Asymptotic Stability Analysis of a Mathematical Model for HIV/AIDS dynamics in the presence of Incomplete Treatment and Public Enlightenment Campaign

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Introduction

- HIV/AIDS.
- Mathematical modelling
- Basic Reproduction number
- Incomplete treatment
- Public enlightenment campaign.

The schematic diagram describing the flow dynamics of the system (1) is depicted in Figure 1, while the description of variables and parameters of the model are presented in Table 1 and Table 2, respectively.

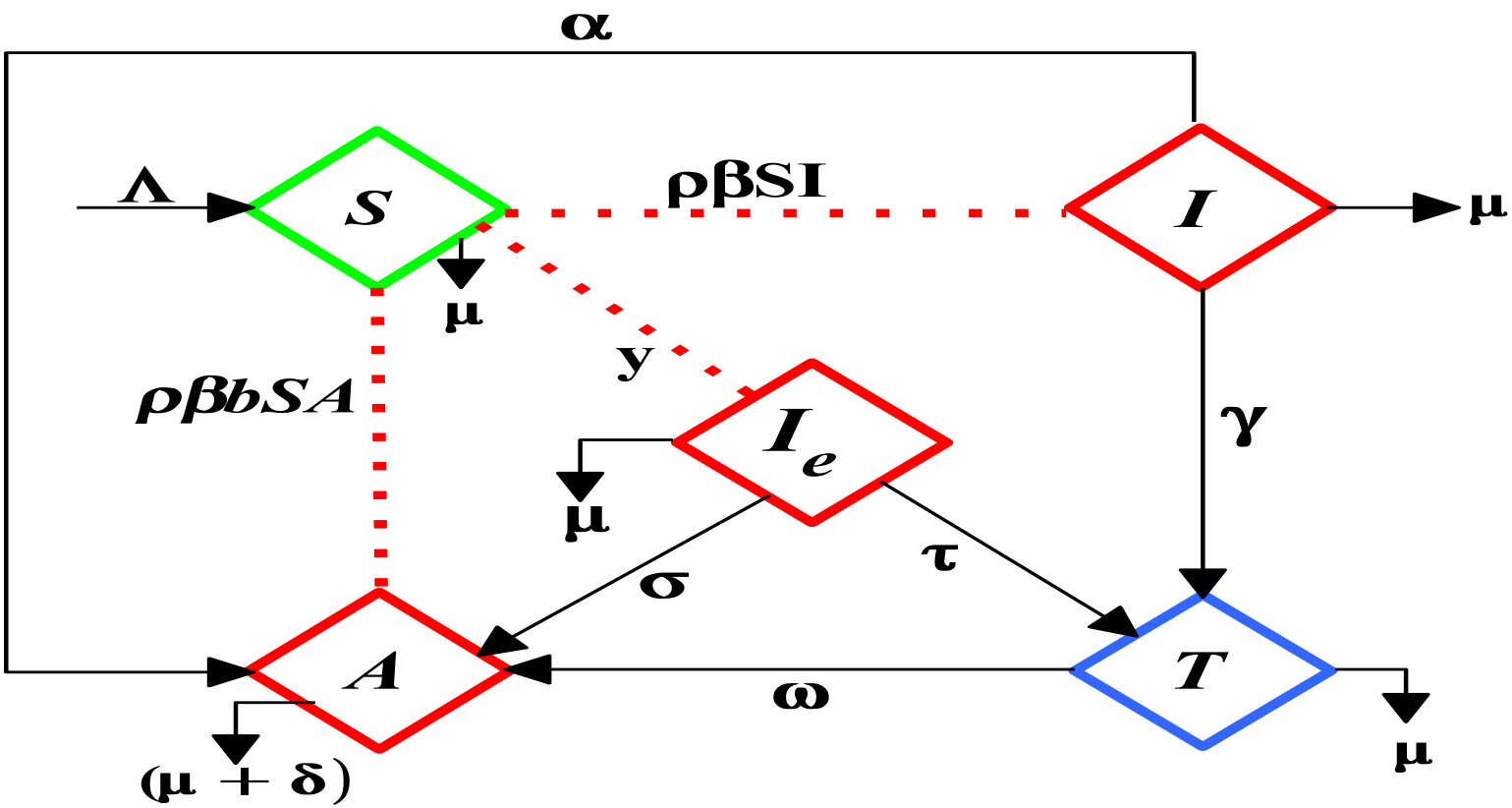

Figure: 1. Schematic diagram for the HIV/AIDS dynamics with incomplete treatment and public enlightenment campaign, where $y = (1 - \rho)\beta S(I + bA)$.

The mathematical model governing the transmission dynamics of HIV/AIDS with incomplete treatment and public enlightenment campaign is given by

$$\begin{aligned}
\frac{dS}{dt} &= \Lambda - \beta SI - \beta bSA - \mu S \\
\frac{dI}{dt} &= \rho\beta S(I + bA) - (\alpha + \gamma + \mu)I \\
\frac{dI_e}{dt} &= (1-\rho)\beta S(I + bA) - (\tau + \sigma + \mu)I_e \qquad (1) \\
\frac{dT}{dt} &= \gamma I + \tau I_e - (\omega + \mu)T \\
\frac{dA}{dt} &= \alpha I + \sigma I_e + \omega T - (\delta + \mu)A.
\end{aligned}$$

Table: 1. The description of variables of the HIV/AIDS model (1).

Variable	Description
$S(t)$	Susceptible population
$I(t)$	HIV-infected class
$I_e(t)$	Enlightened infectious individual
$T(t)$	Population under treatment
$A(t)$	Full blown AIDS class

Table: 2. The description of parameters of the HIV/AIDS model (1).

Parameter	Description
Λ	Birth rate
ρ	Fast progressor rate
$(1-\rho)$	Slow progressor rate
β	Transmission probability of infection
b	Modification parameter responsible for the degree of infectiousness
μ	Natural death rate
τ	HAART treatment rate for enlightened infectious human
γ	HAART Treatment rate for infectious human
α	Progression rate of individuals with HIV to full blown AIDS
ω	Incomplete treatment rate
σ	Progression of enlightened individuals with HIV to full blown AIDS
δ	AIDS-induced death rate

Invariant region

Lemma (1)

The biologically feasible region of the HIV/AIDS model (1), given by

$$\mathfrak{D} = \left\{ (S(t), I(t), I_e(t), T(t), A(t)) \in \mathbb{R}^5_+ : S + I + I_e + T + A \leq \frac{\Lambda}{\mu} \right\},$$

is positively-invariant and attracting.

Proof.

It is apparent from the total population $N(t)$, that the rate of change of the total population yields

$$\frac{dN}{dt} = \Lambda - \mu N - \delta A,$$

such that

$$\frac{dN}{dt} \leq \Lambda - \mu N.$$

Then by standard technique, it follows that

$$N(t) \leq N(0)e^{-\mu t} + \frac{\Lambda}{\mu}(1 - e^{-\mu t}).$$

Accordingly, the feasible region $\mathfrak{D}$ is positively-invariant since $N(t) \leq \Lambda/\mu$ whenever $N(0) \leq \Lambda/\mu$. In addition, it is either the solution enters $\mathfrak{D}$ in finite time, if $N(0) > \Lambda/\mu$, or the total population, $N(t)$, approaches the limit Λ/μ asymptotically as $t \to \infty$. Therefore, the region, $\mathfrak{D}$, attracts all solutions in $\mathbb{R}^5_+$. The implication of this from the epidemiological viewpoint is that all solutions initiated in $\mathbb{R}^5_+$ eventually enter $\mathfrak{D}$.

Positivity and boundedness of solution

Theorem

The solutions $S(t), I(t), I_e(t), T(t)$ *and* $A(t)$, *of the HIV/AIDS model* (1) *with non-negative initial conditions in* $\mathfrak{D}$, *remain non-negative in* $\mathfrak{D}$ *for all time,* $t > 0$.

Proof.

