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Mathematical analysis of sensitive parameters due to dynamic transmission of Ebola virus disease

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Abstract

A mathematical model of Ebola virus disease was formulated, it was shown that the model was well- posed, both disease and endemic equilibria for the models were obtained. The models were analysed for stability and it was established that the disease free equilibrium of model is locally asymptotically stable whenever the basic reproduction number is less than unity. Similarly, there exist endemic point when the basic reproduction numbers of Ebola virus disease is greater than unity. The results obtained so far from sensitivity analysis strongly shows that the spread of Ebola virus disease in the population depend on effective contact rate. Conclusively, in the numerical simulation where Runge –Kutta method of order four via MAPPLE (18) software was adopoted it shows that the best way to control the Ebola virus disease in the population is to minimize the contact rate.

Keywords: Ebola virus disease; Boundedness of solutions; Basic reproduction number; Existence of endemic equilibrium point; Sensitivity indices

1. Introduction

Ebola is a deadly virus that attacks healthy cells and replicates itself in a host's body. The virus, previously known as Ebola hemorrhagic fever, is the deadliest pathogen for humans which affected several African countries. [1-10] performed numerical simulation and sensitivity analysis on a mathematical model of Ebola transmission to determine the biological significance of key model parameters in relation to disease transmissions and prevalence. Result from sensitivity analysis affirm that average contacts and transmission rates championed the disease outbreaks. Similarly, a model with multi-intervention strategies was proved to effectively reduce the contact and prevalence of Ebola virus disease than the models with one intervention at a time. They suggests that strategies targeting contact reduction (such as education and isolation) and those that focus on recovery rates (such as prompt treatment of the infected persons) can be successful in curtailing the Ebola epidemic but they did not consider Ebola-malaria co-infections.[9-19] proposed a mathematical model of Ebola virus (EBOV) using susceptible exposed infected recovered (SEIR) model, their model, the population is affected by animals, EBOV is an infectious agent causing hemorrhagic fever, a severe infectious disease characterized by high fever and bleeding, in humans and some monkeys. The conditions to investigate all possible equilibria of the model in terms of the basic reproduction number (local and global stability) was calculated. [4] formulated a compartmental model of susceptible, exposed, undetected, detected and recovered model to study the dynamical spread of Ebola virus disease which conclude that the rate of public enlightenment and availability of isolation centers can reduce the spread of Ebola virus disease. [10-20] considered a deterministic model of Ebola virus disease incorporating contact tracing and quarantine as interventions. The model was analysed for the existence and

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stability of disease free equilibrium and endemic equilibrium points and numerical simulations were carried out to examine the impact of contact tracing and quarantine measures on the transmission dynamics of Ebola virus disease, the result indicates that Ebola virus disease could be eliminated faster when contact tracing and quarantine measures were implemented together.[13-17]developed a susceptible-exposed-infected-treatment (SEIT) model of Ebola virus transmission. They assumed that some treated individuals will die of the disease while some will recover and loose immunity. [3-19] formulated a susceptible infected-recovered-death model to study the spread of Ebola virus disease transmission in Sub-Saharan African countries. It was assumed that recovered individuals lost immunity and become susceptible again with natural death in susceptible infected recovered (SIR) compartments. [1-2, 20] worked on mathematical analysis of effects of isolation on Ebola transmission dynamics, it shows that if the detection rate of infected undetected individuals is sufficiently large, then the isolation technique can lead to elimination of Ebola in the population, this work is modified by adding the treated class into their model and performed the stability analysis and sensitivity indices on formulated model.

2. Descriptions of Mathematical Model of Ebola Virus Disease

A mathematical model is proposed to consider the dynamics spread of Ebola virus disease The human population is divided into six classes, susceptible individuals $S_H(t)$, Ebola virus disease latently infected individuals $L_E(t)$, Ebola virus disease infected undetected Individuals $I_U(t)$, infected detected Ebola virus disease individuals $I_D(t)$, individuals under treatment for Ebola virus disease $I_T(t)$, individuals isolated for Ebola virus disease J .

Therefore the total population of human denoted

$$N_H(t) = S_H(t) + L_E(t) + I_U(t) + I_D(t) + I_T(t) + J(t) \quad (1)$$

It assumed that susceptible humans are recruited into the population at the constant rate π_H , it acquires Ebola virus diseases infection following the effective contact with infected undetected, infected detected, infected treated and isolated individual. The population increases by fraction of isolated individual who move to susceptible after test negative of Ebola virus disease infection but natural death occurs in all human (at the rate μ), which decreases the population. The force of infection associated with Ebola virus disease, denoted by;

$$\lambda_E = \beta_E \left(\frac{I_U + \eta_D I_D + \eta_T I_T + \eta_J J}{N_H} \right) \quad (2)$$

where β_E represents the effective contact rate, η_D is modification parameter comparing the individual transmissibility of detected infected individuals in relationship to latently infected. Since detected individuals are under treatment and isolation, it is intuitive to assume that $\eta_D \leq 1$. Similarly η_T and η_J are modification parameters comparing the transmissibility of infected individuals in the treated class and isolated class respectively. Putting these assumptions together, the model is given as;

$$\left.\begin{aligned}
\frac{dS_H}{dt} &= \pi_H - \lambda_E S_H - \mu S_H + \alpha\theta J \\
\frac{dL_E}{dt} &= \varepsilon_1\lambda_E S_H - (\kappa_E + \sigma_1 + \mu)L_E + \phi_2 I_T + (1-\alpha)\theta J \\
\frac{dI_U}{dt} &= (1-\varepsilon_1)\lambda_E S_H + \omega_1\kappa_E L_E - (\gamma_{UE} + \mu + \delta_{UE})I_U \\
\frac{dI_D}{dt} &= (1-\omega_1)\kappa_E L_E - (\tau_1 + \mu + \delta_{DE} + \sigma_2)I_D + \gamma_{UE} I_U \\
\frac{dI_T}{dt} &= \tau_1 I_D - (\phi_2 + \mu)I_T \\
\frac{dJ}{dt} &= \sigma_1 L_E + \sigma_2 I_D - (\mu + \delta j)J - \theta J
\end{aligned}\right\} \quad (3)$$

where λ_E is the force of infection, μ is natural death rate, α is the rate of certified Ebola free, θ is the discharge rate, κ_E is progression rate, σ_1 is isolation rate, ω_1 fraction of detection rate, γ_{UE} is the detection rate, δ is the disease death rate, τ_1 is the treatment rate and ε_1 is fraction of individual with low immunity.

