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The Transmission Dynamics of HPV, HIV/ADS and HSV-II Co-Infection Model

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ABSTRACT

The aim of study is to formulate and analyze a mathematical model for coinfection of sexually transmitted diseases HPV, HIV, and HSV-II. The well possedness of the developed model equations was proved and the equilibrium points of the model have been identified. Qualitative analysis of the formulated model equations was proved and the equilibrium points of the model have been identified. Qualitative analysis of the formulated model was established using basic reproduction number. The results show that the disease free equilibrium is locally asymptotically stable if the basic reproduction is less than one. The endemic states are considered to exist when the basic reproduction number for each disease is greater than one. Finally, numerical simulations of the model equations are carried out using the software MATLAB R2015b with ODE45 solver. Numerical simulations illustrated that all infection solutions converge to zero when the basic reproduction number is less than unity.

1. Introduction

Sexually Transmitted Diseases (STDs) can be transmitted through genital-genital, orogenital, or anogenital contacts and remain to be a public health concern worldwide. In the world, around one million people are believed to be newly infected with each day. Numerous causative agents including bacteria, viruses, protozoa, yeast, and fungi are responsible for sexually transmitted infections. However, viruses exhibit more serious risks, probabilities and outcomes of STDs than other organisms. The most lethal viral STIs are Human Immunodeficiency Virus-1 (HIV), Herpes Simplex viruses 1 and 2 (HSV-1 and HSV-2), and Human Papillomavirus (HPV), which are responsible for major sexually transmitted viral infections including AIDS, herpes simplex, and genital warts, respectively. Despite the fact that several prevention strategies such as vaccination, abstinence from sex, limiting sex partners,

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the use of condoms and a range of therapeutic drugs have drastically reduced the risk of contracting STIs, these three infections continue to spread at an alarming rate [1].

Human Papillomaviruses (HPVs) named for warts (papillomas) are the most common sexually transmitted infectious agents both in men and women across the world. HPV is a small, nonenveloped, and double-stranded DNA virus [1]. Most of the HPV infections are asymptomatic and can feed away without treatment over the course of a few years. About 70% of HPV infections fed away with in a year and 90% within two years. However, in some people infection can persist for many years and can cause warts or low risk genotype of HPV, while other types lead to different kinds of cancers or high risk genotype of HPV, including cervical cancer [2-3]. Statistics show that there are 18.1 million new cases, 9.6 million cancer related deaths, and 43.8 million people living with cancer in 2018. The number of new cases is expected to rise from 18 million to 22 million by 2030 and the number of global cancer deaths is projected to increase by 45% by 2030 [4].

Human Immunodeficiency Viruses (HIV) are an RNA retrovirus. That is, to enter a cell, HIV translates its RNA to DNA with a viral enzyme called reverse transcriptase [5]. The target cell of HIV is CD4 T cells. A healthy human body has about $1000/mm^3$ of CD4 T cells. When the CD4 T cells of a patient decline to $200/mm^3$ or below, then that person is classified as having AIDS [6]. In the world, new HIV infections among young women aged 15–24 years were reduced by 25% between 2010 and 2018. The annual number of deaths from AIDS-related illness among people living with HIV globally has fallen from a peak of 1.7 million in 2004 to 770 000 in 2018. The global decline in deaths has largely been driven by progress in eastern and southern Africa, which is home to 54% of the world's people living with HIV. AIDS-related mortality in the region declined by 44% from 2010 to 2018.The annual number of new infections since 2010 has declined from 2.1 million to 1.7 million in 2018 [7].