From the first compartment of the model (1), it is apparent that the following differential inequality holds

$$\frac{dS(t)}{dt} \geq -\left(\beta I(t) + \beta b A(t) + \mu\right) S(t),$$

which after integrating gives rise to,

$$S(t) \geq S(0) \exp\left[-\left(\int_0^t \left(\beta I(\varphi) + \beta b A(\varphi)\right) d\varphi + \mu t\right)\right] > 0, \quad \text{for all} \quad t > 0.$$

Without re-inventing the wheel, it can be shown, in a similar spirit that the remaining state variables of the HIV model (1) are positive $\forall\ t > 0$. That is, $I(t) > 0$, $I_e(t)$, $T(t) > 0$ and $A(t) > 0$. This ends the proof. □

Based on the above results, it is sufficient to consider the transmission dynamics of HIV/AIDS represented by a system of ordinary differential equations (1) in the biologically feasible region $\mathfrak{D}$, where the model is considered to be mathematically and epidemiologically meaningful.

Equilibria and Basic Reproduction Number

3.1. Disease-free equilibrium

The disease-free equilibrium point of the HIV/AIDS model (1), designated by ε_0 is obtained as

$$\varepsilon_0 = (S^*, I^*, I_e^*, T^*, A^*) = \left(\frac{\Lambda}{\mu}, 0, 0, 0, 0\right). \tag{2}$$

3.2. Basic reproduction number

The basic reproduction number of the HIV model (1), denoted by $\mathcal{R}_0$, is obtained using the next generation matrix approach (Driessche and Watmough, 2002), which is the spectral radius of (FV^{-1}), where F is the appearance of new infection matrix and V is the non-singular matrix for the transfer of infection in and out of the compartments of the model. Thus, matrices F and V evaluated at ε_0, are given, respectively, by

$$F = \begin{pmatrix} \frac{\rho\beta\Lambda}{\mu} & 0 & 0 & \frac{\rho b\beta\Lambda}{\mu} \\ \frac{(1-\rho)\beta\Lambda}{\mu} & 0 & 0 & \frac{(1-\rho)b\beta\Lambda}{\mu} \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}$$

and

$$V = \begin{pmatrix} k_1 & 0 & 0 & 0 \\ 0 & k_2 & 0 & 0 \\ -\gamma & -\tau & k_3 & 0 \\ -\alpha & -\sigma & -\omega & k_4 \end{pmatrix},$$

where $k_1 = (\alpha + \gamma + \mu)$, $k_2 = (\tau + \sigma + \mu)$, $k_3 = (\omega + \mu)$ and $k_4 = (\delta + \mu)$. Therefore, the basic reproduction number, $\mathcal{R}_0$, is obtained as

$$\mathcal{R}_0 = \frac{\Lambda\beta\{b\rho(\alpha k_3 + \omega\gamma)k_2 + bk_1(1-\rho)(\omega\tau + \sigma k_3) + \rho k_2 k_3 k_4\}}{\mu k_1 k_2 k_3 k_4}. \quad (3)$$

Now, following Theorem 2 of Driessche and Watmough, (2002), the local asymptotic stability of the disease-free equilibrium point (DFE) of the HIV/AIDS model (1) is established. And the result is summarized as follows

Lemma (2)

The DFE, denoted by ε_0, of the HIV/AIDS model (1) is locally asymptotically stable in $\mathfrak{D}$ provided that $\mathcal{R}_0 < 1$ and unstable otherwise.

This implies that HIV/AIDS can be controlled in the population whenever the initial sizes of the active HIV cases are in the basin of attraction of the DFE, such that $\mathcal{R}_0 < 1$.

3.3. Endemic equilibrium point

Here, let the endemic equilibrium point of the HIV/AIDS model (1) be denoted by $\varepsilon^{**} = (S^{**}, I^{**}, I_e^{**}, T^{**}, A^{**})$ and represent the force of infection of the model by $\lambda^{**} = \beta(I^{**} + bA^{**})$. Solving and simplifying system (1) at steady state simultaneously gives rise to the following.

$$\begin{cases} S^{**} = \dfrac{\Lambda}{(\lambda^{**} + \mu)}, \\ I^{**} = \dfrac{\rho\Lambda\lambda^{**}}{k_1(\lambda^{**} + \mu)}, \\ I_e^{**} = \dfrac{(1-\rho)\Lambda\lambda^{**}}{k_2(\lambda^{**} + \mu)}, \end{cases} \tag{4}$$

$$\begin{cases} T^{**} = \dfrac{\{\gamma\rho k_2 + \tau(1-\rho)k_1\}\Lambda\lambda^{**}}{k_1 k_2 k_3(\lambda^{**}+\mu)}, \\ A^{**} = \dfrac{\Lambda\lambda^{**}\{k_3(\alpha\rho k_2 + \sigma k_1(1-\rho)) + \omega(\gamma\rho k_2 + \tau(1-\rho)k_1)\}}{k_2(\lambda^{**}+\mu)}. \end{cases}$$

3.4. Sensitivity Analysis

The normalized forward sensitivity indexes of the basic reproduction number $\mathcal{R}_0$ relative to its associated parameters, p, are calculated using

$$\chi_p^{\mathcal{R}_0} = \frac{\partial \mathcal{R}_0}{\partial p} \times \frac{p}{\mathcal{R}_0}. \tag{5}$$

Table: 3. Sensitivity indices of $\mathcal{R}_0$ relative to its parameter values.

Parameters	Values	Sensitivity indices
Λ	0.10	$+1.0000$
β	0.006	$+1.0000$
b	0.45	$+1.0000$
μ	0.0125	-1.6139
τ	0.2	-0.0593
ρ	0.004	-0.0012
δ	0.01	-0.4444
γ	0.8	-0.0001
ω	0.02	$+0.0471$
α	0.03	$+0.0001$
σ	0.9	$+0.0705$

