MATHEMATICAL MODEL FOR THE SPREAD AND CONTROL OF EBOLA VIRUS BY QUARANTINE TECHNIQUES

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ABSTRACT: Mathematical model for the control of Ebola Virus by Quarantine Technique method have been developed. The model is first order non-linear differential equation, in which the model has been divided into six compartments; exposed individual (S_H). Exposed Vector (S_V), individual with infection (I_H), Quarantine individual (Q_H), Recovered individual (R_H) and vector with the disease (I_V). The Equilibrium State were Obtained and their Stabilities were analyzed by using A domain Decomposition Method (ADM). The result shows that when treatment rate is high, population of the infected human and quarantine human will be reduced. However, early detection of infected individual as well as treatment in time led to the reduction of Ebola Virus transmission in the Population respectively.
KEYWORDS: Ebola-Virus, Mathematical Model, Quarantine-Technique and ADM

1. INTRODUCTION

Ebola is an acute illness that is very fatal. Ebola was first appeared in 1976 in two outbreaks one in, Nzara, South Sudan, while the other in Yambuku in Congo. which latter occurs in a village close to Ebola River, in which the disease generates its name.

The outbreaks that follows in West Africa was in March, 2014, and was the largest and the most difficult outbreak of Ebola than the two others outbreaks (1). Which later spread among countries like Guinea and spread through land borders of Sierra–leone and Liberia, to Nigeria one parson by air and USA one traveller, to Senegal 1 traveller by land and two travellers to Mali.

Fruit bats of the *Pteropodidae* family group are Ebola virus hosts. Ebola was transferred in to human through contact with fluids of infected vectors like forest antelope, chimpanzees, gorillas, , monkeys, Porcupine that are ill or dead in the forest and fruit bats. Through contact in human it then spreads through human to human transmission by, organs, and other bodily fluids of infected people and with surfaces or materials such as contaminated beddings or clothing with the fluids (11).

The time interval between infection and onset of symptoms in human is between one to two weeks and the signs are sudden onset of headache, fever fatigue, sore throat and muscle pain. This is followed by symptoms of kidney and liver function and in some times both internal and external bleeding such as oozing from the gums, blood in the stools. (4).

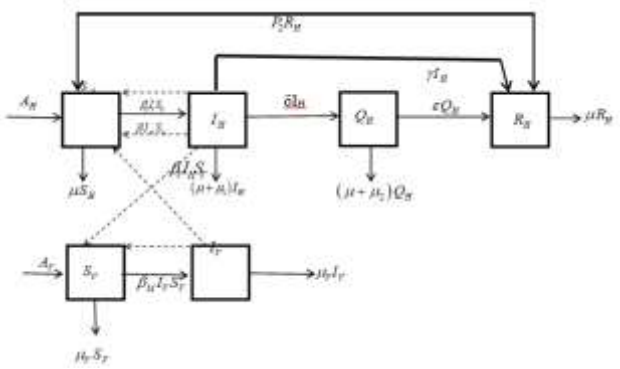
2. PROBLEM FORMATION

In this work, the population have been divided into six compartments, exposed individuals (S_H), exposed Vector (S_V). Human population with infection (I_H), Quarantine individuals (Q_H), Recovered individual from the disease (R_H) Vector population with infection (I_V).

The parameters are; increase in population of human by natural birth and immigration (A_H), contact rate between individuals (β_H). Vector and human contact level (β_V)natural death rate individual in human (μ), rate in which recovered individual in human becomes exposed (P_2). Movement rate of infectious individuals in human to quarantine compartment (δ) movement from quarantine to recovered compartment (ε), movement from infectious to quarantine compartment (γ), death by infection is giving by (μ_1), death by quarantine compartment is giving by(μ_2), vector population increase rate (A_V) and vector dies naturally at the rate (μ_V). However, these can be shown in the

below diagram in which the squares stands for the compartments and transition between the compartments is shown by the this can be shown in a diagram bellow.

