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Transmission of HIV/AIDS with Drug Resistance and Local Stability Analysis

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Abstract: *In this paper a mathematical model is formulated to analyze the transmission of AIDS with drug resistance. The total population under consideration is divided into seven compartments viz., Susceptable, Primary, Asymptomatic, Symptomatic, Resistant, and AIDS compartments. The well-possedness of the formulated model isproved. The local stabilities of the model are analyzed using Routh Hurwitz criterion. Next generation matrix method is used to find the basic reproduction number. The study has shwn that natural death rate is the most sensitive parameter in the model formulated.The transmission rate is one of the factors that determines the extinction or persistence of disease in the population. Finally, numerical solutions of the model equations are simulated using MATLAB.*

Keywords: *HIV, Basic Reproduction Number, Stability Analysis, Routh Hurwitz criterion, well-possedness*

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I. Introduction

Beginning from its discovery in early 1980s, AIDS (Acquired Immunodeficiency syndrome) and its causing virus, HIV (Human Immunodeficiency Virus) has brought a great impact around the world both as disease and source of stigma and discrimination (Cheneke et al. [1]. In 2016, it is estimated that 36.7 million people were living as HIV positive, including 1.8 million a newly infected people in the same year, and 1 million people died because of AIDS related illness. Since the appearance of the epidemic, it is estimated that 76.1 million people have been infected with HIV and about 35 million individuals has been died of AIDS related illness [3]. HIV is a virus that slowly attacks the immune system. This immune system is our body's natural defense toward illness. If a person becomes infected with HIV virus, her or his immune system become weak which leads to poor healthy and hard to fight off infections and diseases [4]. The virus has potential to destroys or reduce a type of white blood cell called T-helper cells and makes copies of itself inside these cells. T-helper cells are also known as CD4 cells and There is no cure or vaccine to permanently eradicate AIDS from human [3].

Based on WHO clinical staging of HIV/AIDS disease, the HIV infection is classified into four distinct stages viz., (i) Primary/Acute stage (ii) Asymptomatic stage (iii) Symptomatic stage and (iv) Advanced AIDS stage [2, 4].

Organization of the paper: In Section 2, assumptions of the model are stated and based on which a mathematical model fordescribing the population dynamics of human population related to HIV/AIDS disease is formulated. In section 3, well possedness of the model formulation, stability analysisof the equilibrium points and reproduction number are included. In Section 4, numerical simulationstudiesof the model equations are performed by assigning various sets of numerical values to the model parameters.In Section 5 sensitivity analysis of model parameters towards the reproduction number is carried out. In section 6 Result and Discussion are presented. Finally, the paper ends with concluding remarks in Section 7.

II. Model Formulation

In this study the dynamical systemof ordinary differential equations is formulated to show the dynamics of human population in the presence of Human Immunodeficiency Virus (HIV)ART as combined treatments. This model is modifcation of the works done in [4]. This previous work is six compartmental model. Here, a deterministic model is formulated in which human population is divided into seven compartments. The descriptions of compartments areas follows:(i) Susceptible compartment. It is denoted by $S(t)$. These are humans who are free of HIV infection but are capable of becoming infected future in infectious environment(ii) Primary compartment. It is denoted by $P(t)$.This compartment includes all humans who infected with HIV for the first time and that do not know their HIV status but transmit the disease to others with effective contact (iii) Asymptomaticcompartment. It is denoted by $A(t)$. This compartment includes all humans who know that they are infected with virus but no signs of infections is visible and abstain from transmitting virus to others.Theyjoin the treatment compartement at a rate $\emptyset$ and Sypmtomatic compartement at

the rate η (iv) Symptomatic compartment. It is denoted by $J(t)$. This compartment includes of infectious humansand they show signs of infections. Such humans manifest their weakness as they harmed by virus and abstain from transmitting virus to others and join treatment compartment at some rateω (v) Treatment compartment. It is denoted by $T(t)$. This compartment includes portion of asymptomatic and symptomatic compartments that join it because of infection (vi) Drug resistant compartment. This compartement includes portion of individuals from treatment class that are resistant to ART. (vii) AIDS compartment.It is denoted by $V(t)$. This compartment includes who are at last stage or advanced stage of HIV.

Now, a mathematical model of Human Immunodeficiency virus (HIV) is formulated based on the stated assumptions on the human population as listed below:

(i) The total size of human's population under considerationis assumed to be constant.
(ii) The numbers of births and deathsof human'spopulation are assumed to be equal.
(iii) Deterministic dynamical system in the presence of Human Immunodeficiency virus (HIV) classifies human population under observation into sixcompartments as SPAJTV at any time.
(iv) Susceptible humans are recruited to the compartment $S(t)$ at some constant rate τ.
(v) Susceptible humanscan be infected if they make effective contact withprimary infected population whose status of HIV is not known yet and joinprimary infected compartment at a constant rate β.
(vi) Primary infected humanstransfer into asymptomatic compartment at a constant rate κ.
(vii) Asymptomatic humanstransfer into symptomatic humans at a rate η and to treatment compartment at the rate of ϕ.
(viii) The symptomatic humanstransfer intotreatment compartment at the rate ω.
(ix) The treated and drug resistant humans transfer into resistant compartment at the rate of γ.
(x) Resistant compartment individuals transfer to AIDS compartment at the rate of ρ.
(xi) All categories of human's compartmentsface the same natural mortality with a rate μ.
(xii) All AIDS humanssuffer disease induced death at a constant rate δ.
(xiii) All parameters used in the dynamical system are positive.

Table 1 Notations and description of model variables

Variable	Description
$\mathbf{S(t)}$	Population size of susceptible humans
$\boldsymbol{P(t)}$	Population size of primary infected humans
$\mathbf{A(t)}$	Population size of asymptomatic humans
$\mathbf{J(t)}$	Population size of symptomatic humans
$\mathbf{T(t)}$	Population size of humans under treatment
$\boldsymbol{R(t)}$	Populatin size of humans under treatment
$\mathbf{V(t)}$	Population size of AIDS humans

Table 2 Model parameters notations and description

Parameter	Description
τ	Recruitment rate of susceptible human population. With this constant rate new humans will born and enter into susceptible compartment
$\boldsymbol{\beta}$	Transmission rate of primaryinfected humans. With this rate primary infected humans transfer into P
$\boldsymbol{\kappa}$	Rate of humans transferring from compartment P to A
$\boldsymbol{\eta}$	Rate of humans transferring from compartment A to J
$\boldsymbol{\omega}$	Rate of humans transferring from compartment J to T
$\boldsymbol{\phi}$	Rate of humans transferring from compartment A to T
$\boldsymbol{\mu}$	Natural death rate. With this rate humansinallcompartments die naturally
$\boldsymbol{\gamma}$	Rate of humans transferring from compartment T to R.
$\boldsymbol{\rho}$	Rate of humans transferring from compartment R to V.
$\boldsymbol{\delta}$	Disease induced death rate of AIDS humans

Now considering basic assumptions and description of both model variables and parameters given the schematic diagram of the formulated deterministic dynamical system is described in the Figure 1.

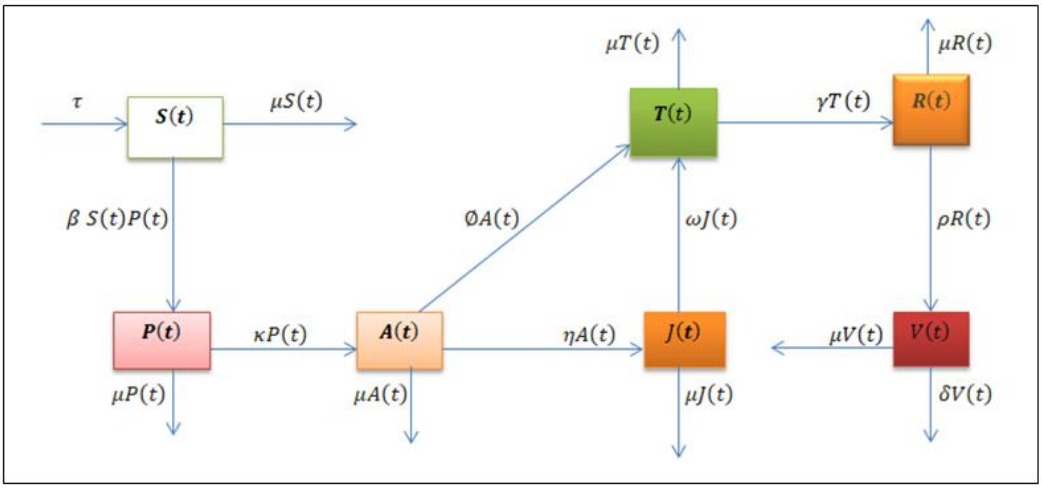

Figure 1 Schematic diagram of compartmental structure of the model

Based on the model assumptions, the notations of variables and parameters and the schematic diagram, the model equations are formulated and are given as follows:

$$dS/dt = \tau - \beta SP - S \quad (1)$$
$$dP/dt = \beta SP - (\kappa + \mu)P \quad (2)$$
$$dA/dt = \kappa P - (\phi + \eta + \mu)A \quad (3)$$
$$dJ/dt = \eta A - (\omega + \mu)J \quad (4)$$
$$dT/dt = \phi A + \omega J - (\gamma + \mu)T \quad (5)$$
$$dR/dt = \gamma T - (\rho + \mu)R \quad (6)$$
$$dV/dt = \rho R - (\delta + \mu)V \quad (7)$$

The non-negative initial conditions of the model equations (1) – (7) are denoted by $S(0) \geq 0,\ P(0) \geq 0,\ A(0) \geq 0,\ J(0) \geq 0, T(0) \geq 0,\ R(0) \geq 0,\ V(0) \geq 0$. This system consists of seven first order non-linear ordinary differential equations.