2.1 Boundedness Solutions of Ebola Virus Disease

For the Ebola virus disease transmission model (3) to be epidemiologically meaningful, it is important to prove that all solutions with nonnegative initial data will remain nonnegative for all time $t \geq 0$.

Theorem 1.

If $S_H(0)$, $L_E(0)$, $I_U(0)$, $I_D(0)$, $I_T(0)$ and $J(0)$ are non-negative, then the solutions S_H, L_E, I_U, I_D, I_T and J of the Ebola virus disease model (3) are non-negative for all $t \geq 0$.

Proof:

Consider the biologically-feasible region, $\prod = \left\{(S_H, L_E, I_U, I_D, I_T, J)\varepsilon\Re_+^6 : N_H \leq \frac{\pi_H}{\mu}\right\}$, it will be proved that $\prod$ is positively invariant.

The total population of Ebola virus disease transmission of sub-model is obtained by adding all the model equation (9) is given by;

$$\frac{dN_H}{dt} = \pi_H - \mu N_H - \left(\delta_{UE} I_U + \delta_{DE} I_D + \delta_j J\right) \quad (4)$$

In the absence of mortality due to Ebola virus disease, equation (4) become

$$\frac{dN_H}{dt} \leq \pi_H - \mu N_H \quad (5)$$

Solve (5) and re-arrange, upon taking the limit as $t \to \infty$ obtain,

$$\left.\begin{aligned}
\frac{dS_H}{dt} &= \pi_H - \lambda_E S_H - \mu S_H + \alpha\theta J \\
\frac{dL_E}{dt} &= \varepsilon_1\lambda_E S_H - (\kappa_E + \sigma_1 + \mu)L_E + \phi_2 I_T + (1-\alpha)\theta J \\
\frac{dI_U}{dt} &= (1-\varepsilon_1)\lambda_E S_H + \omega_1\kappa_E L_E - (\gamma_{UE} + \mu + \delta_{UE})I_U \\
\frac{dI_D}{dt} &= (1-\omega_1)\kappa_E L_E - (\tau_1 + \mu + \delta_{DE} + \sigma_2)I_D + \gamma_{UE} I_U \\
\frac{dI_T}{dt} &= \tau_1 I_D - (\phi_2 + \mu)I_T \\
\frac{dJ}{dt} &= \sigma_1 L_E + \sigma_2 I_D - (\mu + \delta j)J - \theta J
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$$\frac{dN_H}{dt} \leq \pi_H - \mu N_H \quad (5)$$

Solve (5) and re-arrange, upon taking the limit as $t \to \infty$ obtain,

$$R_E = \beta_E \frac{\begin{pmatrix} a_1a_7b_1\eta_D\gamma_{UE} + a_1a_7\eta_T\gamma_{UE}\tau_1 + a_1b_1\eta_j\gamma_{UE}\sigma_2 - a_2b_1\eta_D\gamma_{UE}\sigma_1 - a_2\eta_T\gamma_{UE}\sigma_1\tau_1 + \eta_j\gamma_{UE}\phi_2\sigma_1\tau_1 - \\ \varepsilon_1a_1a_6a_7b_1 + \varepsilon_1a_2a_5b_1\sigma_2 + \varepsilon_1a_2a_6b_1\sigma_1 + \varepsilon_1a_5a_7\phi_2\tau_1 + a_3a_6a_7b_1\varepsilon_1 - \varepsilon_1a_1a_7b_1\eta_D\gamma_{UE} - \varepsilon_1a_1a_7\eta_T\gamma_{UE}\tau_1 \\ -\varepsilon_1a_1b_1\eta_j\gamma_{UE}\sigma_2 + \varepsilon_1a_2b_1\eta_D\gamma_{UE}\sigma_1 + \varepsilon_1a_2\eta_T\gamma_{UE}\sigma_1\tau_1 - \varepsilon_1\eta_j\gamma_{UE}\phi_2\sigma_1\tau_1 + \varepsilon_1a_4a_5b_1\eta_j\sigma_2 + \varepsilon_1a_4a_6b_1\eta_j\sigma_1 \\ a_1a_6a_7b_1 - a_2a_5\sigma_2b_1 - a_2a_6b_1\sigma_1 - a_5a_7\phi_2\tau_1 \end{pmatrix}}{a_1a_4a_6a_7b_1 - a_2a_3b_1\gamma_{UE}\sigma_2 - a_2a_4a_5b_1\sigma_2 - a_2a_4a_6b_1\sigma_1 - a_3a_7\gamma_{UE}\phi_2\tau_1 - a_4a_5a_7\phi_2\tau_1}$$

The reproduction number for Ebola virus disease is given as R_E, where denotes the spectral radius of the dominant eigenvalue of the next generation matrix. Therefore, this measure the average number of new infectious generated by a single infectious individual in a population consisting of susceptible.