A. Model Formulation



$$(2.1)\ \frac{dS_H}{dt} = A_H + P_2R_H - \mu S_H - \beta_H I_V S_H - \beta I_H S_H$$

$$(2.2)\ \frac{dI(H)_H}{dt} = \beta_H I_V S(H)_H + \beta I(H)_H S(H)_H - (\mu + \mu_1 + \delta + \gamma) I(H)_H$$

$$(2.3)\ \frac{dQ(H)_H}{dt} = \delta I(H)_H - (\mu + \mu_2 + \varepsilon) Q(H)_H$$

$$(2.4)\ \frac{dR(H)_H}{dt} = \gamma I_H + \varepsilon Q_H - (\mu + P_2) R(h)_H$$

$$(2.5)\ \frac{dS_V}{dt} = A_V - (\mu_V + \beta_V I_H) S(V)_V - \beta_m I(V)_V S(V)_V$$

$$(2.6)\ \frac{dI_V}{dt} = \beta_V I(H)_H S(V)_V + \beta_m I(V)_V S(V)_V - \mu_V I(V)_V$$

B. Positivity Solutions

Theorem

Let $\{(S(0), S(0) > 0, (I(0), Q(0), R(0), I(0))\} \geq O$ the solution $\{S_H, I_H, Q_H, R_H, S_H, I_V\}(t)$ of the equations is positive for all $t > 0$

From (3.1)

$$(3.1)\ \frac{dS_H}{dt} = A_H + P_2R_H - \mu S_H - \beta_H I_V S_H - \beta I_H S_H \geq -(\mu + \beta_H I_V + \beta I_H) S_H$$

$$(3.2)\ \frac{dS_H}{dt} \geq -(\mu + \beta_H I_V + PI_H) S_H$$

Separation of variables we have:

$$(3.3)\ \frac{(dS_H)}{S_H} \geq -(\mu + \beta_H I_V + \beta I_H)\, dt$$

By taking the Integral 0f both sides gives:

$$(3.4)\ log\ S_H(t) \geq -(\mu + \beta_H I_V + \beta I_H)t + C$$

$$(3.5)\ S_H(t) \geq \ell^{-\mu - \beta_H I_V - \beta I_H)t} \times \ell^C$$

$$(3.6)\ S_H(t) \geq M\ell^{-(\mu + \beta_H I_V + \beta I_H)t}$$

$$but\ M = \ell^C$$

Substituting the initial condition $t = 0$

$$S_H(0) \geq M$$

$$(3.7)\ S_H(t) \geq S_H(0)\ell^{-(\mu + \beta_H I_H + \beta I_H)t \geq 0}$$

$$from\ equation\ (3.2)$$

$$(3.8)\ \frac{dI_H}{dt} = \beta_H I_V S_H + \beta I_H S_H - (\mu + \mu_1 + \delta + \gamma) I_H \geq -(\mu + \mu_1 + \delta + \gamma) I_H$$

$$(3.9)\ \frac{dI_H}{dt} \geq -(\mu + \mu_1 + \delta + \gamma) I_H$$

$$by\ var\ i\ ables\ sepration:$$

$$(3.10)\ \frac{dI_H}{I_H} \geq -(\mu + \mu_1 + \delta + \gamma) dt$$

integrate equation 3.10:

$$(3.11)\ Lin\ I_H \geq -(\mu + \mu_1 + \delta + \gamma)t + c$$

$$(3.12)\ I_H(t) = \ell^{-(\mu + \mu_1 + \delta + \gamma)t} \times \ell^C$$

$$I_H(t) = M\ell^{-(\mu + \mu_1 + \delta + \gamma)t}$$

$$by\ the\ initial\ condition: t = 0$$

however, the remaining equations are positive for $t > 0$ since

$$\ell^w > 0\ w\ \varepsilon R\ for\ all.$$

C. Disease free equilibrium states.

Equilibrium state with no infection is called zero equilibrium state or disease free equilibrium state(point).

Let E_0 denote the disease free equilibrium point or state i.e in the absence of disease or infection $I_V = I_H = 0$

however

$$(4.1)\ \Gamma_1 = \Gamma_2 = 0.$$

$$(4.2)\ Q_H = 0$$

$$(4.3)\ R_H = 0$$

$$(4.4)\ A_H - \mu S_H = 0$$

$$\Rightarrow S_H = \frac{A_H}{\mu}$$

$$(4.5)\ A_V - \mu_V S_V = 0$$

$$\Rightarrow S_V = \frac{A_V}{\mu_V}$$

$$(4.6)\ \therefore E_0 = \left(S^o{}_H, I^o{}_H, Q^o{}_H, R^o{}_H, S^o{}_V, I^o{}_V\right) = \left(\frac{A_H}{\mu}, 000, \frac{A_V}{\mu_V}, 0\right)$$

D. The Endemic Equilibrium point

Equilibrium with the existence of infection is called endemic equilibrium state from our equations (3.1) to (3.6)

At equilibrium:

