International Journal of
Mathematical Modelling &Computations
Vol. 10, No. 04, Fall 2020, 361- 383

Mathematical Model of Herpes Simplex Virus – II (HSV-II) with Global Stability Analysis

E. Gurmu[a,*], B. K. Bole[a] and P. R. Koya[a]

[a]*Department of Mathematics, Wollega University, Nekemte, Ethiopia.*

Abstract. In this paper, a nonlinear deterministic mathematical model of ordinary differential equations has been formulated to describe the transmission dynamics of HSV-II. The well possedness of the formulated model equations was proved and the equilibrium points of the model have been identified. In addition, the basic reproduction number that governs the disease transmission was obtained from the largest eigenvalue of the next-generation matrix. Both local and global stability of the disease free equilibrium and endemic equilibrium point of the model equation was established using basic reproduction number. The results show that, if the basic reproduction is less than one then the solution converges to the disease free steady state and the disease free equilibrium is locally asymptotically stable. On the other hand, if the basic reproduction number is greater than one the solution converges to endemic equilibrium point and the endemic equilibrium is locally asymptotically stable. Also, sensitivity analysis of the model equation was performed on the key parameters to find out their relative significance and potential impact on the transmission dynamics of HSV-II. Finally, numerical simulations of the model equations are carried out using the software DE Discover 2.6.4 and MATLAB R2015b with ODE45 solver. The Results of simulation show that treatment minimizes the risk of HSV-II transmission from the community and the stability of disease free equilibrium is achievable when $\Re_0 < 1$.

Received: 13 April 2020, Revised: 10 June 2020, Accepted: 30 June 2020.

Keywords: HSV; Reproductive number; Stability analysis; Sensitivity.

Index to information contained in this paper

1. Introduction

Sexually transmitted infections (STIs) are a major public health problem worldwide, affecting quality of life and causing serious morbidity and mortality. Herpes is caused by Herpes simplex virus (HSV) [9]. There are two types of herpes, herpes simplex type -I (HSV-I) and herpes simplex type -II (HSV-II). HSV-I is predominantly orally transmitted and it causes orolabial herpes (i.e., cold sores) and HSV-II is one of the most common sexually transmitted infections worldwide and it cause genital herpes. The majority of herpes simplex types -II infections are transmitted by persons who are unaware that they have the infection or who are asymptomatic when transmission occurs [10].

Worldwide, an estimated 19.2 million new HSV-2 infections occurred among adults and adolescents aged 15-49 years in 2012 with the highest rates among younger age groups. HSV-2 is a lifelong infection and the estimated global HSV-2 prevalence of 11.3% translates into an estimated 417 million people with the infection in 2012. The prevalence of HSV-2 is highest in the African Region (31.5%), followed by the Region of the Americas (14.4%). Despite lower prevalence, in the South-East Asia and Western Pacific

Regions also harbour a large number of people with the infection due to the large populations of some countries in the region. The HSV-2 infection rate is consistently higher in females compared to males; there were an estimated 11.8 million new infections and 267 million prevalent infections among women in 2012 versus 7.4 million new and 150 million prevalent infections among men. The higher infection rate among women is most likely due to their greater biological susceptibility to HSV-2 infection [15].

Mathematical models have been used extensively in research into the epidemiology of Herpes Simplex Virus-II to improve our understanding of the major contributing factors [12]. A lot of scholars developed a mathematical model to describe the dynamics of the disease that helped them to propose disease control mechanism and also described the transmission dynamics of the diseases. Some of them are [1, 11] developed and analyzed a deterministic model for the transmission dynamics of Herpes Simplex Virus-II. Mhlanga et al. [8] proposed and analysed a mathematical model for the spread of HSV-2 by incorporating all the relevant biological details and poor treatment adherence. The study demonstrates that though time dependent control will be effective on controlling new HSV-2 cases it may not be sustainable for certain time intervals. Recent studies such as [7, 13] construct a mathematical model of HSV-II for vaccination and develop a vaccine against herpes simplex virus type 2 (HSV-2) to reduce the infection from the community.

All the above studies have been developed a deterministic as well as stochastic mathematical model of Herpes Simplex Virus-II dynamics by subdividing the population into sub-classes of susceptible, infectious, vaccinated and recovered. But none of them considered Herpes Simplex Virus-II class. Therefore, that is motivated us to undertake this study to fulfill this gap.

In this paper, mathematical model of Herpes Simplex Virus-II is formulated and analyzed. This paper is arranged as follows: in Section 2, we derive a model consisting of ordinary differential equations that describes the transmission dynamics of the diseases with the fundamental assumptions. In Section 3, well possedness of the model formulation, stability analysis of the equilibrium points and reproduction number are included. In Section 4, numerical simulation of the model equations are performed by conveying various sets of numerical values to the model parameters. In Section 5 sensitivity analysis of model parameters towards the reproduction number is carried out. Our conclusions are discussed in Section 6.

2. Model formulation

In this study the dynamical system of ordinary differential equations is formulated to show the dynamics of human population in the presence of Human Immunodeficiency Virus (HIV) and ART as combined treatments. This model is modification of the works done in [7]. This previous work is five compartmental model whereas the current study considered deterministic model that consists of eight compartments of human population.

$$N(t) = S(t) + E(t) + A(t) + I\,(t) + H(t) + R(t).$$

In formulating the model, the following assumptions are taken into consideration:

(i) The susceptible individuals are increased by the recruitment of individuals into the population at a rate Π.

(ii) Individuals from susceptible sub compartment move to exposed sub compartment with per capita rate η of becoming infectious (we recall that $1/\eta$ is approximately the length of the latent period).

(iii) Exposed individuals progress to the symptomatic sub compartment with probability p, and to asymptomatic sub compartment with probability $(1-p)$.

(iv) Asymptomatic individuals are typically assumed to be infectious at a reduced transmission rate qA.

(v) The susceptible individuals are acquiring HSV-II infection with force of infection λ which is given by $\lambda = \beta[I + qA]/N$ where, β is the contact rate and q is the transmission coefficient for the asymptomatic individuals. If $q > 1$ then, the asymptomatic infect susceptible more likely than infective. If $q = 1$, then both asymptomatic and infective have equal chance to infect the susceptible, but if $q < 1$ then, the infective have good chance to infect susceptible than asymptomatic.
(vi) Some of the asymptomatic and symptomatic individual's progress to Herpes simplex virus-II at a rate φ, ϕ respectively and others recover naturally through body immune system at a rate γ, α respectively.
(vii) The Herpes Simplex Virus-II individuals are treated at a rate δ and move to recovery sub compartment.
(viii) The recovered individuals may lose immunity and return to the susceptible sub compartment with rate ω.
(ix) Individuals will die due to disease after reaching HSV-II stage with rate ξ.
(x) In all compartments μ is the natural mortality rate of individuals.
(xi) All parameters and variables of the model are considered to be positive.

2.1 *Description of variables and parameters*

The variables and parameters used in this model are introduced in Table 1 and 2. Their notations and descriptions are also included.

Table 1. Description of Variables used in the model equations.

Variable	Description
$\mathbf{N(t)}$	The total population at time t
$\mathbf{S(t)}$	Susceptible Individuals
$\mathbf{E(t)}$	Exposed Individuals
$\mathbf{A(t)}$	Asymptomatic Individuals
$\mathbf{I(t)}$	Symptomatic Individuals
$\mathbf{H(t)}$	Herpes Simplex Virus-II Individuals
$\mathbf{R(t)}$	Recovered Individuals

Table 2. Description of parameters used in the model equations.

Parameter	Description
$\mathbf{\Pi}$	Recruited rate of susceptible individuals
$\boldsymbol{\beta}$	Contact rate
$\boldsymbol{\eta}$	Per capita rate of becoming infectious
$\mathbf{p}$	Probability of exposed joining symptomatic
$\mathbf{q}$	Transmission rate of asymptomatic
$\boldsymbol{\lambda}$	Force of infection
$\boldsymbol{\varphi}$	Progression rate from A to H
$\boldsymbol{\phi}$	Progression rate from I to H
$\boldsymbol{\gamma}$	Recovery rate of asymptomatic
$\boldsymbol{\alpha}$	Recovery rate of symptomatic
$\boldsymbol{\delta}$	Treatment rate of HSV-II
$\boldsymbol{\omega}$	Recovery rate of recovered individuals
$\boldsymbol{\mu}$	Natural death rate

Taking into account of the above consideration, we then have the following transfer diagram of the model which is show in Figure 1.

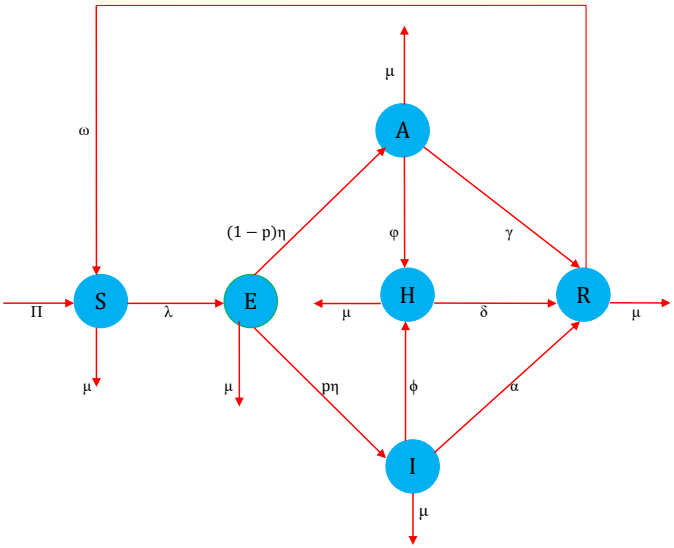

Figure 1. Schematic diagram for HSV-II model.

