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Mathematical Modeling and Analysis of HIV/AIDS with Herbal Medicine and Antiretroviral Treatment

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Abstract. In this paper, a deterministic mathematical model is formulated to study the dynamics of human population subjected to HIV/AIDS with Herbal medicine and ART as treatments. The total population is divided into eight compartments. The existence, uniqueness, positivity, and boundedness of the solutions are shown. Both treatments have a positive impact on the reduction of viral load in the body. The stability analysis of equilibrium points are done. Disease free equilibrium point is locally asymptotically stable if the reproduction number is less than unity and unstable for greater than unity.

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Index to information contained in this paper

1. Introduction

In their study, Kermack and McKendrick described the dynamics of the population pertaining an infectious disease using system of non-linear ordinary differential equations [1, 2, 11]. HIV is one of such infectious disease that can be described with their modeling science. Now a days there are traditional herbal medicine that most commonly used in places where it is difficult to get HIV medicine or ART [8]. In fact, the reason to use alternative therapies is because of expensive antiretroviral therapies or unavailable in resource constrained areas which helps to reduce mortality due to HIV infection. Thus, it is important to develop a model that depict that describes ART and Herbal medicine as treatments of HIV disease. HIV is a virus that attacks the immune system [4, 8, 9]. If a person is infected with HIV virus, then body immune system become weak. This weakness of immune system leads to healthy problem and unable to fight off infections and diseases [3, 7, 10]. The virus has potential to kill or reduce a type of white blood cell known as T-helper cells and multiply itself inside host cells. T-helper cells are also called CD4 cells and there is no vaccine or cure to permanently destroy AIDS from human [4].

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 [8]. This previous work is five compartmental model whereas the current study considered deterministic model that consists of eight compartments of human population.

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The descriptions of compartments are as 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) Secondary compartment. It is denoted by $I(t)$. This compartment includes all humans who know that they are infected with virus. They join either ART or Herbal medicine user(iv) Herbs user compartment. It is denoted by $A(t)$. This compartment includes of infectious humans that uses only herbal medicine as a treatment. They join both treatment compartment at some rate ω (v) ART user compartment. It is denoted by $J(t)$. This compartment includes of infectious humans that uses only ART medicine as a treatment. They join both treatment compartment at some rate κ (vi) Treatment compartment. It is denoted by $T(t)$. This compartment includes all HIV infected population who use both ART and Herbs as a treatment. (vii) Drug resistant compartment. This compartment includes portion of individuals from treatment class that are resistant to both ART and Herbs medicine. (viii) 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) Deterministic dynamical system in the presence of Human Immunodeficiency virus (HIV) classifies human population under observation into eight compartments as SPIAJTRV model at any time.
(ii) Susceptible humans are recruited to the compartment $S(t)$ at some constant rate τ.
(iii) Susceptible humans can be infected if they make effective contact with primary infected population whose status of HIV is not known yet and join primary infected compartment at a constant rate β.
(iv) Primary infected humans transfer into secondary compartment at a constant rate α.
(v) Secondary infected humans transfer into herbs compartment at a constant rate ρ and transfer into ART compartment at a constant rate θ.
(vi) Herbs compartment humans transfer into treatment compartment at a constant rate ω.
(vii) ART user human compartment transfer into treatment compartment at the rate κ.
(viii) Humans in treatment compartment transfer into resistant compartment at the constant rate of ϕ.
(ix) Resistant compartment individuals transfer to AIDS compartment at the rate of γ.
(x) All categories of human's compartments face the same natural mortality with a rate μ.
(xi) All AIDS humans suffer disease induced death at a constant rate δ.All parameters used in the dynamical system are positive.

Table 1. Notations and description of model variables.