(5.1) $A_H + P_2P_H - \mu S_H - \Gamma_1 S_H = 0$

(5.2) $\Gamma_1 S(H)_H - K_1 I(H)_H = 0$

(5.3) $\delta I(H)_H - K_2 Q(H)_H = 0$

(5.4) $\gamma I(H)_H + \varepsilon Q(H)_H - K_3 R(H)_H = 0$

(5.5) $A_V - \mu_V S_V - \Gamma_2 S_V = 0$

(5.6) $\Gamma_2 S_V - \mu_V I_V = 0$

When:

$$\left.\begin{array}{l} \Gamma_1 = \beta_H I_V + \beta I_H \\ \Gamma_2 = \beta_V I_H + \beta_m I_V \\ K_1 = \mu + \mu_1 + (1-\delta) + \gamma + 0 \\ K_2 = \mu + \mu_1 + \varepsilon \\ K_3 = \mu + P_2 \end{array}\right\} \quad (5.7)$$

equation gives (5.1), *we have*:

(5.8) $S(H)_H = \dfrac{A_H + P_2 R_H}{\Gamma_1 + \mu}$

equation (5.2) *gives*:

(5.9) $I(H)_H = \dfrac{\Gamma_1 S_H}{K_1}$

From (5.3) *we have*

(5.10) $Q(H)_H = \dfrac{\delta I_H}{K_2}$ *THAT IS* $\dfrac{\delta \Gamma_1 S_H}{K_1 K_2}$

it follows from (5.4):

(5.11) $R(H)_H = \dfrac{\gamma I_H + \varepsilon Q_H}{K_3}$

Then we have

(5.12) $I_V = \dfrac{A_V \Gamma_2}{\mu_V(\mu_V + \Gamma_2)}$

We denote the Endemic equilibrium state by E, which the components ofthe endemic equilibrium state must satisfy the following:

(5.13) $S(H)_H + \dfrac{A_H + P_2 R(H)_H}{\Gamma_1 \mu}$

(5.14) $I(H)_H = \dfrac{\Gamma_1 S(H)_H}{k_1}$

(5.15), *gives* $Q(H)_H = \dfrac{\delta I(H)_H}{k_2} \Rightarrow \dfrac{\delta \Gamma_1 S(H)_H}{k_1 k_2}$

(5.16) *gives* $R(H)_H = \dfrac{[k_2\gamma + \varepsilon\delta]\Gamma_1 S(H)_H}{k_1 k_2 k_3}$

(5.17) *gives* $S(V)_V = \dfrac{A_V}{\mu_V + \Gamma_2}$

(5.18) *gives* $I(V)_V = \dfrac{A_V \Gamma_2}{\mu_V(\mu_V + \Gamma_2)}$

(5.19) *gives* $R(v)_V = \dfrac{\gamma \Gamma_1 S(H)_H}{k_1} + \dfrac{\varepsilon\delta\Gamma_1 S(H)_H}{k_1 k_2}$

(5.20) $R(H)_H = \dfrac{[k_2\gamma\Gamma_1 + \varepsilon\delta\Gamma_1]S(H)_H}{k_1 k_2 k_3}$

(5.21) $R(H)_H = \dfrac{[k_2\gamma + \varepsilon\delta]\Gamma_1 S(H)_H}{k_1 k_2 k_3}$

equation (3.4) *gives*

(5.22) $S(v)_V = \dfrac{A_V}{\mu_1 + \Gamma_2}$

From (3.45), *we have*:

(5.23) $I(V)_V = \dfrac{\Gamma_2 S(V)_V}{\mu_V}$

Substitute equation (5.22) *in* (5.23) *we have*:

(5.24) $I(V)_V = \frac{\Gamma_2}{\mu_V} \frac{A_V}{\mu_V + \Gamma_2}$

3. THE BASIC EFFECTIVE REPRODUCTION NUMBER (R_0)

(6.1) the value of F is given as

$$F = \begin{bmatrix} \beta_H S_H & 0 & \beta_H S_H \\ 0 & 0 & 0 \\ \beta_V S_V & 0 & \beta_M S_V \end{bmatrix}$$

and

(6.2) the value of V is given as

$$V = \begin{bmatrix} K_1 & 0 & 0 \\ -\delta & K_2 & 0 \\ 0 & 0 & \mu_V \end{bmatrix}$$

(6.3) $\lambda\left[\frac{\beta_M S_V}{\mu_v}\lambda - + \frac{\beta_H \beta_V S_H S_V}{K_1 \mu_v} + \frac{\beta_H S_H}{K_1}\lambda - \lambda^2 + \frac{\beta_H \beta_V S_H S_V}{K_1 \mu_v}\right] = 0$

