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Ebola Epidemic Disease: Modelling, Stability Analysis, Spread Control Technique, Simulation Study and Data Fitting

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***Abstract*—In this paper, we proposed (S-E-I-I_h-R) mathematical model and conducted stability analysis. Disease Free Equilibrium (DFE) point of the model has been identified. Stability analysis at the disease free equilibrium point is studied. Formula for the basic reproductive number is obtained. It is shown that DFE point is locally and globally asymptotically stable for $R_0 < 1$, whereas it is unstable for $R_0 > 1$. Disease spread controlling technique called 'Isolation' is also proposed. Isolation of exposed and infected individuals is a powerful technique and can be used to control the spreading of the epidemic. Simulation study of the model is conducted. Data fitting of Ebola epidemic is done. For this purpose the data of infected and death cases found in West African countries is taken into consideration. The best fit of cumulative infected case is computed to follow simulated curve with R_0 =1.5. Further, the present study supports that the cumulative death cases due to Ebola epidemic is 65% of the infected individuals.**

Keywords—Ebola disease, SEII_hR model, Basic reproductive number, Stability Analysis, Simulation study

1. Introduction

The infectious diseases will be transmitted directly or indirectly from person to person and / or from animals and birds to human beings. These infectious diseases would be a cause of deaths in worldwide [1]. Ebola is one of infection dieses caused by Ebola viruses. Ebola virus causes a hemorrhagic fever syndrome in humans. It is found in previous outbreaks that fatality rate is about 90% among the infected individuals. The current outbreak in the West African countries has spread over a large geographical region and is causing a high number of infection and death cases [4]. Even though the death rate is well below 90% in the West African Ebola outbreak the disaster is not out of danger. Among the West African countries viz., Guinea, Liberia and Sierra Leone the Ebola virus outbreak is being overspread [1-6]. In addition to the loss of life, the outbreak has significant impact on all the socio-economical activities [2]. Even though the present outbreak is restricted to a particular region but its impact spreads limitlessly around the globe.

Mathematical modeling is a significant and powerful tool that can be employed in analyzing the spread and control of infectious diseases such as Ebola [4-7]. Model simulation and data fitting of epidemics are assumed to provide understanding of methods and suggest prevention, control strategies and helps to recognize removing policy development. The basic concept in mathematical modeling is stability analysis of the equilibrium point of the epidemic models. Many epidemic models have a disease free equilibrium point at which the population remains in the absence of disease. These models typically have a threshold parameter, called the basic reproduction number and denoted by R_0. The basic reproduction number R_0 is defined as the expected number of secondary cases produced by a single (typical) infection in a completely susceptible population [10-11]. If $R_0 < 1$ then the DFE point is locally asymptotically stable, whereas if $R_0 > 1$, then the DFE is unstable [11-17]. By using appropriate Lyapunov functions and LaSalle's invariance principle, we prove the disease free equilibrium point is globally asymptotically stable when the basic reproduction number $R_0 < 1$ [17].

Contact tracing or Isolation mechanism is an essential technique of the overall strategy for controlling the outbreak of Ebola virus disease (EVD). Contact tracing is defined as the identification and follow up of persons who comes in direct contact with a sick Ebola patient or an infected person. As a result that there has not been any well know vaccination or medicine, contact tracing proves to be an important measurement of epidemic investigation and active inspection [8]. In this study also the model simulation supports the use of contact tracing process in controlling of Ebola virus disease outbreak. The isolation is made from exposed and infected compartments with different rates.

In section 2, we constructed Mathematical modeling of SEII_hR epidemics. Assumptions and description of the model are provided. Bounds of the model variables are identified. Formula for the basic reproductive number is obtained and dimensionless variables of the system are introduced. In section 3, equilibrium points are identified and the stability analysis is made. In section 4, simulation study of the model is taken up. In section 5, data of Ebola virus epidemic infected and death cases found in West

Africa is fitted into the model and observations are made. The paper ends in Section 6 with concluding remarks.

2. Mathematical modeling of $SEII_hR$ epidemics

The mathematical model that describes the $SEII_hR$ epidemics can be expressed as the following systems of non-linear ordinary differential equations:

$$\frac{dS}{dt} = \Lambda - \frac{\beta(t)SI}{N} - \mu S \quad (1a)$$

$$\frac{dE}{dt} = \frac{\beta(t)SI}{N} - \sigma E - \eta E - \mu E \quad (1b)$$

$$\frac{dI}{dt} = \sigma E - \gamma I - \alpha I - \mu I \quad (1c)$$

$$\frac{dI_h}{dt} = \eta E + \alpha I - \omega I_h - \mu I_h \quad (1d)$$

$$\frac{dR}{dt} = \gamma I + \omega I_h - \mu R \quad (1e)$$

2.1 Assumptions of the model

The $SEII_hR$ model that described Ebola epidemic outbreak is constructed based on the following assumptions which are made since the duration of the Ebola epidemic outbreak is considerably small and during the short periods these assumptions hold good [1]. (i) The population is homogeneously distributed in the sense that each individual has the same probability of entering into a compartment. (ii) The total population at any point of time is considered to be a constant and is represented by the parameter N = S (t) + E (t) + I (t) +I_h (t) + R (t). (iii) The numbers of both births and deaths are equal. (iv) Migration and immigration of individuals are not considered as their influence on the result is small.

2.2 Description of $SEII_hR$ model

The model assumes that the total population N is divided in to five groups which we call here as compartments. The population size of each of the five compartments is represented by one letter from the name of the model sequence $SEII_hR$ at the time t . Thus, the names of the compartments denote S for Susceptible, E for Exposed, I for Infected, I_h for Isolated, and R for Removed respectively.