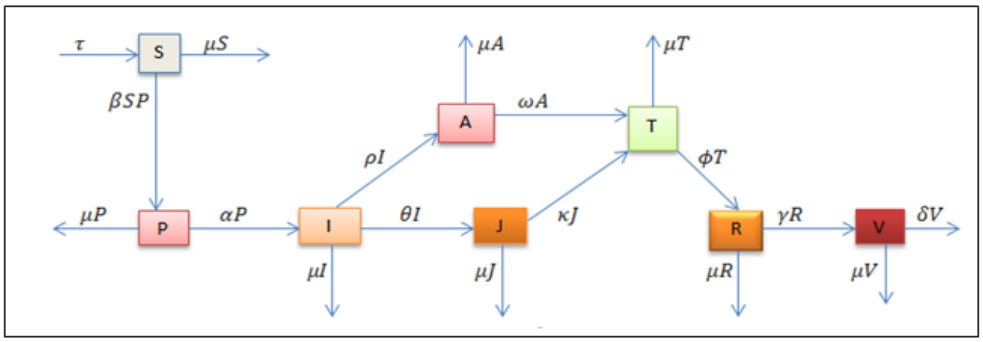
Variable	Description
$S(t)$	Population size of susceptible humans
$P(t)$	Population size of primary infected humans
$I(t)$	Population size of secondary infected population
$A(t)$	Population size of Herbs user humans
$J(t)$	Population size of ART user humans
$T(t)$	Population size of both ART and Herbs user
$R(t)$	Population size of resistant to both treatment
$V(t)$	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
β	Transmission rate of primary infected humans. With this rate primary infected humans transfer into P
α	Rate of humans transferring from compartment P to I
ρ	Rate of humans transferring from compartment I to A
θ	Rate of humans transferring from compartment I to J
ω	Rate of humans transferring from compartment A to T
κ	Rate of humans transferring from compartment J to T
ϕ	Rate of humans transferring from compartment T to R
γ	Rate of humans transferring from compartment R to V
μ	Natural death rate. With this rate humans in all compartments die naturally
δ	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:

$$dS/dt = \tau - \beta SP - \mu S \quad (1)$$
$$dP/dt = \beta SP - (\alpha + \mu)P \quad (2)$$
$$dI/dt = \alpha P - (\rho + \theta + \mu)I \quad (3)$$
$$dA/dt = \rho I - (\omega + \mu)A \quad (4)$$
$$dJ/dt = \theta I - (\kappa + \mu)J \quad (5)$$
$$dT/dt = \omega A + \kappa J - (\phi + \mu)T \quad (6)$$
$$dR/dt = \phi T - (\gamma + \mu)R \quad (7)$$
$$dV/dt = \gamma R - (\delta + \mu)V \quad (8)$$

The non-negative initial conditions of the model equations (1)-(8) are denoted by $S(0) > 0,\ P(0) \geq 0,\ I(0) \geq 0,\ A(0) \geq 0,\ J(0) \geq 0,\ T(0) \geq 0,\ R(0) \geq 0,\ V(0) \geq 0.$

This system consists of seven first order non-linear ordinary differential equations.

3. Mathematical analysis of the model

In this section we describe the mathematical analysis of the present improved 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, uniqueness, positivity and boundedness of solution*

In order to say that the formulated dynamical system is biologically valid and mathematically well-posed, it is required to show that the solutions of the system of differential equations (1)-(8) exist, non-negative and bounded for all time t. The details are given as the followings:

Theorem 3.1 ([5]) Suppose the system of first order differential equation has the form,

$$\left.\begin{array}{l} x_1' = f_1(x_1, \ x_2, \ x_3, . \ . \ ., \ x_n, \ t), \ x_1(t_0) = x_{10} \\ x_2' = f_2(x_1, \ x_2, \ x_3, . \ . \ ., \ x_n, \ t), \ x_2(t_0) = x_{20} \\ x_3' = f_3(x_1, \ x_2, \ x_3, . \ . \ ., \ x_n, \ t), \ x_3(t_0) = x_{30} \\ \vdots \\ x_n' = f_n(x_1, \ x_2, \ x_3, . \ . \ ., \ x_n, \ t), \ x_n(t_0) = x_{n0} \end{array}\right\}$$

or in compact form can be written as

$$x' = f(t, x), \quad x(t_0) = x_0$$

Let D denote the region in $(n+1)$-dimensional space given by

$$R = \{(t, x): \ |t - t_0| \leq a, \qquad |x - x_0| \leq b, \}$$

If the partial derivatives $\partial f_i / \partial x_j$, $i, j = 1,2,3, \dots, n$ are continuous and bounded in D, then there exists a unique continuous vector solution $x^* = \left(x_1(t), x_2(t), \dots, x_n(t)\right)$ in the interval $|t - t_0| \leq \delta$, where δ is a positive constant.