III. Mathematical analysis of the model

In this section we describe the mathematical analysis of the presentimproved and modified model. The analysis consists of the following points(i) existence, positivity and boundedness of solutions (ii) Equilibrium points (iii) disease free equilibrium points (iv) endemic equilibrium points (v) basic reproduction number(vi)stability analysis of the disease free equilibrium points(vii)local stability of disease free equilibrium point (viii) global stability of disease free equilibrium point. These mathematical aspects of the model are presented and discussed in the following sub-sections respectively.

3.1 Existence, Positivity and Boundedness of solution

In order to say that the formulateddynamical system is biologically valid and mathematically well-posed, it is required to show that the solutions of the system of differential equations (1) – (7) exist,non-negative and bounded for all time t . It is done starting with proving Lemma 1.

Lemma 1 (Existence) Solutions of the model equations (1) – (7) together with the initial conditions$S(0) \geq 0,\ P(0) \geq 0,\ A(0) \geq 0,\ J(0) \geq 0,\ T(t),\ R(t), V(0) \geq 0$ exist in$\mathbb{R}_+^7$i.e. the model variables $S(t),\ P(t),\ A(t),\ J(t),\ T(t),\ R(t),$ and $V(t)$ exist for all t and will remain in $\mathbb{R}_+^7$.

Proof: Let the right hand sides of the system of equations (1) – (7) are expressed as follows:

$$dS/dt = \tau - \beta SP - S \equiv g_1(S,\ P,\ A,\ J,\ T,\ R,\ V)$$
$$dP/dt = \beta SP - (\kappa + \mu)P \equiv g_2(S,\ P,\ A,\ J,\ T,\ R,\ V)$$
$$dA/dt = \kappa P - (\phi + \eta + \mu)A \equiv g_3(S,\ P,\ A,\ J,\ T,\ R,\ V)$$
$$dJ/dt = \eta A - (\omega + \mu)J \equiv g_4(S,\ P,\ A,\ J,\ T,\ R,\ V)$$
$$dT/dt = \phi A + \omega J - (\gamma + \mu)T \equiv g_5(S,\ P,\ A,\ J,\ T,\ R,\ V)$$
$$dR/dt = \gamma T - (\rho + \mu)R \equiv g_6(S,\ P,\ A,\ J,\ T,\ R,\ V)$$
$$dV/dt = \rho R - (\delta + \mu)V \equiv g_7(S,\ P,\ A,\ J,\ T,\ R,\ V)$$

According to Derrick and Groosman theorem, let R denote the region$R = \{(S,\ P,\ A,\ J,\ T,\ R,\ V) \in \mathbb{R}_+^7;\ N \leq \tau/\mu\}$. Then equations (1) – (7) have a unique solution if $(\partial g_i)/(\partial x_j),\ \forall\ i, j = 1, 2, 3, 4, 5, 6, 7$ are continuous and bounded in$R$. Here, the notations$x_1 = S,\ x_2 = P,\ x_3 = A,\ x_4 = J,\ x_5 = T,\ x_6 = R,$

$x_7 = V$, are employed. The Existence, continuity and the boundedness of$g_1,\ g_2,\ g_3,\ \ g_4,\ g_5,\ g_6$ and $g_7$are verified as here under:

Table 2 Verification of Continuity and Boundedness of the Function

Function	Existence and Continuity	Boundedness
g_1	$(\partial g_1)/(\partial S) = -[\beta P + \mu]$ $(\partial g_1)/(\partial P) = -\beta S$ $(\partial g_1)/(\partial A) = 0$ $(\partial g_1)/(\partial J) = 0$ $(\partial g_1)/(\partial T) = 0$ $(\partial g_1)/(\partial R) = 0$ $(\partial g_1)/(\partial V) = 0$	$\lvert(\partial g_1)/(\partial S)\rvert = \lvert-[\beta P + \mu]\rvert < \infty$ $\lvert(\partial g_1)/(\partial P)\rvert = \lvert-\beta S\rvert < \infty$ $\lvert(\partial g_1)/(\partial A)\rvert = 0 < \infty$ $\lvert(\partial g_1)/(\partial J)\rvert = 0 < \infty$ $\lvert(\partial g_1)/(\partial T)\rvert = 0 < \infty$ $\lvert(\partial g_1)/(\partial T)\rvert = 0 < \infty$ $\lvert(\partial g_1)/(\partial V)\rvert = 0 < \infty$
g_2	$(\partial g_2)/(\partial S) = \beta P$ $(\partial g_2)/(\partial P) = \beta S - (\kappa + \mu)$ $(\partial g_2)/(\partial A) = 0$ $(\partial g_2)/(\partial J) = 0$ $(\partial g_2)/(\partial T) = 0$ $(\partial g_2)/(\partial R) = 0$ $(\partial g_2)/(\partial V) = 0$	$\lvert(\partial g_2)/(\partial S)\rvert = \lvert\beta P\rvert < \infty$ $\lvert(\partial g_2)/(\partial P)\rvert = \lvert\beta S - (\kappa + \mu)\rvert < \infty$ $\lvert(\partial g_2)/(\partial A)\rvert = 0 < \infty$ $\lvert(\partial g_2)/(\partial J)\rvert = 0 < \infty$ $\lvert(\partial g_2)/(\partial T)\rvert = 0 < \infty$ $\lvert(\partial g_2)/(\partial T)\rvert = 0 < \infty$ $\lvert(\partial g_2)/(\partial V)\rvert = 0 < \infty$
g_3	$(\partial g_3)/(\partial S) = 0$ $(\partial g_3)/(\partial P) = \kappa$ $(\partial g_3)/(\partial A) = -(\phi + \eta + \mu)$ $(\partial g_3)/(\partial J) = 0$ $(\partial g_3)/(\partial T) = 0$ $(\partial g_3)/(\partial R) = 0$ $(\partial g_3)/(\partial V) = 0$	$\lvert(\partial g_3)/(\partial S)\rvert = 0 < \infty$ $\lvert(\partial g_3)/(\partial P)\rvert = \kappa < \infty$ $\lvert(\partial g_3)/(\partial A)\rvert = \phi + \eta + \mu < \infty$ $\lvert(\partial g_3)/(\partial J)\rvert = 0 < \infty$ $\lvert(\partial g_3)/(\partial T)\rvert = 0 < \infty$ $\lvert(\partial g_3)/(\partial R)\rvert = 0 < \infty$ $\lvert(\partial g_3)/(\partial V)\rvert = 0 < \infty$
g_4	$(\partial g_4)/(\partial S) = 0$ $(\partial g_4)/(\partial P) = 0$ $(\partial g_4)/(\partial A) = \eta$ $(\partial g_4)/(\partial J) = -(\omega + \mu)$ $(\partial g_4)/(\partial T) = 0$ $(\partial g_4)/(\partial R) = 0$ $(\partial g_4)/(\partial V) = 0$	$\lvert(\partial g_4)/(\partial S)\rvert = 0 < \infty$ $\lvert(\partial g_4)/(\partial P)\rvert = 0 < \infty$ $\lvert(\partial g_4)/(\partial A)\rvert = \eta < \infty$ $\lvert(\partial g_4)/(\partial J)\rvert = \omega + \mu < \infty$ $\lvert(\partial g_4)/(\partial T)\rvert = 0 < \infty$ $(\partial g_4)/(\partial R) = 0$ $\lvert(\partial g_4)/(\partial V)\rvert = 0 < \infty$
g_5	$(\partial g_5)/(\partial S) = 0$ $(\partial g_5)/(\partial P) = 0$ $(\partial g_5)/(\partial A) = \phi$ $(\partial g_5)/(\partial J) = \omega$ $(\partial g_5)/(\partial T) = -(\gamma + \mu)$ $(\partial g_5)/(\partial R) = 0$ $(\partial g_5)/(\partial V) = 0$	$\lvert(\partial g_5)/(\partial S)\rvert = 0 < \infty$ $\lvert(\partial g_5)/(\partial P)\rvert = 0 < \infty$ $\lvert(\partial g_5)/(\partial A)\rvert = \phi < \infty$ $\lvert(\partial g_5)/(\partial J)\rvert = \omega < \infty$ $\lvert(\partial g_5)/(\partial T)\rvert = (\gamma + \mu) < \infty$ $\lvert(\partial g_5)/(\partial R)\rvert = 0 < \infty$ $\lvert(\partial g_5)/(\partial V)\rvert = 0 < \infty$
g_6	$(\partial g_6)/(\partial S) = 0$ $(\partial g_6)/(\partial P) = 0$ $(\partial g_6)/(\partial A) = 0$ $(\partial g_6)/(\partial J) = 0$ $(\partial g_6)/(\partial T) = \gamma$ $(\partial g_6)/(\partial R) = -(\rho + \mu)$ $(\partial g_6)/(\partial V) = -(\delta + \mu)$	$\lvert(\partial g_6)/(\partial S)\rvert = 0 < \infty$ $\lvert(\partial g_6)/(\partial P)\rvert = 0 < \infty$ $\lvert(\partial g_6)/(\partial A)\rvert = 0 < \infty$ $\lvert(\partial g_6)/(\partial J)\rvert = 0 < \infty$ $\lvert(\partial g_6)/(\partial T)\rvert = \gamma < \infty$ $\lvert(\partial g_6)/(\partial R)\rvert = \rho + \mu < \infty$ $\lvert(\partial g_6)/(\partial V)\rvert = \delta + \mu < \infty$
g_7	$(\partial g_7)/(\partial S) = 0$ $(\partial g_7)/(\partial P) = 0$ $(\partial g_7)/(\partial A) = 0$ $(\partial g_7)/(\partial J) = 0$ $(\partial g_7)/(\partial T) = 0$ $(\partial g_7)/(\partial R) = \rho$ $(\partial g_7)/(\partial V) = -(\delta + \mu)$	$\lvert(\partial g_7)/(\partial S)\rvert = 0 < \infty$ $\lvert(\partial g_7)/(\partial P)\rvert = 0 < \infty$ $\lvert(\partial g_7)/(\partial A)\rvert = 0 < \infty$ $\lvert(\partial g_7)/(\partial J)\rvert = 0 < \infty$ $\lvert(\partial g_7)/(\partial T)\rvert = 0 < \infty$ $\lvert(\partial g_7)/(\partial R)\rvert = \rho < \infty$ $\lvert(\partial g_7)/(\partial V)\rvert = \delta + \mu < \infty$

Thus, all the partial derivatives $(\partial g_i)/(\partial x_j)\colon\ i,\ j = 1,\ 2,\ 3,\ 4, 5, 6, 7$ exist, and are both continuous and bounded in$R$. Hence, by Derrick and Groosman theorem, a solution for the model (1) – (7) exists and is unique.

