\gamma+\kappa)I \end{pmatrix}$$

To obtain the next generation matrices F and V we find the Jacobian of $\mathscr{F}$ and $\mathscr{V}$ at D.F.E. This yields;

$$F = \begin{pmatrix} 0 & \frac{\theta\sigma\Lambda}{\mu} \\ 0 & 0 \end{pmatrix}$$

$$V = \begin{pmatrix} \beta+\mu & 0 \\ -\beta & \mu+\gamma+\alpha \end{pmatrix}$$

The eigenvalues of the matrix FV^{-1} are $\{0, \frac{\beta\theta\Lambda\sigma}{\mu(\beta+\mu)(\alpha+\gamma+\mu)}\}$

$$\text{Therefore,} \quad R_0 = \frac{\beta\theta\Lambda\sigma}{\mu(\beta+\mu)(\alpha+\gamma+\mu)}. \tag{3.10}$$

Theorem 3.3.1. *The DFE of the model (3.8) is locally asymptotically stable whenever* $R_0 < 1$ *and unstable whenever* $R_0 > 1$

Proof. The Jacobian of (3.8) is given by

$$J = \begin{pmatrix} -(\theta I+\mu) & 0 & \theta S \\ \theta I & -(\beta+\mu) & \theta S \\ 0 & \beta & -(\mu+\gamma+\alpha) \end{pmatrix}$$

Evaluating this Jacobian at the disease free equilibrium point ($(S^0, E^0, I^0) = (\frac{\sigma\Lambda}{\mu}, 0, 0)$) we obtain,

$$J_{DFE} = \begin{pmatrix} -\mu & 0 & -\frac{\theta\sigma\Lambda}{\mu} \\ 0 & -(\beta+\mu) & \frac{\theta\sigma\Lambda}{\mu} \\ 0 & \beta & -(\mu+\gamma+\alpha) \end{pmatrix}$$

For the local stability of $D.F.E$, the eigenvalues of the matrix J_{DFE} should all have negative real parts. Clearly one of the eigenvalues of J_{DFE} is $-\mu$. The other eigenvalues are obtained from the reduced 2×2 block matrix given by

$$B = \begin{pmatrix} -(\beta+\mu) & \frac{\theta\sigma\Lambda}{\mu} \\ \beta & -(\mu+\gamma+\alpha) \end{pmatrix}$$

We can apply the Routh-Hurwitz Criterion of: A negative trace and a positive determinant on the B which guarantees that the eigenvalues of B will have negative real parts. Clearly the trace of B is negative since the elements in the main diagonal are negative. The determinant of B is given by:

$$det = (\beta+\mu)(\mu+\gamma+\alpha) - \frac{\beta\theta\sigma\Lambda}{\mu} \tag{3.11}$$

□

From (3.10) $(\beta+\mu)(\mu+\gamma+\alpha) = \frac{\beta\theta\sigma\Lambda}{\mu R_0}$

Substituting this in equation (3.11),

$det = \frac{\beta\theta\sigma\Lambda}{\mu R_0} - \frac{\beta\theta\sigma\Lambda}{\mu}$

$det = \frac{\beta\theta\sigma\Lambda}{\mu}(\frac{1}{R_0} - 1)$

which is positive whenever $R_0 < 1$

The Routh-Hurwitz Criterion is met on condition that $R_0 < 1$. Therefore the eigenvalues of J_{DFE} will have negative real parts whenever $R_0 < 1$ and this implies that D.F.E is locally asymptotically stable whenever $R_0 < 1$ and unstable otherwise.

3.3.2 THE GLOBAL STABILITY OF D.F.E.

To study the global stability of D.F.E we use the technique by [5]. This requires that (3.8) be written in the form;

$$\begin{aligned} \frac{dX}{dt} &= F(X;Z) \\ \frac{dZ}{dt} &= G(X;Z); G(X;\mathbf{0}) = 0 \end{aligned} \tag{3.12}$$

where $X \in \mathbb{R}$, denotes uninfected compartments (S) and, $Z \in \mathbb{R}^2$ denotes infected compartments(E,I). The disease-free equilibrium is now denoted as

$$D.F.E = (X^*, 0), X^* = (\frac{\sigma\Lambda}{\mu}). \tag{3.13}$$

The technique stipulates that the following conditions H1 and H2 must be met to guarantee global asymptotic stability.

H1: For $\frac{dX}{dt} = F(X;0), D.F.Eis(G.A.S)$

H2: $G(X;Z) = AZ - \hat{G}(X,Z), \hat{G}(X,Z) \geq 0.$

where $A = D_z G(X^*, 0)$ is an M-matrix (the off-diagonal elements of A are non-negative).