The time dependent parameter notations: (i) $S(t)$ denotes the number of people in the susceptible compartment where the people are capable of infected, (ii) $E(t)$ denotes the number of people in the exposed compartment where the people are incubating the infection, (iii) $I(t)$ denotes the number of people in the infected compartment where the people are infected with the virus [4], (iv) $I_h(t)$ denotes the number of people in the isolated compartment brought from the infected and exposed compartments and (v) $R(t)$ is the number of people in the removed compartment where the people are considered to be recovered from the epidemic or died. The transmission of Ebola Virus (EBOV) is considered to follow the multistoried sequence flow [1].

The time independent parameter (i) μ represents the death rate or equivalently the birth rate of the population during the short span of the epidemic outbreak, (ii) β represents the transmission rate of the disease that is the rate of transferring people from the compartment $S(t)$ to $E(t)$, (iii) $1/\sigma$ and $1/\gamma$ represent the average durations of stay in the compartments of E(t) and $I(t)$, (iv) $1/\omega$ represent the average time that takes for a patient to get transferred from isolation $I_h(t)$ to death $R(t)$ and (v) η and α are the probabilities of individual isolated from exposed and infected compartments respectively.

2.3 Bounds of the model variables

To understand the behavior of the $SEII_hR$ model properly it is needed to perform a complete stability analysis of the model. This task includes (i) computing the limits of the system variables (ii) identifying equilibrium points and applying on them the appropriate theorems to determine whether these points are stable locally or globally or not and (iii) verifying whether the equilibrium points are stable or asymptotically stable.

On differentiating the population conservative equation $N(t) = S(t) + E(t) + I(t) + I_h(t) + R(t)$ with respect to time we get $N'(t) = S'(t) + E'(t) + I'(t) + I'_h(t)) + R'(t)$and summing up the differentials of (1) leads to $N'(t) = \Lambda - \mu$ or equivalently $N'(t) + \mu N = \Lambda$. Its general solution can be obtained as $N(t) = [(\Lambda/\mu) + (c/e^{\mu t})]$. The result $\lim_{t\to\infty} N(t) = \lim_{t\to\infty}[(\Lambda/\mu) + (c/e^{\mu t})] = (\Lambda/\mu)$ indicates that the upper bound of the total population is (Λ/μ) .

The total population $N(t)$ is must always be positive because a negative population does not make any sense. Therefore, $N(t) > 0$, and that implies $S(t) > 0, E(t) > 0, I(t) > 0, I_h(t) > 0,$ and $R(t) > 0$. Hence, the lower bound for $S, E, I, I_h,$ and R is 0. However, the total population of the system at any point of time t is given by $N = [(\Lambda/\mu) + (c/e^{\mu t})]$ and the corresponding population sizes in the compartments $S, E, I, I_h,$ and R are separately less than or equal to N. Therefore, each of $S, E, I, I_h,$ and R is less than or equal to $[(\Lambda/\mu) + (c/e^{\mu t})]$. That is, each of $S, E, I, I_h,$ and R is a positive quantity with upper bound as$[(\Lambda/\mu) + (c/e^{\mu t})]$.

We observe from the system (1) that the last two compartments are not involved in the expressions for the first three compartments which indicates that the study of first three equations alone can reveal the inter relationship among all the compartments. Hence, it is appropriate to study (1) in the bounded set $\Gamma = \{(S, E, I) \in R^3_+ : 0 \le S + E + I \le N \le (\Lambda/\mu)\}$ where R^3_+ denotes the non-negative three dimensional space. It can be verified that Γ is positively invariant with respect to system (1), [11-12].

2.4 Basic reproductive number

The basic reproduction number denoted by R_0 and is defined as the expected number of people getting secondary infection among the whole susceptible population [9-10]. This number determines the potential for the spread of disease within a population.

If $R_0 < 1$ then the spread of the disease decelerate and ultimately dies down. On the other hand if $R_0 > 1$ then the spread of the disease accelerates and spreads rapidly [11]. We now find the Disease Free Equilibrium (DFE) point as it is required to compute R_0. For the purpose we set the right hand sides of the system (1) to zero and use the fact that the infected compartment is empty, i.e., $\mathrm{I} = 0$ and upon simple algebraic manipulation gives us the disease free equilibrium point of system (1) as $E_0 = (S, E, I) = (\Lambda/\mu, 0, 0)$.

The basic reproductive number R_0 can be determined using the next generation matrix. From the system (1) the first three equations are considered and decomposed into two groups; F contains newly infected cases and V contains the remaining terms. Let $X = [E \quad I \quad S]^T$ be a column vector and the differential equations of the first three compartments are rewritten as $F(X) - V(X)$. That is $F(X) = [F_1 \quad F_2 \quad F_3]^T$. Here (i) $F_1 = (\beta SI/N)$ denote newly infected cases which arrive into the exposed comportment, (ii) $F_2 = 0$ denotes newly infected cases arrived into the infected compartment, and (ii) $F_3 = 0$ denotes newly infected case from susceptible compartment [3]. Further $V(X) = [V_1 \quad V_2 \quad V_3]^T$. Here $V_1 = aE$, $V_2 = -\sigma E + bI$ and $V_3 = -\Lambda + (\beta SI/N) + \mu S$. The parameters a and b denote $a = (\sigma + \eta + \mu)$ and $b = (\gamma + \alpha + \mu)$ respectively.