Lemma 2 (Positivity) Solutions of the model equations (1) – (7) together with the initial conditions $S(0) \geq 0,\ P(0) \geq 0,\ A(0) \geq 0,\ J(0) \geq 0,\ T(0) \geq 0,\ R(0) \geq 0,\ V(0) \geq 0$ are always non-negative (OR) the model variables $S,\ P,\ A,\ J,\ T,\ R$and $V$are non-negative for all t and will remain in $\mathbb{R}_+^7$.

Proof: Positivity of the solutions of model equations is shown separately for each of the model variables $S,\ P,\ A,\ J,\ T,\ R,$ and V.

Positivity of $S(t)$*:* The model equation (1) given by $dS/dt = \tau - \beta SP - S$ can be expressed without loss of generality, after eliminating the positive termτ appearing on the right hand side, as an inequality as $dS/dt \geq -[\beta P + \mu]S$. Using variables separable method and on applying integration, the solution of the foregoing differentially inequality can be obtained as $S(t) \geq S(0)e^{-\mu t - \beta \int P dt}$. Recall that an exponential

function is always non–negative irrespective of the sign of the exponent i.e. the exponential function $e^{-\mu t-\beta \int P dt}$ is a non-negative quantity. Hence, it can be concluded that $S(t) \geq 0$.

Positivity of $P(t)$*:* The model equation (2) given by $dP/dt = \beta SP - (\kappa + \mu)P$can be expressed without loss of generality, after eliminating positive term βSP which is appearing on the right hand side, as an inequality as$dP/dt \geq -(\kappa + \mu)P$. Using variables separable method and on applying integration, the solution of the foregoing differentially inequality can be obtained as $P(t) \geq P(0)e^{-(\kappa+\mu)t}$. Recall that an exponential function is always non–negative irrespective of the sign of the exponent i.e. the exponential function $e^{-(\kappa+\mu)t}$ is a non-negative quantity. Hence, it can be concluded that $P(t) \geq 0$.

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

Positivity of $J(t)$*:* The model equation (4) given by$dJ/dt = \eta A - (\omega + \mu)J$ can be expressed without loss of generality, after eliminating the positive term θA which is appearing on the right hand side, as an inequality as $dJ/dt \geq -(\omega + \mu)J$. Using variables separable method and on applying integration, the solution of the foregoing differentially inequality can be obtained as $J(t) \geq J(0)e^{-(\omega+\mu)t}$. Recall that an exponential function is always non–negative irrespective of the sign of the exponent i.e. the exponential function$e^{-(\omega+\mu)t}$is a non-negative quantity. Hence, it can be concluded that $J(t) \geq 0$.

Positivity of $T(t)$*:* The model equation (5) given by$dJ/dt = \phi A + \omega J - (\gamma + \mu)T$ can be expressed without loss of generality, after eliminating the positive terms $\omega J$and ϕA which is appearing on the right hand side, as an inequality as $dT/dt \geq -(\gamma + \mu)T$. Using variables separable method and on applying integration, the solution of the foregoing differentially inequality can be obtained as $T(t) \geq J(0)e^{-(\gamma+\mu)t}$. Recall that an exponential function is always non–negative irrespective of the sign of the exponent i.e. the exponential function$e^{-(\gamma+\mu)t}$is a non-negative quantity. Hence, it can be concluded that $T(t) \geq 0$.

Positivity of $R(t)$*:* The model equation (6) given by$dR/dt = \gamma T - (\rho + \mu)R$ can be expressed without loss of generality, after eliminating the positive terms γT which is appearing on the right hand side, as an inequality as $dR/dt \geq -(\rho + \mu)R$. Using variables separable method and on applying integration, the solution of the foregoing differentially inequality can be obtained as $R(t) \geq J(0)e^{-(\rho+\mu)t}$. Recall that an exponential function is always non–negative irrespective of the sign of the exponent i.e. the exponential function$e^{-(\rho+\mu)t}$is a non-negative quantity. Hence, it can be concluded that $T(t) \geq 0$.

Positivity of $V(t)$*:* The model equation (7) given by $dV/dt = \rho R - (\delta + \mu)V$ can be expressed without loss of generality, after eliminating the positive termρR which is appearing on the right hand side, as an inequality as $dV/dt \geq -(\delta + \mu)V$. Using variables separable method and on applying integration, the solution of the foregoing differentially inequality can be obtained as $V(t) \geq V(0)e^{-(\delta+\mu)t}$. Recall that an exponential function is always non–negative irrespective of the sign of the exponent i.e. the exponential function$e^{-(\delta+\mu)t}$is a non-negative quantity. Hence, it can be concluded that $V(t) \geq 0$.

Thus, the model variables $S,\ P,\ A,\ J,\ T,\ R$ and V representing population sizes of various types of human population are positive quantities and will remain in $\mathbb{R}_+^7$for all$t$.

Lemma 2 (Boundedness) Thenon-negative solutions of the system of model equations (1) – (7) are bounded. That is the model variables $S,\ P,\ A,\ J,\ T,$ R and V are all bounded for all[3].

Proof: Recall that each population size is bounded if and only if the total population size is bounded. Hence, in the present case it is sufficient to prove that the total population size $N(t) = S(t) + P(t) + A(t) + J(t) + T(t) + \mathrm{R}(t) + V(t)$ is bounded for all t. It can be begun by showing that all feasible solutions are uniformly bounded in a proper subset $R \in \mathbb{R}_+^7$where the feasible region D is given by$D = \{(S,\ P,\ A,\ J,\ T,\ R,\ V) \in \mathbb{R}_+^7\ ;\ \mathrm{N} \leq \tau/\mu\}$.

Now, summation of all the five equations (1) – (7) of the model gives $\mathrm{dN(t)/dt} = \tau - \mu\mathrm{N(t)}$. Again considering total population N and subpopulation V further we can write the equation as inequality of the form$\mathrm{dN/dt} \leq \tau - \mu\mathrm{N(t)}$. Equivalently this inequality can be expressed as a linear ordinary differential inequality as $\mathrm{dN/dt} + \mu\mathrm{N} \leq \tau$ giving general solution upon solving as$\mathrm{N(t)} \leq \tau/\mu + ce^{-\mu t}$. But, the term $N(0)$ denotes the initial values of the respective variable$\mathrm{N(t)} = \mathrm{N(0)}$at $\mathrm{t} = 0$. Thus, the particular solution can be expressed as$\mathrm{N(t)} \leq \tau/\mu + [\mathrm{N(0)} - (\tau/\mu)]e^{-\mu t}$. Further, it can be observed that $N(t) \to \tau/\mu$as $t \to \infty$. That is, total population size $N(t)$takes off from a value $\mathrm{N(0)}$ at the initial time $\mathrm{t} = 0$ and ends up with a bounded valueτ/μ as the time t progresses to infinity. Thus, it can be concluded that $N(t)$ is bounded within a pair of values as $0 \leq N(t) \leq \tau/\mu$.

Therefore, $\tau/\mu$is an upper bound of $N(t)$. Hence, feasible solution of the system of model equations (1) – (7) remains in the region R which is a positively invariant set. Thus, the system is biologically meaningful in the domain$R$. Further, it is sufficient to consider the dynamics of the populations represented by the model system (1) – (7) in that domain.

Therefore, it can be summarized the result of Lemma 2 as "the model variables $S,\ P,\ A,\ J,\ T,\ R$ and V are bounded for all t".

Therefore, the formulated model is biologically meaningful and mathematically well-posed.

3.2 Equilibrium points

In order to understand the 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) – (7) 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. Equilibrium points of the model are found, categorized, stability analysis is conducted and the results have been presented in the following sub-sections:

3.2.1 Disease free equilibrium point

Disease free equilibrium point is a steady state solution where there is no disease in the population. Now, absence of disease implies that $P = A = J = T = R = V = 0$ and also setting the right hand sides of the model equations (1) – (6) equal to zero results in giving $\tau - \mu S = 0$, solution of which is the population size of the susceptible humans at the disease free equilibrium and is given by $S^0 = (\tau/\mu)$.Thus, the disease free equilibrium point of the model equations(1) – (7) is given by

$$E_0 = (S^0,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0) = (\tau/\mu,\ 0,\ 0,\ 0,\ 0,\ 0,\ 0)$$

3.2.2

Endemic equilibrium point

The endemic equilibrium point $E_1 = \{S^1,\ P^1,\ A^1,\ J^1,\ T^1,\ R^1,\ V^1\}$ is a steady state solution when the disease persists in the population. The endemic equilibrium point is obtained by setting rates of changes of variables with respect to time of model equations (1) – (7) to zero. That is, setting $dS/dt = dA/dt = dJ/dt = dT/dt = dV/dt = 0$ the model equations take the form as

$$\tau - \beta SP - \mu S = 0 \quad (8)$$
$$\beta SP - aP = 0 \quad (9)$$
$$\kappa P - bA = 0 \quad (10)$$
$$\eta A - cJ = 0 \quad (11)$$
$$\phi A + \omega J - dT = 0 \quad (12)$$
$$\gamma T - eR = 0 \quad (13)$$
$$\rho R - fV = 0 \quad (14)$$

Here in (8) – (14), the quantities $a,\ b,\ c$ represent the parametric expressions as $a = \kappa + \mu,\ b = \phi + \eta + \mu,\ c = \omega + \mu,\ d = \gamma + \mu,\ e = \rho + \mu,\ f = \delta + \mu$. Clearly, solutions of (8) – (14) will provide endemic equilibrium of the model equations and that is obtained as follows:

(i) Equations (9) can be rearranged as $[\beta S - a]P = 0$ leading to the solutions $\beta S - a = 0$ or $P = 0$ or both. However, P does not vanish since the disease is assumed to persist. Thus, it leads to the only meaningful solution $\beta S - a = 0$ or equivalently $S = (a/\beta)$. That is, S^1 component of E_1 is given by

$$S^1 \equiv S = (a/\beta) = (\tau/\mu R_0) \quad (15)$$

(ii) Now the solution for P can be obtained by substituting equation (15) into equation (8) and rewriting the resulting equation as $\tau - \beta(\tau/\mu R_0)P - \mu(\tau/\mu R_0) = 0$ giving

$$P^1 \equiv P = (\mu/\beta)(R_0 - 1) \quad (16)$$

(iii) Substituting P^1 value from (16) into (10) and solving for A we get the following

$$A^1 \equiv A = (k\mu/b\beta)(R_0 - 1) \quad (17)$$

(iv) Substituting J^1 value from (17) into (11) and solving for J we get the following

$$J^1 \equiv J = (\eta k\mu/bc\beta)(R_0 - 1) \quad (18)$$

(v) Substituting T^1 value from (18) into (12) and solving for T we get the following

$$T^1 \equiv T = (k\mu/bd\beta)\big(\phi + (\omega\eta/c)\big)(R_0 - 1) \quad (19)$$

(vi) SubstitutingT^1 value from (19) into (13) and solving for R we get the following

$$R^1 \equiv R = ((\gamma k\mu)/(ebd\beta))\big(\phi + (\omega\eta/c)\big)(R_0 - 1) \quad (20)$$

(vii) SubstitutingR^1 value from (20) into (13) and solving for V we get the following

$$V^1 \equiv V = ((\rho\gamma k\mu)/(febd\beta))\big(\phi + (\omega\eta/c)\big)(R_0 - 1) \quad (21)$$

3.3 Basic Reproduction Number

The basic reproduction number is denoted by R_0 and is defined as the expected number of people getting secondary infection because of infected person enters into wholly susceptible population [2, 3, 7]. This number determines the potential for the spread of disease within a population. When$R_0 < 1$ 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 $R_0 > 1$ 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 R_0 to less than one.

The basic reproductive number R_0 can be determined using the next generation matrix. In this method$R_0$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.

Assume that there are n compartments in the model and of which the first m compartments are with infected individuals [7]. From the system (1) – (7) the five equations of infected individuals are considered and decomposed into two groups: F contains newly infected cases and v contains the remaining terms. Let $X = [S,\ P,\ A,\ J,\ T,\ R,\ V]^t$ be a column vector and the differential equations of the first four compartments are rewritten as $F(X) - T(X)$.

Now, let $F(X) = [F_1,\ F_2,\ F_3,\ F_4,\ F_5,\ F_6]^t$. Here (i) $F_1 = \beta SP$ denotes newly infected cases which arrive into primary infected compartment (ii) $F_2 = 0$ denotes newly infected cases arrivedinto the infectious asymptomatic compartment (iii) $F_3 = 0$ denotes newly infected cases arrived into the infectious symptomatic compartment, (iv) $F_4 = 0$ denotes newly infected case from susceptible compartment into treatment compartment, (v)$F_5 = 0$ denotes newly infected case from susceptible compartment into drug resistant compartment and (vi) $F_6 = 0$ denotes newly infected case from susceptible compartment into AIDS compartment. Further, let $T(X) = [T_1,\ T_2,\ T_3,\ T_4,\ T_5,\ T_6]^t$. Here $T_1 = aP,\ T_2 = -\kappa P + bA,\ T_3 = -\eta A + cJ, T_4 = -\phi A - \omega J + cT,\ T_5 = -\gamma T + dR$ and$T_6 = -\rho R + eV$. Here, the values of $a,\ b,\ c,\ d, e$ and f are as defined above.

The next step is the computation of square matrices F and T of order $m \times m$, where m is the number of infected classes, defined by $F = \left[\frac{\partial F_i(E_0)}{\partial x_j}\right]$ and $T = \left[\frac{\partial T_i(E_0)}{\partial x_j}\right]$ with $1 \le i,\ j \le m$, such that F is non-negative, V is a non-singular matrices and E_0 is the disease free equilibrium point DFE. If F and $T$are non-negative and T is non-singular then T^{-1} is non-negative and thus $FT^{-1}$is also non-negative. Also, the matrix FT^{-1} is called the next generation matrix for the model. Finally, the basic reproduction number $R_0$is given by $R_0 = \rho(\mathrm{F}T^{-1})$.In general, $\rho(A)$ denotes the spectral radius of matrix A and the spectral radius is the biggest non-negative eigenvalue of the next generation matrix.

The Jacobian of F and T at the disease free equilibrium point E_0 takes the form respectively as

$$F \equiv \begin{bmatrix} \beta\tau/\mu & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix},\ T \equiv \begin{bmatrix} a & 0 & 0 & 0 & 0 & 0 \\ -\kappa & b & 0 & 0 & 0 & 0 \\ 0 & -\eta & c & 0 & 0 & 0 \\ 0 & -\phi & -\omega & d & 0 & 0 \\ 0 & 0 & 0 & -\gamma & e & 0 \\ 0 & 0 & 0 & 0 & -p & f \end{bmatrix} \quad (22)$$

It can be verified that the matrix T is non-singular as its determinantis non-zero and after some algebraic computations the next generation matrix is constructed as

$$[J_F(E_0)][J_T(E_0)]^{-1} =$$

$$\begin{bmatrix} \beta\tau/\mu & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix} \begin{bmatrix} a & 0 & 0 & 0 & 0 & 0 \\ -\kappa & b & 0 & 0 & 0 & 0 \\ 0 & -\eta & c & 0 & 0 & 0 \\ 0 & -\phi & -\omega & d & 0 & 0 \\ 0 & 0 & 0 & -\gamma & e & 0 \\ 0 & 0 & 0 & 0 & -p & f \end{bmatrix}^{-1}$$

$$= \begin{bmatrix} (\beta\tau)/(a\mu) & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix}$$

Now, it is possible to calculate the eigenvaluesof the matrix$[F][T]^{-1}$ to determine the basic reproduction number R_0 which is the spectral radius or the largest eigenvalue. Thus, the eigenvalues are computed by evaluating the characteristic equation $det[F[T]^{-1} - \lambda I] = 0$ or equivalently solving

$$\begin{vmatrix} (\beta\tau)/(a\mu) & 0 & 0 & 0 & 0 & 0 \\ 0 & -\lambda & 0 & 0 & 0 & 0 \\ 0 & 0 & -\lambda & 0 & 0 & 0 \\ 0 & 0 & 0 & -\lambda & 0 & 0 \\ 0 & 0 & 0 & 0 & -\lambda & 0 \\ 0 & 0 & 0 & 0 & 0 & -\lambda \end{vmatrix} = 0$$

It reduces to theequation as $\lambda^5[(\beta\tau/\mu\, a) - \lambda] = 0$ giving the six eigenvalues as

$$\lambda_1 = (\beta\tau/\mu\, a), \quad \lambda_2 = 0, \quad \lambda_3 = 0, \quad \lambda_4 = 0\,, \quad \lambda_5 = 0, \quad \lambda_6 = 0.$$

However, the largest eigenvalue here is and is the spectral radius or the threshold value or the basic reproductive number. Thus, the reproduction number of the model is $R_0 = (\beta\tau/\mu\, a)$.

3.4 Stability analysis of the disease free equilibrium

In absence of the infectious disease, the model populations have a unique disease free steady state E_0. To find the local stability of E_0, the Jacobian method of the model equations evaluated at DEF $E_0$is used. Also, to determine the global stability at E_0 M-matrix method given in [3] is used. It is already shown that the DFE of model (1) – (7) is given by $E_0 = \{\tau/\mu\,, \quad 0, \quad 0, \quad 0, \quad 0, \quad 0\}$. Now, following [4] the stability analysis of DFE is conducted and the results are presented in the form of theorems and proofs in the following sub-sections.

3.4.1 Local Stability of Disease Free Equilibrium point

Theorem 1: The DFE E_0 of the system (1) – (7) is locally asymptotically stable if $R_0 < 1$ and unstableif $R_0 > 1$.

Proof: Consider the right hand side expressions of the equations (1) – (7) as functions so as to find the Jacobian matrix as follows:

$$g_1(S, \quad P, \quad A, \quad J, \quad T, \quad R, \quad V) = \tau - \beta SP - S$$
$$g_2(S, \quad P, \quad A, \quad J, \quad T, \quad R, \quad V) = \beta SP - (\kappa + \mu)P$$
$$g_3(S, \quad P, \quad A, \quad J, \quad T, \quad R, \quad V) = \kappa P - (\phi + \eta + \mu)A$$
$$g_4(S, \quad P, \quad A, \quad J, \quad T, \quad R, \quad V) = \eta A - (\omega + \mu)J$$

$$g_5(S,\ P,\ A,\ J,\ T,\ R,\ V) = \phi A + \omega J - (\gamma + \mu)T$$
$$g_6(S,\ P,\ A,\ J,\ T,\ R,\ V) = \gamma T - (\rho + \mu)R$$
$$g_7(S,\ P,\ A,\ J,\ T,\ R,\ V) = \rho R - (\delta + \mu)V$$