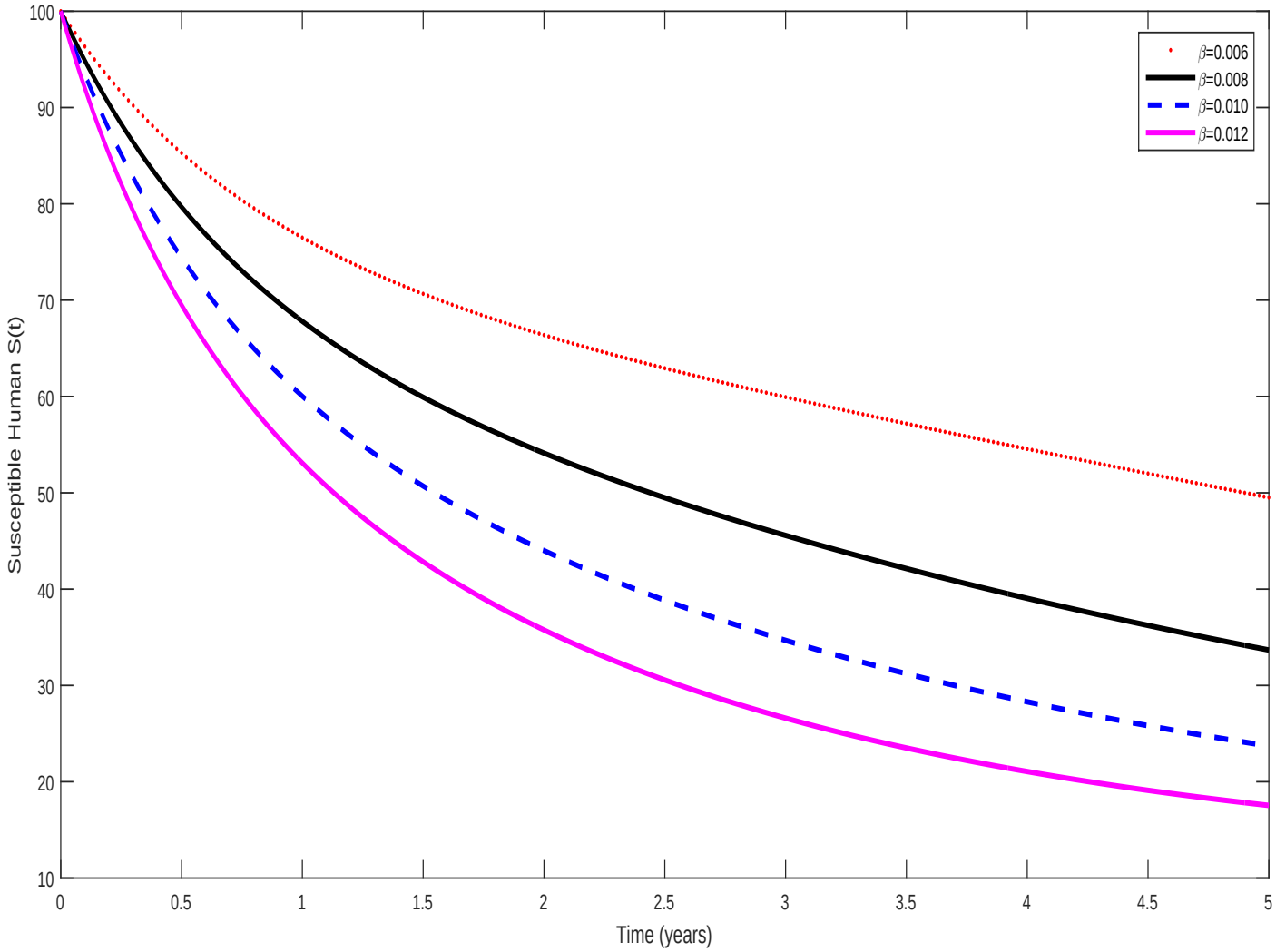

Figure: 2. Effect of transmission rate on the incidence of susceptible class.

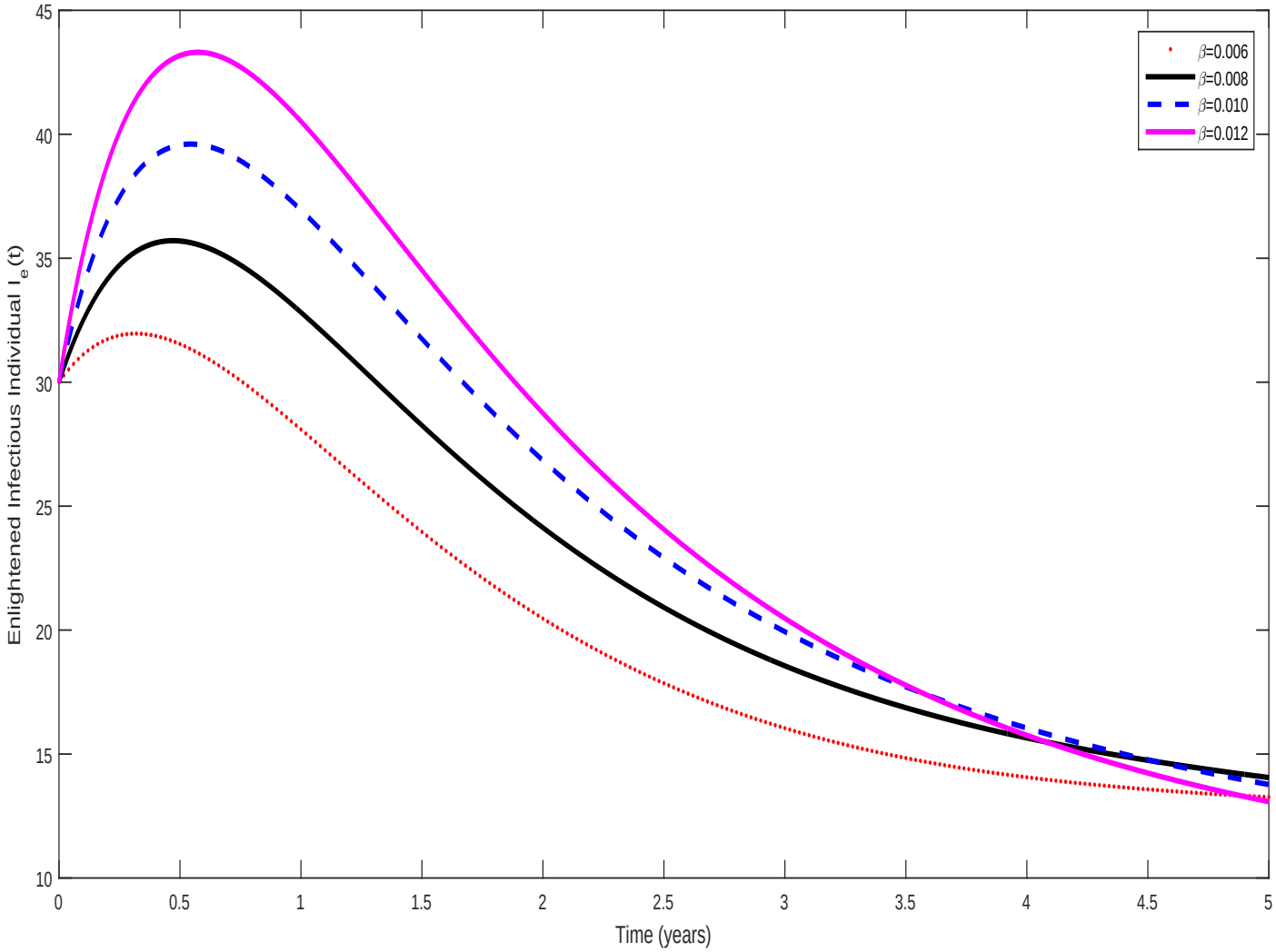

Figure: 3. Effects of transmission rate on the incidence of enlightened infectious class.

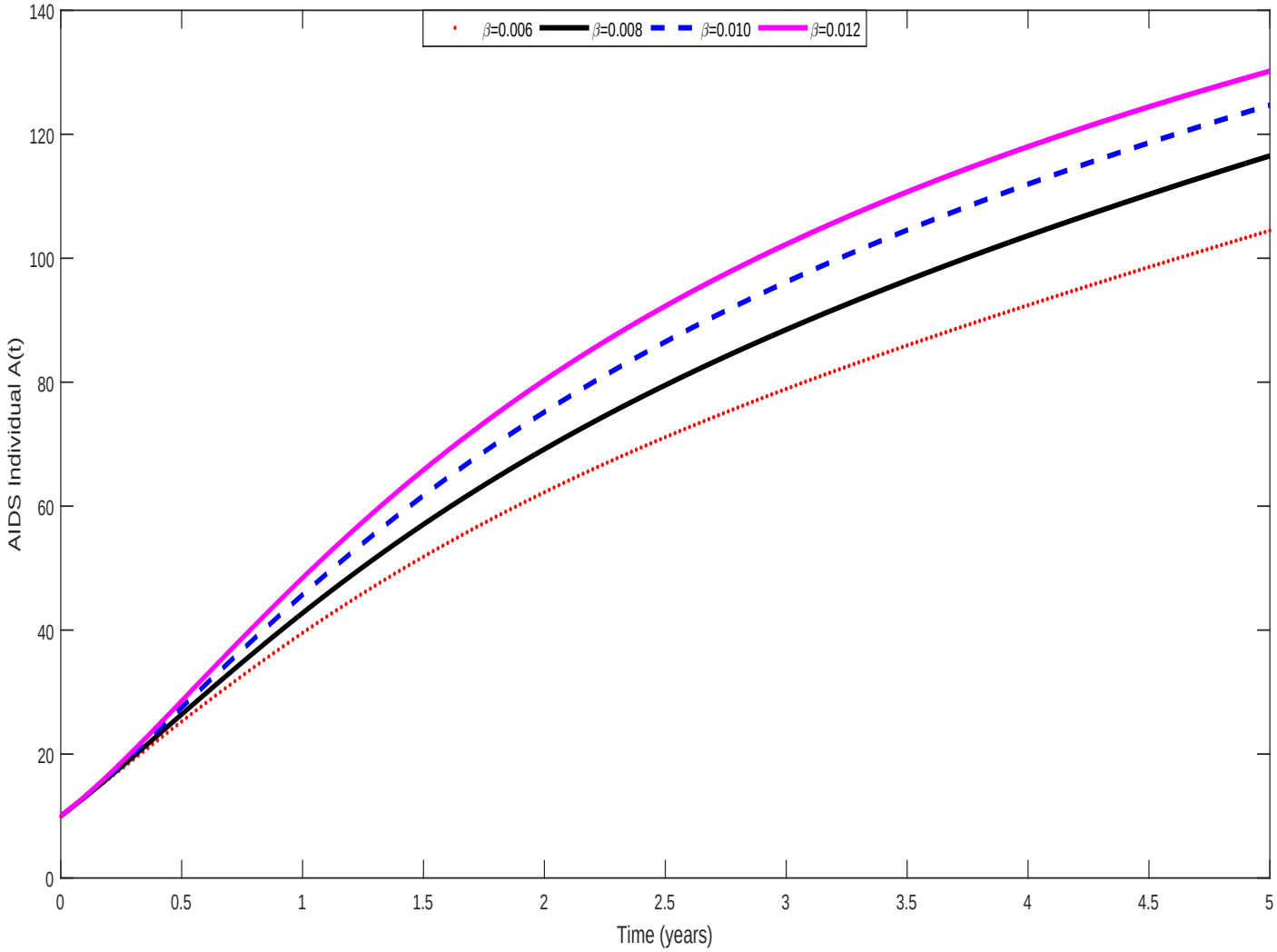

Figure: 4. Effects of transmission rate on the incidence of AIDS class.