(6.4) $-\lambda^2\left[\lambda - \left(\frac{\beta_H S_H}{K_1} + \frac{\beta_M S_V}{\mu_v}\right)\right] = 0$

(6.5) $-\lambda^2 = 0$ or

(6.6) $\lambda - \left(\frac{\beta_H S_H}{K_1} + \frac{\beta_M S_V}{\mu_v}\right) = 0$

(6.7) $\lambda_1 = \lambda_2 = 0$

(6.8) $\lambda_3 = \left(\frac{\beta_H S_H}{K_1} + \frac{\beta_M S_V}{\mu_v}\right)$

the dominant eigen value λ_3 is our

$R_0 = \left(\frac{\beta_H S_H}{K_1} + \frac{\beta_M S_V}{\mu_v}\right)$

A. The Stability Analysis of Disease Free Equilibrium State (DFE)

Theorem (3.1): Disease free equilibrium E^o of the model equations (3.1) to (3.6) given is locally asymptotically stable if and only if $R_0<1$

Proof:

Linearization of equations (3.1) to (3.6) at the point of equilibrium (E) is given by the Jacobian matrix bellow:

$$(7.1)\ J(E^0) = \begin{bmatrix} -(\mu + \beta_H I_V + \beta I_H) & -\beta_H S_H & 0 & P_2 & 0 & -\beta_H S_H \\ \beta_H I_V + \beta_H I_V & \beta_H S_H - K_I & 0 & 0 & 0 & \beta_H S_H \\ 0 & \delta & -K_2 & 0 & 0 & 0 \\ 0 & \gamma & \varepsilon & -K_3 & 0 & 0 \\ 0 & \beta_V S_V & 0 & 0 & [(-\mu_V + \beta_V I_V) - \beta_M I_V] & -\beta_V S_V \\ 0 & \beta_V S_V & 0 & 0 & \beta_V I_H + \beta_V I_V & \beta_M S_V - \mu_V \end{bmatrix}$$

evaluating the Jacobin matrix to determine the Local stability of the model equations gives the following,

$$(7.2)\ J(E^0) = \begin{bmatrix} -\mu & -\beta_H S_H & 0 & P_2 & 0 & \beta S_H \\ 0 & \beta_H S_H - K_1 & 0 & 0 & 0 & \beta_H S_H \\ 0 & \delta & -k_2 & 0 & 0 & 0 \\ 0 & \gamma & \varepsilon & -k_3 & 0 & 0 \\ 0 & -B_V S_V & 0 & 0 & -\mu_V & -B_M S_V \\ 0 & B_V S_V & 0 & 0 & 0 & B_M S_V - \mu_V \end{bmatrix}$$

by elementary transformation, the above matrix (7.2) gives

$$(7.3)\ J(E^0) = \begin{bmatrix} -\mu & -\beta_H S_H & 0 & P_2 & 0 & -\beta S_H \\ 0 & \beta_H S_H - K_1 & 0 & 0 & 0 & \beta_H S_H \\ 0 & 0 & -k_2 & 0 & 0 & \frac{-\delta \beta_H S_H}{-\beta_H S_H - K_1} \\ 0 & 0 & 0 & -k_3 & 0 & -\frac{\beta_H S_H (\delta_E + \gamma K_2)}{K_2 (-\beta_H S_H - K_1)} \\ 0 & 0 & 0 & 0 & -\mu_V & \frac{\beta_V S_H (2 - \beta_H S_H - K_1)}{\beta_H S_H - K_1} \\ 0 & 0 & 0 & 0 & 0 & \frac{-\beta_H S_H \mu_V + K_1 B_M S_V}{-B_H S_H - K_1} \end{bmatrix}$$

For $|A - I\lambda|$ we have (7.4) $J(E^0) =$

$$\begin{bmatrix} -(\mu + \lambda) & -\beta_H S_H & 0 & P_2 & 0 & -\beta_H S_H \\ 0 & -(K_1 - \beta_H S_H + \lambda) & 0 & 0 & 0 & \beta_H S_H \\ 0 & 0 & -(K_2 + \lambda) & 0 & 0 & -\frac{\delta \beta_H S_H}{\beta_H S_H - K} \\ 0 & 0 & 0 & -(K_3 + \lambda) & 0 & \frac{-\beta_H S_H (\delta E + R K_2)}{K_2 (\beta_H S_H - K_1)} \\ 0 & 0 & 0 & 0 & -(\mu_V + \lambda) & \frac{\beta_V S_V (2\beta_H S_H + K_1)}{\beta_H S_H - K_1} \\ 0 & 0 & 0 & 0 & 0 & \frac{-\beta_H S_H \mu_V + K_1 \beta_M S_V - \mu_V K_1}{\beta_H S_H - K_1} - \lambda \end{bmatrix}$$