The model is thus governed by the following system of non-linear ordinary differential equations:

$$dS/dt = \Pi - \lambda S - \mu S + \omega R \quad (1)$$

$$dE/dt = \lambda S - (\eta + \mu)E \quad (2)$$

$$dA/dt = (1-p)\eta E - (\varphi + \gamma + \mu)A \quad (3)$$

$$dI/dt = p\eta E - (\phi + \alpha + \mu)I \quad (4)$$

$$dH/dt = \varphi A + \phi I - (\delta + \mu + \xi)H \quad (5)$$

$$dR/dt = \gamma A + \alpha I + \delta H - (\omega + \mu)R \quad (6)$$

The non-negative initial conditions of the system of model equations (1)-(6) are denoted by $S(0) = S_0,\ E(0) = E_0,\ A(0) = A_0,\ I(0) = I_0,\ H(0) = H_0,\ R(0) = R_0$.

3. Basic properties of the model

3.1 *Invariant region*

Lemma 3.1 (Boundedness) The non-negative solutions of the system of model equations (1)-(6) are bounded. That is the model variables $S(t), E(t), A(t), I(t), H(t)$ and $R(t)$ are all bounded for all t [14].

Proof The dynamic system is uniformly bounded in the proper subset $\Omega \subset \mathbb{R}_+^6$, under consideration that the total population at any time t is given by:

$$N(t) = S(t) + E(t) + A(t) + I(t) + H(t) + R(t)$$

Differentiating $N(t)$ with respect to t leads to;

$$dN/dt = (dS/dt) + (dE/dt) + (dA/dt) + (dI/dt) + (dH/dt) + (dR/dt) \quad (7)$$

By combining model equation (1)-(6) and (7), we can get

$$dN/dt = \Pi - \mu N - \xi H \tag{8}$$

In the absence of mortality due to HSV-II (8) becomes

$$dN/dt = \Pi - \mu N$$

Equivalently this inequality can be expressed as a linear ordinary differential inequality as $[\mathrm{dN(t)/dt}] + \mu \mathrm{N(t)} \leq \Pi$ giving general solution upon solving as $\mathrm{N(t)} \leq (\Pi/\mu) + ce^{-\mu t}$. But, the term $N(0)$ denotes the initial values of the respective variable i.e., $\mathrm{N(t)} = \mathrm{N(0)}$ at $\mathrm{t} = 0$. Thus, the particular solution can be expressed as $\mathrm{N(t)} \leq (\Pi/\mu) + [\mathrm{N(0)} - (\Pi/\mu)]e^{-\mu t}$. Further, it can be observed that $N(t) \to (\Pi/\mu)$ as $t \to \infty$. That is, the total population size $N(t)$ takes off from the value $\mathrm{N(0)}$ at the initial time $\mathrm{t} = 0$ and ends up with the bounded value (Π/μ) as the time t grows to infinity. Thus, it can be concluded that $N(t)$ is bounded as $0 \leq N(t) \leq (\Pi/\mu)$. Thus, the feasible solution set of the system equation of the model enters and remains in the region:

$$\Omega = \{(S, E, A, I, H, R) \in \Re_+^6 \ : \ N \leq \Pi/\mu\}$$

The solution set of the dynamic system of the equation in the model is bounded in the region such that Ω. This implies that the dynamic system of the model in the region is well posed epidemiologically and mathematically. Hence, it is sufficient to study the dynamics of the basic model in the region Ω.

3.2 *Existence of the solution*

Lemma 3.2 (Existence) Solutions of the model equations (1)-(6) together with the initial conditions $S(0) > 0, E(0) > 0, A(0) > 0, I(0) > 0, H(0) > 0, R(0) > 0$ exist in $\mathbb{R}_+^6$ i.e., the model variables $S(t), E(t), A(t), I(t), H(t)$ and $R(t)$ exist for all t and will remain in $\mathbb{R}_+^6$.

Proof The right-hand sides of the system of equations (1)-(6) can be expressed as follows:

$$f_1(S, E, A, I, H, R) = \Pi - \lambda S - \mu S + \omega R$$
$$f_2(S, E, A, I, H, R) = \lambda S - (\eta + \mu)E$$
$$f_3(S, E, A, I, H, R) = (1 - p)\eta E - (\varphi + \gamma + \mu)A$$
$$f_4(S, E, A, I, H, R) = p\eta E - (\phi + \alpha + \mu)I$$
$$f_5(S, E, A, I, H, R) = \varphi A + \phi I - (\delta + \mu + \xi)H$$
$$f_6(S, E, A, I, H, R) = \gamma A + \alpha I + \delta H - (\omega + \mu)R$$

According to Derrick and Groosman theorem, let Ω denote the region $\Omega = \{(S, E, A, I, H, R) \in \Re_+^6 : N \leq \Pi/\mu\}$. Then equations (1)-(6) have a unique solution if $(\partial f_i)/(\partial x_j)$, $i, j = 1, 2, 3, 4, 5, 6$ are continuous and bounded in Ω. Here, $x_1 = S$, $x_2 = E$, $x_3 = A$, $x_4 = I$, $x_5 = H$ and $x_6 = R$. The continuity and the boundedness are shown in Table 3.

Thus, all the partial derivatives $(\partial f_i)/(\partial x_j), i, j = 1, 2, 3, 4, 5, 6$ exist, continuous and bounded in Ω as shown in Table 3. Hence, by Derrick and Groosman theorem, a solution for the model (1)-(6) exists and is unique.

Table 3. Continuity and boundedness of the model solution.

$\lvert(\partial f_1)/(\partial S)\rvert = \lvert-(\lambda+\mu)\rvert < \infty$	$\lvert(\partial f_2)/(\partial S)\rvert = \lvert\lambda\rvert < \infty$
$\lvert(\partial f_1)/(\partial E)\rvert = 0 < \infty$	$\lvert(\partial f_2)/(\partial E)\rvert = \lvert-(\eta+\mu)\rvert < \infty$
$\lvert(\partial f_1)/(\partial A)\rvert = \lvert-(\beta q/N)\rvert < \infty$	$\lvert(\partial f_2)/(\partial A)\rvert = \lvert(\beta q/N)\rvert < \infty$
$\lvert(\partial f_1)/(\partial I)\rvert = \lvert-(\beta/N)\rvert < \infty$	$\lvert(\partial f_2)/(\partial I)\rvert = \lvert(\beta/N)\rvert < \infty$
$\lvert(\partial f_1)/(\partial H)\rvert = 0 < \infty$	$\lvert(\partial f_2)/(\partial H)\rvert = 0 < \infty$
$\lvert(\partial f_1)/(\partial R)\rvert = \omega < \infty.$	$\lvert(\partial f_2)/(\partial R)\rvert = 0 < \infty.$
$\lvert(\partial f_3)/(\partial S)\rvert = 0 < \infty$	$\lvert(\partial f_4)/(\partial S)\rvert = 0 < \infty$
$\lvert(\partial f_3)/(\partial E)\rvert = \lvert(1-p)\eta\rvert < \infty$	$\lvert(\partial f_4)/(\partial E)\rvert = \lvert p\eta\rvert < \infty$
$\lvert(\partial f_3)/(\partial A)\rvert = \lvert-(\varphi+\gamma+\mu)\rvert < \infty$	$\lvert(\partial f_4)/(\partial A)\rvert = 0 < \infty$
$\lvert(\partial f_3)/(\partial I)\rvert = 0 < \infty$	$\lvert(\partial f_4)/(\partial I)\rvert = \lvert-(\phi+\alpha+\mu)\rvert < \infty$
$\lvert(\partial f_3)/(\partial H)\rvert = 0 < \infty$	$\lvert(\partial f_4)/(\partial H)\rvert = 0 < \infty$
$\lvert(\partial f_3)/(\partial R)\rvert = 0 < \infty.$	$\lvert(\partial f_4)/(\partial R)\rvert = 0 < \infty.$
$\lvert(\partial f_5)/(\partial S)\rvert = 0 < \infty$	$\lvert(\partial f_6)/(\partial S)\rvert = 0 < \infty$
$\lvert(\partial f_5)/(\partial E)\rvert = 0 < \infty$	$\lvert(\partial f_6)/(\partial E)\rvert = 0 < \infty$
$\lvert(\partial f_5)/(\partial A)\rvert = \lvert p\rvert < \infty$	$\lvert(\partial f_6)/(\partial A)\rvert = \lvert\gamma\rvert < \infty$
$\lvert(\partial f_5)/(\partial I)\rvert = \lvert\phi\rvert < \infty$	$\lvert(\partial f_6)/(\partial I)\rvert = \lvert\alpha\rvert < \infty$
$\lvert(\partial f_5)/(\partial H)\rvert = \lvert-(\delta+\mu+\xi)\rvert < \infty$	$\lvert(\partial f_6)/(\partial H)\rvert = \lvert\delta\rvert < \infty$
$\lvert(\partial f_5)/(\partial R)\rvert = 0 < \infty.$	$\lvert(\partial f_6)/(\partial R)\rvert = \lvert-(\omega+\mu)\rvert < \infty.$

3.3 *Positivity of the solution*

The solution of the system remains positive at any point in time t, if the initial values of all the variables are positive.

Lemma 3.3 Let $\Omega = \{(S,E,A,I,H,R) \in \mathbb{R}^6_+; S_0 > 0,\ E_0 > 0,\ A_0 > 0,\ I_0 > 0,\ H_0 > 0, R_0 > 0\}$; then the solutions of $\{S,E,A,I,H,R\}$ are positive for all $t \geq 0$.

Proof Positivity is verified separately for each of the model $S(t)$, $E(t), A(t)$, $I(t)$, $H(t)$ and $R(t)$.

Positivity of $S(t)$: The model equation (1) given by $dS/dt = \Pi - \lambda S - \mu S + \omega R$ can be expressed without loss of generality, after eliminating the positive terms $\Pi + \omega R$ which are appearing on the right-hand side, as an inequality as $dS/dt \geq -[\lambda+\mu]S$. Using variables separable method and on applying integration, the solution of the foregoing differentially inequality can be obtained as $S(t) \geq S_0[exp-(\lambda+\mu)t]$. Recall that an exponential function is always non–negative irrespective of the sign of the exponent, i.e., the exponential function $[exp-(\lambda+\mu)t]$ is a non-negative quantity. Hence, it can be concluded that $S(t) \geq 0$.