The Jacobian matrices for $F(X)$ and $V(X)$ at any point can be constructed as

$$J_F(X) = \begin{bmatrix} \frac{\partial F_1}{\partial E} & \frac{\partial F_1}{\partial I} & \frac{\partial F_1}{\partial S} \\ \frac{\partial F_2}{\partial E} & \frac{\partial F_2}{\partial I} & \frac{\partial F_2}{\partial S} \\ \frac{\partial F_3}{\partial E} & \frac{\partial F_3}{\partial I} & \frac{\partial F_3}{\partial S} \end{bmatrix} = \begin{bmatrix} 0 & \frac{\beta S}{N} & \frac{\beta I}{N} \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}$$

and

$$J_V(X) = \begin{bmatrix} \frac{\partial V_1}{\partial E} & \frac{\partial V_1}{\partial I} & \frac{\partial V_1}{\partial S} \\ \frac{\partial V_2}{\partial E} & \frac{\partial V_2}{\partial I} & \frac{\partial V_2}{\partial S} \\ \frac{\partial V_3}{\partial E} & \frac{\partial V_3}{\partial I} & \frac{\partial V_3}{\partial S} \end{bmatrix} = \begin{bmatrix} a & 0 & 0 \\ -\sigma & b & 0 \\ 0 & \frac{\beta S}{N} & \frac{\beta I}{N} + \mu \end{bmatrix}$$

The Jacobian of F and V at the disease free equilibrium point E_0 take the form respectively $J_F(E_0) = \begin{bmatrix} 0 & \beta & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}$ and $J_V(E_0) = \begin{bmatrix} a & 0 & 0 \\ -\sigma & b & 0 \\ 0 & \beta & \mu \end{bmatrix}$. It can be verified that the matrix $J_V(E_0)$ is nonsingular as its determinant $\det(J_V(E_0)) = ab\mu$ is non zero and after some algebraic computations the inverse is constructed as $[J_V(E_0)]^{-1} = \begin{bmatrix} \frac{1}{a} & 0 & 0 \\ \frac{\sigma}{ab} & \frac{1}{b} & 0 \\ \frac{-\beta\sigma}{a\mu b} & \frac{-\beta}{b\mu} & \frac{1}{\mu} \end{bmatrix}$. The product of the matrices $[J_F(E_0)]$ and $[J_V(E_0)]^{-1}$ is $[J_F(E_0)]\,[J_V(E_0)]^{-1} = \begin{bmatrix} \frac{\beta\sigma}{ab} & \frac{\beta}{b} & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}$ and the latter product's spectral radius $\rho([J_F(E_0)]\,[J_V(E_0)]^{-1}) = (\beta\sigma/ab)$. Hence, we call the said spectral radius as the threshold value or the basic reproductive number $\mathrm{R}_0 = (\beta\sigma/ab)$.

2.5 Non-dimensionalization of the system

Non-dimensionalization is the method to reduce the number of parameters in the system of equations. In addition to this we can eliminate the units since the units are not important for the dynamical analysis of the system. The dimensionless form of the model can be express including the parameter R_0, and this is interesting and useful for model simulation. For the said purpose we introduce the dimensionless quantities $\mathrm{u}, \mathrm{v}, \mathrm{w}, \mathrm{z}, \mathrm{m}$, and τ defined in terms of the model parameters as $\mathrm{S} = \mathrm{uN}, \mathrm{E} = \mathrm{vN}, \mathrm{I} = \mathrm{wN}, \mathrm{I_h} = \mathrm{zN}, \mathrm{R} = \mathrm{mN}, \text{and } \tau = (\mathrm{ab}/\sigma)\mathrm{t}$.

Thus the dimensionless form of system (1) can be express as

$$\frac{\mathrm{du}}{\mathrm{d}\tau} = (1 - \mathrm{u})\mathrm{K}\mu - \mathrm{R_0 uw} \tag{3a}$$

$$\frac{\mathrm{dv}}{\mathrm{d}\tau} = \mathrm{R_0 uw} - \mathrm{K_2 v} \tag{3b}$$

$$\frac{\mathrm{dw}}{\mathrm{d}\tau} = \mathrm{K_1 K_2 v} - \mathrm{K_1 w} \tag{3c}$$

$$\frac{\mathrm{dz}}{\mathrm{d}\tau} = \mathrm{K}(\eta \mathrm{v} + \alpha \mathrm{w} - \mathrm{cz}) \tag{3d}$$

$$\mathrm{m} = 1 - \mathrm{u} - \mathrm{v} - \mathrm{w} - \mathrm{z} \tag{3e}$$

where $\mathrm{K_1} = (\sigma/\mathrm{a})$, $\mathrm{K_2} = (\sigma/\mathrm{b})\,\mathrm{K} = (\mathrm{K_1}/\mathrm{b})$ and $\mathrm{c} = (\omega + \mu)$.

3. Stability analysis of the model at DFE point

In this section, stability analysis of the system (1) is considered and discussed. We mainly focus on DFE point alone. The endemic equilibrium points (non DFE) are not acceptable on the reality grounds since Ebola virus is an epidemic disease and is a short time outbreak. We now analyze the local and global stability of DFE point of the system (1) by analyzing the characteristic equation.

3.1 Locally but asymptotically stability

In the absence of the infectious disease, the model has a unique disease free steady state E_0. To find the local stability of E_0, we use the Jacobian of the model evaluated at E_0. Stability of this steady state is then determined based on the eigenvalues of the corresponding Jacobian which are functions of the model parameters [9]. The Jacobian matrix for the system (1) is given by

$$\mathrm{J(S, E, I)} = \begin{bmatrix} \frac{-\beta I}{N} - \mu & 0 & \frac{-\beta S}{N} \\ \frac{\beta I}{N} & -a & \frac{\beta S}{N} \\ 0 & \sigma & -b \end{bmatrix}$$ and this implies

$$J(E_0) = \begin{bmatrix} -\mu & 0 & -\beta \\ 0 & -a & \beta \\ 0 & \sigma & -b \end{bmatrix}.$$

The DFE point E_0 is not locally stability because $R_0 \neq 1$ but it is locally asymptotically stable since $R_0 < 1$. The validity of $R_0 < 1$ is verified in Theorem 1.

Theorem 1 If $R_0 < 1$, then the disease free equilibrium point E_0 of system (1) is locally asymptotically stable.