Herpes Simplex Virus Type II (HSV-II) infections are the primary cause of genital herpes. Genital herpes is a chronic, life-long viral infection caused by Herpes Simplex Virus-I (HSV-I) and Herpes Simplex Virus-II (HSV-II). HSV-II can be transmitted during sexual contact with someone who has a genital HSV-II infection [8]. Worldwide, an estimated 19.2 million new HSV-II infections occurred among adults and adolescents aged 15-49 years in 2012 with the highest rates among younger age groups. HSV-II is a lifelong infection and the estimated global HSV-II prevalence of 11.3% translates into an estimated 417 million people with the infection in 2012. The prevalence of HSV-II is highest in the WHO African Region (31.5%), followed by the Region of the Americas (14.4%) [9].

Co-infection is more than one disease co-existing within a single host. HPV, HIV and HSV-II are among the diseases that contaminate a large number of individuals worldwide. People with a weakened immune system such as those with HIV/AIDS are susceptible to diseases such as HPV, HSV-II. HPV-HIV-HSV-II is the co-infection of three of diseases responsible for loss of many lives. When an individual is co-infected with HPV-HIV, HPV-HSV-II, HIV-HSV-II and HPV-HIV-HSV-II at acute and clinical latency stages is called the initial stage. The final stage of the co-infection of HPV-HIV, HPV-HSV-II, HIV-HSV-II and HPV-HIV-HSV-II involves AIDS with Cervical cancer, cervical cancer with Herpes Simplex Virus-II, AIDS with HSV-II and Cervical Cancer-AIDS-HSV-II. This paper develops and analyses the mathematical model of HPV-HIV-HSV-II co-infection.

Mathematical modelling plays an important role in increasing our understanding of the dynamics of co-infectious diseases and also to investigate the optimal use of intervention strategies to control the spread of infectious diseases. Old and recent studies such as [10-12] developed a mathematical model of Human Papillomavirus to understand the transmission dynamics of the disease. A lot of scholars [13,

15] developed a mathematical model of HIV to describe the dynamics of the disease that helped them to propose disease control mechanism and also described the transmission dynamics of the diseases. Some of them are [16, 24] developed and analyzed a deterministic model for the transmission dynamics of Herpes Simplex Virus-II. Mhlanga et al. [17] proposed and analyzed a mathematical model for the spread of HSV-2 by incorporating all the relevant biological details and poor treatment adherence.

Furthermore, a lot of scholars developed a mathematical model to illustrate the dynamics of the co-infection with other infectious diseases and to suggest disease control mechanism. Some of them are [18, 19] the co-dynamics of HPV and HIV Disease. In their study, it was found that if the basic reproduction number of HPV becomes very small approaching zero, there is no new HPV infection which reduces the rate of AIDS progression. There are also some findings on coinfection of HPV and HSV-II by authors [20, 21]. The analysis of their study showed that HPV infection increases the risk of HSV-II similarly; HSV-II infection increases the risk for HPV. Moreover, Mhlanga [22] proposed a deterministic mathematical model for the co-interaction of HIV and HSV-II in a community, with all the relevant biological detail and poor HSV-II treatment adherence. In this study threshold parameters of the model are determined and stabilities are analyzed. Results from their simulation suggests that more effort should be devoted to monitoring and counseling of individuals dually infected with HIV and HSV-II as compared to those infected with HSV-II only.

So far, several mathematical studies have been undertaken to understand the transmission dynamics HPV, HIV, HSV-II, but they did not considered the coinfection of three disease i.e. coinfection of HPV-HIV-HSV-II in their studies.