Let $J(S,\ P,\ A,\ J,\ T,\ R,\ V)$ be aJacobian matrix of $g_1,\ g_2,\ g_3,\ g_4,\ g_5,\ g_6,\ g_7$ with respect to$S,\ P,\ A,\ J,\ T,\ R,\ V$. Thus,

$$J(S,\ P,\ A,\ J,\ T,\ R,\ V) = \begin{bmatrix} -\beta P - \mu & -\beta S & 0 & 0 & 0 & 0 & 0 \\ \beta P & \beta S - a & 0 & 0 & 0 & 0 & 0 \\ 0 & \kappa & -b & 0 & \emptyset & 0 & 0 \\ 0 & 0 & \eta & -c & 0 & 0 & 0 \\ 0 & 0 & \phi & \omega & -d & 0 & 0 \\ 0 & 0 & 0 & 0 & \gamma & -e & 0 \\ 0 & 0 & 0 & 0 & 0 & \rho & -f \end{bmatrix} \quad (23)$$

Now, the Jacobian matrix of $g_1,\ g_2,\ g_3,\ g_4,\ g_5,\ g_6,\ g_7$ with respect to $S,\ P,\ A,\ J,\ T,\ R,\ V$ at the disease free equilibrium E_0 is given by

$$J(E_0) = \begin{bmatrix} -\mu & -\tau\beta/\mu & 0 & 0 & 0 & 0 & 0 \\ 0 & a(R_0 - 1) & 0 & 0 & 0 & 0 & 0 \\ 0 & \kappa & -b & 0 & \emptyset & 0 & 0 \\ 0 & 0 & \eta & -c & 0 & 0 & 0 \\ 0 & 0 & \phi & \omega & -d & 0 & 0 \\ 0 & 0 & 0 & 0 & \gamma & -e & 0 \\ 0 & 0 & 0 & 0 & 0 & \rho & -f \end{bmatrix}$$

Now, to determine the signs of eigenvalues we use the concept of trace and determinant of a given matrix as mentioned in the [7].

(a) Trace of $J(E_0) = a(R_0 - 1) - \mu - b - c - d - e - f < 0$, if $R_0 < 1$.

(b) Determinant of $J(E_0) = -a\mu(R - 1)(cef\phi^2 + ef\eta\omega\phi - bcdef) > 0$,Provided that either of the following conditions is satisfied: (i) $bcdef < cef\phi^2 + ef\eta\omega\phi$ and $R_0 < 1$ and (ii) $bcdef > cef\phi^2 + ef\eta\omega\phi$ and $R_0 > 1$.

Now, from trace and determinant obtained in (1) and (2) with the given conditions we conclude that all eigenvalues of a matrix $J(E_0)$ are negative provided the mentioned conditions are satisfied. Thus, from Hurwitz Routh principle disease free equilibrium point is locally asymptotically stable if $R_0 < 1$ and unstable if $R_0 > 1$.

3.4.2 Global Stability of Disease Free Equilibrium Point

Here, we follow the procedure given in [7, 3]. That is, let $x \in R^n$ is disease compartment and $y \in R^m$be disease free compartment the disease transmission model (1) – (7) can be written in the form:

$$\dot{x} = -(T - F)x - h(x, y) \quad (24)$$
$$\dot{y} = g(x, y) \quad (25)$$

Here in (24), the notations$F$ and T are given in (20).

Theorem 2: If $T - F$ is a nonsingular M-matrix and $h \geq 0$ then the disease-free equilibrium point of model equations (1) – (6) is globally asymptotically stable.

Proof: Using the procedure given in [3, 7] the rate of change of the variables in the model equations (1) – (5) can be rewritten as

$$\dot{x} = -(T - F)x - \begin{bmatrix} \beta(S_0 - S)P \\ \\ 0 \end{bmatrix}$$
$$\dot{S} = \tau - \beta SP - \mu S$$

Now, it is to be shown that $T - F$ is nonsingular M-matrix. From the previous computations (19) we have

$$F \equiv \begin{bmatrix} \beta\tau/\mu & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix},\ T \equiv \begin{bmatrix} a & 0 & 0 & 0 & 0 & 0 \\ -\kappa & b & 0 & 0 & 0 & 0 \\ 0 & -\eta & c & 0 & 0 & 0 \\ 0 & -\phi & -\omega & d & 0 & 0 \\ 0 & 0 & 0 & -\gamma & e & 0 \\ 0 & 0 & 0 & 0 & -p & f \end{bmatrix}.$$

$$T-F=\begin{bmatrix} a & 0 & 0 & 0 & 0 & 0 \\ -\kappa & b & 0 & 0 & 0 & 0 \\ 0 & -\eta & c & 0 & 0 & 0 \\ 0 & -\phi & -\omega & d & 0 & 0 \\ 0 & 0 & 0 & -\gamma & e & 0 \\ 0 & 0 & 0 & 0 & -p & f \end{bmatrix} \equiv sI-\begin{bmatrix} \beta\tau/\mu & 0 & 0 & 0 & 0 & 0 \\ \kappa & 0 & 0 & 0 & 0 & 0 \\ 0 & \eta & 0 & 0 & 0 & 0 \\ 0 & \phi & \omega & 0 & 0 & 0 \\ 0 & 0 & 0 & \gamma & 0 & 0 \\ 0 & 0 & 0 & 0 & p & 0 \end{bmatrix}$$
$$= sI-B$$

Here, $s=\max(a,\ b,\ c,\ d,\ e,\ f)$ and

$$B=\begin{bmatrix} \beta\tau/\mu & 0 & 0 & 0 & 0 & 0 \\ \kappa & 0 & 0 & 0 & 0 & 0 \\ 0 & \eta & 0 & 0 & 0 & 0 \\ 0 & \phi & \omega & 0 & 0 & 0 \\ 0 & 0 & 0 & \gamma & 0 & 0 \\ 0 & 0 & 0 & 0 & p & 0 \end{bmatrix}$$

Now, $\det(T-F)=-bcdef(\beta\tau-a\mu)/\mu$ and $\rho(B)=\beta(\tau/\mu)$ and $T-F$ is nonsingular matrix provided that the conditions$\beta\tau\neq a\mu$ are satisfied. Further, off diagonal elements of $T-F$ are non-positive numbers. Thus, $T-F$ is non-singular M-matrix if $s\geq\rho(B)$.

Following procedures given in [3] one can easily show that $S\leq S_0$. Therefore, from the above hypothesis disease-free equilibrium point of model equations (1) – (7) is globally asymptotically stable for$R_0<1$.

3.5 Stability Analysis of Endemic Equilibrium Point

By definition it is true that at the endemic equilibrium point $E_1=\{S^1,\ P^1,\ A^1,\ J^1,\ T^1,\ R^1,\ V^1\}$ is the point where the disease persists or exists. To analyze the local stability ofE_1, Jacobian matrix of the model that evaluated at this equilibrium point is used. Further, remember that the endemic equilibrium point $E_1=\{S^1,\ P^1,\ A^1,\ J^1,\ T^1,\ R^1,\ V^1\}$ of the given model (1) – (7) is already computed.

3.5.1 Local Stability of Endemic Equilibrium Point

The local stability of endemic equilibrium point is stated and proved in Theorem 3.

Theorem 3: The endemic equilibrium point is locally asymptotically stable if$R_0>1$ and unstable if $R_0<1$.

Proof: The stability analysis of E_1 is conducted by following the similar procedure adopted as in the case of E_0. Thus, the procedure starts with the construction of Jacobian matrix at E_1. Now, the Jacobian matrix of the model given in (20) at endemic equilibrium point E_1 takes the form as

$$J(S,\ P,\ A,\ J,\ T,\ R,\ V)=\begin{bmatrix} -\beta P-\mu & -\beta S & 0 & 0 & 0 & 0 & 0 \\ \beta P & \beta S-a & 0 & 0 & 0 & 0 & 0 \\ 0 & \kappa & -b & 0 & \emptyset & 0 & 0 \\ 0 & 0 & \eta & -c & 0 & 0 & 0 \\ 0 & 0 & \phi & \omega & -d & 0 & 0 \\ 0 & 0 & 0 & 0 & \gamma & -e & 0 \\ 0 & 0 & 0 & 0 & 0 & \rho & -f \end{bmatrix}$$

Hence, $$J(E_1)=\begin{bmatrix} -\mu R_0 & -(\beta\tau/\mu R_0) & 0 & 0 & 0 & 0 & 0 \\ \mu(R_0-1) & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \kappa & -b & 0 & \emptyset & 0 & 0 \\ 0 & 0 & \eta & -c & 0 & 0 & 0 \\ 0 & 0 & \phi & \omega & -d & 0 & 0 \\ 0 & 0 & 0 & 0 & \gamma & -e & 0 \\ 0 & 0 & 0 & 0 & 0 & \rho & -f \end{bmatrix}$$

Now the trace of $J(E_1)$ is a negative quantity while determinant of $J(E_1)$ computed as $\beta\tau(R_0-1)(cef\phi^2+ef\eta\omega\phi-bcdef)/R_0$ and is a positive quantity provided that either of the following conditions are satisfied,

(i) $bcdef < cef\phi^2+ef\eta\omega\phi$ and $R_0 > 1$

(ii) $bcdef > cef\phi^2+ef\eta\omega\phi$ and $R_0 < 1$

Hence, the endemic equilibrium point$E_1$is locally asymptotically unstable if $R_0 < 1$.and stable if $R_0 > 1$ provided that the afro mentioned conditions are satisfied.

IV. Numerical Simulations

In this section, numerical simulation study of model equations (1) – (7) is carried out using the software MATLAB. 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. These sets of parametric values are given under figures.