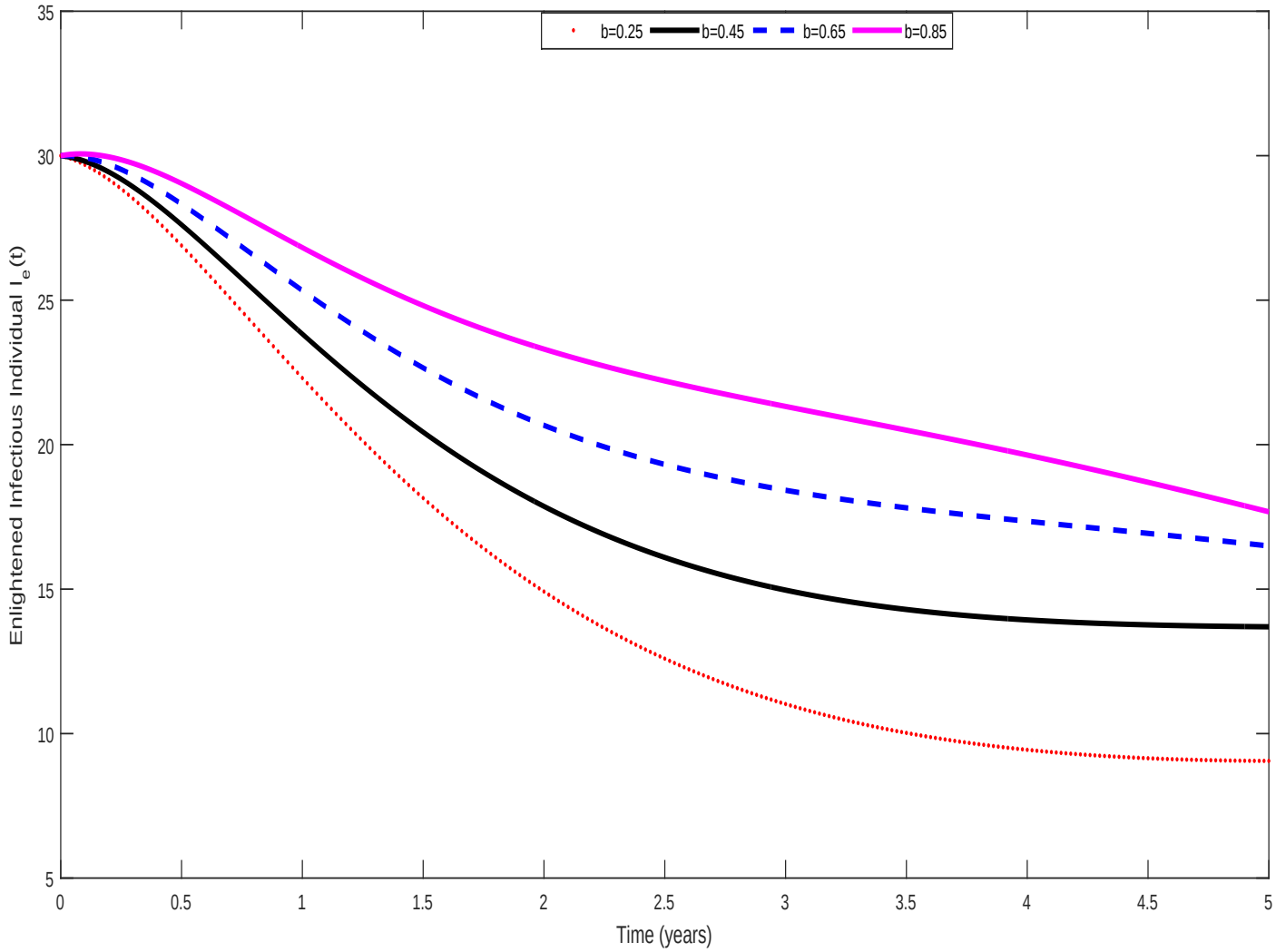

Figure: 5. Effects of modification parameter on the incidence of enlightened infected class.

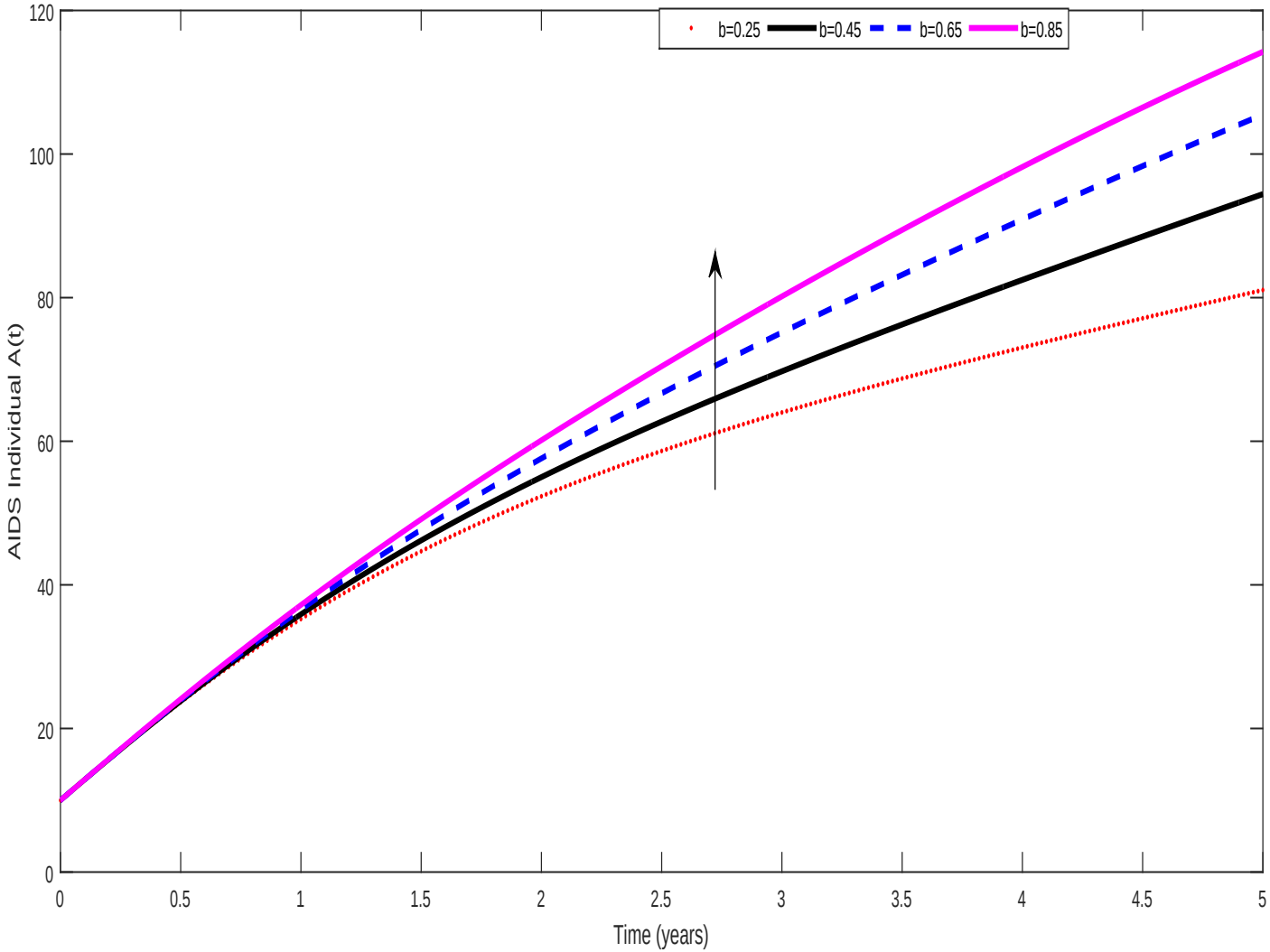

Figure: 6. Effects of modification parameter on the incidence of full blown AIDS class.