Lemma 3.1 (Existence and uniqueness) Solutions of the model equations (1)-(8) together with the initial conditions $S(0) > 0,\ P(0) \geq 0,\ I(0) \geq 0, A(0) \geq 0,\ J(0) \geq 0,$ $T(t),\ R(t), V(0) \geq 0,$ exist in $\mathbb{R}_+^8$ 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 $\mathbb{R}_+^8$.

Proof Let the right hand sides of the system of equations (1)-(8) are expressed as follows:

$$\begin{array}{l} dS/dt = \tau - \beta SP - \mu S \equiv g_1(S, P, I, A, J, T, R, V) \\ dP/dt = \beta SP - (\alpha + \mu)P \equiv g_2(S, P, I, A, J, T, R, V) \\ dI/dt = \alpha P - (\rho + \theta + \mu)I \equiv g_3(S, P, I, A, J, T, R, V) \\ dA/dt = \rho I - (\omega + \mu)A \equiv g_4(S, P, I, A, J, T, R, V) \\ dJ/dt = \theta I - (\kappa + \mu)J \equiv g_5(S, P, I, A, J, T, R, V) \\ dT/dt = \omega A + \kappa J - (\phi + \mu)T \equiv g_6(S, P, I, A, J, T, R, V) \\ dR/dt = \phi T - (\gamma + \mu)R \equiv g_7(S, P, I, A, J, T, R, V) \end{array}$$

$$dV/dt = \gamma R - (\delta + \mu)V \equiv g_8(S, P, I, A, J, T, R, V)$$

Let R denote the region $R = \{(S, P, I, A, J, T, R, V) \in \mathbb{R}_+^8 ; \ N \leq \tau/\mu\}$. Then according to Theorem 3.1 equations (1)-(8) have a unique solution if $(\partial g_i)/(\partial x_j)$, $\forall\ i, j = 1,2,3,4,5,6,7,8$ are continuous and bounded in R. Here, the notations $x_1 = S$, $x_2 = P$, $x_3 = I$, $x_4 = A$, $x_5 = J$, $x_6 = T$, $x_7 = R$, and $x_8 = V$ are employed. The existence, continuity and the boundedness of g_1, g_2, g_3, g_4, g_5, g_6, g_7 and g_8 are verified as here under:

Table 3. Verification of Continuity and Boundedness of the Function.

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

g_6	$(\partial g_6)/(\partial S) = 0$ $(\partial g_6)/(\partial P) = 0$ $(\partial g_6)/(\partial I) = 0$ $(\partial g_6)/(\partial A) = \omega$ $(\partial g_6)/(\partial J) = \kappa$ $(\partial g_6)/(\partial T) = -(\phi + \mu)$ $(\partial g_6)/(\partial R) = 0$ $(\partial g_6)/(\partial V) = 0$	$\lvert(\partial g_6)/(\partial S)\rvert = 0 < \infty$ $\lvert(\partial g_6)/(\partial P)\rvert = 0 < \infty$ $(\partial g_6)/(\partial I) = 0$ $\lvert(\partial g_6)/(\partial A)\rvert = \omega < \infty$ $\lvert(\partial g_6)/(\partial J)\rvert = \kappa < \infty$ $\lvert(\partial g_6)/(\partial T)\rvert = \phi + \mu < \infty$ $\lvert(\partial g_6)/(\partial R)\rvert = 0 < \infty$ $\lvert(\partial g_6)/(\partial V)\rvert = 0 < \infty$
g_7	$(\partial g_7)/(\partial S) = 0$ $(\partial g_7)/(\partial P) = 0$ $(\partial g_7)/(\partial I) = 0$ $(\partial g_7)/(\partial A) = 0$ $(\partial g_7)/(\partial J) = 0$ $(\partial g_7)/(\partial T) = \phi$ $(\partial g_7)/(\partial R) = -(\gamma + \mu)$ $(\partial g_7)/(\partial V) = 0$	$\lvert(\partial g_7)/(\partial S)\rvert = 0 < \infty$ $\lvert(\partial g_7)/(\partial P)\rvert = 0 < \infty$ $(\partial g_7)/(\partial I) = 0$ $\lvert(\partial g_7)/(\partial A)\rvert = 0 < \infty$ $\lvert(\partial g_7)/(\partial J)\rvert = 0 < \infty$ $\lvert(\partial g_7)/(\partial T)\rvert = \phi < \infty$ $\lvert(\partial g_7)/(\partial R)\rvert = \gamma + \mu < \infty$ $\lvert(\partial g_7)/(\partial V)\rvert = 0 < \infty$
g_8	$(\partial g_8)/(\partial S) = 0$ $(\partial g_8)/(\partial P) = 0$ $(\partial g_8)/(\partial I) = 0$ $(\partial g_8)/(\partial A) = 0$ $(\partial g_8)/(\partial J) = 0$ $(\partial g_8)/(\partial T) = 0$ $(\partial g_8)/(\partial R) = \gamma$ $(\partial g_8)/(\partial V) = -(\delta + \mu)$	$\lvert(\partial g_8)/(\partial S)\rvert = 0 < \infty$ $\lvert(\partial g_8)/(\partial P)\rvert = 0 < \infty$ $\lvert(\partial g_8)/(\partial P)\rvert = 0 < \infty$ $\lvert(\partial g_8)/(\partial A)\rvert = 0 < \infty$ $\lvert(\partial g_8)/(\partial J)\rvert = 0 < \infty$ $\lvert(\partial g_8)/(\partial T)\rvert = 0 < \infty$ $\lvert(\partial g_8)/(\partial R)\rvert = \gamma < \infty$ $\lvert(\partial g_8)/(\partial V)\rvert = \delta + \mu < \infty$