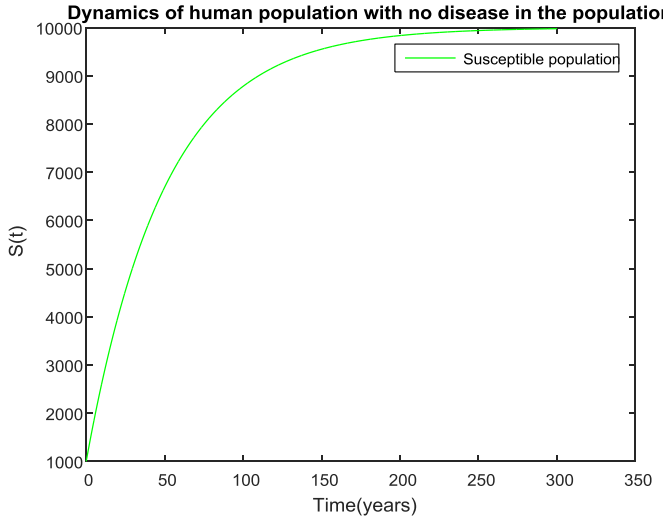

Figure 1 Dynamics of susceptible population with parametric values

$\boldsymbol{\tau = 200}$, $\boldsymbol{ = 0.02}$, $\boldsymbol{\beta = 0.00005}$, $\boldsymbol{\phi = 0.1}$, $\boldsymbol{\eta = 0.06}$, $\boldsymbol{\omega = 0.08}$, $\boldsymbol{\rho = 0.09}$, $\boldsymbol{k = 0.3}$, $\boldsymbol{\gamma = 0.1}$, $\boldsymbol{\delta = 0.08}$

In Figure 1, human population increase for about 300 years then after remain constant over the entire interval of time.

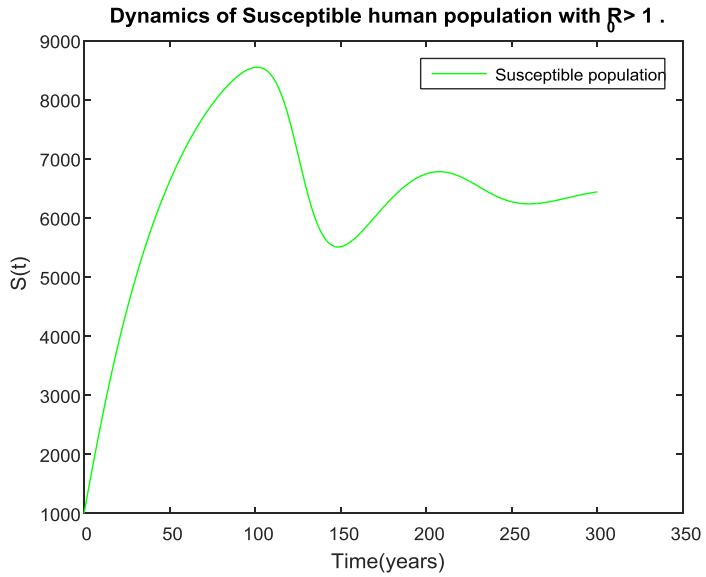

Figure 2 Dynamics of susceptible population with parametric values

$\boldsymbol{\tau = 200}$, $\boldsymbol{ = 0.02}$, $\boldsymbol{\beta = 0.00005}$, $\boldsymbol{\phi = 0.1}$, $\boldsymbol{\eta = 0.06}$, $\boldsymbol{\omega = 0.08}$, $\boldsymbol{\rho = 0.09}$, $\boldsymbol{k = 0.3}$, $\boldsymbol{\gamma = 0.1, \delta = 0.08}$,

In Figure 2, the human population increases over the first hundred years and then decrease for about 50 years. Then followed with increasing and decreasing as time increases which finally shows no change in number as disease persists in the population.

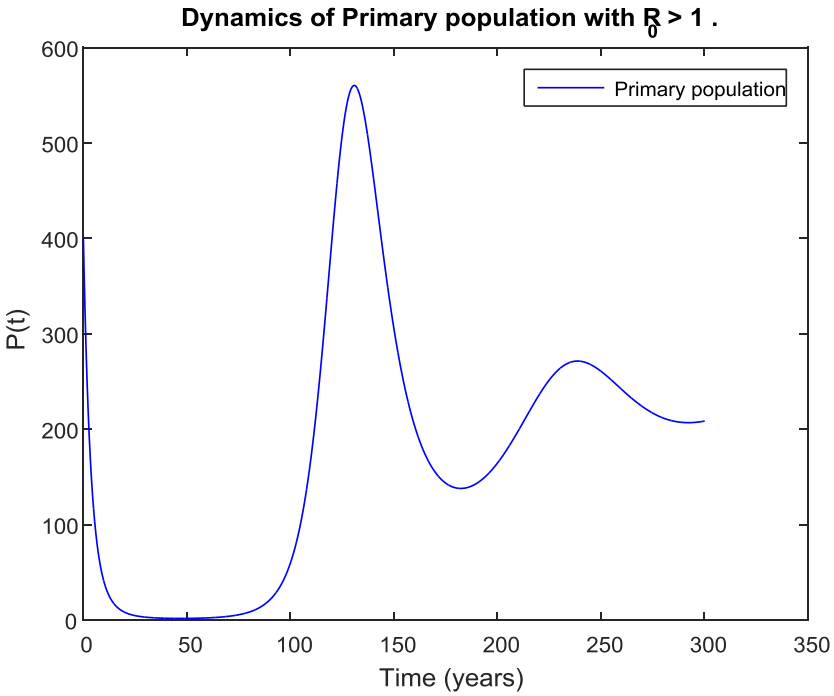

Figure 3 Dynamics of primary population with parametric values
$\tau = 200$, $\square = 0.02$, $\beta = 0.00005$, $\phi = 0.1$, $\eta = 0.06$, $\omega = 0.08$, $\rho = 0.09$, $k = 0.3$, $\gamma = 0.1, \delta = 0.08$,

In Figure 3, it is observed that the primary human populations decreases over the first fifty years. Then increase over the next hundred years. Then decrease for about fifty years wich is followed with small change in the number of population as time increase.

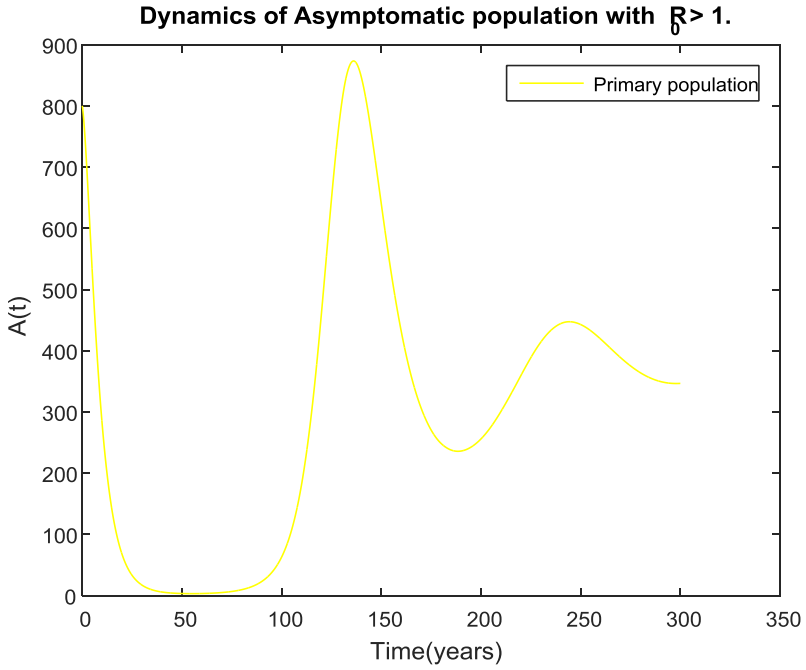

Figure 4 Dynamics of asyptomatic population with parametric values
$\tau = 200$, $\square = 0.02$, $\beta = 0.00005$, $\phi = 0.1$, $\eta = 0.06$, $\omega = 0.08$, $\rho = 0.09$, $k = 0.3$, $\gamma = 0.1, \delta = 0.08$,

In Figure 4, the the number of asyptomatic human populations decrease for about fifty years. Then increase and decrease with oscillation pattern and decreasing applitude that finally show no change in popution number.

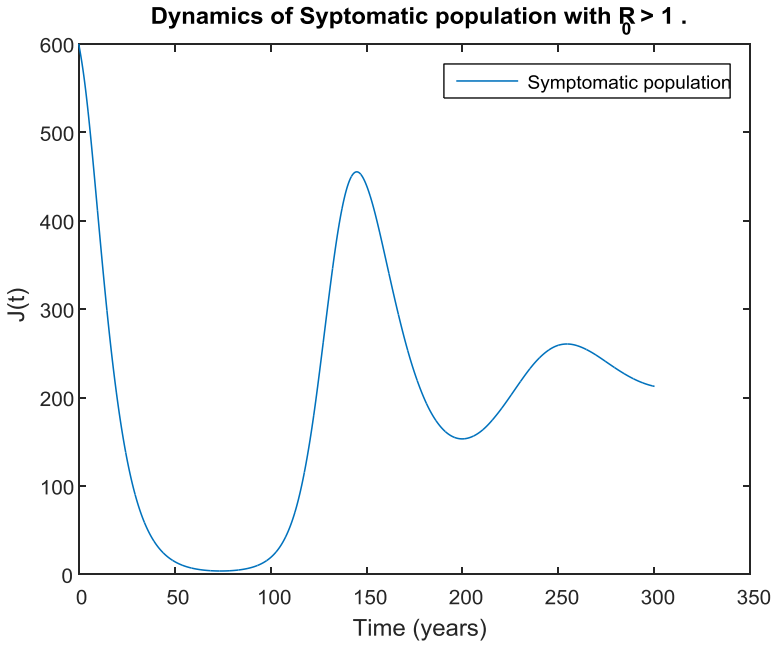

Figure 5 Dynamics of syptomatic population with parametric values
$\boldsymbol{\tau = 200}$, $\boldsymbol{\beta = 0.00005}$, $\boldsymbol{\phi = 0.1}$, $\boldsymbol{\eta = 0.06}$, $\boldsymbol{\omega = 0.08}$, $\boldsymbol{\rho = 0.09}$, $\boldsymbol{k = 0.3}$, $\boldsymbol{\gamma = 0.1, \delta = 0.08}$,

In Figure 5, the symptomatic population decrease initially for about sixty years and then increase for about ninety yearys. Then shows oscillating pattern with finally no change in population size eventhou the disease persists in the population.