Proof The characteristics equation of the Jacobian matrix $(J(E_0)$ at DFE point E_0 is given by $\det(J(E_0) - \lambda I) = 0$ and the corresponding characteristic equations are $[\lambda + \mu]\,[\lambda^2 + (a+b)\lambda + ab(1-R_0)] = 0$. From this it is straight forward to get a root as $\lambda_1 = -\mu$. Since the parameter μ is real but positive, the eigenvalue λ_1 is real but negative. To analyze the nature of the remaining two eigenvalues, we now divide the characteristic equation by $(\lambda + \mu)$ to get the remainder as $\lambda^2 + (a+b)\lambda + ab(1-R_0) = 0$. Since the coefficients of λ^2 and λ are positive, in order to have both roots real but negative, we must have the constant term $ab(1-R_0)$ to be positive. That is, $[ab(1-R_0)] > 0$ or $(1-R_0) > 0$ or $R_0 < 1$. This justifies that the system (1) is locally asymptotically stable at E_0.

3.2 Global stability of DFE

The phase diagram curves representing dynamics of system are attracted towards the equilibrium point while it is stable. But, the curves appear to move away from the equilibrium point while it is unstable [12]. The DFE E_0 in the present case is globally asymptotically stable and the same is proved in Theorem 2 below.

Theorem 2: If $\mathrm{R_0} < 1$ then the disease free equilibrium point $\mathrm{E_0}$ is globally asymptotically stable and at that point the disease dies out.

Proof Let us consider the analogous of Lyapunov function [17] in the present model as $L = (\sigma \mathrm{E} + \mathrm{aI})$ and which on differentiating both sides with respect to time we obtain $\mathrm{L'} = \sigma \mathrm{E'} + \mathrm{aI'}$**.** On substituting for E' and I' from (1) it takes the form $\mathrm{L'} = \sigma[(\beta \mathrm{SI/N}) - \mathrm{aE}] + \mathrm{a}(\sigma \mathrm{E} - \mathrm{bI})$ or equivalently $\mathrm{L'} = (\sigma\, \beta \mathrm{SI/N}) - \mathrm{abI}$. But $\mathrm{L'} = [(\sigma\, \beta \mathrm{S/N}) - \mathrm{ab}]\mathrm{I}$ at DFE $S = N$ and this implies to have $L' = ab[(\sigma\beta/ab) - 1]\mathrm{I}$ or equivalently $L' = ab(R_0 - 1)\mathrm{I}$. It is simple to conclude that $\mathrm{L'} < 0$ whenever $(R_0 - 1) \leq 0$ or equivalently $R_0 \leq 1$. Also, the maximal compact invariant set in $\{(\mathrm{S, E, I}) \in \Gamma, \frac{\mathrm{dL}}{\mathrm{dt}} = 0\}$ is the singleton $\{E_0\}$. Therefore, by Lasalle's invariance principle [16] the statement is proved. However, it is to be noted that if $\mathrm{R_0} > 1$ then $\mathrm{E_0}$ is unstable.

4. Model simulation

Here we consider simulation study of $\mathrm{S\,EI\,I_h\,R}$ model with different values for R_0. The main focus of the simulation study is to investigate the response of model parameters Ebola epidemic outbreak. In mathematical epidemiology the value of the basic reproductive number parameter denoted by R_0 plays an important role. We consider R_0 taking different values less than or greater than a unity and conduct simulation study. For the Ebola epidemic there has not been a well known vaccination or medicine. Hence, the only alternative mechanism to control spreading of the disease is contact tracing (isolation of the infected individuals). We will see the effect of isolation on the spread of the disease using simulation.

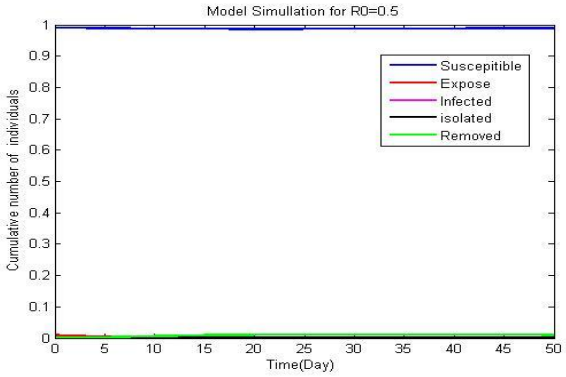

Figure 1: Simulation of $\mathrm{SEII_hR}$ model with the basic reproductive number $\mathrm{R_0} = 0.5$.

In the stability analysis of the model it is shown that the disease dies out whenever $R_0 < 1$ and the same is evident by the simulation given in Figure 1. It is observed that susceptible compartment represented by the blue curve remains at the same level with respect to the progress of time indicating that the susceptible compartment is stable. Further, biologically if there is no new infected case then size of the susceptible population remains the same without any distraction and sizes of the other compartments remain to be at zero level and this fact is very much evident as displayed in the Figure 1. That is, in real life situation as long as a new infected case do not occur the size of susceptible compartment remains the same as the total population N.

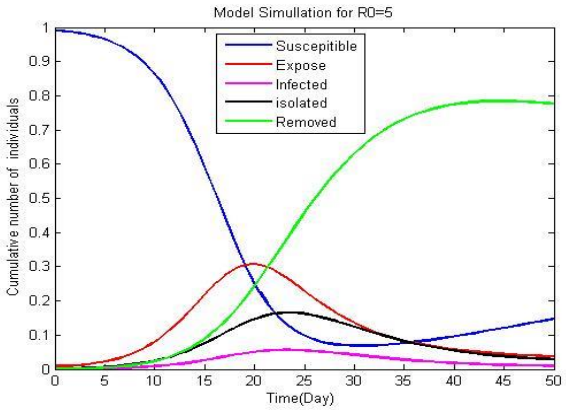

Figure 2: Model simulation for basic reproductive number $\mathrm{R_0} = 5$.

In Figure 2 the simulation study shows that the system is unstable. It is also in support of Theorem 2. The population size of the susceptible compartment

(blue curve) decreases due to spread of the epidemic up to certain point of time and then takes up due to controlling of the spread of disease with the mechanism of isolation. The size of the removed compartment (green curve) grows and asymptotically converges. The sizes of the exposed (red curve), isolated (black curve) and infected (rose curve) compartments follow normal distribution curves with varied mean and standard deviations.