Here, from computations in Table 3, all the partial derivatives $(\partial g_i)/(\partial x_j)$: $i,\ j = 1, 2, 3, 4, 5, 6, 7, 8$ exist, and are both continuous and bounded in R. Hence, by Theorem 3.1, a solution for the model (1)-(8) exists and unique.

Lemma 3.2 (Positivity) Solutions of the model equations (1)-(8) together with the initial conditions $S(0) > 0,\ P(0) \geq 0,\ I(0) \geq 0, A(0) \geq 0,\ J(0) \geq 0,\ T(0) \geq 0,\ R(0) \geq 0,\ V(0) \geq 0$ are always non-negative (OR) the model variables $S,\ P,\ I,\ A,\ J,\ T,\ R$ and V are non-negative for all t and will remain in $\mathbb{R}^8_+$.

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

Positivity of $S(t)$: The model equation (1) given by $dS/dt = \tau - \beta SP - \mu S$ 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 differential 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 $dP/dt = \beta SP - (\alpha + \mu)$can be expressed without loss of generality, after eliminating positive term βSP which is appearing on the right hand side, as an inequality as$dP/dt \geq -(\alpha + \mu)P$. Using variables separable method and on applying integration, the solution of the foregoing differential inequality can be obtained as $P(t) \geq P(0)e^{-(\alpha+\mu)t}$. Recall that an exponential function is always non–negative irrespective of the sign of the exponent i.e., the exponential function $e^{-(\alpha+\mu)t}$ is a non-negative quantity. Hence, it can be concluded that $P(t) \geq 0$.

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

Positivity of $A(t)$: The model equation (4) given by $dA/dt = \rho I - (\omega + \mu)A$ can be expressed without loss of generality, after eliminating the positive terms ρI which is appearing on the right hand side, as an inequality as $dA/dt \geq -(\omega + \mu)A$. Using variables separable method and on applying integration, the solution of the foregoing differential inequality can be obtained as $A(t) \geq A(0)e^{-(\omega+\mu)t}$. 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 $A(t) \geq 0$.

Positivity of $J(t)$: The model equation (5) given by $dJ/dt = \theta I - (\kappa + \mu)J$ can be expressed without loss of generality, after eliminating the positive term θI which is appearing on the right hand side, as an inequality as $dJ/dt \geq -(\kappa + \mu)J$. Using variables separable method and on applying integration, the solution of the foregoing differential inequality can be obtained a $J(t) \geq J(0)e^{-(\kappa+\mu)t}$. 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 $J(t) \geq 0$.

Positivity of $T(t)$: The model equation (6) given by $dT/dt = \omega A + \kappa J - (\phi + \mu)T$ can be expressed without loss of generality, after eliminating the positive terms ωA and κJ which is appearing on the right hand side, as an inequality as $dT/dt \geq -(\phi + \mu)T$. Using variables separable method and on applying integration, the solution of the foregoing differential inequality can be obtained as $T(t) \geq J(0)e^{-(\phi+\mu)t}$. 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 (7) given by $dR/dt = \phi T - (\gamma + \mu)R$ can be expressed without loss of generality, after eliminating the positive terms ϕT which is appearing on the right hand side, as an inequality as $dR/dt \geq -(\gamma + \mu)R$. Using variables separable method and on applying integration, the solution of the foregoing differential inequality can be obtained as $R(t) \geq R(0)e^{-(\gamma+\mu)t}$. 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 $R(t) \geq 0$.