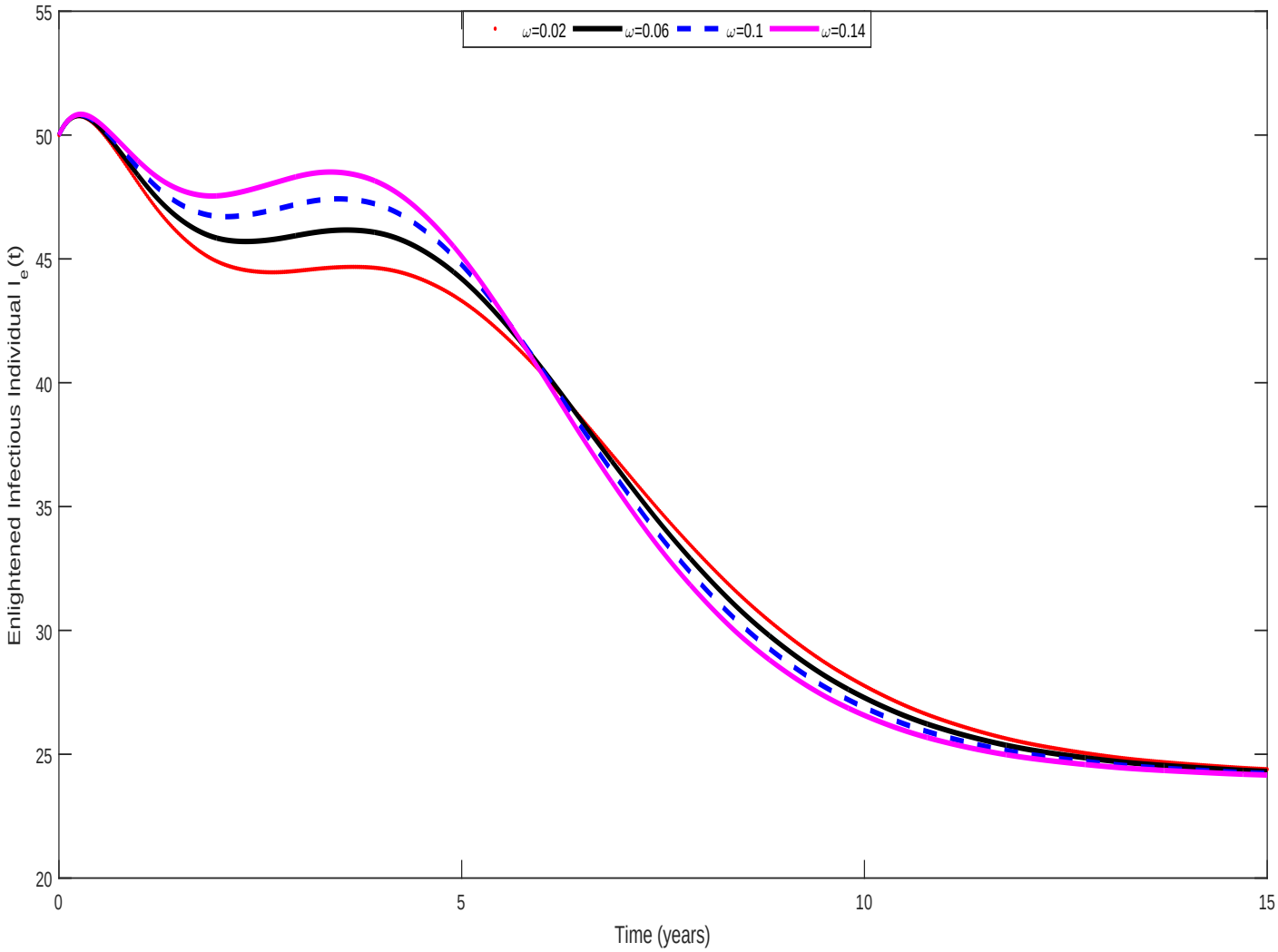

Figure: 7. Effects of incomplete treatment rate on the incidence of enlightened infectious class.

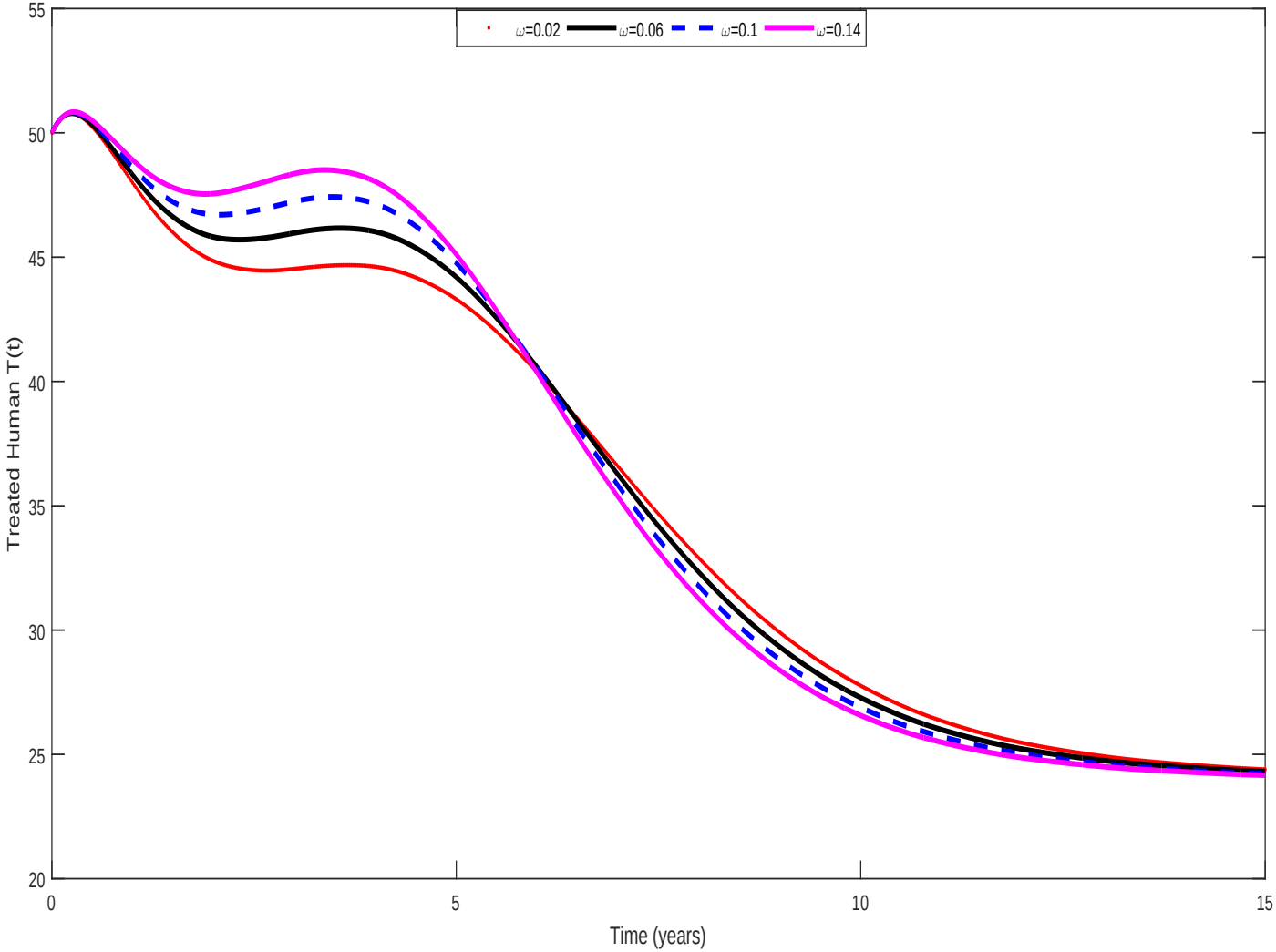

Figure: 8. Effects of incomplete treatment rate on the incidence of treatment class.