Positivity of $E(t)$: The model equation (2) given by $dE/dt = \lambda S - (\eta+\mu)E$ can be expressed without loss of generality, after eliminating the positive term $[\lambda S]$ which are appearing on the right hand side, as an inequality as $dE/dt \geq [-(\eta+\mu)]E$ sing variables

separable method and on applying integration, the solution of the foregoing differentially inequality can be obtained as $E(t) \geq E_0[exp-(\eta+\mu)t]$. Recall that an exponential function is always non–negative irrespective of the sign of the exponent, i.e., the exponential function $[exp-(\eta+\mu)t]$ is a non-negative quantity. Hence, it can be concluded that $E(t) \geq 0$.

Positivity of $A(t)$: The model equation (3) given by $dA/dt = (1-p)\eta E-(\varphi+\gamma+\mu)A$ can be expressed without loss of generality, after eliminating the positive term $[(1-p)\eta E]$ which are appearing on the right-hand side, as an inequality as $dA/dt \geq [-(\varphi+\gamma+\mu)]A$. Using variables separable method and on applying integration, the solution of the foregoing differentially inequality can be obtained as $A(t) \geq A_0[exp-(\varphi+\gamma+\mu)t]$. Recall that an exponential function is always non–negative irrespective of the sign of the exponent, i.e., the exponential function $[exp-(\varphi+\gamma+\mu)t]$ is a non-negative quantity. Hence, it can be concluded that $A(t) \geq 0$.

Positivity of $I(t)$: The model equation (4) given by $dI/dt = p\eta E-(\phi+\alpha+\mu)I$ can be expressed without loss of generality, after eliminating the positive term $[p\eta E]$which are appearing on the right-hand side, as an inequality as $dI/dt \geq -[(\phi+\alpha+\mu)]I$. Using variables separable method and on applying integration, the solution of the foregoing differentially inequality can be obtained as $I(t) \geq I_0[exp-(\phi+\alpha+\mu)t]$. Recall that an exponential function is always non–negative irrespective of the sign of the exponent, i.e., the exponential function $[exp-(\phi+\alpha+\mu)]$ is a non-negative quantity. Hence, it can be concluded that $I(t) \geq 0$.

Positivity of $H(t)$: The model equation (5) given by $dH/dt = \varphi A+\phi I-(\delta+\mu+\xi)H$ can be expressed without loss of generality, after eliminating the positive term $[\varphi A+\phi I]$ which are appearing on the right-hand side, as an inequality as $dH/dt \geq [-(\delta+\mu+\xi)]H$. Using variables separable method and on applying integration, the solution of the foregoing differentially inequality can be obtained as $H(t) \geq H_0[exp-(\delta+\mu+\xi)t]$. Recall that an exponential function is always non–negative irrespective of the sign of the exponent, i.e., the exponential function $[exp-(\delta+\mu+\xi)t]$. is a non-negative quantity. Hence, it can be concluded that $H(t) \geq 0$.

Positivity of $R(t)$: The model equation (5) given by $dR/dt = \gamma A+\alpha I+\delta H-(\omega+\mu)R$ can be expressed without loss of generality, after eliminating the positive term $[\gamma A+\alpha I+\delta H]$ which are appearing on the right-hand side, as an inequality as $dR/dt \geq [-(\omega+\mu)]R$. Using variables separable method and on applying integration, the solution of the foregoing differentially inequality can be obtained as $R(t) \geq R_0[exp-(\omega+\mu)t]$. Recall that an exponential function is always non–negative irrespective of the sign of the exponent, i.e., the exponential function $[-(\omega+\mu)t]$. is a non-negative quantity. Hence, it can be concluded that $R(t) \geq 0$.

Thus, the model variables $S(t)$, $E(t)$, $A(t)$, $I(t)$, $H(t)$ and $R(t)$ representing population sizes of various types of cells are positive quantities and will remain in $\mathbb{R}_+^6$ for all t.

3.4 *The disease free equilibrium (DFE)*

In order to understand the transmission dynamics of the model, it is necessary to determine equilibrium points of the solution region. An equilibrium solution is a steady state solution of the model equations (1)-(6) in the sense that if the system begins at such a state, it will remain there for all times. In other words, the population sizes remain unchanged and thus the rate of change for each population vanishes [3].

To find the disease free equilibrium, we equated the right hand sides of model

equations (1)-(6) to zero, evaluating it at $E = I = A = H = 0$ and solving for the symptomatic and non-asymptomatic variables. These requirements reflect in reducing the model equations (1)-(6) as $\Pi - (\lambda + \mu)S = 0$ giving $S^0 = \Pi/(\lambda + \mu) = (\Pi/\mu)$ where $\lambda = \beta(I + qA)/N = \beta(0 + 0)/N = 0$. Thus, the disease-free equilibrium point of the model equation in (1)-(6) above is given by:

$$\varepsilon_0 = \{S^0, E^0, A^0, I^0, H^0, R^0\} = \{(\Pi/\mu),\ \ 0, 0, 0, 0, 0\}.$$

3.5 *The basic reproduction number* ($\mathfrak{R}_0$)

The basic reproduction number denoted by $\mathfrak{R}_0$ and is defined as the expected number of people getting secondary infection among the whole susceptible population. This number determines the potential for the spread of disease within a population. When $\mathfrak{R}_0 < 1$ each infected individual produces on average less than one new infected individual so that the disease is expected to die out. On the other hand, if $\mathfrak{R}_0 > 1$ then each individual produces more than one new infected individual so that the disease is expected to continue spreading in the population. This means that the threshold quantity for eradicating the disease is to reduce the value of $\mathfrak{R}_0$ to less than one [5].

The basic reproductive number $\mathfrak{R}_0$ can be determined using the next generation matrix. In this method, $\mathfrak{R}_0$ is defined as the largest eigenvalue of the next generation matrix. The formulation of this matrix involves classification of all compartments of the model in to two classes: infected and non-infected. That is, the basic reproduction number cannot be determined from the structure of the mathematical model alone but depends on the definition of infected and uninfected compartments.

The model equations are rewritten starting with newly infective classes

$$\begin{aligned} dE/dt &= \lambda S - (\eta + \mu)E \\ dA/dt &= (1 - p)\eta E - (\varphi + \gamma + \mu)A \\ dI/dt &= p\eta E - (\phi + \alpha + \mu)I \\ dH/dt &= \varphi A + \phi I - (\delta + \mu + \xi)H \end{aligned} \tag{9}$$

Then by the principle of next-generation matrix, we obtained

$$f_i = \begin{bmatrix} \beta(I + qA)S/N \\ 0 \\ 0 \\ 0 \end{bmatrix} \quad \text{and} \quad v_i = \begin{bmatrix} (\eta + \mu)E \\ -(1 - p)\eta E + (\varphi + \gamma + \mu)A \\ -p\eta E + (\phi + \alpha + \mu)I \\ -\varphi A - \phi I + (\delta + \mu + \xi)H \end{bmatrix}$$

The Jacobian matrices of f_i and v_i evaluated at DFE are given by F and V, respectively, such that

$$F = \begin{bmatrix} 0 & \beta q & \beta & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \quad \text{and} \quad V = \begin{bmatrix} a & 0 & 0 & 0 \\ -(1 - p)\eta & b & 0 & 0 \\ -p\eta & 0 & c & 0 \\ 0 & -\varphi & -\phi & d \end{bmatrix}$$

It can be verified that the matrix V is non-singular as its determinant $det[V] = abcd$ is non-zero and after some algebraic computations its inverse matrix is constructed as

$$V^{-1} = \begin{bmatrix} [1/a] & 0 & 0 & 0 \\ [(1 - p)\eta/ab] & [1/b] & 0 & 0 \\ [p\eta/ac] & 0 & [1/c] & 0 \\ [-(\phi bp\eta + c\varphi(1 - p)\eta)/abcd] & [\varphi/bd] & [\phi/cd] & [1/d] \end{bmatrix}.$$

The product of the matrices F and V^{-1} can be computed as

$$FV^{-1} = \begin{bmatrix} 0 & \beta q & \beta & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \begin{bmatrix} [1/a] & 0 & 0 & 0 \\ [(1-p)\eta/ab] & [1/b] & 0 & 0 \\ [p\eta/ac] & 0 & [1/c] & 0 \\ [-(\phi bp\eta + c\varphi(1-p)\eta)/abcd] & [\varphi/bd] & [\phi/cd] & [1/d] \end{bmatrix}$$

$$= \begin{bmatrix} [(\eta\beta qc(1-p) + \beta p\eta b)/abc] & [\beta q/b] & [\beta/c] & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}.$$

Now it is possible to calculate the eigenvalue to determine the basic reproduction number $\Re_0$ by taking the spectral radius of the matrix FV^{-1}. Thus, the eigenvalues are computed by evaluating $det[FV^{-1} - \psi I] = 0$ or equivalently solving

$$\begin{vmatrix} [(\eta\beta qc(1-p) + \beta p\eta b)/abc] - \psi & [\beta q/b] & [\beta/c] & 0 \\ 0 & -\psi & 0 & 0 \\ 0 & 0 & -\psi & 0 \\ 0 & 0 & 0 & -\psi \end{vmatrix} = 0.$$

It reduces to the equation for ψ as $-\psi^3\big[[(\eta\beta qc(1-p) + \beta p\eta b)/abc] - \psi\big] = 0$ giving the two eigenvalues as $\psi_1 = [(\eta\beta qc(1-p) + \beta p\eta b)/abc]$, $\psi_2 = \psi_3 = \psi_4 = 0$.

However, the dominant eigenvalue here is $\psi_1 = [(\eta\beta qc(1-p) + \beta p\eta b)/abc]$ and is the spectral radius as the threshold value or the basic reproductive number. Thus, it can be concluded that the reproduction number of the model is $\Re_0 = [\beta\eta[qc(1-p) + pb]/abc]$, where $a = (\eta + \mu)$, $b = (\varphi + \gamma + \mu)$, $c = (\phi + \alpha + \mu)$, $d = (\delta + \mu)$, $e = (\omega + \mu)$.

3.6 *Local stability of disease free equilibrium*

Theorem 3.1 The disease free equilibrium point ε_0 of the system (1)-(6) is locally asymptotically stable if $\Re_0 < 1$ and unstable if $\Re_0 > 1$.