Positivity of $V(t)$: The model equation (7) given by $dV/dt = \gamma R - (\delta + \mu)V$ can be expressed without loss of generality, after eliminating the positive termγR 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 differential 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 $S,\ P,\ I,\ A,\ J,\ T,\ R$ and V representing population sizes of

various types of human population are positive quantities and will remain in $\mathbb{R}_+^8$ for all t.

Lemma 3.3 (Boundedness) The non-negative solutions of the system of model equations (1)-(8) are bounded. That is the model variables S, P, I, A, J, T, R and V are all bounded for all t.

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 $N(t) = S(t) + P(t) + I(t) + A(t) + J(t) + T(t) + R(t) + V(t)$ is bounded for all t. It can be began by showing that all feasible solutions are uniformly bounded in a proper subset D of $\mathbb{R}_+^8$where the feasible region R is given by $R = \{(S, P, I, A, J, T, R, V) \in \mathbb{R}_+^8 ; N \leq \tau/\mu\}$.

Now, summation of all the five equations (1)-(8) of the model gives $dN(t)/dt = \tau - \mu N(t)$. Again, considering total population N and sub-population V further we can write the equation as inequality of the form $dN/dt \leq \tau - \mu N(t)$. Equivalently this inequality can be expressed as a linear ordinary differential inequality as $dN/dt + \mu N \leq \tau$ giving general solution upon solving as $N(t) \leq \tau/\mu + ce^{-\mu t}$. But, the term $N(0)$ denotes the initial values of the respective variable $N(t) = N(0)$ at $t = 0$. Thus, the particular solution can be expressed as $N(t) \leq \tau/\mu + [N(0) - (\tau/\mu)]e^{-\mu t}$. 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 $N(0)$ at the initial time $t = 0$ and ends up with a bounded value τ/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, τ/μ is an upper bound of $N(t)$. Hence, feasible solution of the system of model equations (1)-(8) 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)-(8) in that domain.

Therefore, it can be summarized the result of Lemma 3.3 as "the model variables S, P, I, 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)-(8) 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 $P = I = A = J = T = R = V = 0$ and also setting the right hand sides of the model equations (1)-(8) 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)-(8) is given by

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

3.2.2 Endemic equilibrium point

The endemic equilibrium point $E_1 = \{S^1, P^1, I^1, A^1, J^1, T^1, R^1, V^1\}$ 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)-(8) to zero. That is, setting $dS/dt = dA/dt = dI/dt = dJ/dt = dT/dt = dV/dt = 0$ the model equations take the form as

$$\tau - \beta SP - \mu S = 0 \quad (9)$$
$$\beta SP - aP = 0 \quad (10)$$
$$\alpha P - bI = 0 \quad (11)$$
$$\rho I - cA = 0 \quad (12)$$
$$\theta I - dJ = 0 \quad (13)$$
$$\omega A + \kappa J - eT = 0 \quad (14)$$
$$\phi T - fR = 0 \quad (15)$$
$$\gamma R - gV = 0 \quad (16)$$

Here in (9)-(16), the quantities a, b, c represent the parametric expressions as $a = \alpha + \mu, b = \rho + \theta + \mu, c = \omega + \mu, d = \kappa + \mu, e = \phi + \mu, f = \gamma + \mu, g = \delta + \mu$. Clearly, solutions of (9) – (16) 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

$$S^1 \equiv S = (a/\beta) = (\tau/\mu R_0) \quad (17)$$

(ii) Now the solution for P can be obtained by substituting (17) into equation (9) and rewriting the resulting equation as $\tau - \beta(\tau/\mu R_0)P - \mu(\tau/\mu R_0) = 0$ giving

$$P^1 \equiv P = (\mu/\beta)(R_0 - 1) \quad (18)$$

(iii) Substituting P^1 value from (18) into (11) and solving for I we get the following

$$I^1 \equiv I = (\alpha\mu/b\beta)(R_0 - 1) \quad (19)$$

(iv) Substituting I^1 value from (19) into (12) and solving for A we get the following

$$A^1 \equiv A = (\rho\alpha\mu/cb\beta)(R_0 - 1) \quad (20)$$

(v) Substituting I^1 value from (19) into (13) and solving for J we get the following

$$J^1 \equiv J = (\theta\alpha\mu/db\beta)(R_0 - 1) \quad (21)$$

(vi) Substituting A^1 value from (20) and J^1 value from (21) into (14) and solving for T we get the following

$$T^1 \equiv T = \left(\alpha\omega\rho\mu/ecb\beta + (\kappa\theta\alpha\mu/db\beta)\right)(R_0 - 1) \quad (22)$$