2.3 Local Stability of Disease Free of Ebola Virus Disease

Theorem 2. Disease free equilibrium point is locally asymptotically stable if $R_E < 1$ and unstable if $R_E > 1$. Then the theorem implies the disease can be eliminated from the community.

Proof: To prove local stability of disease free equilibrium, obtain the Jacobian matrix of the system (3) at disease free equilibrium.

$$J(E_1) = \begin{vmatrix} -\mu & 0 & -\beta_E & -\beta_E\eta_D & -\beta_E\eta_T & \alpha\theta - \beta_E\eta_J \\ 0 & -K_1 & \varepsilon_1\beta_E & \varepsilon_1\beta_E\eta_D & \varepsilon_1\beta_E\eta_T + \phi_2 & \varepsilon_1\beta_E\eta_J + (1-\alpha)\theta \\ 0 & \omega_1\kappa_E & -K_2 + (1-\varepsilon_1)\beta_E & (1-\varepsilon_1)\beta_E\eta_D & (1-\varepsilon_1)\beta_E\eta_T & (1-\varepsilon_1)\beta_E\eta_J \\ 0 & (1-\omega_1)\kappa_E & \gamma_{UE} & -K_3 & 0 & 0 \\ 0 & 0 & 0 & \tau_1 & -K_4 & 0 \\ 0 & \sigma_1 & 0 & \sigma_2 & 0 & -K_5 \end{vmatrix}$$

For simplicity

$$K_1 = \kappa_E + \mu + \sigma_1, K_2 = \gamma_{UE} + \mu + \delta_{UE}, K_3 = \tau_1 + \mu + \delta_{DE} + \sigma_2, K_4 = \phi_2 + \mu, K_5 = \mu + \delta_j + \theta$$

Therefore, the eigenvalue of the Jacobian matrix are the solution of the characteristic equation $|J - \lambda I| = 0$

Expand along the first column obtain

$$-\mu - \lambda \begin{vmatrix} -K_1 - \lambda & \varepsilon_1\beta_E & \varepsilon_1\beta_E\eta_D & \varepsilon_1\beta_E\eta_T + \phi_2 & \varepsilon_1\beta_E\eta_J + (1-\alpha)\theta \\ \omega_1\kappa_E & -K_2 + (1-\varepsilon_1)\beta_E - \lambda & (1-\varepsilon_1)\beta_E\eta_D & (1-\varepsilon_1)\beta_E\eta_T & (1-\varepsilon_1)\beta_E\eta_J \\ (1-\omega_1)\kappa_E & \gamma_{UE} & -K_3 - \lambda & 0 & 0 \\ \sigma_1 & 0 & \sigma_2 & 0 & -K_5 - \lambda \end{vmatrix} = 0$$

$\Rightarrow \lambda_1 = \mu$, or

$$\begin{vmatrix} -\mu-\lambda & 0 & -\beta_E & -\beta_E\eta_D & -\beta_E\eta_T & \alpha\theta-\beta_E\eta_J \\ 0 & -K_1-\lambda & \varepsilon_1\beta_E & \varepsilon_1\beta_E\eta_D & \varepsilon_1\beta_E\eta_T+\phi_2 & \varepsilon_1\beta_E\eta_J+(1-\alpha)\theta \\ 0 & \omega_1\kappa_E & -K_2+(1-\varepsilon_1)\beta_E-\lambda & (1-\varepsilon_1)\beta_E\eta_D & (1-\varepsilon_1)\beta_E\eta_T & (1-\varepsilon_1)\beta_E\eta_J \\ 0 & (1-\omega_1)\kappa_E & \gamma_{UE} & -K_3-\lambda & 0 & 0 \\ 0 & 0 & 0 & \tau_1 & -K_4-\lambda & 0 \\ 0 & \sigma_1 & 0 & \sigma_2 & 0 & -K_5-\lambda \end{vmatrix} = 0$$

$$\begin{vmatrix} -K_1-\lambda & \varepsilon_1\beta_E & \varepsilon_1\beta_E\eta_D & \varepsilon_1\beta_E\eta_T+\phi_2 & \varepsilon_1\beta_E\eta_J+(1-\alpha)\theta \\ \omega_1\kappa_E & -K_2+(1-\varepsilon_1)\beta_E-\lambda & (1-\varepsilon_1)\beta_E\eta_D & (1-\varepsilon_1)\beta_E\eta_T & (1-\varepsilon_1)\beta_E\eta_J \\ (1-\omega_1)\kappa_E & \gamma_{UE} & -K_3-\lambda & 0 & 0 \\ \sigma_1 & 0 & \sigma_2 & 0 & -K_5-\lambda \end{vmatrix} = 0$$

Again expand along second column obtain

$$-\varepsilon_1\beta_E \begin{vmatrix} \omega_1\kappa_E & (1-\varepsilon_1)\beta_E\eta_D & (1-\varepsilon_1)\beta_E\eta_T & (1-\varepsilon_1)\beta_E\eta_J \\ (1-\omega_1)\kappa_E & -K_3-\lambda & 0 & 0 \\ 0 & \tau_1 & -K_4-\lambda & 0 \\ \sigma_1 & \sigma_2 & 0 & -K_5-\lambda \end{vmatrix}$$

$-K_2+(1-\varepsilon_1)\beta_E-\lambda)$

$$\begin{vmatrix} -K_1-\lambda & \varepsilon_1\beta_E\eta_D & \varepsilon_1\beta_E\eta_T+\phi_2 & \varepsilon_1\beta_E\eta_J+(1-\alpha)\theta \\ (1-\omega_1)\kappa_E & K_3-\lambda & 0 & 0 \\ 0 & \tau_1 & -K_4-\lambda & 0 \\ \sigma_1 & \sigma_2 & 0 & -K_5-\lambda \end{vmatrix}$$