If the system (3.9) satisfies the conditions above then the theorem below holds.

Theorem 3.3.2. *The fixed point $D.F.E = (X^*, 0)$ is a globally asymptotically stable equilibrium of system (3.8) provided that $R_0 < 1$ and the assumptions in H1 and H2 are satisfied.*

From the system (3.8),

$$F(X;0) = \sigma\Lambda - \mu$$

$$A = \begin{pmatrix} -(\beta+\mu) & 0 \\ \beta & -(\mu+\gamma+\alpha) \end{pmatrix}$$

and

$$\hat{G}(X,Z) = \begin{pmatrix} -(\theta IS) \\ -(1-\rho)(1-\sigma)\Lambda \end{pmatrix}$$

Since $\sigma \leq 1$ and $0 \leq I \leq S \leq N$, then $\hat{G}(X,Z) \leq 0$, therefore D.F.E is not globally asymptotically stable. This means given a large perturbation, the system does not return to DFE.

3.4 THE EXISTENCE OF A UNIQUE POSITIVE ENDEMIC EQUILIBRIUM

The endemic equilibrium state is the state where the disease cannot be totally eradicated but remains in the population at manageable levels. For the disease to persist in the population, the susceptible class, the Exposed and the Infectious class must not be empty at equilibrium state. In other words, if $EE = (S^*, E^*, I^*)$ is the endemic equilibrium state, then $EE = (S^*, E^*, I^*) \neq (0,0,0)$

The endemic equilibrium point of (3.3.1) is obtained by equating the derivatives to zero and solving for the variables S^*, E^*, I^*.

At an endemic state, the first equation of model (3.3.1) becomes

$$\begin{aligned} \sigma\Lambda &= (\theta I + \mu)S \\ S^* &= \frac{\sigma\Lambda}{\theta I^* + \mu} \qquad \forall I^* \geq 0 \end{aligned} \tag{3.14}$$

From the second equation in (3.8),

$$\begin{aligned} \theta I^* S^* &= (\beta + \mu)E^* \\ \frac{\theta I^* \sigma\Lambda}{\theta I^* + \mu} &= (\beta + \mu)E^* \\ E^* &= \frac{\theta I^* \sigma\Lambda}{(\theta I^* + \mu)(\beta + \mu)} \qquad \forall I^* \geq 0 \end{aligned} \tag{3.15}$$

From the third equation in (3.8),

$$
\begin{aligned}
\beta E^* &= (\mu+\gamma+\alpha)I^* - (1-\rho)(1-\sigma)\Lambda \\
E^* &= \frac{1}{\beta}(\mu+\gamma+\alpha)I^* - (1-\rho)(1-\sigma)\Lambda) \\
\frac{\theta I^*\sigma\Lambda}{(\theta I^*+\mu)(\beta+\mu)} &= \frac{1}{\beta}(\mu+\gamma+\alpha)I^* - (1-\rho)(1-\sigma)\Lambda) \\
\frac{\theta I^*\sigma\Lambda\beta}{(\theta I^*+\mu)(\beta+\mu)} &= (\mu+\gamma+\alpha)I^* - (1-\rho)(1-\sigma)\Lambda \qquad (3.16)
\end{aligned}
$$

Multiplying both sides of equation (3.16) by $\frac{\theta I^*+\mu}{(\mu)(\mu+\gamma+\alpha)}$

$$
\frac{\theta I^*\sigma\Lambda\beta}{\mu(\beta+\mu)(\mu+\gamma+\alpha)} = \frac{\theta}{\mu}I^{*2} + I^* - \frac{(1-\rho)(1-\sigma)\Lambda\theta}{(\mu+\gamma+\alpha)(\mu)}I^* - \frac{(1-\rho)(1-\sigma)\Lambda}{\mu+\gamma+\alpha}
$$

$$
R_0 I^* = \frac{\theta}{\mu}I^{*2} + I^* - \frac{(1-\rho)(1-\sigma)\Lambda\theta}{(\mu+\gamma+\alpha)(\mu)}I^* - \frac{(1-\rho)(1-\sigma)\Lambda}{\mu+\gamma+\alpha}
$$

$$
\frac{\theta}{\mu}I^{*2} + [1 - R_0 - \frac{(1-\rho)(1-\sigma)\Lambda\theta}{(\mu+\gamma+\alpha)(\mu)}]I^* - \frac{(1-\rho)(1-\sigma)\Lambda}{\mu+\gamma+\alpha} = 0
$$

which we express as

$$
AI^{*^2} + BI^* - C = 0 \qquad (3.17)
$$

where

$A = \frac{\theta}{\mu}$

$B = 1 - R_0 - \frac{(1-\rho)(1-\sigma)\Lambda\theta}{(\mu+\gamma+\alpha)(\mu)}$

$C = \frac{(1-\rho)(1-\sigma)\Lambda}{\mu+\gamma+\alpha}$

By the Descartes rule of sign change, [7], equation (3.17) has only one variation in sign which implies that there exists only one positive real root. Therefore $I^* > 0$.