(vii) Substituting T^1 value from (22) into (15) and solving for R we get the following

$$R^1 \equiv R = (\phi/f)\left(\alpha\omega\rho\mu/ecb\beta + (\kappa\theta\alpha\mu/db\beta)\right)(R_0 - 1) \quad (23)$$

(viii) Substituting R^1 value from (23) into (16) and solving for V we get the following

$$V^1 \equiv V = (\gamma\,\phi/gf)\left(\alpha\omega\rho\mu/ecb\beta + (\kappa\theta\alpha\mu/db\beta)\right)(R_0 - 1) \quad (24)$$

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 [6, 11]. 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 [11]. The formulation of this matrix involves classification of all compartments of the model in to two classes: infected and non-infected.

Assume that there are n compartments in the model and of which the first m compartments are with infected individuals. From the system (1)-(8) the seven equations of infected individuals are considered and decomposed into two groups: F contains newly infected cases and v contains the remaining terms. Let $X = [P, I, A, J, T, R, V]^t$ be a column vector and the differential equations of the last seven compartments are rewritten as $F(X) - T(X)$.

Now, let $F(X) = [F_1, F_2, F_3, F_4, F_5, F_6, F_7]^t$. Here (i) $F_1 = \beta SP$ denotes newly infected cases which arrived into primary infected compartment (ii) $F_2 = 0$ denotes newly infected cases arrived into the infectious with known status compartment (iii) $F_3 = 0$ denotes newly infected cases arrived into the infectious asymptomatic compartment, (iii) $F_4 = 0$ denotes newly infected cases arrived into the infectious symptomatic compartment, (iv) $F_5 = 0$ denotes newly infected case from susceptible compartment into treatment compartment, (v) $F_6 = 0$ denotes newly infected case from susceptible compartment into drug resistant compartment (vi) $F_7 = 0$ denotes newly infected case from susceptible compartment into AIDS compartment. Further, let $T(X) = [T_1, T_2, T_3, T_4, T_5, T_6, T_7]^t$. Here $T_1 = aP$, $T_2 = -\alpha P + bI$, $T_3 = -\rho I + cA$, $T_4 = -\theta I + dJ$, $T_5 = -\omega A - \kappa J + eT$, $T_6 = -\phi T + fR$, and $T_7 = -\gamma R + gV$. Here, the values of a, b, c, d, e, f and g 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

$$F \equiv \begin{bmatrix} \beta\tau/\mu & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix}, T \equiv \begin{bmatrix} a & 0 & 0 & 0 & 0 & 0 & 0 \\ -\alpha & b & 0 & 0 & 0 & 0 & 0 \\ 0 & -\rho & c & 0 & 0 & 0 & 0 \\ 0 & -\theta & 0 & d & 0 & 0 & 0 \\ 0 & 0 & -\omega & -\kappa & e & 0 & 0 \\ 0 & 0 & 0 & 0 & -\phi & f & 0 \\ 0 & 0 & 0 & 0 & 0 & -\gamma & g \end{bmatrix} \quad (25)$$

It can be verified that the matrix T is non-singular as its determinant is non-zero and after

some algebraic computations the next generation matrix is constructed as

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

$$= \begin{bmatrix} \beta\tau/\mu & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix} \begin{bmatrix} a & 0 & 0 & 0 & 0 & 0 & 0 \\ -\alpha & b & 0 & 0 & 0 & 0 & 0 \\ 0 & -\rho & c & 0 & 0 & 0 & 0 \\ 0 & -\theta & 0 & d & 0 & 0 & 0 \\ 0 & 0 & -\omega & -\kappa & e & 0 & 0 \\ 0 & 0 & 0 & 0 & -\phi & f & 0 \\ 0 & 0 & 0 & 0 & 0 & -\gamma & g \end{bmatrix}^{-1}$$