$-\gamma_{UE}$

$$\begin{vmatrix} -K_1-\lambda & \varepsilon_1\beta_E\eta_D & \varepsilon_1\beta_E\eta_T+\phi_2 & \varepsilon_1\beta_E\eta_J+(1-\alpha)\theta \\ \omega_1\kappa_E & (1-\varepsilon_1)\beta_E\eta_D & (1-\varepsilon_1)\beta_E\eta_T & (1-\varepsilon_1)\beta_E\eta_J \\ 0 & \tau_1 & -K_4-\lambda & 0 \\ \sigma_1 & \sigma_2 & 0 & -K_5-\lambda \end{vmatrix} = 0$$

The characteristics polynomial of the above matrix is given by;

$$B_5\lambda^5 + B_4\lambda^4 + B_3\lambda^3 + B_2\lambda^2 + B_1\lambda + B_0 = 0 \quad (7)$$

where;

$B_5 = 1,$

$B_4 = K_2 + K_4 + K_5 + K_3 + K_1$

$B_3 = -q_1q_4 + b_1K_2 + b_2 + q_3\sigma_1 - \gamma_{UE}C_3 + a_3$

$$B_2 = -C_1q_1q_4 + K_2b_2 + b_3 - q_3\sigma_1K_2 - q_3\sigma_1K_3 - q_3\sigma_1K_4 + q_3q_4\sigma_2 - q_2q_4\tau_1 + \gamma_{UE} - \gamma_{UE}\tau_1C_5 - \gamma_{UE}C_3d_1 - \sigma_2\gamma_{UE}C_7 + a_4 + a_3K_4 - 2K_5a_3$$

$$B_1 = q_1q_4C_2 + K_2b_3 + b_4 - q_3K_2K_3\sigma_1 - q_3K_2K_4\sigma_1 - q_3\sigma_1K_3K_4 - q_3q_4\sigma_2K_4 - q_3q_4k_2\sigma_2 - q_2q_4\tau_1K_2 - q_2q_4\tau_1K_5 + \sigma_1C_7C_1\gamma_{UE} - \gamma_{UE}\sigma_1C_6C_3 + \gamma_{UE}C_2C_4\tau_1 + 2\gamma_{UE}K_5 + \gamma_{UE}C_2C_6\sigma_2 - \gamma_{UE}C_5K_1\tau_1 - \gamma_{UE}\tau_1C_5K_5 - \gamma_{UE}C_3d_2 - \gamma_{UE}C_7K_1\sigma_2 - \gamma_{UE}C_7K_4\sigma_2 + a_5 + a_4K_4 + a_4K_5 + 2a_3K_5K_4 - a_2 - a_1$$

The Routh Hurwitz criterion will be applied to determine the nature of the roots of the polynomial, which state that the roots of the polynomial will be negative if the coefficient

B_i (where *i*=0, 1, 2,...,5) are all positive and that the Hurwitz matrices are greater than zero. The coefficient $B_5 > 0,$ $B_4 > 0,$ $B_3 > 0,$ $B_2 > 0,$ $B_1 > 0$.

Also, the Hurwitz matrices are as follow:

$$\det(H_2) = \begin{pmatrix} B_1 & 1 \\ B_3 & B_2 \end{pmatrix} = B_1B_2 - B_3 > 0, \det(H_3) = \begin{pmatrix} B_1 & 1 & 0 \\ B_3 & B_2 & B_1 \\ 0 & 0 & B_3 \end{pmatrix} = B_1B_2B_3 - B_3^2 > 0 \Rightarrow B_1B_2 - B_3 > 0 \text{ and}$$

$$\det(H_4) = \begin{pmatrix} B_1 & 1 & 0 & 0 \\ B_3 & B_2 & B_1 & 1 \\ 0 & B_4 & B_3 & B_2 \\ 0 & 0 & 0 & B_4 \end{pmatrix} = B_3(B_2B_1 - B_3) - B_4B_1^2 > 0.$$

Now, that all determinants of the Hurwitz matrices are positive, then all the eigenvalues of the Jacobian matrix have negative real roots when $R_E < 1$, therefore, the disease free equilibrium is locally asymptotically stable.

2.4 Existence of Endemic Equilibrium Point of Ebola Virus Disease

Here we consider the possible existence and stability of endemic (positive) equilibria of the model (3) (that is, a case, where equilibria of one of the infected components of the model is non-zero) will be explored.

Let $E_1^{**} = (S_H^{**}, L_E^{**}, I_U^{**}, I_D^{**}, I_T^{**}, J^{**})$ represents any arbitrary endemic equilibrium of model (3) so that $N_H^{**} = S_H^{**} + L_E^{**} + I_U^{**} + I_D^{**} + I_T^{**} + J^{**}$. Solve (3) at steady state obtain $N_H^{**} = S_H^{**} + L_E^{**} + I_U^{**} + I_D^{**} + I_T^{**} + J^{**}$

$$S_H^{**} = \frac{\pi_H + \alpha\theta J^{**}}{\lambda_E^{**} + \mu}, L_E^{**} = \frac{\varepsilon_1\lambda_E^{**}S_H^{**} + \phi^2 I_T^{**} + (1-\alpha)\theta J^{**}}{C_2}, \quad I_U^{**} = \frac{(1-\varepsilon_1)\lambda_E^{**}S_H^{**} + \omega_1\kappa_E L_E^{**}}{C_3}, \tag{8}$$

$$I_D^{**} = \frac{(1-\omega_1)\kappa_E L_E^{**} + \gamma_{UE} I_U^{**}}{C_4}, \quad I_T^{**} = \frac{\tau_1 I_D^{**}}{C_5}, \quad J^{**} = \frac{\sigma_1 L_E^{**} + \sigma_2 I_D^{**}}{C_6}$$