2. Model Description and Formulation

The total human population N is subdivided into 22 subclasses, namely susceptible individuals, which are capable of becoming infected $S(t)$, individuals who are exposed to HPV$E_p(t)$, individuals who are exposed to HIV $E_h(t)$, individuals who are exposed to HSV-II $E_s(t)$, individuals who are exposed to both HPV and HIV $E_{ph}(t)$, individuals who are exposed to both HPV and HSV-II $E_{ps}(t)$, individuals who are exposed to both HIV and HSV-II $E_{hs}(t)$, individuals who are infected with HPV$I_p(t)$, individuals who are infected with HIV $I_h(t)$, individuals who are infected with HSV-II $E_s(t)$, individuals who are coinfected with both HPV and HIV $I_{ph}(t)$, individuals who are coinfected with both HPV and HSV-II $I_{ps}(t)$, individuals who are coinfected with both HIV and HSV-II $I_{hs}(t)$, individuals having cervical cancer $C(t)$, individuals having AIDS $A(t)$, individuals having HSV-II $H(t)$, individuals having both cervical cancer and AIDS $CA(t)$, individuals having both cervical cancer and HSV-II $CH(t)$, individuals having both AIDS and HSV-II $AH(t)$, individuals having cervical cancer AIDS and HSV-II $CAH(t)$, individuals recovered from HPV infection R_p, and individuals recovered from HSV infection R_s are considered.

The whole population is susceptible to human papillomavirus, HIV and HSV-II. It is assumed that individuals enter to the susceptible subclass through birth at a rate Π and the number of susceptible increases by those individuals that lost their temporary immunity from subclass of recovered R_p and R_s with rate χ_p and χ_s respectively. Susceptible individuals may acquire HPV infection, HIV infection, HSV-II infection, HPV-HIV coinfection, HPV-HSV-II coinfection and HIV-HSV-II coinfection with force of infection $\lambda_p = \frac{\beta_p I_p}{N_p}$, $\lambda_h = \frac{\beta_h I_h}{N_h}$, $\lambda_s = \frac{\beta_s I_s}{N_s}$, $\lambda_{ph} = \frac{\beta_{ph} I_{ph}}{N_{ph}}$, $\lambda_{ps} = \frac{\beta_{ps} I_{ps}}{N_{ps}}$ and $\lambda_{hs} = \frac{\beta_{hs} I_{hs}}{N_{hs}}$ respectively. Here β_p, β_h, β_s, β_{ph}, β_{ps} and β_{hs} are transmission coefficient of HPV, HIV, HSV-II, HPV-

HIV coinfection, HPV-HSV-II coinfection and HIV-HSV-II coinfection. Individuals in E_p and E_h subclass move to E_{ph} with rate ν_1 and ν_2. Individuals in E_p and E_s subclass are also move to E_{ps} with rate ν_{19} and ν_{20}. Similarly, individuals in E_h and E_s subclass move to E_{hs} with rate ν_3 and ν_4. Furthermore, individuals in $E_p, E_{ph}, E_{ps}, E_h, E_{hs}$ and E_s sub-class progress to $I_p, I_{ph}, I_{ps}, I_h, I_{hs}$ and I_s sub-class with per capita rate of $\eta_p, \eta_{ph}, \eta_{ps}, \eta_h, \eta_{hs}$ and η_s respectively. Addition to this, individuals in I_p and I_h subclass move to I_{ph} with rate ν_6 and ν_7. Also, Individuals in I_p and I_s subclass are move to I_{ps} with rate ν_{15} and ν_{16}. Similarly, individuals in I_h and I_s subclass move to I_{hs} with rate ν_8 and ν_9. Moreover, individuals in subclass $I_p, I_{ph}, I_{ps}, I_h, I_{hs}$ and I_s may develop cervical cancer, cervical cancer-AIDS coinfection, cervical cancer-HSV-II coinfection, AIDS, AIDS-HSV-II coinfection and HSV-II with progression rates $\alpha_p, \alpha_{ph}, \alpha_{ps}, \alpha_h, \alpha_{hs}$ and α_s respectively. Finally, individuals in C, CA, CH, A, AH and H may developed coinfection of HPV-HIV-HSV-II with rate φ, θ, π, ψ, δ and γ, respectively. All individuals suffer natural mortality at a rate μ and sick, die of cervical cancer, AIDS, HSV-II, cervical cancer-AIDS coinfection, AIDS-HSV-II coinfection, cervical cancer-HSV-II infection and cervical cancer-AIDS-HSV-II coinfection at rate ξ. The schematic diagram that describes the flow of the model is given below in *Fig. 1*.