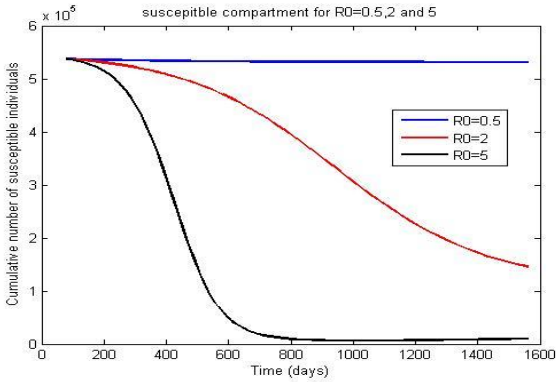

Figure 3 Model simulation of susceptible compartment with $\mathbf{R_0}$=0.5, 2, and 5

The fact that the system is stable if $R_0 < 1$ and unstable if $R_0 > 1$ is evident in Figure 3. The suceptible compartment with $R_0 = 0.5$ is stable (blue) but the same with $R_0 = 2$ (red) and with $R_0 = 5$ (black) are unstable. The unstability converges to zero faster in proportional to increasing of R_0 .

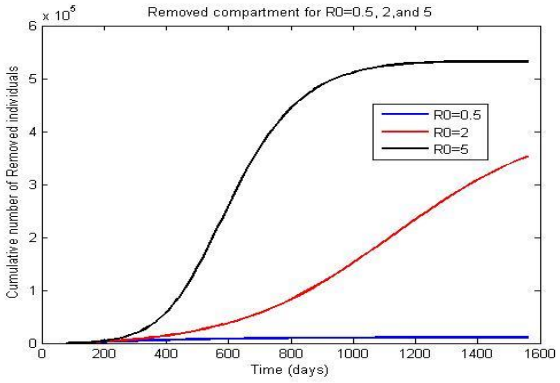

Figure 4 Model simulation of removed compartment $R_0 = 0.5, 2, \& 5$

The fact that the system is stable if $R_0 < 1$ and unstable if $R_0 > 1$ is evident in Figure 4. The removed compartment with $R_0 = 0.5$ is stable (blue) but the same with $R_0 = 2$ (red) and with $R_0 = 5$ (black) are unstable. The unstability converges to upper bound faster in proportional to increasing of R_0 . Note that stability stands for horizontalness of a curve while unstability is reflected in the fall or rise or both of a curve.

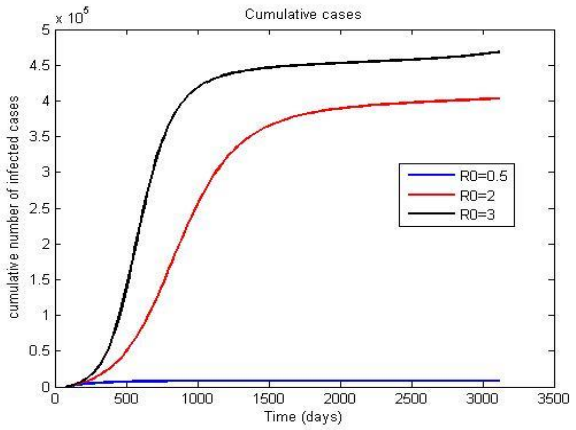

Figure 5 Model simulations of number of infected cases with $R_0 = 0.5, 2, \& 3$

In Figure 5, we have considered the simulation study of total number of infected cases, i.e. the sum of the population sizes of isolated and infected compartments. The fact that the system is stable if $R_0 < 1$ and unstable if $R_0 > 1$ is evident here. Further, it shows that the sum of infected cases with $R_0 = 0.5$ is stable (blue) but the same with $R_0 = 2$ (red) and with $R_0 = 3$ (black) is unstable. The unstability converges to upper bound faster in proportional to increasing of R_0 .

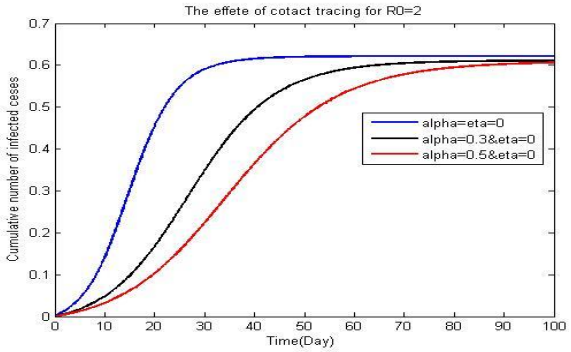

Figure 6 Model simulation of isolation with $\alpha = 0.0, 0.3 \,\&\, 0.5$

The parameter α represents the probability of isolating an infected person i.e. the probability of transferring a person from infected compartment to isolated compartment. As expected, Figure 6 shows that as α grows on its range $[0\,, 1]$ the cumulative number of infected cases approach the upper asymptote with delay in time; blue early, black later and red still lately.

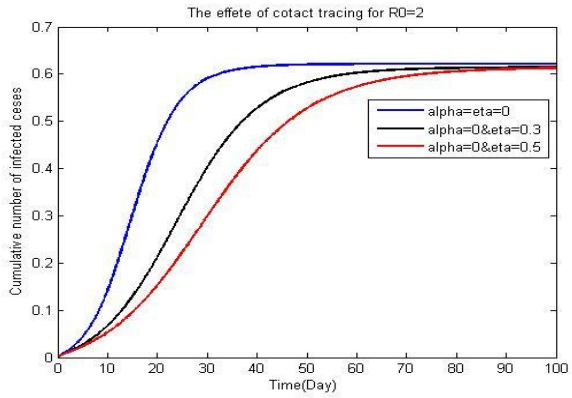

Figure 7 Model simulation of isolation with $\eta = 0.0, 0.3 \& 0.5$

The parameter η represents the probability of isolating an exposed person i.e. the probability of transferring a person from exposed compartment to isolated compartment. As expected, Figure 7 shows that as η grows on its range $[0, 1]$ the cumulative number of infected cases approach the upper asymptote with delay in time; blue early, black later and red still lately.