This confirms the existence of a positive endemic state.

3.4.1 THE LOCAL STABILITY OF ENDEMIC EQUILIBRIUM.

Theorem 3.4.1. *The Endemic Equilibrium (EE) is locally asymptotically stable whenever it exists.*

Proof. Consider the Jacobian of the model (3.8) at the Endemic Equilibrium $EE = (S^*, E^*, I^*)$

$$J_{EE} = \begin{pmatrix} -\theta I^* - \mu & 0 & -\theta S^* \\ \theta I^* & -(\beta+\mu) & \theta S^* \\ 0 & \beta & -(\mu+\gamma+\alpha) \end{pmatrix}$$

Since the diagonal elements of the matrix J_{EE} are negative and the eigenvalues of any square matrix A are the same as those of A^T, an argument using Ger sgorin discs [8] shows that J_{EE} is stable if it is diagonally dominant in columns.

setting $\tau = max\{g_1, g_2, g_3\}$ where

$g_1 = -\theta I^* - \mu + \theta I^* + 0 = -\mu$

$g_2 = 0 + -(\beta+\mu) + \beta = -\mu$

$g_3 = -\theta S^* + \theta S^* - (\mu+\gamma+\alpha) = -(\mu+\gamma+\alpha)$

gives $\tau = max\{-\mu, -(\mu+\gamma+\alpha)\} < 0$; which implies diagonal dominance as claimed, and hence the proof. □

3.5 NUMERICAL SIMULATION

We use Matlab software to illustrate the numerical simulations describing the theoretical results for system 3.1. The parameters used in the simulation are either obtained from literature or estimated. The parameter values have been varied within realistic limits to better understand how screening of immigrants influences the prevalence and transmission of EVD. The parameter values are given in the table 3.2.

3.6 PARAMETER VALUES

Table 3.2: Parameter Values used in simulation

Parameter	**Symbol**	**values per day**	**source**
Recruitment into susceptible	$\sigma\Lambda$	0.000096274	[10]
Natural death rate	μ	0.000039	[10]
Average incubation period	β	0.1429	[10]
Effective contact rate	θ	varies	*Estimated*
Rate of hospitalization of infectives	γ	0.67	[10]
Rate of death of infectives due to disease	α	0.1042	[10]
Rate of death of hospitalized infectives	κ	0.55	[10]
Rate of recovery	η	0.05	[10]
Effectiveness of screening	ρ	varies	Estimated

When screening is highly effective then we expect the number of infected individuals generally having contact with susceptibles to be low. Thus the probability of transmission is low and effectively the effective contact rate becomes low. For numerical simulation of Ebola transmission of the model 3.8, we use the following initial populations. The time t in the simulation is in days. $S_0 = 1000; I_0 = 40$. The Figure (3.2) below shows the effect of varying screening levels on number of infectives.

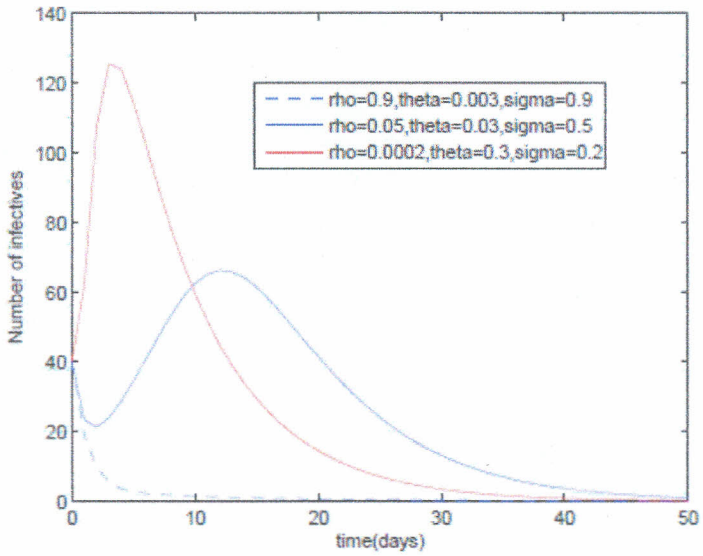

Figure 3.2: Effect of varying screening on number of infectives

The profile for $\rho = 0.0002, \theta = 0.3, \sigma = 0.2$; corresponds to very low levels of screening. It shows the number of infectives initially increasing then coming down steadily to diminishing levels. The rise could be as a result of inability to accurately diagnose the disease at its initial stages since it has clinical symptom overlap with other diseases such as flu, malaria and typhoid. The drop in the number of new infectives may be attributed to the fact that once there are clear manifestations of Ebola symptoms, the susceptible population quickly takes precautionary measures.