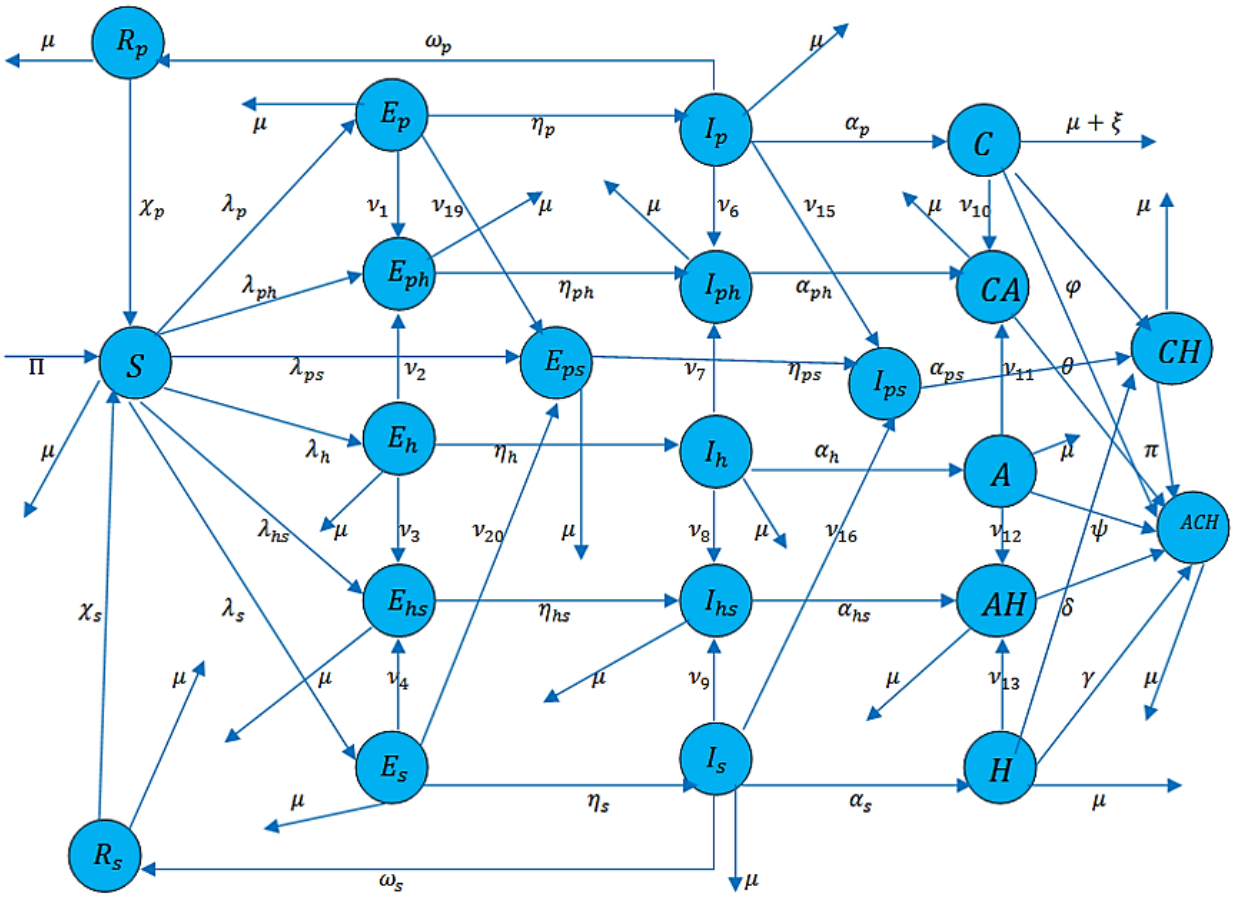

Fig. 1. *Schematic diagram for HPV-HIV-HSV-II coinfection model.*

Based on model assumption and *Fig. 1* we obtain the following system of linear differential equation