Recall that the force of infection λ_E, defined in (3) can be expressed at endemic steady state as

$$\lambda_E^{**} = \beta_E\left(\frac{I_U^{**} + \eta_D I_D^{**} + \eta_T I_T^{**} + \eta_J J^{**}}{N_H^{**}}\right) \tag{9}$$

For computational simplicity (8) can be re-write in terms of $\lambda_E^{**}S_H^{**}$ below

$$L_E^{**} = \frac{(C_3C_4M_1 + M_2K_3)\lambda_E^{**}S_H^{**}}{C_3C_4M_4 - M_2K_1 + C_3C_4M_3} = P_1\lambda_E^{**}S_H^{**}, \; I_U^{**} = \frac{(K_3 + \omega_1\kappa_E P_1)\lambda_E^{**}S_H^{**}}{C_3} = P_5\lambda_E^{**}S_H^{**},$$

$$I_D^{**} = \frac{(K_1P_1 + K_3)\lambda_E^{**}S_H^{**}}{C_3C_4} = P_2\lambda_E^{**}S_H^{**}, I_T^{**} = \frac{(\tau_1K_1P_1 + K_3\tau_1)\lambda_E^{**}S_H^{**}}{C_3C_4C_5} = P_4\lambda_E^{**}S_H^{**} \tag{10}$$

$$J^{**} = \frac{(K_2P_1 + K_3)\lambda_E^{**}S_H^{**}}{C_3C_4C_6} = P_3\lambda_E^{**}S_H^{**}.$$

Where $P_1 = \frac{C_3C_4M_1 + M_2K_3}{C_3C_4M_4 - M_2K_1 + C_3C_4M_3}, P_2 = \frac{K_1P_1 + K_3}{C_3C_4}, P_4 = \frac{\tau_1K_1P_1 + K_3\tau_1}{C_3C_4C_5},$

$$P_3 = \frac{K_2P_1 + K_3}{C_3C_4C_6}, P_5 = \frac{K_3 + \omega_1\kappa_E P_1}{C_3}$$

Now, substituting the above expression into (10) gives,

$$\lambda_E^{**}S_H^{**} \neq 0 \; \begin{matrix} \lambda_E^{**}(S_H^{**} + P_1\lambda_E^{**}S_H^{**} + P_5\lambda_E^{**}S_H^{**} + P_2\lambda_E^{**}S_H^{**} + P_4\lambda_E^{**}S_H^{**} + P_3\lambda_E^{**}S_H^{**}) \\ = \beta_E\lambda_E^{**}(P_5S_H^{**} + \eta_D P_2S_H^{**} + \eta_T P_4S_H^{**} + \eta_J PS_H^{**}) \end{matrix} \tag{11}$$

Dividing each term of (11) by $\lambda_E^{**}S_H^{**}$ (and noting that at the endemic steady-state,) obtain $1 + P_6\lambda_E^{**} = R_E$

where $P_6 = P_1 + P_2 + P_3 + P_4 + P_5 \geq 0$ and $R_E = \beta_E(P_5 + \eta_D P_2 + \eta_T P_4 + \eta_J P_3$

Hence, $\lambda_E^{**} = \frac{R_E - 1}{P_6} > 0$, whenever $R_E > 1$ (12)

The components of E_1 can be obtained by substituting the unique value of λ_E^{**}, obtain in (12) into the expression in (3), then the result is established.

Lemma 1 The model (3) has a unique endemic (positive) equilibrium, given by E_1, whenever $R_E > 1$.

2.5 Sensitivity Analysis of Model Parameters for Ebola Virus Disease

Sensitivity analysis was carried out to determine the model robustness to parameter values. This helps us to identify the parameters that have a significant to the basic reproduction number R_E. Also, Sensitivity indices helps in developing efficient and effective intervention strategies in the control of Ebola virus disease in the community. This is calculated using normalized forward sensitivity method, which is defined as the ratio of the relative change in R_E to the relative change in the parameter "P": $Z_P^{R_E} = \frac{\partial R_E}{\partial P} \times \frac{P}{R_E}$.

Table 1 Sensitivity values of basic reproduction number R_E of Ebola virus disease model

Parameters	Sensitivity indices
β_E	1.0000000000
σ_2	0.5252281866
θ	0.1580601091
α	0.1272806385
η_D	0.009595059744
κ_E	0.003178326922
μ	0.0005554843456
ω_1	0.002846541946
γ_{UE}	0.0003910511435
ε_1	0.0001295977841
ϕ_2	0.00004396024358
σ_1	-0.2704057438
τ_1	-0.0001999572217
η_T	-0.0002006352752
η_J	-0.000002002101128
δ_{UE}	0
δ_{DE}	0
δj	0

3. Numerical Simulation

The analytical results of this study are illustrated by carrying out numerical simulations using parameter values in Table 2 with initial values $S_H(0) = 12000,\ L_E(0) = 2000,\ I_U(0) = 200,\ I_D(0) = 300, I_T(0) = 350,\ J(0) = 180$. The simulations are carried out with the help of MAPLE 18 software and the results are given below

Table 2 Parameters values used for the numerical simulation

Parameters	Values	Sources
π_H	1800	Estimated
μ	0.2	Estimated
τ_1	0.3143	[2,20]
ε_1	0.92	[19, 20]
γ_{UE}	0.2	[2]
κ_E	0.2	[1]
σ_2	0.6	[1-2]
σ_1	0.712	[1-2]
β_E	0.8	Estimated
ω_1	0.2	[2,20
ϕ_2	0.02	[1-2]
θ	0.8	[20]
δ_{UE}	0.01	Estimated
δ_{DE}	0.008	[1,20]
δ_j	0.06	Estimated
η_T, η_D, η_J	0.01	Estimated