We have

(7.5) $\lambda_1 = \mu < 0$

(7.6) $\lambda_2 = \beta_H S_H - K_1$

For λ_2 to be negative, then

(7.7) $\beta_H S_H - K_1 < 0$

(7.8) $\frac{\beta_H S_H}{K_1} < 1$

(7.9) $R_{c\,(H)} < 1$

(7.10) $\lambda_3 = -K_2 < 0 \quad negative$

(7.11) $\lambda_4 = -K_3 < 0 \quad negative$

(7.12) $\lambda_5 = -\mu_v < 0 \quad negative$

(7.13) $\lambda_6 = \frac{\beta_H S_H \mu_V + K_1 \beta_M S_V - \mu_V K_1}{\beta_H S_H - K_1}$

For λ_6 to be negative

(7.14) $\frac{k \beta_H S_H \mu_V + K_1 \beta_V S_V - \mu_V K_1}{\beta_H S_H \mu_V} < 0$

$\beta_H S_H \mu_V + K_1 \beta_V S_V - \mu_V K_1 + K_1 \beta_M S_V < \mu_V K_1$

(7.15) $\frac{\beta_H S_H \mu_V}{\mu_V K_1} + \frac{K_1 \beta_M S_V}{\mu_V K_1} < 1$

(7.16) $\frac{\beta_H S_H}{K_1} + \frac{\beta_M S_V}{\mu_V} < 1$

(7.17) $R_c < 1$

This implies that for $\lambda_6 < 0$ which shows that DFE E^0 of equations (3.1) to (3.6) is locally asymptotically stable. since our $R_0 < 1$ as shown above

B. Using Adomian Decomposition Methods (ADM) to solve the model equations (3.1) to (3.6)

To construct approximate solutions of the model equations, Adomian decomposition method is employed.

(8.1) $S_H = S_H + A_H + P_2 \int_0^t R_H(t)dt - \mu \int_0^t S_H(dt) - \beta_H \int_{T^0}^t I_V S_H \, dt - \beta \int_{T^0}^t I_H S_H \, dt$

(8.2) $i_H(t) = i_H(0) + \beta_H \int_0^t I_v S_H\, dt - \mu \int_0^t I_H\, dt - \mu \int_0^t I_H\, dt\ (1-\beta)\gamma \int_0^t I_H\, dt$

(8.3) $r_H(t) = r(0) + \mu \int_0^t I_H(t)dt + \varepsilon \int_0^t Q_H\, dt - (\mu - P_2) \int_0^t R_H(t)\, dt$

(8.4) $q_H(t) = q(0) + \delta \int_0^t I_H(t)\, dt - (\mu + \mu_2 - \varepsilon) \int_0^t Q_H(t)\, dt$

(8.5) $S_v(t) = S_v(0) + A_V - (\mu_v + \beta_v) \int_0^t I_H S_v(t)dt$

(8.6) $i_v(t) = i_v(0) + \beta_V \int_0^t I_H S_v(t)dt + \beta_m \int_0^t I_v S_v(t)dt - \mu_v \int_0^t I_v(t)dt$

by (ADM) the solutions of equations are reduced to

(8.7) $S_H = \sum_{n=o}^{\infty} S_{n(H)}, i_n = \sum_{n=o}^{\infty} i_{n(H)}, r_H = \sum_{n=o}^{\infty} r_{n(H)} S_v = \sum_{n=0}^{\infty} S_{n(v)}\ and\ l_v = \sum_{n=0}^{\infty} i_{v(v)}$

approximating the non-linear terms in the system gives:

(8.8) $S_H^i = \sum_{n=o}^{\infty} F_n \left(S_{o(H),} \ldots, S_{n(H),} i_{o(V)} \ldots, i_{n(V)}\right)$

(8.9) $r_H^i = \sum_{n=o}^{\infty} F_n \left(r_{o(H),} \ldots, r_{n(H),}\, i_{o(H)} \ldots, i_{n(H)}\right)$

(8.10) $Q_n^i = \sum_{n=o}^{\infty} F_n \left(q_{o(H),} \ldots, q_{n(H),} i_{o(H)} \ldots, i_{n(H)}\right)$