$$\frac{dS}{dt} = \Pi + \chi_p R_p + \chi_s R_s - (\lambda_p + \lambda_{ph} + \lambda_h + \lambda_{ps} + \lambda_{hs} + \lambda_s + \mu)S, \quad (1)$$

$$\frac{dE_p}{dt} = \lambda_p S - (\eta_p + \nu_{19} + \nu_1 + \mu)E_p,$$

$$\frac{dE_{ph}}{dt} = \lambda_{ph} S + \nu_1 E_p + \nu_2 E_h - (\eta_{ph} + \mu)E_{ph},$$

$$\frac{dE_{ps}}{dt} = \lambda_{ps} S + \nu_{19} E_p + \nu_{20} E_s - (\eta_{ps} + \mu)E_{ps},$$

$$\frac{dE_h}{dt} = \lambda_h S - (\eta_h + \nu_2 + \nu_3 + \mu)E_h,$$

$$\frac{dE_{hs}}{dt} = \lambda_{hs} S + \nu_3 E_h + \nu_4 E_s - (\eta_{hs} + \mu)E_{hs},$$

$$\frac{dE_s}{dt} = \lambda_s S - (\eta_s + \nu_4 + \nu_{20} + \mu)E_s,$$

$$\frac{dI_p}{dt} = \eta_p E_p - (\alpha_p + \nu_{15} + \nu_6 + \omega_p + \mu)I_p,$$

$$\frac{dI_{ph}}{dt} = \eta_{ph} E_{ph} + \nu_6 I_p + \nu_7 I_h - (\alpha_{ph} + \mu)I_{ph},$$

$$\frac{dI_{ps}}{dt} = \eta_{ps} E_{ps} + \nu_{15} I_p + \nu_{16} I_s - (\alpha_{ps} + \mu)I_{ps},$$

$$\frac{dI_h}{dt} = \eta_h E_h - (\alpha_h + \nu_7 + \nu_8 + \mu)I_h,$$

$$\frac{dI_{hs}}{dt} = \eta_{hs} E_{hs} + \nu_8 I_h + \nu_9 I_s - (\alpha_{hs} + \mu)I_{hs},$$

$$\frac{dI_s}{dt} = \eta_s E_s - (\omega_s + \nu_9 + \nu_{16} + \mu)I_s,$$

$$\frac{dC}{dt} = \alpha_p I_p - (\nu_{10} + \nu_{17} + \varphi + \mu + \xi)C,$$

$$\frac{dCA}{dt} = \alpha_{ph} I_{ph} + \nu_{10} C + \nu_{11} A - (\theta + \mu + \xi)CA,$$

$$\frac{dCH}{dt} = \alpha_{ps} I_{ps} + \nu_{17} C + \nu_{18} H - (\pi + \mu + \xi)CH,$$

$$\frac{dA}{dt} = \alpha_h I_h - (\nu_{11} + \nu_{12} + \psi + \mu + \xi)A,$$

$$\frac{dAH}{dt} = \alpha_{hs} I_{hs} + \nu_{12} A + \nu_{13} H - (\delta + \mu + \xi)AH,$$

$$\frac{dH}{dt} = \alpha_s I_s - (\nu_{13} + \nu_{18} + \gamma + \mu + \xi)H,$$

$$\frac{dACH}{dt} = \varphi C + \theta CA + \pi CH + \psi A + \delta AH + \gamma H - (\mu + \xi)ACH,$$