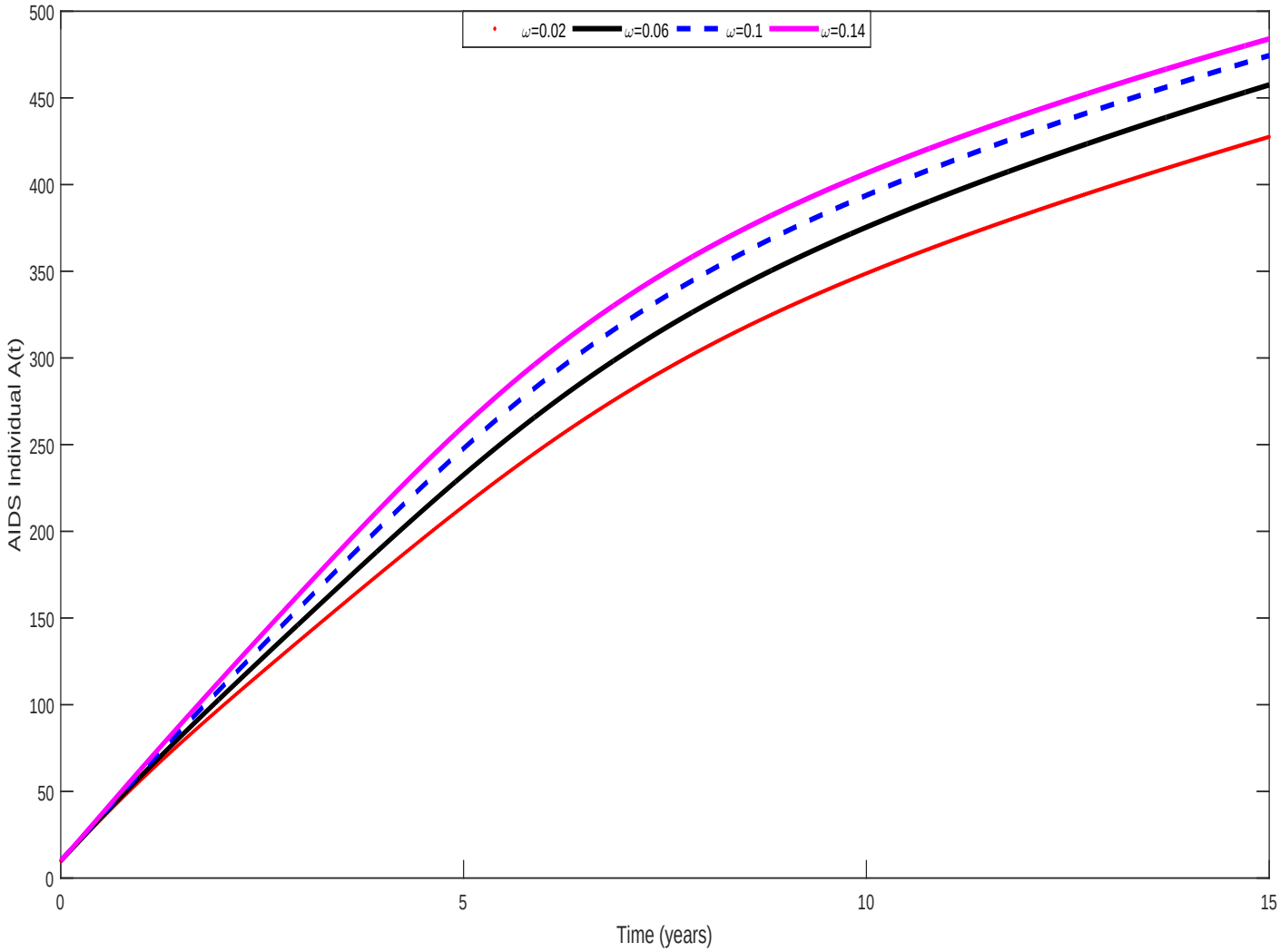

Figure: 9. Effects of incomplete treatment rate on the incidence of full blown AIDS class.

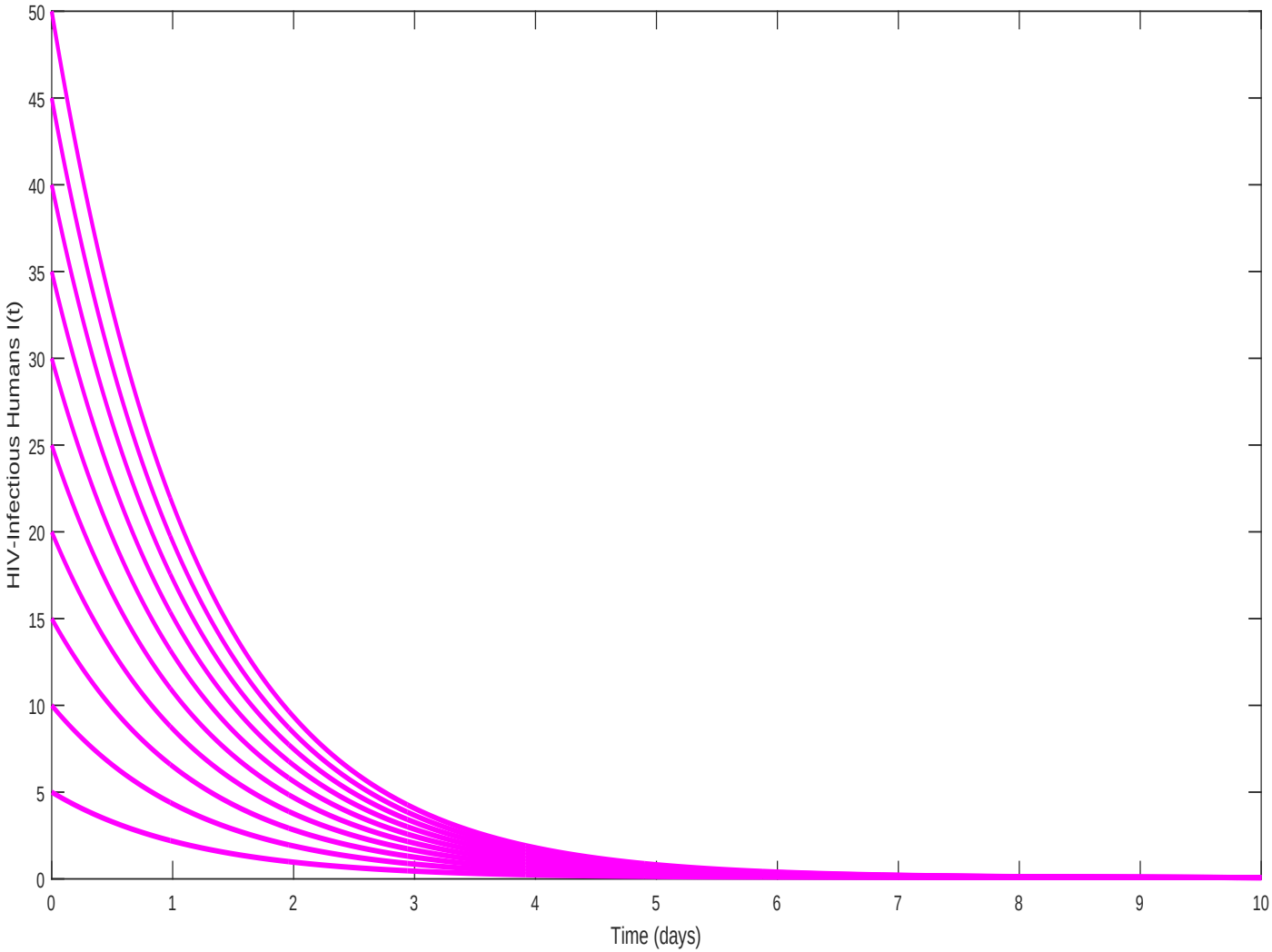

Figure: 10. Convergence of trajectories of HIV-infectious population to a disease-free equilibrium regardless of the values of initial conditions.