Proof To proof this theorem first we obtain the Jacobian matrix of system (9) at the disease free equilibrium ε_0 as follows:

$$J(\varepsilon_0) = \begin{bmatrix} -\mu & 0 & \beta q & \beta & 0 & \omega \\ 0 & -a & \beta q & \beta & 0 & 0 \\ 0 & (1-p)\eta & -b & 0 & 0 & 0 \\ 0 & p\eta & 0 & -c & 0 & 0 \\ 0 & 0 & \varphi & \phi & -d & 0 \\ 0 & 0 & \gamma & \alpha & \delta & -e \end{bmatrix} = 0.$$

Now, the eigenvalues of $J(\varepsilon_0)$ are required to be found. The characteristic equation $det[J(\varepsilon_0) - \psi I] = 0$ is expanded and simplified as follows:

$$\begin{vmatrix} -\mu - \psi & 0 & \beta q & \beta & 0 & \omega \\ 0 & -a - \psi & \beta q & \beta & 0 & 0 \\ 0 & (1-p)\eta & -b - \psi & 0 & 0 & 0 \\ 0 & p\eta & 0 & -c - \psi & 0 & 0 \\ 0 & 0 & \varphi & \phi & -d - \psi & 0 \\ 0 & 0 & \gamma & \alpha & \delta & -e - \psi \end{vmatrix} = 0 \qquad (10)$$

From the characteristic equation of (10), we obtained a characteristic polynomial:

$$[-\mu-\psi][-e-\psi][-d-\psi][\psi^3+L_1\psi^2+L_2\psi+L_3]=0, \tag{11}$$

where

$$L_1=a+b+c$$
$$L_2=ab+ac+bc-\beta\eta(p+q)$$
$$L_3=abc(1-\Re_0)$$

Thus, from equation (11) clearly, we see that:

$$\psi_1=-\mu$$
$$\psi_2=-d$$
$$\psi_3=-e$$

It can be observed that the eigenvalues $\psi_1,\ \psi_2$ and ψ_3 are absolutely negative quantities.

For the last expression, that is,

$$\psi^3+L_1\psi^2+L_2\psi+L_3=0 \tag{12}$$

We applied Routh-Hurwitz criteria. By the principle of Routh-Hurwitz criteria, (12) has strictly negative real root if and only if $L_1>0,\ L_3>0$ and $L_1L_2>L_3$.

Therefore, it is concluded that the DFE ε_0 of the system of differential equations (1)-(6) is locally asymptotically stable if $\Re_0<1$ and unstable if $\Re_0>1$.

3.7 *Global stability of disease free equilibrium*

To investigate the global stability of disease free equilibrium we used technique implemented by Castillo-Chavez and Song [2]. First the model equation (1)-(6) can be re-written as

$$dX/dt=F(X,Z)$$

$$dZ/dt=G(X,Z),\ G(X,0)=0$$

Where, X stands for the uninfected population, that is $X=(S,R)$ and Z also stands for the infected population, that is $Z=(E,\ A,\ I,\ H)$. The disease free equilibrium point of the model is denoted by $U=(X^*,0)$. The point $U=(X^*,0)$ to be globally asymptotically stable equilibrium for the model provided that $\Re_0<1$ and the following conditions must be met:

(H_1). For $dX/dt=F(X,0),\quad X^*$ is globally asymptotically stable.

(H_2). $G(X,Z)=AZ-\tilde{G}(X,Z),\quad \tilde{G}(X,Z)\geq 0$ for $(X,Z)\in\Omega$.

Where $A=D_ZG(U,0)$ is a Metzler matrix (the off diagonal elements of A are non-negative) and G is the region where the model makes biological sense.

If the model (1)-(6) met the above two criteria, then the following theorem holds.

Theorem 3.2 The point $U=(X^*,0)$ is globally asymptotically stable equilibrium provided that $\Re_0<1$ and the condition (H_1) and (H_2) are satisfied.

Proof From system (1)-(6) we can get $F(X,Z)$ and $G(X,Z)$;

$$(X,Z)=\begin{bmatrix}\Pi-\lambda S-\mu S+\omega R\\ \gamma A+\alpha I+\delta H-(\omega+\mu)R\end{bmatrix}\ \text{and}\ G(X,Z)=\begin{bmatrix}\lambda S-(\eta+\mu)E\\ (1-p)\eta E-(\varphi+\gamma+\mu)A\\ p\eta E-(\phi+\alpha+\mu)I\\ \varphi A+\phi I-(\delta+\mu)H\end{bmatrix}$$

Consider the reduced system

$$\frac{dX}{dt}_{|Z=0} = \begin{bmatrix} \Pi - \mu S \\ 0 \end{bmatrix} \tag{13}$$

From (13), it is obvious that $X^* = [(\Pi/\mu), 0]$ is the global asymptotic point. This can be verified from the solution, namely $S = [\Pi/\mu] + [S(0) - (\Pi/\mu)]e^{-\mu t}$. As $t \to \infty$, the solution $(S) \to [\Pi/\mu]$, implying that the global convergence of (15) in Ω.

From the equation for infected compartments in the model we have:

$$A = \begin{bmatrix} (\eta+\mu) & \beta q & \beta & 0 \\ (1-p)\eta & -(\varphi+\gamma+\mu) & 0 & 0 \\ p\eta & 0 & -(\phi+\alpha+\mu) & 0 \\ 0 & \varphi & \phi & -(\delta+\mu) \end{bmatrix}$$

Since A is Metzler matrix, i.e., all off diagonal elements are nonnegative. Then, $G(X,Z)$ can be written as, $G(X,Z) = AZ - \tilde{G}(X,Z)$, where

$$\tilde{G}(X,Z) = \begin{bmatrix} \beta(\mathrm{I} + \mathrm{qA})(1 - [\mathrm{S/N}]) \\ 0 \\ 0 \\ 0 \end{bmatrix} = \begin{bmatrix} \tilde{G}_1(X,Z) \\ \tilde{G}_2(X,Z) \\ \tilde{G}_3(X,Z) \\ \tilde{G}_4(X,Z) \end{bmatrix}$$

It follows that $\tilde{G}_1(X,Z) \geq 0$, $\tilde{G}_2(X,Z) = \tilde{G}_3(X,Z) = \tilde{G}_4(X,Z) = 0$. Thus, $\tilde{G}(X,Z) \geq 0$. Conditions (H_1) and (H_2) are satisfied and we conclude that U is globally asymptotically stable for $\mathfrak{R}_0 < 1$.

3.8 *Stability analysis of endemic equilibrium*

Existence: We find an equilibrium where at least A^* or E^* or I^* or H^* is non zero. Let the endemic equilibrium point of the model equation (1)-(6) be denoted by:

$$\varepsilon^* = (S^*,\ E^*,\ A^*,\ I^*,\ H^*,\ R^*),$$

and consider the force of infection

$$\lambda^* = [\beta(I^* + qA^*)]/[N^*] \tag{14}$$

Solving the equations in system (1)-(6) interms of the force of infection by setting the right-hand sides of equations in (1)-(6) to zero, gives:

$$\begin{aligned}
S^* &= [abcde\Pi]/\left[abcde(\lambda^*+\mu) + \lambda^*\eta\omega[cf(1-p) - gbp]\right] \\
E^* &= [bcde\Pi\lambda^*]/\left[abcde(\lambda^*+\mu) + \lambda^*\eta\omega[cf(1-p) - gbp]\right] \\
A^* &= [cde\Pi\eta\lambda^*(1-p)]/\left[abcde(\lambda^*+\mu) + \lambda^*\eta\omega[cf(1-p) - gbp]\right] \\
I^* &= [bdep\Pi\eta\lambda^*]/\left[abcde(\lambda^*+\mu) + \lambda^*\eta\omega[cf(1-p) - gbp]\right] \\
H^* &= [\Pi\eta\lambda^*[\varphi c(1-p) + \phi bp]]/\left[abcde(\lambda^*+\mu) + \lambda^*\eta\omega[cf(1-p) - gbp]\right] \\
R^* &= \left[\Pi\eta\lambda^*[\mathrm{dc}\gamma(1-p) + \alpha\mathrm{bd}p + \delta\varphi c(1-p) + \delta\phi\mathrm{b}p]\right] \\
&\qquad /\left[abcde(\lambda^*+\mu) + \lambda^*\eta\omega[cf(1-p) - gbp]\right]
\end{aligned} \tag{15}$$

Substituting (15) and in equation (14) gives

$$\lambda^* = [\mathrm{de}\beta\mu\eta\lambda^*[\mathrm{b}p + \mathrm{qc}(1-p)]]/\left[abcde\mu + abcde\lambda^* + \lambda^*\eta\omega[cf(1-p) - gbp]\right] \tag{16}$$

After some rearrangement equation (16) becomes

$$[abcde + \eta\omega cf(1-p) - \eta\omega gbd]\lambda^* + abcde\mu[1 - \mathfrak{R}_0] = 0$$

This shows that the non-zero (positive endemic) equilibrium point of the model satisfy

$$D_1\lambda^* + D_2 = 0, \tag{17}$$

where, $D_1 = abcde + \eta\omega cf(1-p) - \eta\omega gbd$ and $D_2 = abcde\mu[1-\Re_0]$.

It is clear that $D_1 > 0$ and $D_2 < 0$ when $\Re_0 > 1$. Thus, the linear system (17) has a unique positive solution, given by $\lambda^* = -D_2/D_1$ whenever $\Re_0 > 1$. On the other hand, when $\Re_0 < 1$, $D_2 > 0$. In this case, the force of infection at steady state is negative. Hence the model has no positive equilibrium point in this case.

Lemma 3.4 The model equation (1)-(6) has a unique positive endemic equilibrium whenever $\Re_0 > 1$ and no positive endemic equilibrium whenever $\Re_0 < 1$.

The local stability property of this endemic equilibrium is now explored.

Theorem 3.3 The unique endemic equilibrium of model equation (1)-(6) is locally asymptotically stable if $\Re_0 > 1$.