(8.11) $S_v^i = \sum_{n=o}^{\infty} F_n \left(S_{o(v),} \ldots, S_{n(v),} i_{o(H)} \ldots, i_{n(H)}\right)$

(8.12)

Where, $F_n = \frac{1}{n!}\left[\frac{d^n \left(\sum_{k=o}^{\infty} S_k^{\lambda^k}\right)\left(\sum_{k=o}^{\infty} i_k^{\lambda^k}\right)}{d\lambda^k}\right]_{\lambda=o}$

non-linear function F_n is the Adomian polynomial substituting equations we have

(8.13) $\sum_{n=o}^{\infty} S_{n(H)} = S(O) + A_H + P_2 \int_v^t \sum_{n=o}^{\infty} r_{n(H)} dt - \mu \int_o^t \sum_{n=o}^{\infty} S_{n(H)} dt - \beta_H \int_o^t \sum_{n=o}^{\infty} F_n\, dt - \beta \int_o^t \sum_{n=o}^{\infty} F_n\, dt$

(8.14) $\sum_{n=o}^{\infty} i_{n(H)} i(O) + \beta_H \int_v^t \sum_{n=o}^{\infty} F_n dt \int_o^t \sum_{n=o}^{\infty} i_{n(H)} dt - \mu \int_o^t \sum_{n=o}^{\infty} i_{n(v)}\, dt\ (1-5) - \gamma \int_o^t \sum_{n=o}^{\infty} i_{n(H)}\, dt$

(8.15) $\sum_{n=o}^{\infty} r_{n(H)} = r(O) + \gamma \int_v^t \sum_{n=o}^{\infty} i_{n(H)} dt\ \varepsilon \int_o^t \sum_{n=o}^{\infty} q_{n(H)} dt - (\mu + P_2 \int_o^t \sum_{n=o}^{\infty} r_{n(H)}\, dt$

(8.16) $\sum_{n=o}^{\infty} q_{n(H)} = q_H(O) + \delta \int_v^t \sum_{n=o}^{\infty} i_{n(H)} dt - (\mu + \mu_2 + \varepsilon) \int_o^t \sum_{n=o}^{\infty} q_{n(H)} dt$

(8.17) $\sum_{n=o}^{\infty} s_{n(v)} = S_v(O) + A_v - (\mu_v + \beta_v) \int_v^t \sum_{n=o}^{\infty} F_n dt - \beta_M \int_o^t \sum_{n=o}^{\infty} F_n\, dt$

(8.18) $\sum_{n=o}^{\infty} i_{n(v)} = i_r(O) + \beta_v \int_v^t \sum_{n=o}^{\infty} F_n dt - \mu_2 \int_o^t \sum_{n=o}^{\infty} i_{n(H)} + \beta_M \int_o^t \sum_{n=o}^{\infty} F_n\, dt$

Using equation (8.12), we compute some of the domain polynomials as follows:

$Fo = \frac{1}{0!}\left[\frac{d^0}{d\lambda^0}\left(\sum_{K=d}^{0}(S_K\lambda^K)(i_k\lambda^k)\right)\right]$

$Fo = 1\left[\sum_{K=d}^{0}(S_0\lambda^0)(i_0\lambda^0)\right]$

(8.19) $Fo = S_0 i_0$

$F_1 = \frac{d}{d_\lambda}\left[\left(\sum_{k=0}^{1} S_K\lambda^K\right)\left(\sum_{K=0}^{1} i_K\lambda^K\right)\right]$

but $\sum_{k=0}^{1} S_K\lambda^K = S_0 + S_1\lambda$

also $\sum_{k=0}^{1} i_K\lambda^k = i_0 + i_1\lambda$

$\left(\sum_{k=0}^{1} S_K\lambda^K\right)\left(\sum_{k=0}^{1} i_K\lambda_K\right) = (S_0 + S_1\lambda)(i_0 + i_1\lambda)$

$= (S_0 i_0 + S_0 i_1\lambda + i_0 S_1\lambda + i_1 S_1\lambda^2)$

$F_1 = \frac{d}{d_\lambda}(S_0 i_1 + S_0 i_1\lambda + i_0 S_1\lambda + i_1 S_1\lambda^2)|\lambda = 0$

$F_1 = [S_0 i_1 + i_0 S_1 + Z\lambda i_1 S_1]\lambda = 0$

(8.20) $F_1 = S_0 i_1 + i_0 S_1$

It follows that:

(8.21) $F_0 = S_0 i_0 +, F_1 = S_0 i_1 + S_1 i_0, F_2 = S_0 i_2 + S_1 i_1 + S_2 i_0, F_3 = S_0 i_3 + S_1 i_2 + S_2 i_1, + S_3 i_0, F_4 = S_0 i_4 + S_1 i_3 + S_2 i_2 + S_3 i_1 + S_4 i_0, F_5 = S_0 i_5 + S_1 i_4 + S_2 i_3 + S_3 i_5 + S_4 i_1, S_5 i_0$

By the use of Maple we obtained approximate solutions as given bellow:

$S_{n(H)} = \sum_{n=1}^{N} S_{n(H),} i_{N(H)} = \sum_{n=0}^{N} i_{n(H)}$,

$R_{n(H)} \sum_{n=0}^{N} R_{n(H)},\ Q_{n(H)} \sum_{n=0}^{N} q_{n(H)},$

(8.22) $S_{n(v)} = \sum_{n=0}^{N} S_{n(v)},\ and\ i_{N(v)} = \sum_{n=0}^{N} i_{n(v)}$.

4. RESULTS AND DISCUSSION

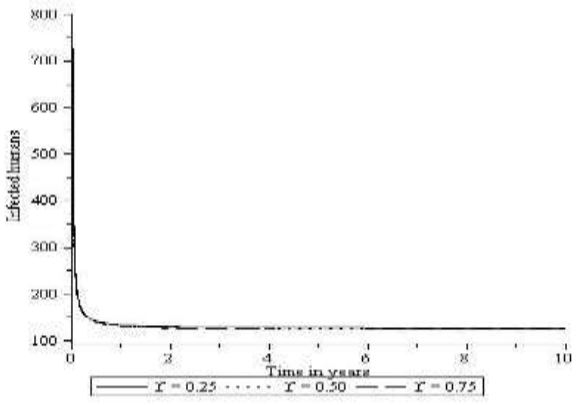


Fig: 4.1 Infected human I_H against time(t) for contact rate between infected human and exposed human

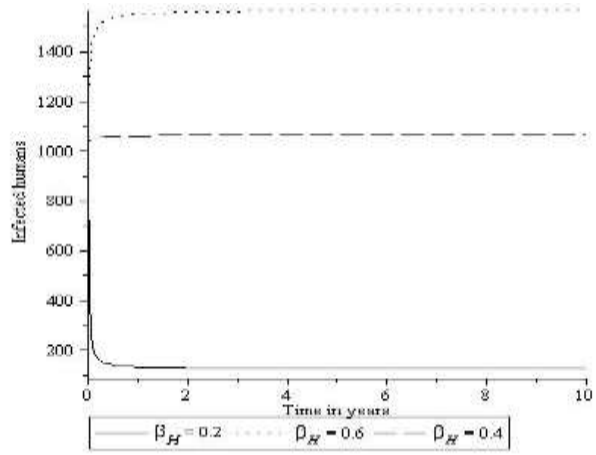


Fig: 4.2 Infected individuals in human with time(t) in terms of treatment

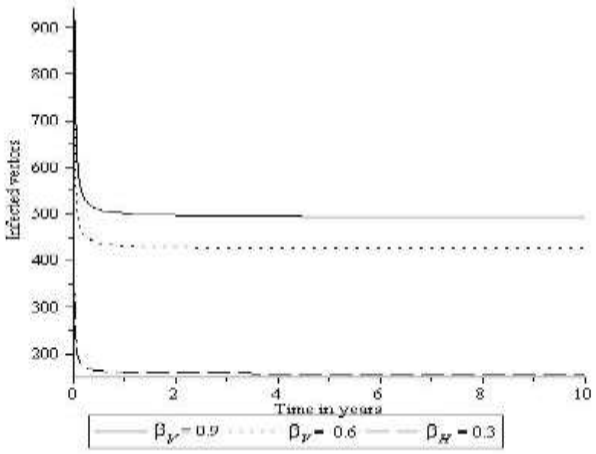


Fig:4.5 Infected vector against time(t) for contact rate of vectors

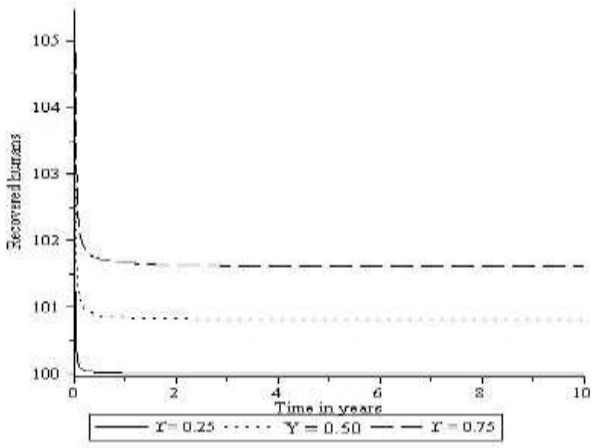


Fig:4.3 Recovered individuals in human with time(t) in terms of treatment of infected individuals