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

Now, it is possible to calculate the eigenvalues of 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

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

It reduces to the equation as $\lambda^6[(\beta\tau/\mu\, a) - \lambda] = 0$ giving the seven eigenvalues as

$$\lambda_1 = (\beta\tau/a\mu),\ \ \lambda_2 = 0,\ \ \lambda_3 = 0,\ \ \lambda_4 = 0,\ \ \lambda_5 = 0,\ \ \lambda_6 = 0,\ \ \lambda_7 = 0.$$

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 DFE E_0 is used. Also, to determine the global stability at E_0 the steps given in [2, 4] are used. It is already shown that the DFE of model (1)-(8) is given by$E_0 = \{\tau/\mu\,, 0,0,0,0,0,0,0\}$. Now, 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 3.2 The DFE E_0 of the system (1)-(8) is locally asymptotically stable if $R_0 < 1$ and unstable if $R_0 > 1$.

Proof Consider the right hand side expressions of the equations (1)-(8) as functions so as to find the Jacobian matrix from the functions. Now let,

$$g_1(S,P,I,A,J,T,R,V) = \tau - \beta SP - \mu S$$
$$g_2(S,P,I,A,J,T,R,V) = \beta SP - aP$$
$$g_3(S,P,I,A,J,T,R,V) = \alpha P - bI$$
$$g_4(S,P,I,A,J,T,R,V) = \rho I - cA$$
$$g_5(S,P,I,A,J,T,R,V) = \theta I - dJ$$
$$g_6(S,P,I,A,J,T,R,V) = \omega A + \kappa J - eT$$
$$g_7(S,P,I,A,J,T,R,V) = \phi T - fR$$
$$g_8(S,P,I,A,J,T,R,V) = \gamma R - gV$$

Let $J(S,P,I,A,J,T,R,V)$ be a Jacobian matrix of g_1, g_2, g_3, g_4, g_5, g_6, g_7, g_8 with respect to S, P, I, J, T, R, V. Thus,

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

Now, the Jacobian matrix of g_1, g_2, g_3, g_4, g_5, g_6, g_7, g_8 with respect to S, P, I, J, T, R, V at the disease free equilibrium E_0 is given by

$$J(E_0) = \begin{bmatrix} -\mu & -aR_0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & a(R_0 - 1) & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \alpha & -b & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \rho & -c & 0 & 0 & 0 & 0 \\ 0 & 0 & \theta & 0 & -d & 0 & 0 & 0 \\ 0 & 0 & 0 & \omega & \kappa & -e & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & \phi & -f & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \gamma & -g \end{bmatrix}$$

Now, to determine the signs of eigenvalues we use the concept of trace and determinant of a given matrix. Now,

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

Since trace is negative and determinant is positive for $R_0 < 1$. We can conclude that all eigenvalues of a matrix $J(E_0)$ are negative provided the mentioned condition is 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, 7, 6].

3.4.2 Global stability of disease free equilibrium point

Let $x \in R^n$ is disease compartment and $y \in R^m$ be disease free compartment the disease transmission model (1)-(8) can be written in the form:

$$\dot{x} = -(T - F)x - h(x,y) \quad (26)$$
$$\dot{y} = g(x,y) \quad (27)$$

Here in (24), the notations F and T are given in (25).

Theorem 3.3 If $T-F$ is a non-singular M-matrix and $h \geq 0$ then the disease-free equilibrium point of model equations (1)-(8) is globally asymptotically stable.

Proof Using the procedure given in [1, 10] the rate of change of the variables in the model equations (1)-(8) 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 non-singular M-matrix. From the previous computations (25) we have

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

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

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

$$B = \begin{bmatrix} \beta\tau/\mu & 0 & 0 & 0 & 0 & 0 & 0 \\ \alpha & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \rho & 0 & 0 & 0 & 0 & 0 \\ 0 & \theta & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \omega & \kappa & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \phi & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & \gamma & 0 \end{bmatrix}$$

Now, $\det(T-F) = -bcdefg(\beta\tau - a\mu)/\mu$ and $\rho(B) = \beta\tau/\mu$ and $T-F$ is non-singular 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 $s \geq \rho(B)$.