Proof The proof is based on transforming the problem of analysing the stability of an equilibrium point to that of analysing the stability of a fixed point. Equation (16) gives a fixed point problem of the form:

$$f(\lambda^*) = [\mathrm{de}\beta\mu\eta\lambda^*[\mathrm{b}p + \mathrm{qc}(1-p)]]/[abcde\mu + [abcde + \eta\omega[cf(1-p) - gbp]]\lambda^*]$$

It follows that

$$f(\lambda^*) = [\mathrm{de}\mu\lambda^*[\mathrm{abc}\Re_0]]/[abcde\mu + [abcde + \eta\omega[cf(1-p) - gbp]]\lambda^*]$$

Then, derivative of $f(\lambda^*)$ become:

$$f'(\lambda^*) = [(\mathrm{abcde}\mu)^2\Re_0]/[[abcde\mu + [abcde + \eta\omega[cf(1-p) - gbp]]\lambda^*]^2]$$

Evaluating $f'(\lambda^*)$ at $\lambda^* = -D_2/D_1$ gives:

$$f'(-D_2/D_1) = [(\mathrm{abcde}\mu)^2\Re_0]/[(\mathrm{abcde}\mu\Re_0)^2] = \frac{1}{\Re_0}.$$

It is clear that

$$|f'(\lambda^*)| < 1 \text{ at } \lambda^* = -D_2/D_1 \text{ , whenever } \Re_0 > 1.$$

Thus, the unique endemic equilibrium is locally asymptotically stable if $\Re_0 > 1$.

Theorem 3.4 The endemic equilibrium point of the model equation (1)-(6) is globally asymptotically stable whenever $\Re_0 > 1$.

Proof To prove the global asymptotic stability of the endemic equilibrium we use the method of Lyapunov functions. Define

$$\begin{aligned}(S^*, E^*, A^*, I^*, H^*, R^*) = {} & [M - M^* - M^* ln(M^*/M)] + [S - S^* - S^* ln(S^*/S)] \\ & + [I - I^* - I^* ln(I^*/I)] + [A - A^* - A^* ln(A^*/A)] \\ & + [H - H^* - H^* ln(H^*/H)] + [R - R^* - R^* ln(R)]\end{aligned}$$

By direct calculating the derivative of F along the solution (1)-(6) we have

$$\begin{aligned}dF/dt = {} & [(S - S^*)/S]\, dS/dt + [(E - E^*)/E]\, dE/dt + [(A - A^*)/A]\, dA/dt \\ & + [(I - I^*)/I]\, dI/dt + [(H - H^*)/H]\, dH/dt + [(R - R^*)/R]\, dR/dt\end{aligned}$$

$$= [(S - S^*)/S][\Pi - \lambda S - \mu S + \omega R] + [(E - E^*)/E][\lambda S - (\eta + \mu)E] + [(A - A^*)/A][(1 - p)\eta E - (\varphi + \gamma + \mu)A] + [(I - I^*)/I][p\eta E - (\phi + \alpha + \mu)I\ ] + [(H - H^*)/H][\varphi A + \phi I - (\delta + \mu + \xi)H] + [(R - R^*)/R][\gamma A + \alpha I + \delta H - (\omega + \mu)R$$

$$= [1 - S^*/S][\Pi - \lambda S - \mu S + \omega R] + [1 - E^*/E][\lambda S - (\eta + \mu)E] + [1 - A^*/A][(1 - p)\eta E - (\varphi + \gamma + \mu)A\ ] + [1 - I^*/I][p\eta E - (\phi + \alpha + \mu)I] + [1 - H^*/H][\varphi A + \phi I - (\delta + \mu + \xi)H] + [1 - R^*/R][\gamma A + \alpha I + \delta H - (\omega + \mu)R]$$

$$dF/dt = [\Pi + \lambda S^* + \eta E^* + (\varphi + \gamma)A^* + (\phi + \alpha)I^* + \delta H^* + \omega R^* + (N^* - N)\mu] - [(\Pi + \omega R)\,[S^*/S] + \lambda S[E^*/E] + (1 - p)\eta E[A^*/A] + p\eta E[I^*/I] + (\varphi A + \phi I + \gamma A + \alpha I + \delta H)[R^*/R]]$$

Thus, collecting positive and negative terms together we obtain

$$dF/dt = Q - K.$$

Here,

$$Q = \Pi + \lambda S^* + \eta E^* + (\varphi + \gamma)A^* + (\phi + \alpha)I^* + \delta H^* + \omega R^* + (N^* - N)\mu,$$

$$K = [(\Pi + \omega R)\,[S^*/S] + \lambda S[E^*/E] + (1 - p)\eta E[A^*/A] + p\eta E[I^*/I] + (\varphi A + \phi I + \gamma A + \alpha I + \delta H)[R^*/R]]$$

$$N = S + E + A + I + H + R \quad \text{and} \quad N^* = S^* + E^* + A^* + I^* + H^* + R^*$$

Thus if $Q < K$, then $dF/dt \leq 0$. Noting that $dF/dt = 0$ if and only if $S = S^*,\ E = E^*,\ A = A^*,\ I = I^*,\ H = H^*,\ R = R^*$. Therefore, the largest compact invariant set in $\{(S^*, E^*, A^*, I^*, H^*, R^*) \in \Omega:\ dF/dt = 0\}$ is the singleton ε^* is the endemic equilibrium of the system (1)-(6). By LaSalle's invariant principle (LaSalle's, 1976), it implies that ε^* is globally asymptotically stable in Ω if $Q < K$.

4. Sensitivity analysis

In this section we perform the sensitivity analysis of the basic reproduction number. Sensitivity analysis tells us how important each parameter is to disease transmission. Such information is crucial not only for experimental design, but also to data assimilation and reduction of complex nonlinear models. Sensitivity analysis is commonly used to determine the robustness of model predictions to parameter values, since there are usually errors in data collection and presumed parameter values. It is used to discover parameters that have a high impact on $\mathfrak{R}_0$ and should be targeted by intervention strategies. Following Eshetu and Koya [6], we present the normalized forward sensitivity indices of $\mathfrak{R}_0$ with respect to model parameter values $\mu = 0.02,\ \beta = 0.68,\ \phi = 0.004,\ \varphi = 0.003,\ \gamma = 0.58,\ \alpha = 0.89,\ \eta = 0.006,\ q = 0.04,\ p = 0.48$. The explicit expression of $\mathfrak{R}_0$ is given by

$$\mathfrak{R}_0 = \beta\eta[q(1 - p)(\phi + \alpha + \mu) + p(\varphi + \gamma + \mu)]/[(\eta + \mu)(\varphi + \gamma + \mu)(\phi + \alpha + \mu)].$$

Since $\mathfrak{R}_0$ depends only on nine parameters, we derive an analytical expression for its sensitivity to each parameter using the normalized forward sensitivity index as follows in Table 4 [4]. The sensitivity indices of the basic reproduction number with respect to main parameters are arranged orderly in Table 4. The parameters are arranged from the most

sensitive one to the least sensitive one. Those parameters that have positive indices i.e., φ, β, p, η, γ, q and ϕ show that they have great impact on expanding the disease in the community if their values are increasing. Due to the reason that the basic reproduction number increases as their values increase, it means that the average number of secondary cases of infection increases in the community. Furthermore, those parameters in which their sensitivity indices are negative i.e., α and μ have an influence of minimizing the burden of the disease in the community as their values increase while the others are left constant. And also, as their values increase, the basic reproduction number decreases, which leads to minimizing then endemicity of the disease in the community.

Table 4. Sensitivity index and indices table.

Parameter Symbol	Sensitivity index	Sensitivity indices
φ	$\Upsilon_{\varphi}^{\Re_0} = [\partial\, \Re_0/\varphi] \times [\varphi/\, \Re_0]$	1.13926
β	$\Upsilon_{\beta}^{\Re_0} = [\partial\, \Re_0/\beta] \times [\beta/\, \Re_0]$	11
p	$\Upsilon_{p}^{\Re_0} = [\partial\, \Re_0/p] \times [p/\, \Re_0]$	0.93836
η	$\Upsilon_{\eta}^{\Re_0} = [\partial\, \Re_0/\eta] \times [\eta/\, \Re_0]$	0.769232
γ	$\Upsilon_{\gamma}^{\Re_0} = [\partial\, \Re_0/\gamma] \times [\gamma/\, \Re_0]$	0.220
q	$\Upsilon_{q}^{\Re_0} = [\partial\, \Re_0/q] \times [q/\, \Re_0]$	0.01616
ϕ	$\Upsilon_{\phi}^{\Re_0} = [\partial\, \Re_0/\phi] \times [\phi/\, \Re_0]$	0.0002697
α	$\Upsilon_{\alpha}^{\Re_0} = [\partial\, \Re_0/\alpha] \times [\alpha/\, \Re_0]$	-0.9137
μ	$\Upsilon_{\mu}^{\Re_0} = [\partial\, \Re_0/\mu] \times [\mu/\, \Re_0]$	-1.363231

5. Numerical simulation

In this section, numerical simulation study of model equations (1)-(6) is carried out using the software DE Discover 2.6.4 and MATLAB R2015b with ODE45 solver. To conduct the study, a set of physically meaningful values are assigned to the model parameters. These values are either taken from literature or assumed on the basis of reality. Using the parameter values given in Table 5 and the initial conditions $S(0) = 300$, $E(0) = 50$, $A(0) = 120$, $A(0) = 100$, $H(0) = 90$ and $R(0) = 140$ in the model equations (1)-(6) a simulation study is conducted and the results are given in the following Figures.

Table 5. Parameter values used in model equations.

Parameter	Value	Source
$\boldsymbol{\Pi}$	0.0015	[6]
$\boldsymbol{\mu}$	0.002	[6]
$\boldsymbol{\beta}$	0.68	Assumed
$\boldsymbol{\phi}$	0.004	Assumed
$\boldsymbol{\varphi}$	0.003	Assumed
$\boldsymbol{\gamma}$	0.058	Assumed
$\boldsymbol{\alpha}$	0.089	Assumed
$\boldsymbol{\omega}$	0.09	Assumed
$\boldsymbol{\xi}$	0.001	[6]
$\boldsymbol{\eta}$	0.006	Assumed
$\boldsymbol{q}$	0.004	Assumed
$\boldsymbol{\delta}$	0.078	Assumed
$\boldsymbol{p}$	0.048	Assumed

Figure 2 illustrated that the susceptible individuals growing up to equilibrium level in the absence of HSV-II infection and decreases at a later time because of HSV-II infection but did not die out over time.