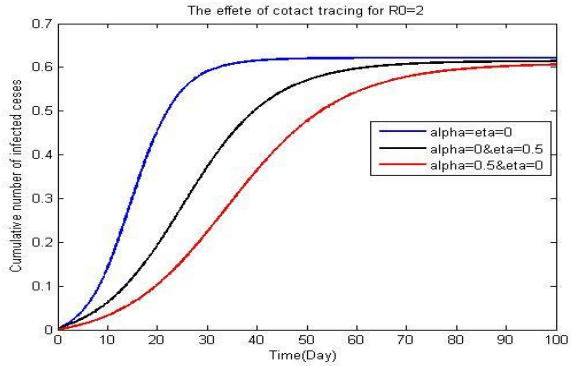

Figure 8 Model simulation of isolation with varied combinations of $\alpha \& \eta$

The influence of the parameter α is more than that of the parameter η on converging of cumulative number of infected cases to an upper asymptote with delay in time. This fact is evident in figure 8 as the curves converge asymptotically; blue early, black later and red still lately.

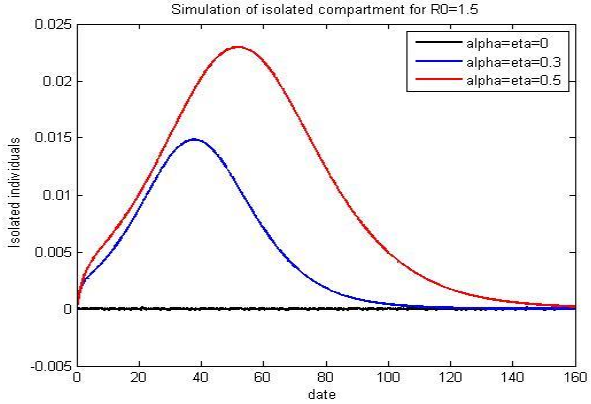

Figure 9 Model simulation of isolation compartment

The cumulative number of isolated individual cases with the increasing values of the parameters α and η grows faster during the initial times but fall down lately to zero. This fact is evident in Figure 9. The simulated curve (red) with $\alpha = \eta = 0.5$ grows faster and falls later in comparison with the simulated curve (blue) with $\alpha = \eta = 0.3$. The simulated curve (black) with $\alpha = \eta = 0$ neither rises nor falls but remains at zero level as there has not been any kind of isolation.

5. Data fitting

For the fitting data in the present model we have considered the data of Ebola epidemic disease. The data includes the infected and death cases recorded in the countries Guinea, Liberia and Sierra Leon up to March 8, 2015 [2-3]. In this subsection, we focus on data fitting in the model and predict the cases using the best fit. In the data fitting the cumulative infected and death cases are considered. The study is applicable for a total population size of $N = 542580$.

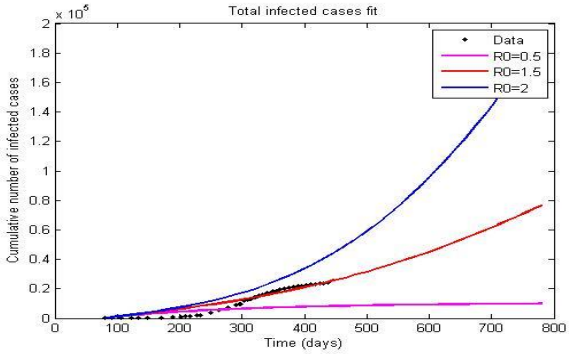

Figure 10 Data fitting of cumulative infected cases with $R_0 = 0.5, 1.5, \& 2, N = 542580$

In figure 10, we have fitted cumulative infected cases 24282 found in West Africa up to March 8, 2015. The parametric values are set as $R_0 = 0.5, 1.5, \& 2$ and $\eta = 0.2, \alpha = 0.3, \sigma = 0.1783, \gamma = 0.1887, \mu = 0.001$. It can be observed that for the best fit $R_0 = 1.5$. But the theory predicts that as long as $R_0 > 1$ the epidemic grows without any interruption and spreads to the whole population. Thus, the data fitting up to March 8, 2015 is suggests that the epidemic spreads to the whole population with the progressive time unless control measurements are taken.

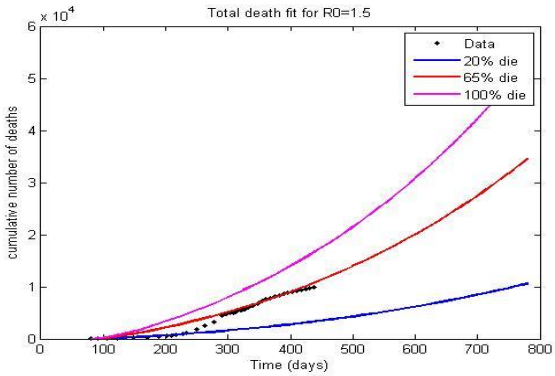

Figure 11 Data fitting of total cumulative death cases

In figure 11, we have fitted cumulative death cases 9976 found in West Africa up to March 8, 2015. The parametric values are set as $R_0 = 1.5, \eta = 0.2, \alpha = 0.4, \sigma = 0.1783, \gamma = 0.1887, \mu = 0.001$. It can be observed that for the best fit for $R_0 = 1.5$ is 65%. That is, it can be interpreted that from the population of the Removed compartment, 65% are died and the remaining 35% are recovered from the epidemic. The data fitting suggests that this ratio of death and recovered cases 65:35 will continue unless any remedial control measurements are pressed in.