$$\frac{dR_p}{dt} = \omega_p I_p - (\chi_p + \mu)R_p,$$

$$\frac{dR_s}{dt} = \omega_s I_s - (\chi_s + \mu)R_s.$$

With initial condition

$S(0) = S_0,\ E_p(0) = E_{p0},\ E_{ph}(0) = E_{ph0},\ E_{ps}(0) = E_{ps0}, E_h(0) = E_{h0},\ E_{hs}(0) = E_{hs0},\ E_s(0) = E_{s0},\ I_p(0) = I_{p0},\ I_{ph}(0) = I_{ph0},\ I_{ps}(0) = I_{ps0}, I_h(0) = I_{h0},\ I_{hs}(0) = I_{hs0}, I_s(0) = I_{s0},\ A(0) = A_0,\ C(0) = C_0,\ CA(0) = CA_0,\ AH(0) = AH_0,\ CH(0) = CH_0,\ H(0) = H_0\ , ACH(0) = ACH_0, R_p = R_{p0}, R_s = R_{s0}.$

3. Analysis HPV only Model

Here analysis of HVP only model is considered and model equation obtained from *Eq. (1)*. This is

$$\begin{aligned}
\frac{dS}{dt} &= \Pi + \chi_p R_p - (\lambda_p + \mu)S, \qquad (2)\\
\frac{dE_p}{dt} &= \lambda_p S - (\eta_p + \mu)E_p,\\
\frac{dI_p}{dt} &= \eta_p E_p - (\alpha_p + \omega_p + \mu)I_p,\\
\frac{dC}{dt} &= \alpha_p I_p - (\mu + \xi)C,\\
\frac{dR_p}{dt} &= \omega_p I_p - (\chi_p + \mu)R_p.
\end{aligned}$$

3.1. Invariant Region

In this section, we get a region in which the solution of *Eq. (2)* is bounded. To obtain this, first we considered the total population (N_p), where $(N_p) = S + E_p + I_p + C + R_p$. Then, differentiating (N_p) both sides with respect to t leads

$$\frac{dN_p}{dt} = \frac{dS}{dt} + \frac{dE_p}{dt} + \frac{dI_p}{dt} + \frac{dC}{dt} + \frac{dR_p}{dt}. \qquad (3)$$

Substituting *Eq. (2)* into *Eq. (3)*, we can get

$$\frac{dN_p}{dt} = \Pi - \mu N_p - \xi C,$$

$$\Rightarrow \frac{dN_p}{dt} \leq \Pi - \mu N_p,$$

where $(\xi = 0)$ i.e., in the absence of mortality

$$\int \frac{dN_p}{\Pi - \mu N_p} \leq \int dt,$$

$$\Leftrightarrow \frac{-1}{\mu}\ln(\Pi - \mu N_p) \leq t + c_1,$$

where c_1 is integration constant

$$\Rightarrow (\Pi - \mu N_p) \geq ce^{-\mu t},$$

where $c = e^{-c_1}$.

Then, applying initial condition $N_p(0) = N_{p0}$, we obtain

$$\Rightarrow \mathrm{N_p} \leq \frac{\Pi}{\mu} - [\frac{\Pi - \mu \mathrm{N_p}}{\mu}]\mathrm{e}^{-\mu \mathrm{t}}. \quad (4)$$

Further, it can be observed that $N_p(t) \to (\Pi/\mu)$ as $t \to \infty$. That is, the total population size $N_p(t)$ takes off from the value $N_p(0)$ at the initial time $t = 0$ and ends up with the bounded value (Π/μ) as the time t grows to infinity. Thus, it can be concluded that $N_p(t)$ is bounded as $0 \leq N_p(t) \leq (\Pi/\mu)$. Thus, the feasible solution set of the system equation of the model enters and remains in the region:

$$\Omega_{\mathrm{p}} = \{(\mathrm{S}, \quad \mathrm{E_p}, \quad \mathrm{I_p}, \quad \mathrm{C}, \quad \mathrm{R_p}) \in \Re_+^5 \ : \ \mathrm{N_p} \leq \Pi/\mu\}.$$

Therefore, the *Eq. (2)* is well posed epidemiologically and mathematically. Hence, it is sufficient to study the dynamics of the basic model in the region Ω_p.