When the screening is very effective almost no new infected individuals enter the susceptible population, as indicated by the profile for $\rho = 0.9, \theta = 0.003, \sigma = 0.9$. Therefore there's no increase in the number of infectives, instead there's a decrease.

This figure 3.2 therefore shows a significant decrease in the number of Ebola infec-

tives with an increase in rate of screening. Hence, we can conclude that screening of immigrants should be adopted by policy makers as a control measure for the effective management and control of the spread of Ebola.

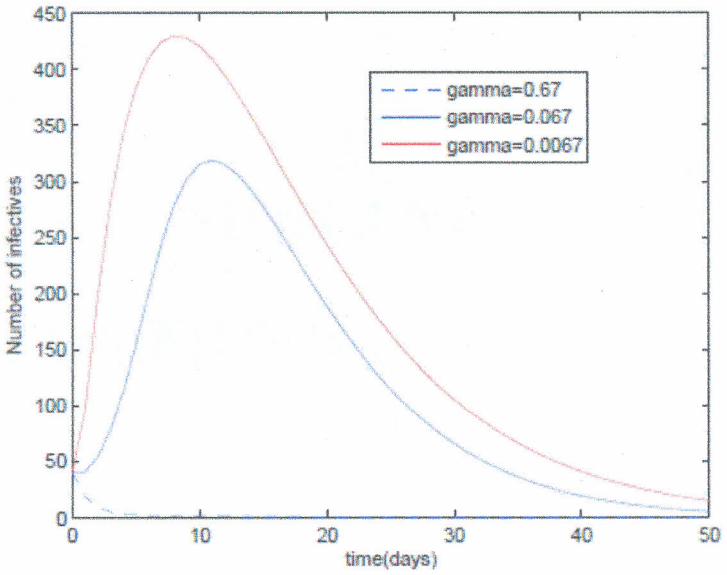

Figure 3.3: Effect of varying rate of hospitalization

We expect that during screening the infectives found in the population are quarantined in a hospital and given treatment. The Figure 3.3 below indicates that when the rate of hospitalization is very low say, $\gamma = 0.0067$, the number of infectives rises sharply before falling. This may be attributed to the unrestricted contacts made between the susceptible population and the infected individuals. The fall in the number of new infectives is due to control measures being employed.

When the rate of hospitalization is high say $\gamma = 0.67$, the number of infectives drops. This is because of the expected reduced contact between the susceptibles and the infectives.

Chapter 4

CONCLUSION AND RECOMMENDATIONS

4.1 CONCLUSION

A deterministic model for the dynamics of ebola is presented and analysed. We established the basic reproduction number R_0 of the model, which is the expected number of secondary infections produced by an infective in a completely susceptible population, during his/her infective period. The analysis shows that the disease free equilibrium of the model is locally asymptotically stable but may not be globally asymptotically stable whenever R_0 is less than unity. This means that given a small perturbation near the DFE, the system returns to DFE while given a big perturbation the system does not return to DFE. The Centre Manifold theorem is used to show that the model has a unique endemic equilibrium which is locally asymptotically stable when$R_0 < 1$ and unstable when $R_0 > 1$.

The numerical simulation as presented in figure 3.1 showed that the screening of Ebola infected immigrants plays a very important role in controlling the spread of this disease. From the presented results it can be seen that there's a significant decrease in the number of Ebola infectives with an increase in rate of screening. Hence, we can conclude that screening of immigrants should be adopted by policy makers as a control measure for the

effective management and control of the spread of Ebola.

4.2 RECOMMENDATIONS

We conclude by providing the following list of recommendations, mostly directly borne out of the simulation results derived from this study.

- Screening- From the findings of this study,as in figure 3.1, it is clear that there's a significant decrease in the number of Ebola infectives with an increase in rate of screening. It is recommended that screening of immigrants should be adopted as a control measure for the effective management and control of the spread of Ebola.

- Hospitalization- From figure 3.2, we see that a high rate of hospitalization of Ebola infectives also significantly decreases the number of infectives in the population. Hospitalization of the infectives after screening is therefore highly recommended.

- Future work- Reports of Ebola vaccine trials have indicated very promising results due to high vaccine efficacy levels [17]. Future studies should emphasize the formulation and analysis of vaccine models with different vaccine strategies e.g Pulse vaccination, Mass vaccination, Routine vaccination etc.

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