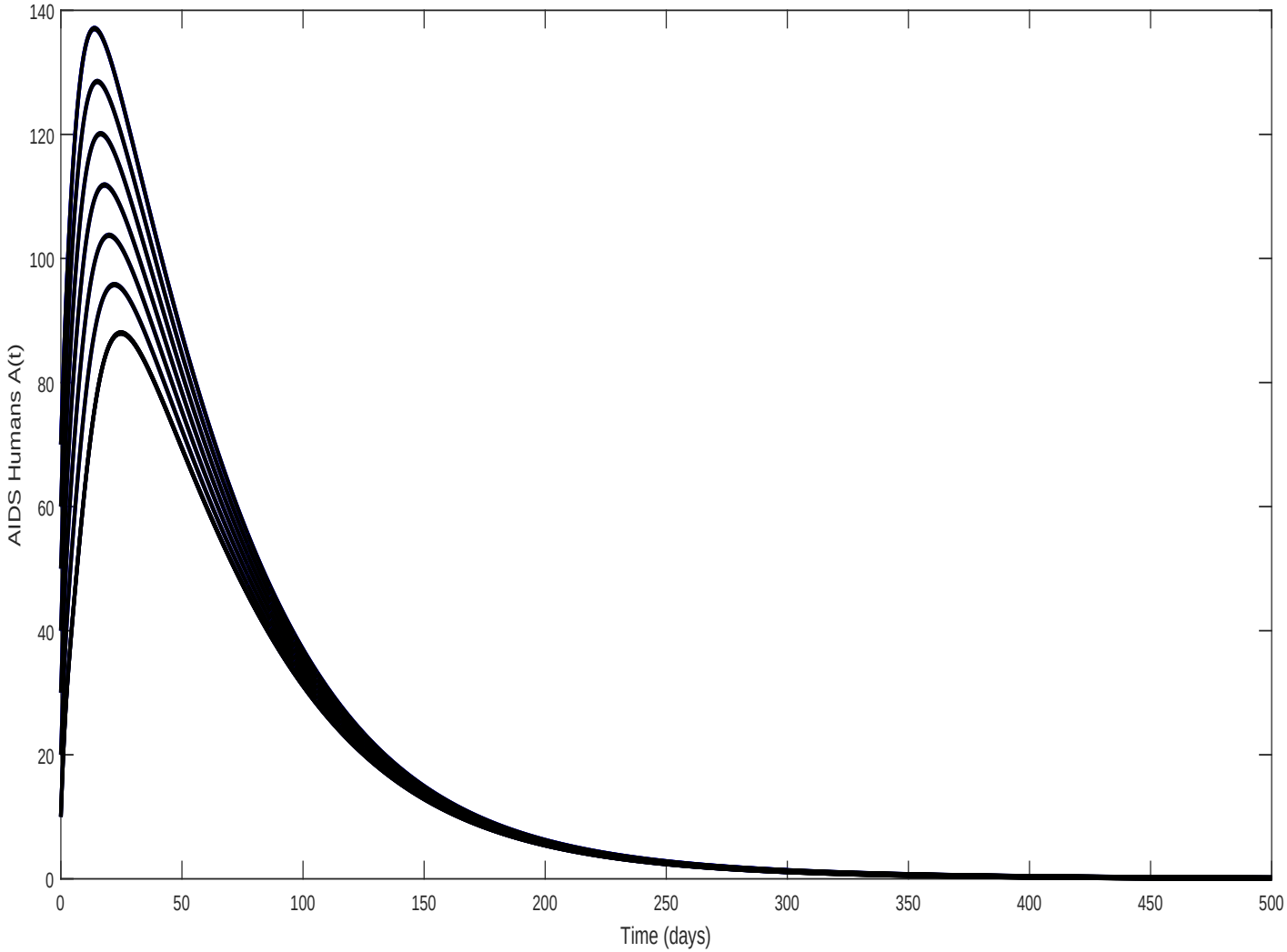

Figure: 11. Convergence of trajectories of full blown AIDS population to a disease-free equilibrium regardless of the values of initial conditions.

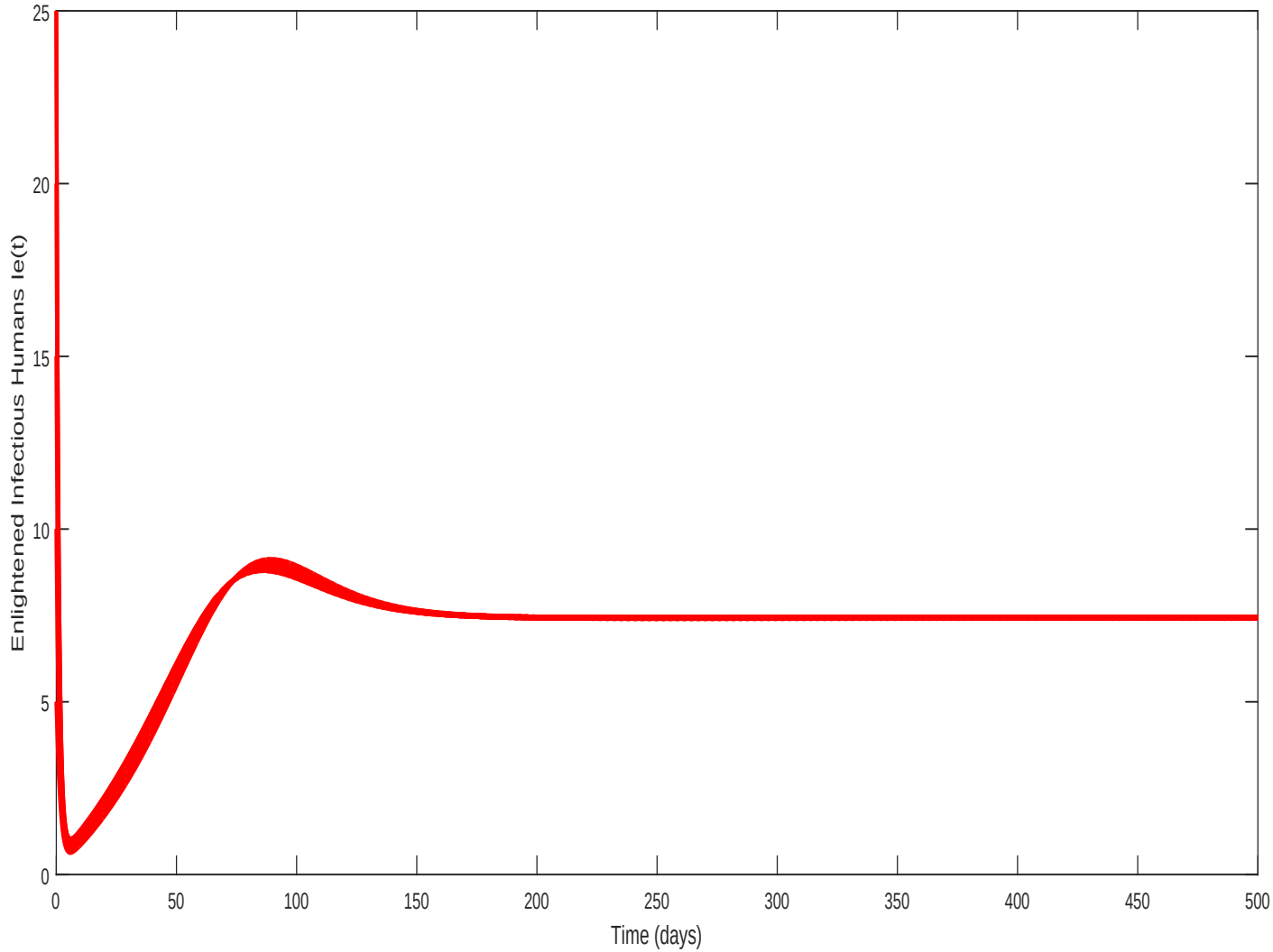

Figure: 12. Convergence of trajectories of enlightened infectious population to a unique endemic equilibrium regardless of the values of initial conditions.