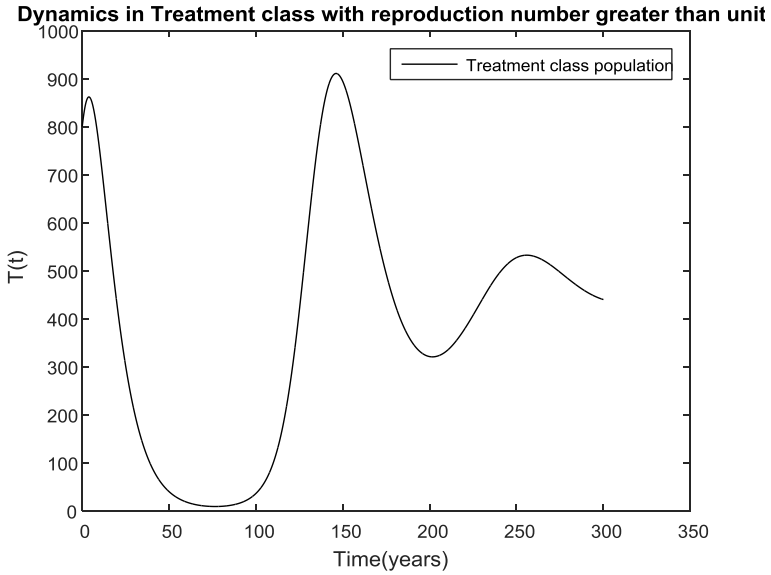

Figure 6 Dynamics of treatment population with parametric values
$\boldsymbol{\tau = 200}$, $\boldsymbol{\beta = 0.00005}$, $\boldsymbol{\phi = 0.1}$, $\boldsymbol{\eta = 0.06}$, $\boldsymbol{\omega = 0.08}$, $\boldsymbol{\rho = 0.09}$, $\boldsymbol{k = 0.3}$, $\boldsymbol{\gamma = 0.1, \delta = 0.08}$,

In Figure 6, it is observed that initially treatment class human population increase followed with decreasing and increasing pattern in which there is no significant changes in the number of population for time interval above hundred years.

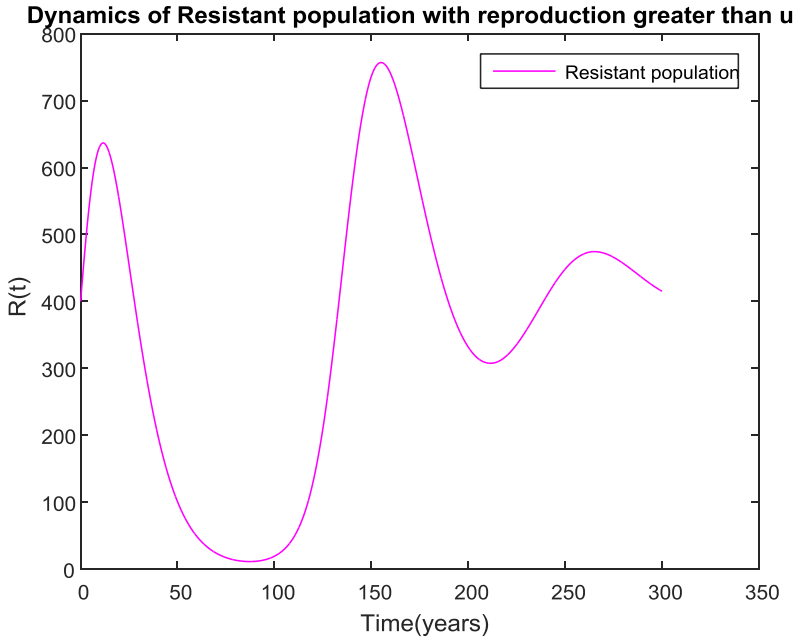

Figure 7 Dynamics of resistant population with parametric values
$\boldsymbol{\tau = 200}$, $\boldsymbol{\beta = 0.00005}$, $\boldsymbol{\phi = 0.1}$, $\boldsymbol{\eta = 0.06}$, $\boldsymbol{\omega = 0.08}$, $\boldsymbol{\rho = 0.09}$, $\boldsymbol{k = 0.3}$, $\boldsymbol{\gamma = 0.1, \delta = 0.08}$,

In Figure 7, initially the number of drug resistant population increases. Then their number drops to the least then increase to the maximum. Then decrease upto some interval followed with increament upto some interval which is oscillating with decreasing changes in number of population.Finally, there is no change in the number of population as time increases.

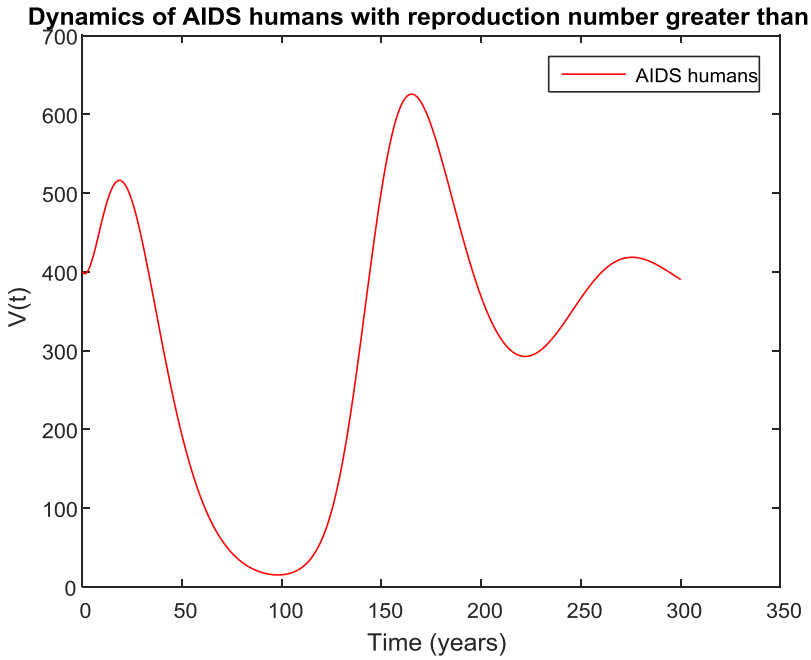

Figure 8 Dynamics of AIDS population with parametric values
$\boldsymbol{\tau = 200}$, $\boldsymbol{\beta = 0.00005}$, $\boldsymbol{\phi = 0.1}$, $\boldsymbol{\eta = 0.06}$, $\boldsymbol{\omega = 0.08}$, $\boldsymbol{\rho = 0.09}$, $\boldsymbol{k = 0.3}$, $\boldsymbol{\gamma = 0.1, \delta = 0.08}$,

In Figure 8, initially the number of human population at the advanced stage of HIV increases. Then decrease to the minimum number of AIDS humans and followed with increasing upto some maximum number. Then decrease upto some number then increase for some interval. Finally, there is no change in the number of AIDS patients.

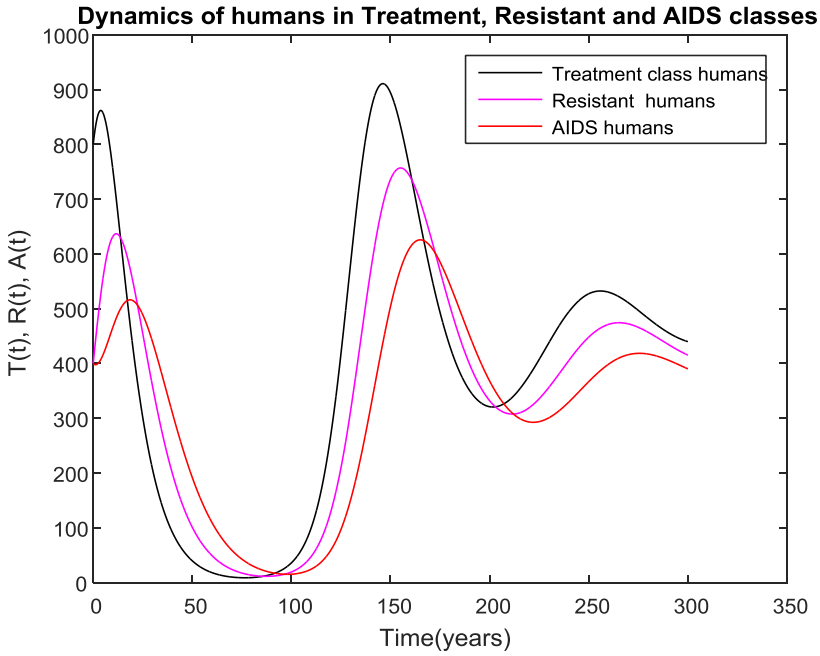

Figure 9 Dynamics of treatment, resistance and AIDS populations with parametric values $\tau = 200$, $\Lambda = 0.02$, $\beta = 0.00005$, $\phi = 0.1$, $\eta = 0.06$, $\omega = 0.08$, $\rho = 0.09$, $k = 0.3$, $\gamma = 0.1, \delta = 0.08$,

Figure 9 describes initially treatment class population, resistant population, and AIDS class population increase for some time interval. But the increasing time interval of treatment class population is less than the number of drug resistant population and the time interval of drug resistant population is less than the time interval of AIDS population. Then decrease and increase within some time interval alternatively. Finally, the changes in the number of each population is not recognizable.