Additionally, one can easily show that $S \leq S_0$. Therefore, from the above hypothesis disease-free equilibrium point of model equations (1)-(8) 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 $E_1 = \{S^1, P^1, I^1, A^1, J^1, T^1, R^1, V^1\}$ 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 $E_1 =$

$\{S^1, P^1, I^1, A^1, J^1, T^1, R^1, V^1\}$ of the given model (1)-(8) 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 3.4.

Theorem 3.4 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 ofE_0. Thus, the procedure starts with the construction of Jacobian matrix at E_1. Now, the Jacobian matrix of the model given at endemic equilibrium point E_1 takes the form as

$$J(S^1, P^1, I^1, A^1, J^1, T^1, R^1, V^1)$$

$$= \begin{bmatrix} -\mu R_0 & -\tau\beta/\mu R_0 & 0 & 0 & 0 & 0 & 0 & 0 \\ \mu(R_0 - 1) & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \alpha & -b & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \rho & -c & 0 & 0 & 0 & 0 \\ 0 & 0 & \theta & 0 & -d & 0 & 0 & 0 \\ 0 & 0 & 0 & \omega & \kappa & -e & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & \phi & -f & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \gamma & -g \end{bmatrix}$$

Now the trace of $J(E_1)$ is a negative quantity while determinant of $J(E_1)$ computed as $-\beta\theta bcdR_0(eg\phi - ef\gamma)(R_0 - 1)$ and is a positive quantity provided that either of the following conditions are satisfied,

(i) $eg\phi < ef\gamma$ and $R_0 > 1$.
(ii) $eg\phi > ef\gamma$ 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.

4. Result and discussion

In this study, a model describing the dynamics of eight compartments human population pertaining to HIV (Human Immunodeficiency Virus) with treatments are formulated and analyzed. ART only users and Herbs only users joins treatment compartment to use both alternatives for better medifications. 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. 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.

5. Conclusion

In this study, a mathematical model of eight compartments has been formulated to show the dynamics of human populations subjected to HIV/AIDS. Moreover, the formulated model is verified as biologically meaningful and mathematically well posed. The reproduction number is directly proportional to recruitment and probability of transmission rates. From computation of reproduction number, we observed that natural

death rate is indirectly proportional to the propagation of the disease. It is also observed that the equilibrium points of model equations are locally asymptotically stable. Further, the Global stability of disease free equilibrium points are described.

References

[1] L. J. S. Allen, An Introduction to mathematical biology, Prentice Hall, USA, (2007).

[2] F. Brauer and C. Castillo-Chavez, Mathematical Models in Population Biology and Epidemiology, Springer-Verlag, New York, (2001).

[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, doi:10.9790/5728-1506033451.

[4] K. R. Cheneke, G. K. Edessa and P. R. Koya, Impact of Treatment and Isolation on the Dynamics of HIV Transmission, IOSR Journal of Mathematics (IOSR-JM), **15 (6)** (2019) 73-72, doi:10.9790/5728-1506055372.

[5] N. R. Derrick and S. L. Grossman, Differential Equation with Application, Addison Wesley Publishing Company, Inc., Philippines, (1976).

[6] O. Diekmann, J. A. P. Heesterbeek and M. G. Roberts, The construction of next-generation matrices for compartmental epidemic models, Journal of The Royal Society Interface, **7 (47)** (2010) 873-885.

[7] Fatmawati, Windarto and L. Hanif, Application of optimal control strategies to HIV-malaria co-infection dynamics, Journal of Physics: Conference Series, **974** (2018) 012057, doi:10.1088/1742-6596/974/1/012057.

[8] A. Y. A. Mukhtar, P. J. Witbooi and G. Hughes, Mathematical modeling of population dynamics of HIV with antiretroviral treatment and herbal medicine, MSc diss., University of the Western Cape, (2014).

[9] S. Noeiaghdam and E. Khoshrouye Ghiasi, An efficient method to solve the mathematical model of HIV infection for CD8T-cells, International Journal of Mathematical Modelling & Computations, **9 (4)** (2019) 267-281.

[10] K. Regassa and P. R. Koya, Modeling and Analysis of Population Dynamics of Human Cells Pertaining to HIV/AIDS with treatment, American Journal of Applied Mathematics, **7 (4)** (2019) 127-136, doi:10.11648/j.ajam.20190704.14.

[11] P. Van den Driessche and J. Watmough, Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission, Mathematical Biosciences, **180** (2002) 29-48.