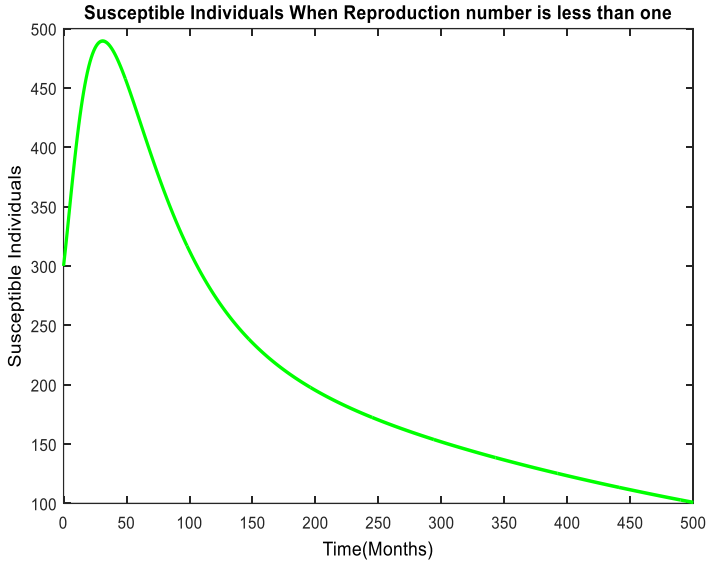

Figure 2. Susceptible individuals.

Figure 3 shows that the exposed individuals increase initially due to a smaller number of asymptomatic and symptomatic individuals and decreases at a later time due to more infectious individuals but did not die out over time.

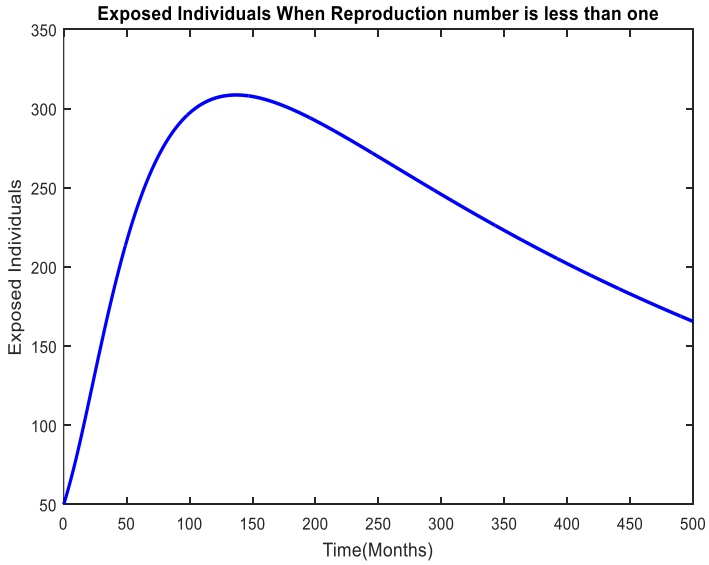

Figure 3. Exposed individuals.

Figure 4 illustrated that the asymptomatic individual increases at the start as the result of a greater number of exposed individuals joined the asymptomatic class but decline

because of some asymptomatic individuals joined HSV-II class and due to recovery.

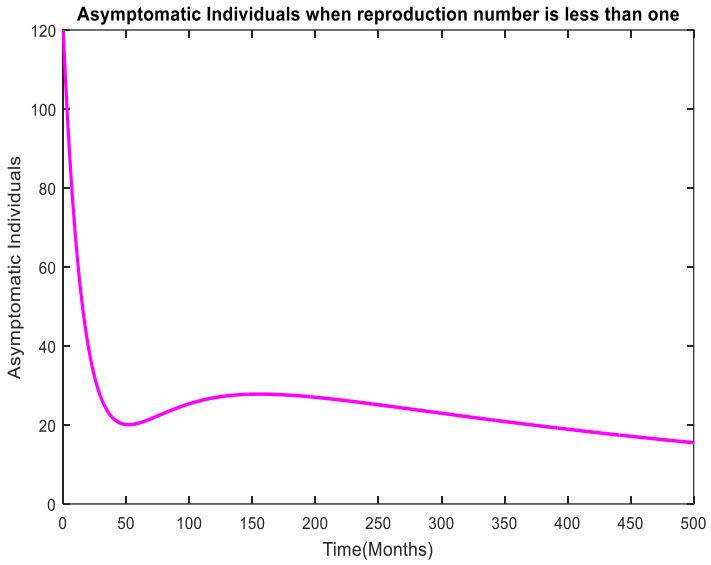

Figure 4. Asymptomatic individuals.

Figure 5 shows that the symptomatic individual decline for the reason that some symptomatic individuals joined HSV-II class and due to recovery.

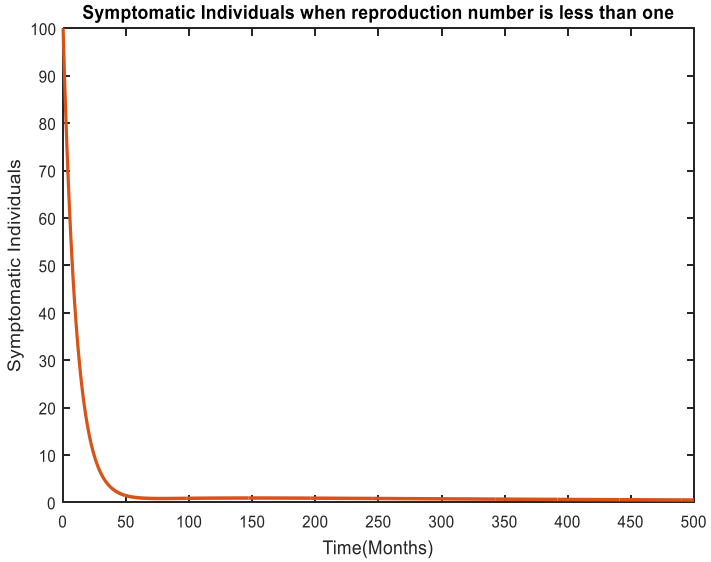

Figure 5. Symptomatic individuals.

Figure 6 shows that the number of HSV-II individual decreases due to treatment and recovered individuals.

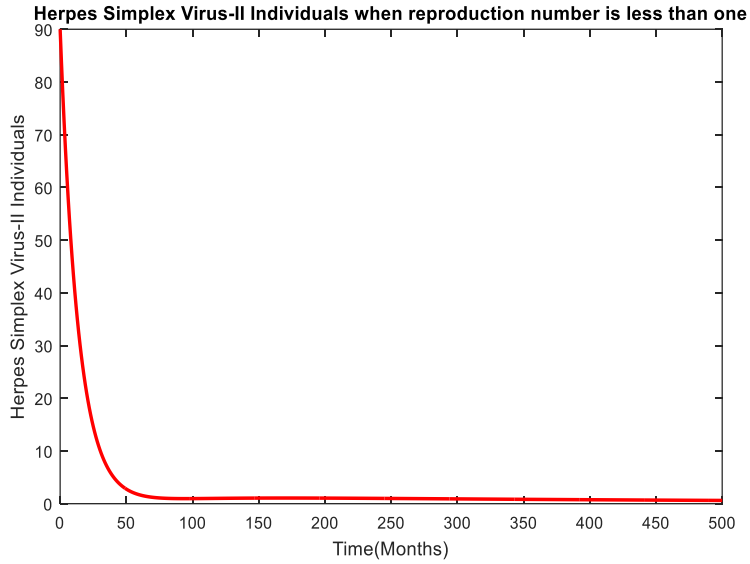

Figure 6. Herpes simplex virus-II individuals.

Figure 7 illustrated that recovered individuals increases initially as the result of asymptomatic, symptomatic and HSV-II individuals are recovered and decreases due to natural death.

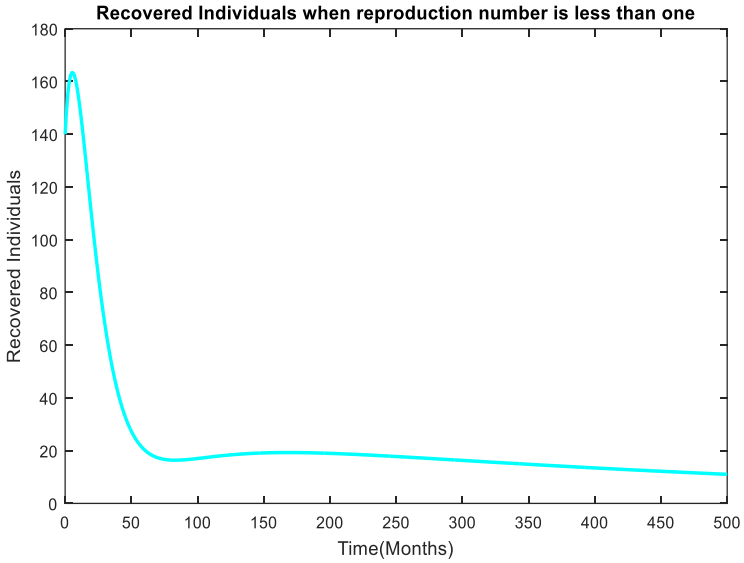

Figure 7. Recovered individuals.

The asymptomatic, symptomatic, HSV-II, and recovered individuals grows exponentially in which, after reaching equilibrium level, and died out over time as seen the results of the simulations in Figure 8. The results of simulation for the susceptible and exposed individuals shows that in the absence of the HSV-II infection, grows up to equilibrium level, achieved asymptotic stability and did not die out over time.