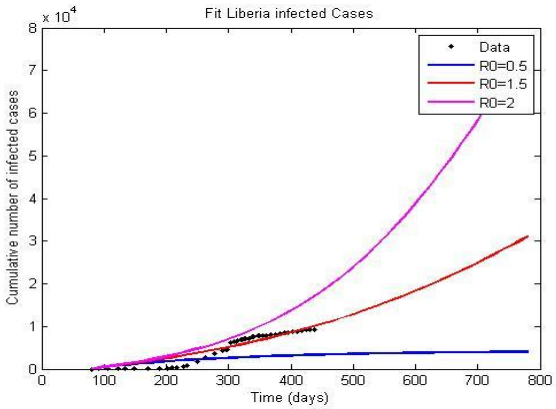

Figure 12 Data fitting of cumulative infected cases of Liberia with $R_0 = 0.5, 1.5 \& 2, N = 220180$.

In figure 12, we have fitted cumulative infected cases 9343 found in Liberia up to March 8, 2015. The parametric values are set as $R_0 = 0.5, 1.5 \& 2$and $\eta = 0.2, \alpha = 0.3, \sigma = 0.1783, \gamma = 0.1887, \mu = 0.001$. It can be observed that for the best fit $R_0 = 1.5$. But the theory predicts that as long as $R_0 > 1$ the epidemic grows without any interruption and spreads to the whole population. Thus, the data fitting suggests that the epidemic spreads to the whole population of Liberia with the progressive time unless control measurements are taken.

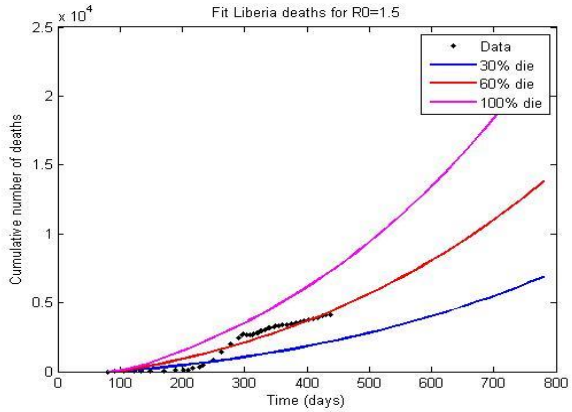

Figure 13 Data fitting of cumulative death cases of Liberia

In figure 13, we have fitted cumulative death cases 4162 found in Liberia up to March 8, 2015. The parametric values are set as $R_0 = 1.5, \eta = 0.3, \alpha = 0.3, \sigma = 0.1783, \gamma = 0.1887, \mu = 0.001$. It can be observed that for the best fit for $R_0 = 1.5$ is 60%. That is, it can be interpreted that from the population of the Removed compartment corresponding to Liberia, 60% are died and the remaining 40% are recovered from the epidemic. The data fitting suggests that this ratio of death and recovered cases 60:40 will continue unless any remedial control measurements are pressed in.

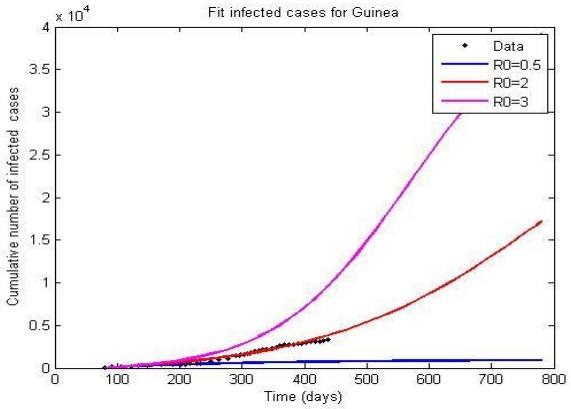

Figure 14 Data fitting of cumulative infected cases of Guinea with $R_0 = 0.5, 2 \& 3, N = 49400$.

In figure 14, we have fitted cumulative infected cases 3285 found in Guinea up to March 8, 2015. The parametric values are set as $R_0 = 0.5, 2 \& 3$ and $\eta = 0.2, \alpha = 0.3, \sigma = 0.1783, \gamma = 0.1887, \mu = 0.001$. It can be observed that for the best fit $R_0 = 2$. But the theory predicts that as long as $R_0 > 1$ the epidemic grows without any interruption and spreads to the whole population. Thus, the data considering up to March 8, 2015 and fitting suggests that the epidemic spreads to the whole population of Guinea with the progressive time unless control measurements are taken.

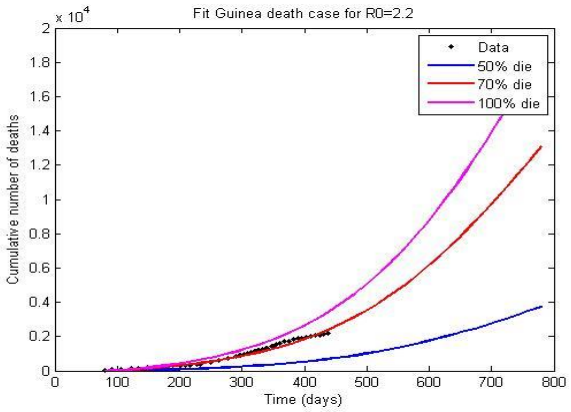

Figure 15 Data fitting of cumulative death cases of Guinea

In figure 15, we have fitted cumulative death cases 2170 found in Guinea up to March 8, 2015. The parametric values are set as $R_0 = 2.2, \eta = 0.2, \alpha = 0.3, \sigma = 0.1783, \gamma = 0.1887, \mu = 0.001$. It can be observed that for the best fit for $R_0 = 2.2$ is 70%. That is, it can be interpreted that from the population of the Removed compartment corresponding to Guinea, 70% are died and the remaining 30% are recovered from the epidemic. The data fitting suggests that this ratio of death and recovered cases 70:30 will continue

unless any remedial control measurements are pressed in.