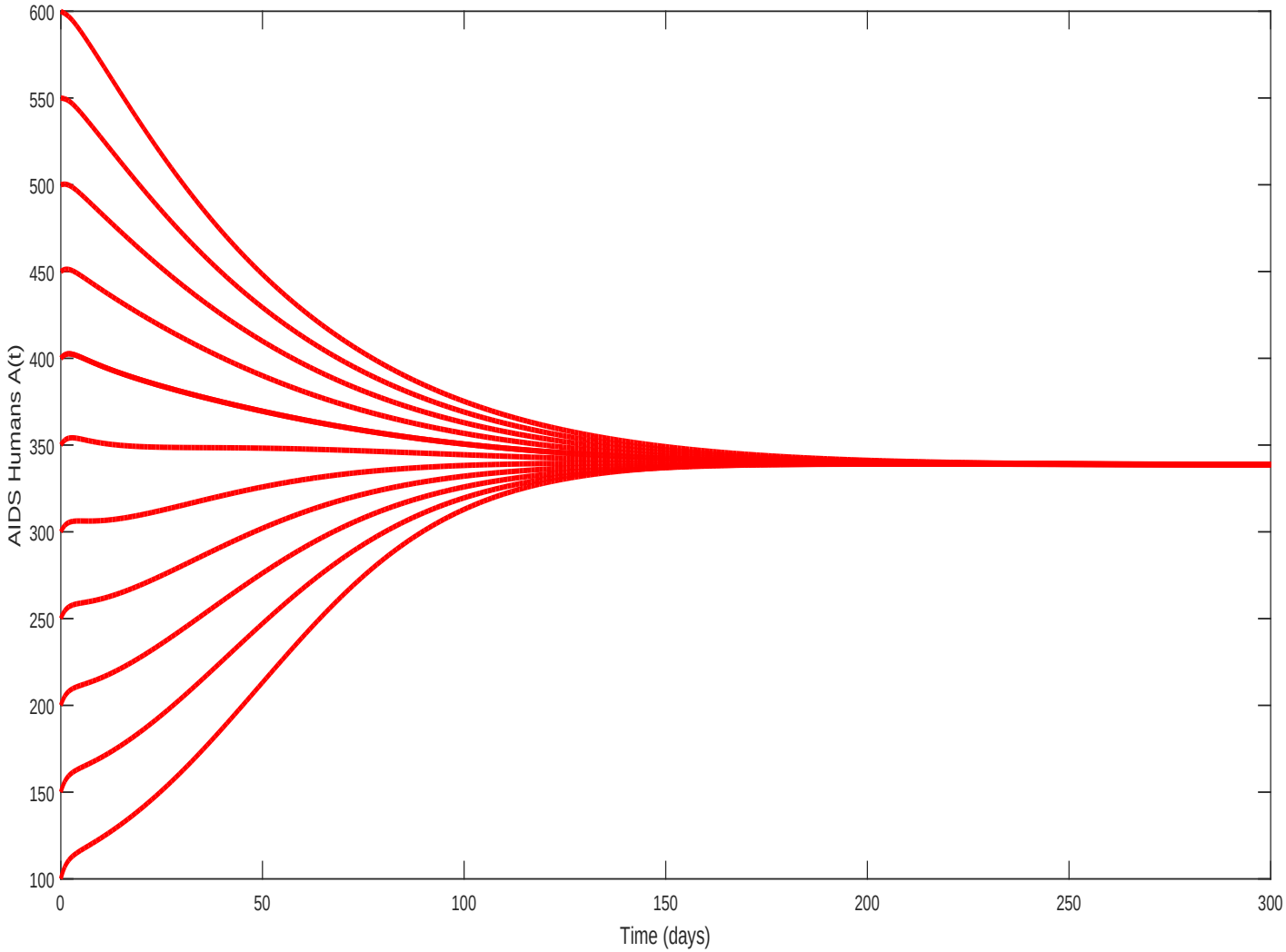

Figure: 13. Convergence of trajectories of full blown AIDS population to a unique endemic equilibrium regardless of the values of initial conditions.

3.8. Conclusion

A five-dimensional system of ordinary differential equations incorporating two distinguishing factors namely, incomplete treatment and public enlightenment campaign was formulated and analysed. Basic properties exhibited by the model was investigated using the theory of positivity and boundedness of solutions.

Consequently, the global dynamics of the model around the disease-free and endemic equilibrium points were explored. And it was shown that the model has a globally-asymptotically stable disease-free equilibrium (endemic equilibrium) whenever the basic reproduction number is less than (greater than) unity accordingly.

Furthermore, the sensitivity analysis of the model was conducted and positive and negative sensitivity indices were obatined for the parameters associated with the basic reproduction number. Parameters with positive indices tends to increase the value of basic reproduction number when increased, while parameters with negative indices reduces the value of basic reproduction number when increased.

Conclusively, it suffices to mention that proper and effective treatment of HIV infection would go a long way in suppressing the prevalence of the disease transmission in the population.

Abimbade, S.F., Olaniyi, S., and Ajala, O. A. (2022). Recurrent malaria dynamics: insight from mathematical modelling. *Eur Phys J Plus* 137:292. https://doi.org/10.1140/epjp/s13360-022-02510-3

Abdulahi, J. T., and Cerna, D.P. (2017). Prediction of antiretroviral drug consumption for HIV patient in hospital pharmacy using data mining technique. International journal of information technology and computer science.DOI.10.5815/IJITCS.2016.02.07

Adepoju, O. A., and Olaniyi, S. (2021). Stability and optimal control of a disease model with vertical transmission and saturated incidence. *Sci. Afr.* **12**:e00800. https://doi.org/10.1016/j.sciaf.2021.e00800

Arafa, A. M., Rida, S. Z., and Khalili, M. A. (2013). Fractional-order of HIV infection with drug therapy effect. *J. Egypt Math Soc* **22**(3):538-543

Arias, R., Angeles, K. D., Maleki, S., and Ahangar, R. R. (2022). Mathematical modeling of HIV-AIDS epidemic. *Open Access Libr J* **9**:e7972. https://doi.org/10.4236/oalib.1107972

Centers for Diseases Control and Prevention (CDC) (2023) National Center for Emerging and Infectious Diseases (NCEZID). Accessed: January, 202.

Cheneke, K. R., Rao, K. P., and Edessa, G. K. (2021). Bifurcation and stability analysis of HIV transmission model with optimal control. *J. Math.* https://doi.org/10.1155/2021/7471290

Cheneke, K. R. (2023). Optimal control and bifurcation analysis of HIV model. *Comput Math Meth Med.* https://doi.org/10.1155/2023/4754426

Alade, T. O., Alnegga, M., Olaniyi, S., and Abidemi, A. (2023). Mathematical modelling of within-host chikungunya virus dynamics with adaptive immune response. *Model Earth Syst Environ*. https://doi.org/10.1007/s40808-023-01737-y

Castillo-Chavez, C., Feng, Z., Hunag, W. (2002). On the computation of $\mathcal{R}_0$ and its role on global stability. Mathematical Approaches for Emmerging and Re-emmerging Infectious Diseases: an introduction 1(29)

Chuma, F. M., Musa, Z. S. (2021). Campylobacteriosis transmission dynamics in humans: modeling the effects of public health education, treatment, and sanitation. Tanzania *J. Sci* **47**(1):315–331. https://dx.doi.org/10.4314/tjs.v47i1.27

van den Driessche, P., and Watmough, J. (2002). Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission. *Math Biosci* **180**:29âĂŞ48. https://doi.org/10.1016/S0025-5564(02)00108-6

Lasalle, J. P. (1976). The Stability of Dynamical Systems. Philadelphia, *PA SIAM*. https://doi.org/10.1137/1.9781611970432.

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