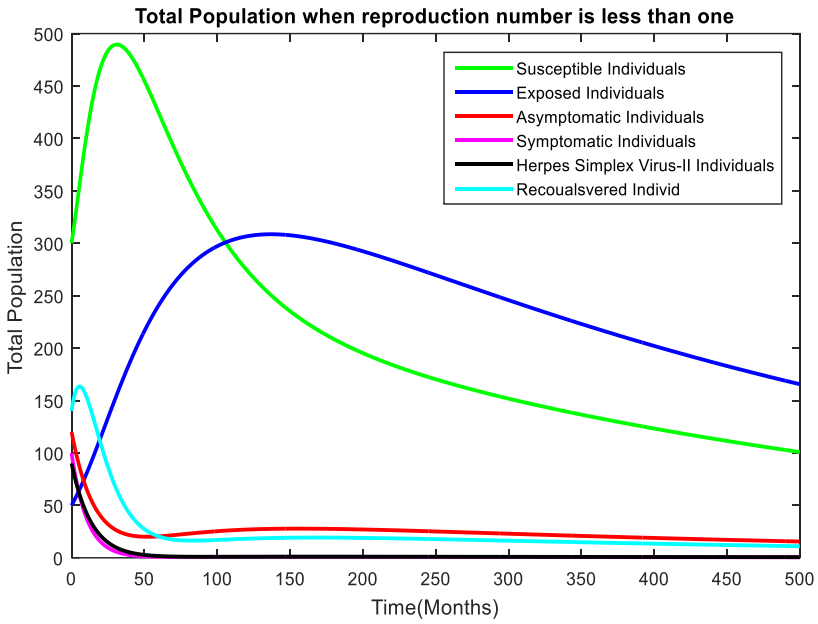

Figure 8. Total population of individuals.

Figure 9 presents the graph of variation of treatment rate on human population infected with Herpes Simplex Virus – II against time. We see that as the treatment rates increases the number of HSV-II infections decreases. This implies that treatment reduces the viral load in the HSV-II individuals and minimizes the risk of HSV-II transmission from the community.

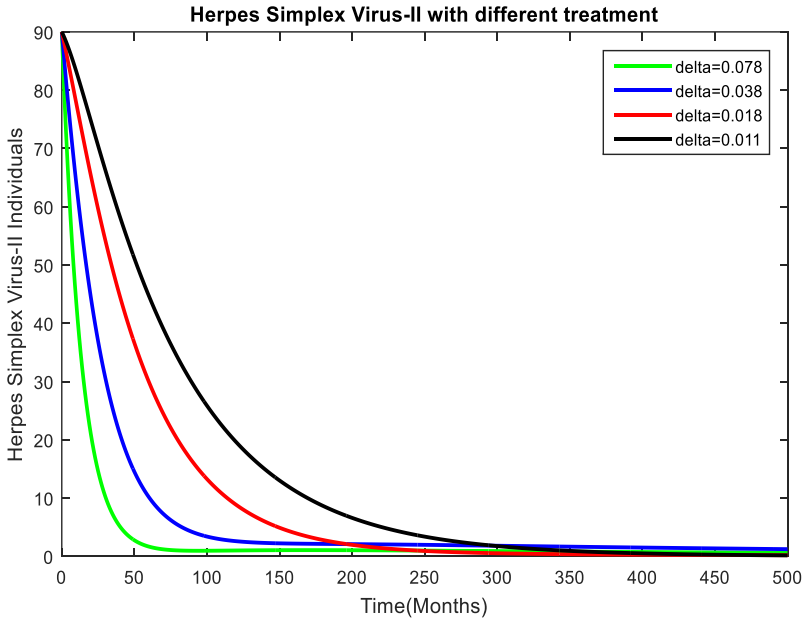

Figure 9. Variation of HSV-II individuals for different values of treatment.

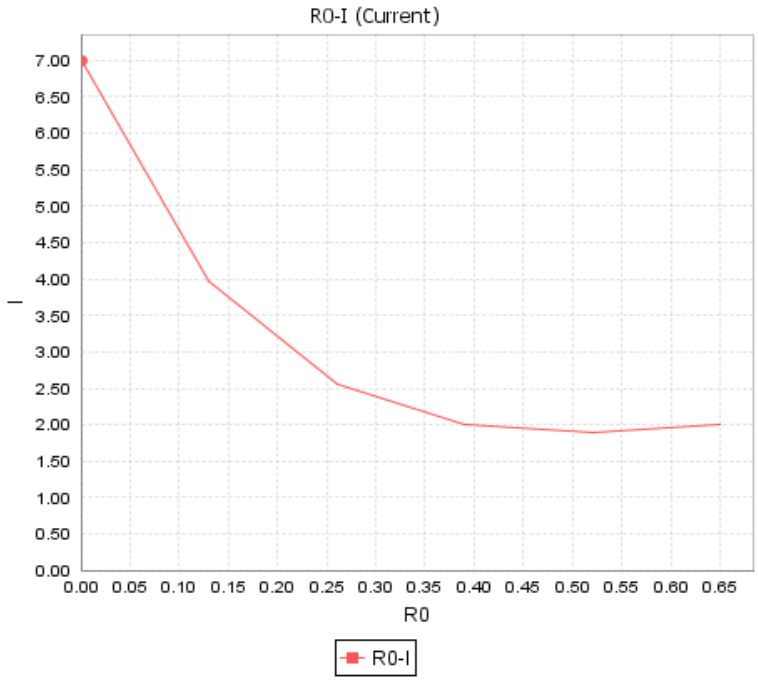

Figure 10. Figure showing $\mathfrak{R}_0$ with respect to symptomatic individuals.

Figure 10 shows that the basic reproduction number with respect to symptomatic individuals. It is evident that stability to be achieved when $\mathfrak{R}_0 < 1$.

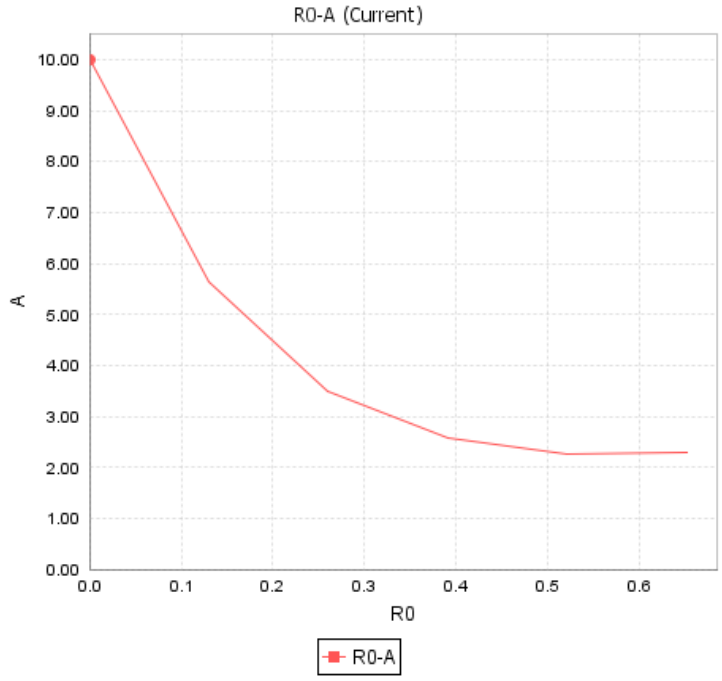

Figure 11. Figure showing $\mathfrak{R}_0$ with respect to asymptomatic individuals.

Figure 11 shows that the basic reproduction number with asymptomatic individuals. Clearly, the stability of disease free equilibrium is achievable when $\mathfrak{R}_0 < 1$.

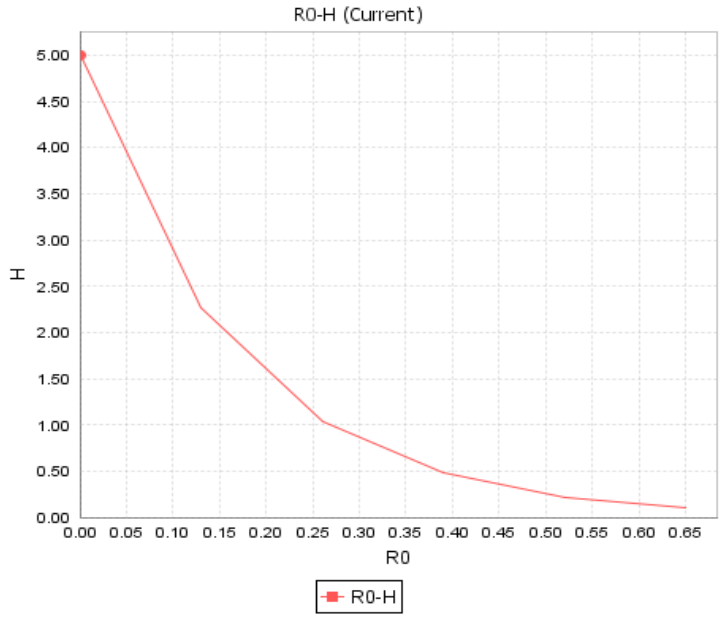

Figure 12. Figure showing $\Re_0$ with respect to HSV-II individuals.

Figure 12 shows that the basic reproduction number with HSV-II. It is evident that the stability of disease free equilibrium is achievable when $\Re_0 < 1$.

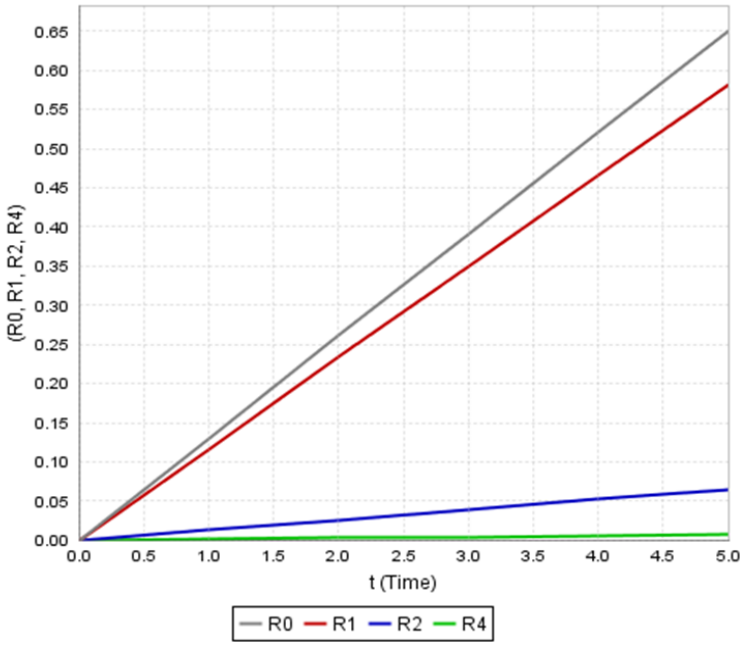

Figure 13. Effect of varying the contact rate β on $\Re_0$.