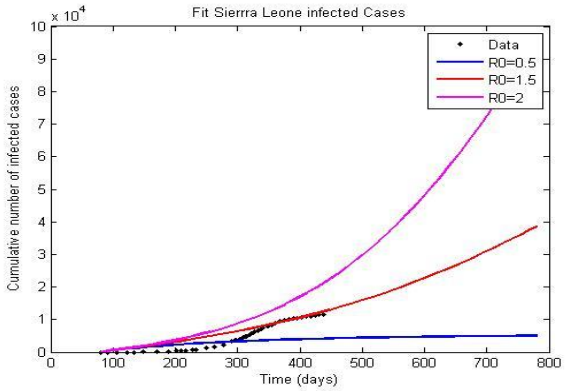

Figure 16 Fitting of cumulative infected cases of Sierra Leon with $\mathrm{R}_0 = 0.5, 1.5 \,\&\, 2, \mathrm{N} = 273180$.

In figure 16, we have fitted cumulative infected cases 11619 found in Sierra Leon up to March 8, 2015. The parametric values are set as $\mathrm{R}_0 = 0.5, 1.5 \,\&\, 2$ and $\eta = 0.2, \alpha = 0.3, \sigma = 0.1783, \gamma = 0.1887, \mu = 0.001$. It can be observed that for the best fit $\mathrm{R}_0 = 1.5$. But the theory predicts that as long as $\mathrm{R}_0 > 1$ the epidemic grows without any interruption and spreads to the whole population. Thus, the data considering up to March 8, 2015 and fitting suggests that the epidemic spreads to the whole population of Sierra Leon with the progressive time unless control measurements are taken.

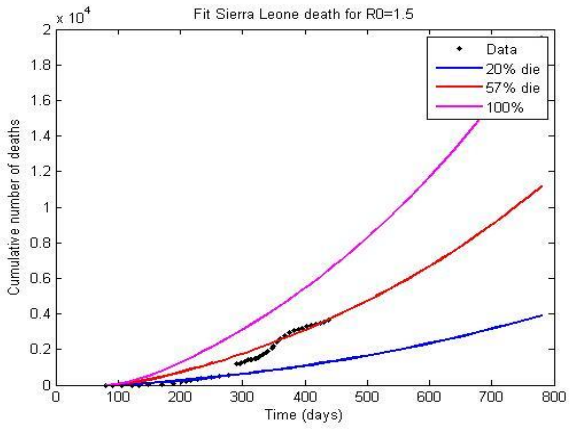

Figure 17 Data fitting of cumulative death cases of Sierra Leon

In figure 17, we have fitted cumulative death cases 3629 found in Sierra Leon up to March 8, 2015. The parametric values are set as $\mathrm{R}_0 = 1.5, \eta = 0.3, \alpha = 0.5, \sigma = 0.1783, \gamma = 0.1887, \mu = 0.001$. It can be observed that for the best fit for $\mathrm{R}_0 = 1.5$ is 57%. That is, it can be interpreted that from the population of the Removed compartment corresponding to Sierra Leon, 57% are died and the remaining 43% are recovered from the epidemic. The data fitting suggests that this ratio of death and recovered cases 57:43 will continue unless any remedial control measurements are pressed in.

6. Comparison between $SEIR$ and $SEII_hR$ models

The same authors in [1] in their $SEIR$ model have not considered the inclusion of 'isolation' compartment and hence missed accounting the powerful controlling technique of disease propagation. We here in this $SEII_hR$ model included the 'isolation' compartment and shown a way to reduce the rate of propagation of the disease. The main observations and comparisons of both the models are presented in the form of a table below:

SEIR Model	$SEII_hR$ Model
It is a four compartment model containing: Susceptible, Exposed, Infected and Removed compartments	It is a five compartment model containing: Susceptible, Exposed, Infected, Isolated and Removed compartments
As isolation of the exposed or infected individual is not included, the disease outbreak spreads faster.	As isolation of the exposed or infected individual is included, the disease outbreak spread is slowed down.
The population size of the susceptible compartment falls down and gradually tends to zero over a period of time (see Fig 3 [1]).	The population size of the susceptible compartment falls down to certain level and from then instead of going to zero it takes off and grows with normal rates. That is, the isolation technique is contributing for the control of disease spread (see Fig2).
In this model the data of total infected cases fits well for $R_0 = 3$. That is, every infected individual propagates the disease to three susceptible individuals.	In this model the data of total infected cases fits well for $R_0 = 1.5$. That is, every infected individual propagates the disease to 1.5 susceptible individuals. That is, the propagation due to the inclusion of isolation compartment is decreased by half.
In this model the data of total death cases fits well for $R_0 = 2.6$ with 70% deaths. That is, disease is spreading with a rate of 2.6 and the fatal rate is 0.7.	In this model the data of total death cases fits well for $R_0 = 1.5$ with 65% deaths. That is, disease is spreading with a rate of 1.5 and the fatal rate is 0.65.

Table 1 Comparison of non-inclusion and inclusion of 'Isolation' compartment

7. Conclusions

Mathematical models are useful to describe the spreading and control mechanism of epidemics including Ebola virus disease. In the present study $SEII_hR$ model is formulated with an intention of describing Ebola virus epidemic outbreak. We have studied the local and global stabilities of the model at the disease free equilibrium point E_0. At DFE, the value of R_0 is calculated as $R_0 = (\delta\beta/ab)$ using second generation matrix. It is shown that for $R_0 < 1$ at DFE point, the $SEII_hR$ model is locally asymptotically stable.

Disease spread controlling technique called 'Isolation' is proposed and included in this study. Isolation of exposed and infected individuals is a powerful technique and can be used to control the spreading of the epidemic.

Further, using Lyapunov function it is shown that the model is globally asymptotically stable for $R_0 < 1$ whereas it is unstable for $R_0 > 1$. It is interpreted that the Ebola virus disease outbreak vanishes over evolution of time for $R_0 < 1$ but remains alive among the population for $R_0 > 1$.

The data fit for the cumulative infected cases in the model suggests that the basic reproductive number takes the value R_0 =1.5. The data fit of the cumulative death cases in the model suggests that 65% of the persons enter into the removed compartment will die unless remedial measurements are adopted. Similar conclusions for the three countries viz., Liberia Guinea and Sierra Leon are drawn.

8. Acknowledgements

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