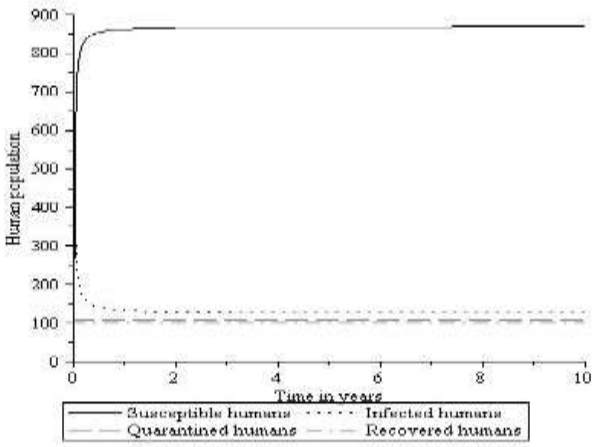


Fig: 4.6 Human population against time (t) for the compartments

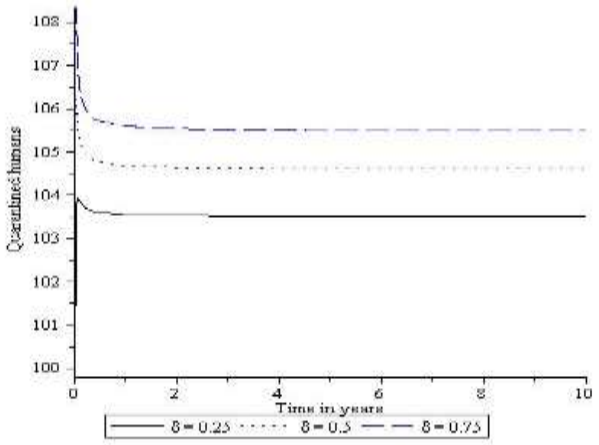


Fig:4.4 Quarantine individuals in human with time(t) in terms of treatment of individuals

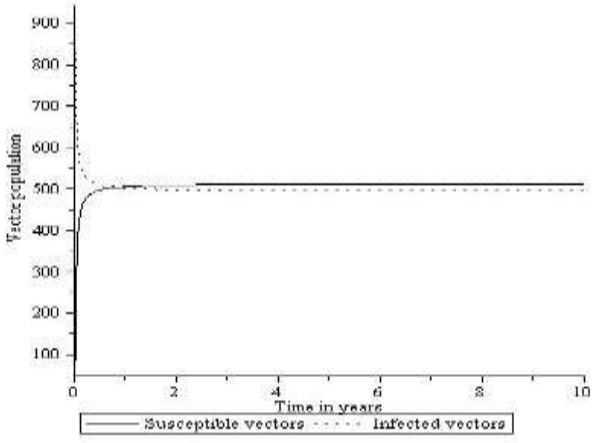


Fig: 4.7 Vector population against time(t) for exposed vector and infected vector

5. DISCUSSIONS

The mathematical model of Ebola virus have been developed in the study, in which the Zero equilibrium state(DFE) have been solved for stability and shows that is stable. Similarly, endemic equilibrium state was found and tested for stability which prove that is stable. However, we suggests Ebola virus can be controlled. The simulation help us understand the time to time nature of the population.

6. CONCLUSIONS

It is shown however, from the graph Figures (4.2) and (4.4) that when the treatment rate is high, Ebola virus will be eradicated from the population completely and there will be no infections, detection of infection in time, isolating and treatment of infected individuals helps in reducing the Ebola virus transmission in the population as shown at the Figures (4.1) and (4.5) respectively .With these facts, we can conclude that, the population is stable and free from infection of Ebola virus in the community, Below are the findings:

1. Presence of non-infection in the population (equilibrium state wit out infection)
2. presence of infection in the population (equilibrium stat wit infection)
3. Inadequate response in terms of treatment of Ebola virus of both infected and quarantined individuals will not control the Ebola virus in the population.
4. Limited response in treatment of infected and quarantined individuals in human will not control Ebola virus in human population.
   While if it is High, it brings significant control of Ebola virus or infection in any human population.

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