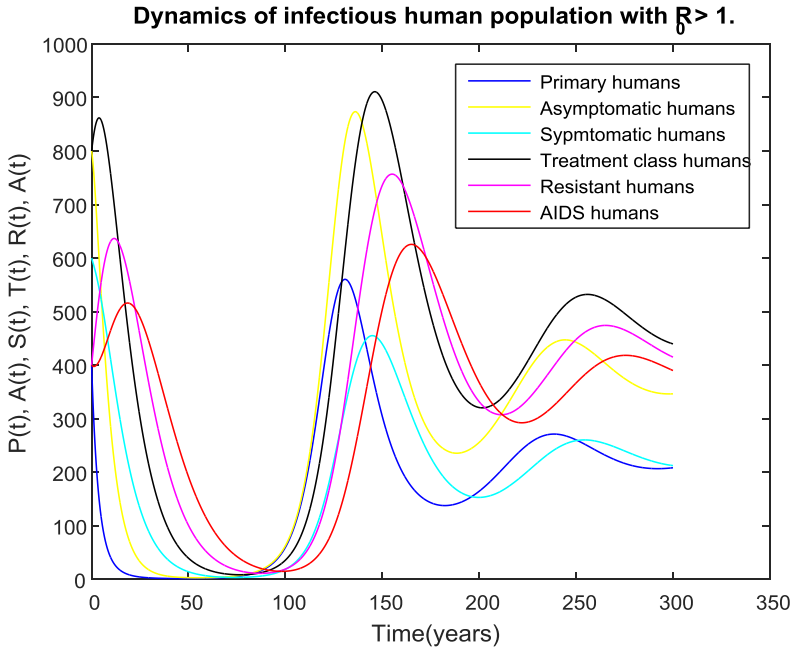

Figure 10 Dynamics of susceptible population with parametric values $\tau = 200$, $\Lambda = 0.02$, $\beta = 0.00005$, $\phi = 0.1$, $\eta = 0.06$, $\omega = 0.08$, $\rho = 0.09$, $k = 0.3$, $\gamma = 0.1, \delta = 0.08$.

In Figure 10, it is observable that initially populations in treatment, resistant, and AIDS class population increases but the number of population in susceptible, primary, asyptomatic, symptomatic classes decrease for some interval. Then increase and decrease alternatively which finally shows insignificant changes in each class population.

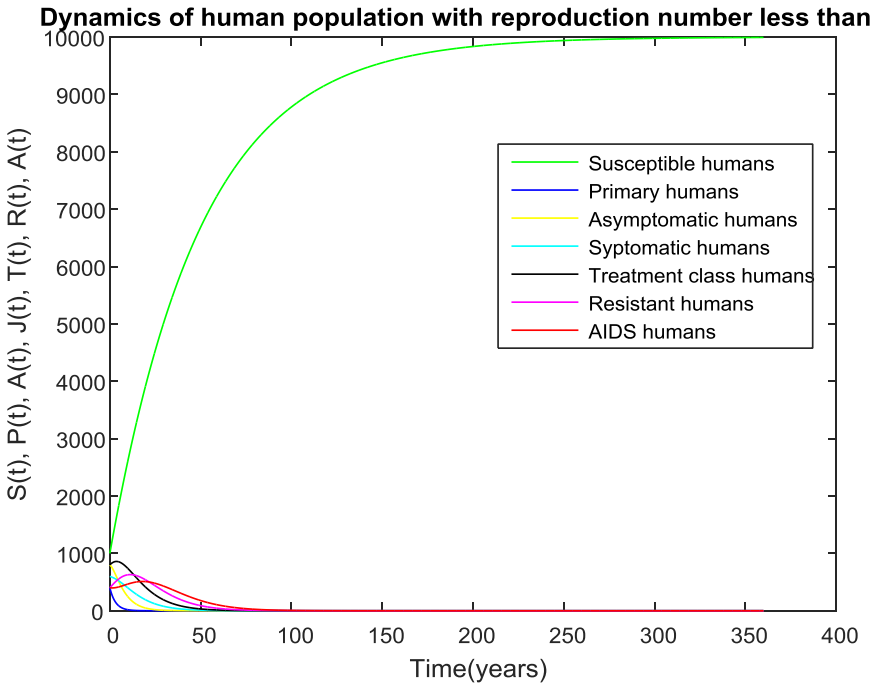

Figure 11 Dynamics of susceptible population with parametric values
$\tau = 200$, $\square = 0.02$, $\beta = 0.000005$, $\phi = 0.1$, $\eta = 0.06$, $\omega = 0.08$, $\rho = 0.09$, $k = 0.3$, $\gamma = 0.1, \delta = 0.08$,

In Figure 11, it is observable that the number of HIV infected population is almost decreases for about hundred years. Then the number of HIV infected population are invisible. It is also observable that the number of susceptible population increases on the given time interval. Finally, there is no visible changes in number of population as time increase.

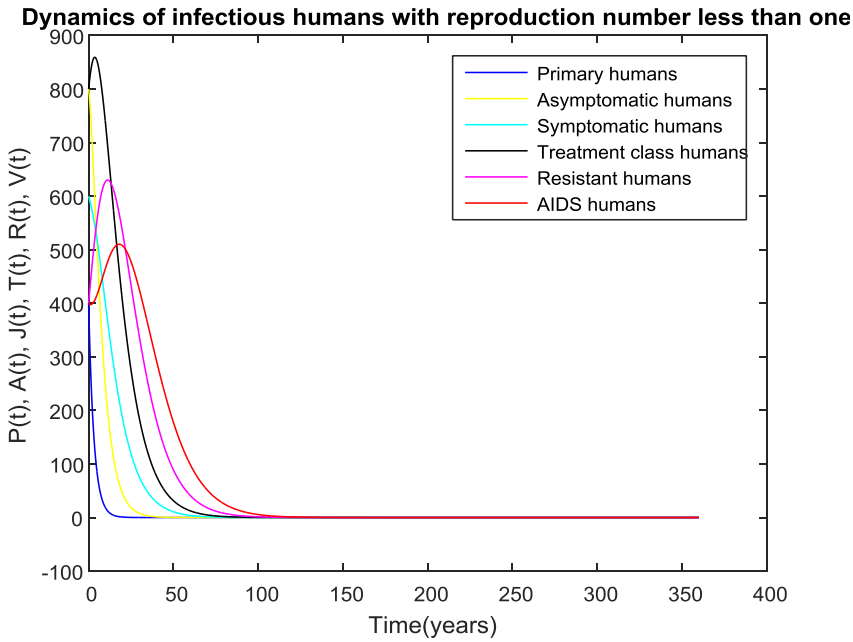

Figure 12 Dynamics of susceptible population with parametric values
$\tau = 200$, $\square = 0.02$, $\beta = 0.00005$, $\phi = 0.1$, $\eta = 0.06$, $\omega = 0.08$, $\rho = 0.09$, $k = 0.3$, $\gamma = 0.1, \delta = 0.08$,

In Figure 12, it is observable that initially human population in three comprtments increase whereas the four compartment population decrease strictly. Finally, the number of human population in diseasecompartment decrease which leads to zero after hundred years.

V. Sensitivity Analysis

Sensitivity analysis is used to determine the sensitivity of the model with respect to the parameters involved in it. That is, how changes in the value of the parameters of the model result in changing the dynamics of the infection. It is used to discover parameters that have a high impact on $R_0$and should be targeted by intervention strategies. More precisely, sensitivity indices allowmeasuring the relative change in a variable when parameter changes [3, 6].If the result is negative, then the relationship between the parameters and $R_0$is inversely proportional. In this case, the modulus of the sensitivity index will be taken so that the size of the effect of changing that parameter can be deduced.

On the other hand, a positive sensitivity index means that both the function and the parameter are proportional to each otheri.e. both of them grow or decay together.

It is already shown that the explicit expression of $R_0$is given by $R_0 = \beta\tau/\mu a$. Since, R_0 depends only on four parameters, an analytical expression will be derived for its sensitivity to each of the parameters using the normalized forward sensitivity index as given by Chitnis [3].

$$\Upsilon_{\beta}^{R_0} = [\partial R_0/\partial\beta] \times [\beta/R_0]$$
$$\Upsilon_{\mu}^{R_0} = [\partial R_0/\partial\mu] \times [\mu/R_0]$$
$$\Upsilon_{\eta}^{R_0} = [\partial R_0/\partial\eta] \times [\eta/R_0]$$
$$\Upsilon_{\tau}^{R_0} = [\partial R_0/\partial\tau] \times [\tau/R_0]$$
$$\Upsilon_{\kappa}^{R_0} = [\partial R_0/\partial\kappa] \times [\kappa/R_0]$$

Table 3 Sensitivity of R_0 evaluated for the parametric values given under Figure 1

Parameter	Sensitivity index
μ	-83
β	+1
κ	- 4.8828
τ	+1

From Table 3, it can be observed that parametersτ andβhave positive sensitivity indicesand values of the remaining two parameters κ andμ get negative sensitivity indices.

As it is observed from the table the parameter with large magnitude areμ and κ . Hence,they are most sensitive parameter in the model equations. On the other hand an increase in these positive parameter values will cause an increasingR_0 this implies that disease transmission in human population. Similarly, a decrease in negative parameter values will cause a decrease inR_0 which means the disease transmission decreases in human population.

VI. Result and Discussion

In this study, a model describing the dynamics of seven compartment human population pertaining to HIV(Human Immunodeficiency Virus)with treatment is formulated and analyzed. Further, it is observed that the disease transmission decreases with decreased transmission rate value and disease persist in the population with increasing transmission rate value.Figure 1 shows that with no disease the population growth to the upper bond exponentially. Figures 2 – 10 describes the dynamics of human population with the persistence of the disease in the population. Figures 11 – 12 describes the dynamics of human population with extinction of disease out of the population. The mathematical analysis has shown that if the reproduction number $R_0 < 1$ then the disease free equilibrium point is locally and globally asymptotically stable. Also the disease free equilibrium point is unstable if $R_0 > 1$ implying that the transmission of disease increases.

VII. Conclusions

In this study, a deterministic mathematical model of seven compartments has been formulated to describe the dynamics of human populations pertaing to HIV/AIDS. Moreover, the formulated model is biologically meaningful and mathematically well posed. The simulation shows as the number of drug resistant population increases the number of HIV population also increases. The equilibrium points of model equations are locally stable. Further, the Global stability of disease free equilibrium points are described.and Also, the solution of the model equations is numerically simulatedandsensitivity analysis of the model is conducted. Furthermore, results of the research work presented in this paper reveal that transmission rate has natural death rate is the most sensitive parameter.

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