Figure 13 show that $\Re_0 > \Re_1 > \Re_2 > \Re_4$, indicating that contact rate has an effect on reducing the reproduction number. An increase in level of contact rate among individuals in a community has an effect on reducing the prevalence of the disease.

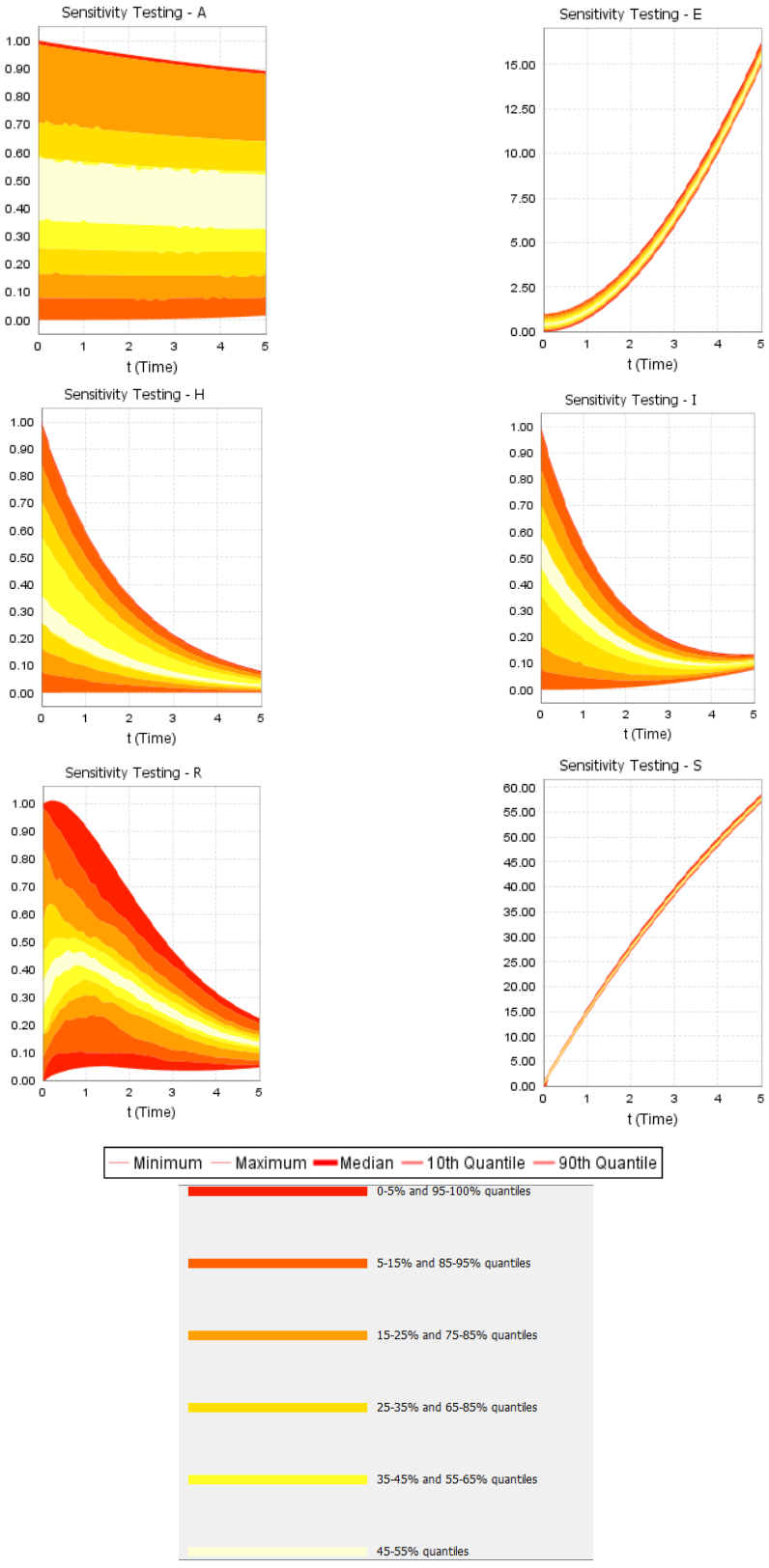

Figure14. Sensitivity testing of S, E, A, I, H, R.

Figure 14 illustrate that sensitivity testing of S, E, A, I, H, R. This explain that susceptible individuals, exposed individuals and removed compartment are medium, i.e., which leads to minimizing the endemicity of the disease in the community. Furthermore, those variables I, H and A (in some interval) in which their status are maximum, i.e., which have an influence of minimizing the burden of the disease in the community.

6. Discussions and conclusions

In this study, a mathematical model on the Herpes Simplex Virus-II (HSV-II) governed by a system of ordinary differential equations is formulated. The qualitative analysis of the model shows that there exists a domain where the model is epidemiologically and mathematically well-posed. The equilibria points of the model are obtained and their local as well as global stability conditions are established. The stability analysis of the model was investigated using the threshold parameter that governs the disease transmission. It was established that the disease free equilibrium is locally stable if the basic reproduction number $\Re_0 < 1$ and unstable if the basic reproduction number $\Re_0 > 1$. The endemic equilibrium, which exist only when $\Re_0 > 1$, is globally asymptotically stable. Sensitivity analysis of the reproduction number suggested that increasing the rate of contact has high impact on the transmission of the diseases. Furthermore, analysis of the reproduction number through simulation shows that the reproduction number can be reduced to very low levels by decreasing contact rate. Therefore, these findings conclude that using different treatment would be a very effective way for reducing the disease from community.

References

[1] L. J. Abu-Raddad, J. T. Schiffer, R. Ashley, G. Mumtaz, R. A. Alsallaq, F. A. Akala, I. Semini, G. Riedner and D. Wilson, HSV-2 serology can be predictive of HIV epidemic potential and hidden sexual risk behavior in the Middle East and North Africa, Epidemics, **2** (2010) 173–182.

[2] C. Castillo-Chavez and B. Song, Dynamical models of tuberculosis and their applications, Mathematical Biosciences and Engineering, **1 (2)** (2004) 361–404, doi:10.3934/mbe.2004.1.361.

[3] K. R. Cheneke, G. K. Edessa and P. R. Koya, Global stability and sensitivity analysis of the dynamics of human population subjected to HIV/AIDS with treatment, IOSR Journal of Mathematics (IOSR-JM), **15 (6)** (2019) 34–51.

[4] N. Chitnis, J. M. Hyman andJ. M. Cusching (2008). Determining important Parameters in the spread of malaria through the sensitivity analysis of a mathematical model, Bulletin of Mathematical Biology, **70 (5)** (2008) 1272-1296, doi:10.1007/s11538-008-9299-0.

[5] E. D. Gurmu and P. R. Koya, Impact of chemotherapy treatment of SITR compartmentalization and modeling of human papilloma virus (HPV), IOSR Journal of Mathematics (IOSR – JM), **15 (3)** (2019) 17–29.

[6] E. D. Gurmu and P. R. Koya, Sensitivity analysis and modeling the impact of screening on the transmission dynamics of human papilloma virus (HPV), American Journal of Applied Mathematics, **7 (3)** (2019) 70–79.

[7] C. Johnston, S. L. Gottlieb and A. Wald, Status of vaccine research and development of vaccines for herpes simplex virus, Vaccine, **34 (26)** (2016) 2948–2952, doi:10.1016/j.vaccine.2015.12.076.

[8] A. Mhlanga, C. P. Bhunu and S. Mushayabasa, A computational study of HSV-2 with poor treatment adherence, Abstract and Applied Analysis, **2015** (2015), Article ID 850670, http://dx.doi.org/10.1155/2015/850670.

[9] M. Mustafa, E. M. Illzam, R. K. Muniandy, A. M. Sharifah, M. K. Nang and B. Ramesh, Herpes simplex virus infections, pathophysiology and management, IOSR Journal of Dental and Medical Sciences (IOSR-JDMS), **15 (7)** (2016) 85–91.

[10] R. Patel, O. J. Kennedy, E. Clarke, A. Geretti, A. Nilsen, S. Lautenschlager, J. Green, G. Donders, W. van der Meijden, M. Gomberg, H. Moi and E. Foley, 2017 European guidelines for the management of genital herpes, International Journal of STD & AIDS, **28 (14)** (2017) 1366–1379.

[11] J. T. Schiffer, D. A. Swan, A. Magaret, T. W. Schacker, A. Wald and L. Corey, Mathematical modeling predicts that increased HSV-2 shedding in HIV-1 infected persons is due to poor immunologic control in ganglia and genital mucosa, PLoS ONE, **11 (6)** (2016) e0155124, doi:10.1371/journal.pone.0155124.

[12] R. J. Smith, J. Li, J. Mao and B. Sahai, Using within-host mathematical modelling to predict the long-term outcome of human papillomavirus vaccines, Canadian Applied Mathematics Quarterly, **21 (2)** (2013) 281–299.

[13] I. H. Spicknall, K. J. Looker, S. L. Gottlieb, H. W. Chesson, J. T. Schiffer, J. Elmes and M. C. Boily, Review of mathematical models of HSV-2 vaccination: Implications for vaccine development, Vaccine, **37 (50)** (2019) 7396–7407, doi:10.1016/j.vaccine.2018.02.067.

[14] A. G. Wedajo, B. K. Bole and P. R. Koya, The impact of susceptible human immigrants on the spread and dynamics of Malaria transmission, American Journal of Applied Mathematics, **6 (3)** (2018) 117–127.

[15] World Health Organization, WHO guidelines for the treatment of genital herpes simplex virus, (2016).