3.2. Existence of Solution

Lemma 1. Solutions of the model *Eq. (2)* together with the initial conditions $S(0) > 0, S, E_p(0) > 0, I_p(0) >), C(0) > 0, \quad R_p(0) > 0$ exist in $\mathbb{R}_+^5$ i.e., the model variables $S(t), E_p(t), I_p(t), C(t)$ and $R_p(t)$ exist for all t and will remain in $\mathbb{R}_+^5$.

Proof. The right hand sides of the system of *Eq. (2)* can be expressed as follows:

$$\mathrm{f_1(S, E_p, I_p, C, R_p)} = \Pi + \chi_{\mathrm{p}}\mathrm{R_p} - (\lambda_{\mathrm{p}} + \mu)\mathrm{S},$$

$$\mathrm{f_2(S, E_p, I_p, C, R_p)} = \lambda_{\mathrm{p}}\mathrm{S} - (\eta_{\mathrm{p}} + \mu)\mathrm{E_p},$$

$$\mathrm{f_3(S, E_p, I_p, C, R_p)} = \eta_{\mathrm{p}}\mathrm{E_p} - (\alpha_{\mathrm{p}} + \omega_{\mathrm{p}} + \mu)\mathrm{I_p},$$

$$\mathrm{f_4(S, E_p, I_p, C, R_p)} = \alpha_{\mathrm{p}}\mathrm{I_p} - (\mu + \xi)\mathrm{C},$$

$$\mathrm{f_5(S, E_p, I_p, C, R_p)} = \omega_{\mathrm{p}}\mathrm{I_p} - (\chi_{\mathrm{p}} + \mu)\mathrm{R_p}.$$

According to Derrick and Groosman theorem, let Ω_p denote the region $\Omega_p = \{(S, E_p, I_p, C, \quad R_p) \in \Re_+^5 \ : N_p \leq \Pi/\mu\}$. Then *Eq. (1)* have a unique solution if $(\partial f_i)/(\partial x_j)$, $i, j = 1, 2, 3, 4, 5$ are continuous and bounded in Ω_p. Here, $x_1 = S, \ x_2 = E_p, \ x_3 = I_p, \ x_4 = C$ and $x_6 = R_p$. The continuity and the boundedness are verified as here under in *Table 1*.

Table 1. *Continuity and boundedness of the model solution.*

$\lvert(\partial f_1)/(\partial S)\rvert = \lvert-(\lambda_p+\mu)\rvert < \infty$	$\lvert(\partial f_2)/(\partial S)\rvert = \lvert\lambda_p\rvert < \infty.$	$\lvert(\partial f_3)/(\partial S)\rvert = 0 < \infty.$
$\lvert(\partial f_1)/(\partial I_p)\rvert = \lvert-(\beta_1 S/N_p)\rvert < \infty.$	$\lvert(\partial f_2)/(\partial E_p)\rvert = \lvert-(\eta_p+\mu)\rvert < \infty.$	$\lvert(\partial f_3)/(\partial E_p)\rvert = \lvert\eta_p\rvert < \infty.$
$\lvert(\partial f_1)/(\partial R_p)\rvert = \lvert\eta\rvert < \infty.$	$\lvert(\partial f_2)/(\partial I_p)\rvert = \lvert\beta_1 S/N_p\rvert < \infty.$	$\lvert(\partial f_3)/(\partial I_p)\rvert = \lvert-(\alpha_p+\omega_p+\mu)\rvert < \infty.$
$\lvert(\partial f_1)/(\partial E_p)\rvert = \lvert(\partial f_1)/(\partial C)\rvert = 0 < \infty.$	$\lvert(\partial f_2)/(\partial C)\rvert = \lvert(\partial f_2)/(\partial R_p)\rvert = 0 < \infty.$	$\lvert(\partial f_3)/(\partial C)\rvert = \lvert(\partial f_2)/(\partial R_p)\rvert = 0 < \infty.$
$\lvert(\partial f_4)/(\partial S)\rvert = \lvert(\partial f_4)/(\partial E_p)\rvert = 0 < \infty.$	$\lvert(\partial f_4)/(\partial R_p)\rvert = 0 < \infty.$	$\lvert(\partial f_5)/(\partial C)\rvert = 0 < \infty.$
$\lvert(\partial f_4)/(\partial I_p)\rvert = \lvert\alpha_p\rvert < \infty.$	$\lvert(\partial f_5)/(\partial S)\rvert = \lvert(\partial f_5)/(\partial E_p)\rvert = 0 < \infty.$	$\lvert(\partial f_5)/(\partial R_p)\rvert = \lvert-(\chi_p+\mu)\rvert < \infty.$
$\lvert(\partial f_4)/(\partial C)\rvert = \lvert-(\mu+\xi)\rvert < \infty.$	$\lvert(\partial f_5)/(\partial I_p)\rvert = \lvert\omega_p\rvert < \infty.$	