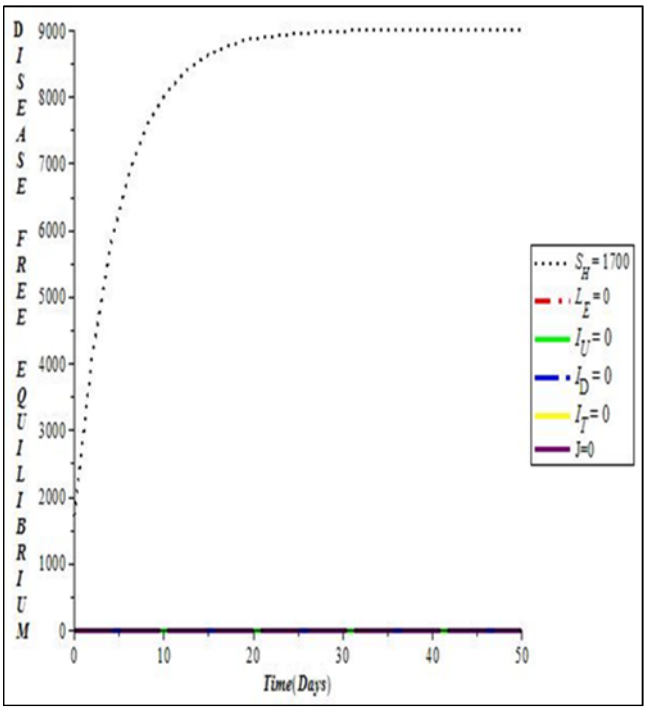

Figure 1 Graph shows DFE point at different time

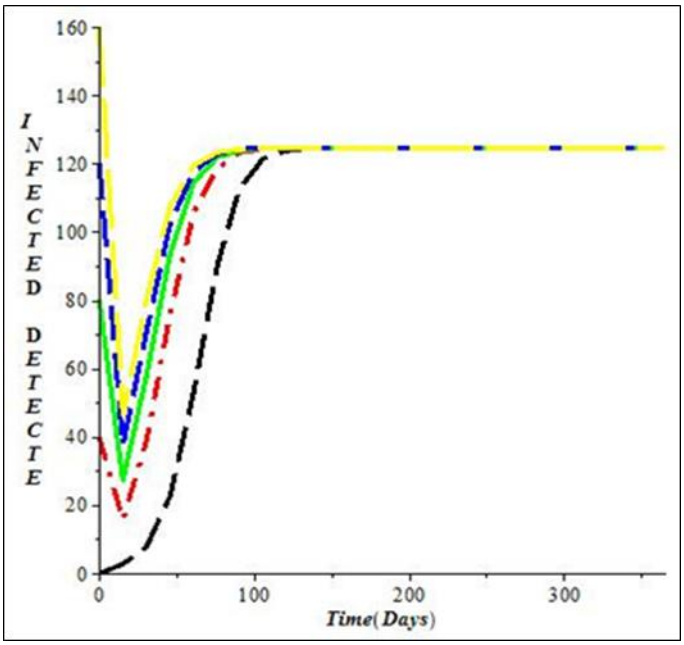

Figure 2 Graph shows global stability of EE point at different time

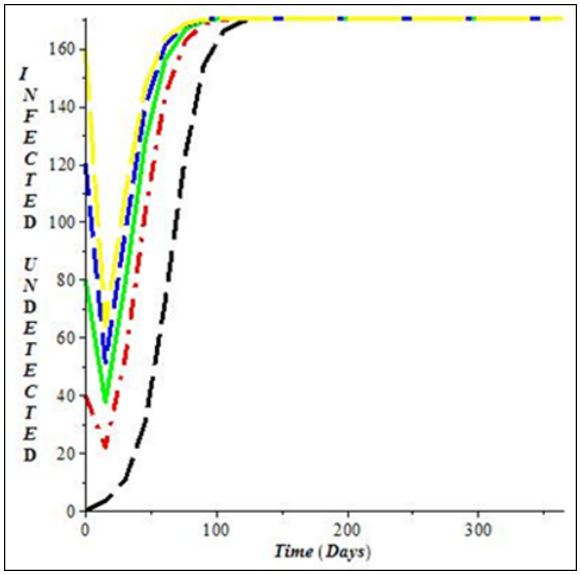

Figure 3 Graph shows global stability of EE point at different time

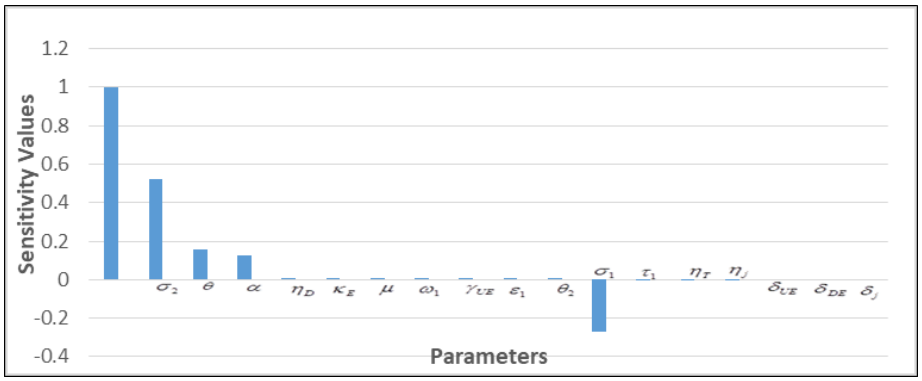

Figure 4 Chart of sensitivity indices on basic reproduction number

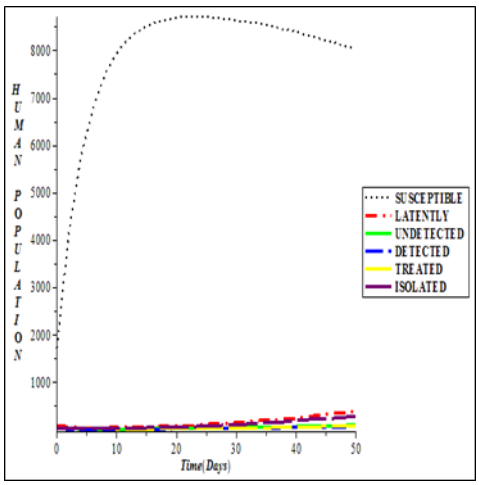

Figure 5 Represents the initial behavior of the Ebola virus disease model

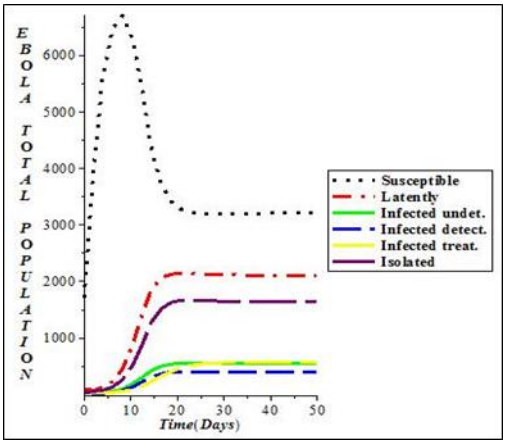

Figure 6 Graph of increasing the most positive sensitive index value which is contact rate on Ebola virus disease model

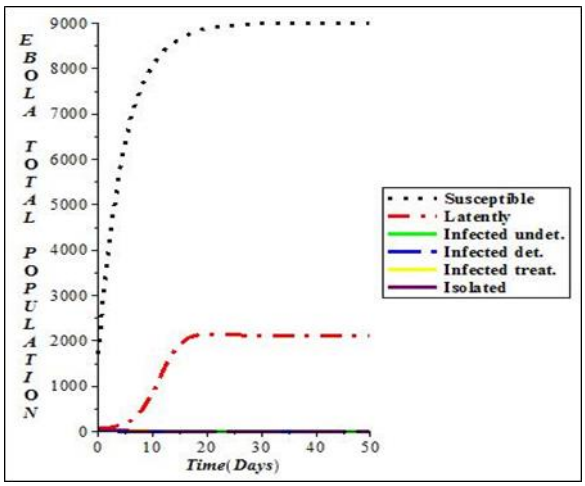

Figure 7 Graph of reducing the most positive sensitive index value which is contact rate from Ebola virus disease model

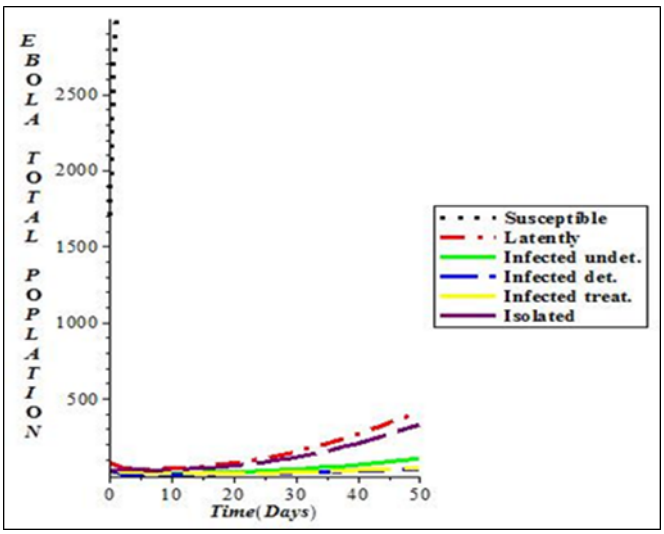

Figure 8 Graph of increasing the most second positive sensitive index value which is isolation rate on Ebola virus disease model

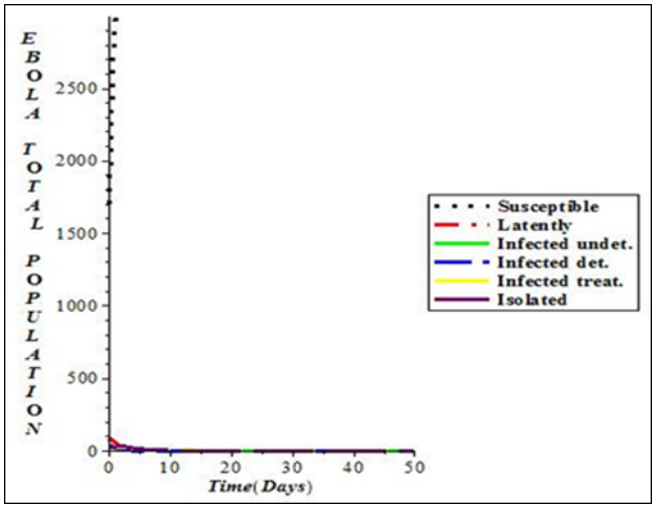

Figure 9 Graph of eliminating the most positive sensitive index value (contact rate) and increasing the most second sensitive value index (isolation rate) on Ebola virus disease model

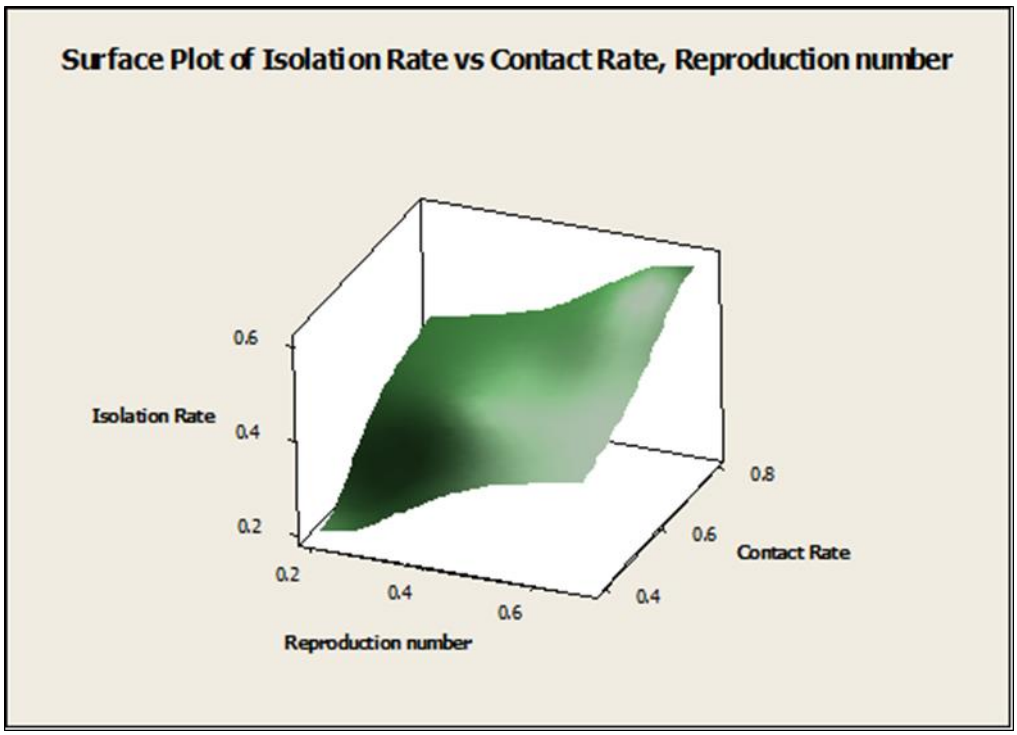

Figure 10 Graph of decreasing the sensitive index value contact rate and isolation rate and their effect on reproduction number

4. Results

Figure 1 depicts the disease-free equilibrium point of the Ebola virus disease, demonstrating that while latent, infected identified, infected undetected, infected treated, and isolated individuals die out, there is always a susceptible population as a whole. According to Figure 2, the system will converge to the same point at a maximum of 120 infected detected classes after 149 days, regardless of the beginning values. Figure 2 illustrates the global stability of endemic equilibrium point of infected detected person. Figure 3 depicts the global stability of the infected undiscovered individual endemic equilibrium point, which illustrates that regardless of the initial values, the system also converges after 149 days to the same position at a maximum of 165 infected undetected classes. The chart of sensitivity indices on the fundamental reproduction is shown in Figure 4. Figure 5 shows the initial behavior of the total population of the various Ebola virus classes. The susceptible population increases initially, then declines slightly due to the natural death rate and remains stable due to the percentage of infected isolated people who become susceptible after testing, while

the latently infected class decreases due to progression, isolation rate, and increases slightly due to discharge rate and treatment progression rate. Individuals' detection causes them to leave the class and join the discovered class, which diminishes the undetected class.

The treated class later reduces as a result of therapy, which causes them to migrate from the undetected class, which initially increases due to the rapid detection of undiscovered individuals. Due to advancement and death rate, the treated class decreases. Due to contributions from latent and observed class isolation rates, the isolated class initially falls and then occasionally increases. As the contact rate increases, it starts to decline due to an increase in infection in the compartment (Figure 6), while the initial susceptible population increases to a peak of 6,700 at just 10 days. Latent, infected undetected, infected detected, infected treated, and isolated individuals increase and remain constant after 20 days. Figure 7 when contact rate was abolished in the community, susceptible human grows to 8600 its highest at 11 days and remain consistent as the day advances while latent population reduces a bit and remain constant as a result of persistence of virus in latent individual. However, the number of isolated, treated, and infected people remained the same throughout and did not significantly affect the compartment.

Figure 8 shows that as the isolation rate rises, the susceptible population grows significantly while the latent and isolated populations also advance. However, the population has a very small number of infected who have been identified, undetected, and treated. Figure 9 shows the effects of reducing contact rates and raising isolation rates. The vulnerable human population reaches its peak without ever declining because there is no infection in the population, while other compartments do not actually exist.

5. Conclusion

In order to incorporate the treated of infected class into [2], a mathematical model was built in this work. The results of the research demonstrated that the model is correctly posed; both endemic and disease equilibria for the models were found. The fundamental Ebola virus disease reproduction number is $R_E = 0.6870878144$ obtained using the newest matrix technique. When the fundamental reproduction number is less than unity, the disease-free equilibrium of the model is locally asymptotically stable, according to the analysis of the models' stability. Similar to this, there are endemic areas where the Ebola virus disease's fundamental reproduction numbers are more than unity. The results of the sensitivity analysis thus far strongly suggest that the effective contact rate β_E is a key factor in the spread of the Ebola virus disease within the population. The elimination of contact rates is the greatest strategy to control the Ebola virus Disease in the population, according to the graphical results in Figure 9. The 3D plots of the inverse relationship between the fundamental reproduction number, contact rate, and isolation rate are shown in Figures 10 and 11.

Compliance with ethical standards

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Disclosure of conflict of interest

No conflict of interest was declared by the authors.

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