Thus, all the partial derivatives $(\partial f_i)/(\partial x_j), i,j = 1,2,3,4,5$ exist, continuous and bounded in Ω_p. Hence, by Derrick and Groosman theorem, a solution for the *Model (2)* exists and is unique.

3.3. Positivity of Solution

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

Lemma 2. Let $\Omega_{\mathrm{p}} = \{(S,\ E_p,\ I_p,\ C,\quad R_p) \in \mathbb{R}^5_+;\ S_0(0) > 0,\ E_{p0}(0) > 0,\ I_{p0}(0) >),\ C_0(0) > 0,\quad R_{p0}(0) > 0\}$; then the solutions of $\{S,\ E_p,\ I_p,\ C,\ R_p\}$ are positive for all $t \geq 0$.

Proof: Positivity is verified separately for each of the model $S(t),\ E_p(t),\ I_p(t),\ C(t)$ and $R_p(t)$.

Positivity of$S(t)$: From *Eq. (2)* we have:

$\frac{dS}{dt} = \Pi + \chi_p R_p - (\lambda_p+\mu)S$, eliminating the positive terms $(\Pi + \chi_p R_p)$ we get,

$\Leftrightarrow \frac{dS}{dt} \geq -(\lambda_p+\mu)S$, using variables separable method we get,

$$\Rightarrow \int \frac{\mathrm{dS}}{\mathrm{S}} \geq -\int (\lambda_{\mathrm{p}}+\mu)\,\mathrm{dt},$$

$$\Rightarrow \ln \mathrm{S} \geq -(\lambda_{\mathrm{p}}+\mu)\mathrm{t} + \mathrm{c}_3,$$

where c_3 is integration constant.

$\Rightarrow S(t) \geq S_0 \mathrm{e}^{-(\lambda_p+\mu)t}$,$S_0 = \mathrm{e}^{\mathrm{c}_3}$ and $\mathrm{e}^{-(\lambda_p+\mu)t} \geq 0$, for all $t \geq 0$.

Hence, it can be concluded that $S(t) \geq 0$.

Positivity of $E_p(t)$: From *Eq. (2)* we have:

$\frac{dE_p}{dt} = \lambda_p S - (\eta_p+\mu)E_p$, eliminating the positive terms $(\lambda_p S)$ we get,

$\Leftrightarrow \frac{dE_p}{dt} \geq -(\eta_p+\mu)E_p$, using variables separable method we get,

$\Rightarrow \frac{dE_p}{E_p} \geq -(\eta_p + \mu)dt$, integrating both side we can get,

$$\Rightarrow \int \frac{dE_p}{E_p} \geq -\int (\eta_p + \mu)\, dt,$$

$$\Rightarrow \ln E_p \geq -(\eta_p + \mu)t + c_4,$$

where c_4 is integration constant

$\Rightarrow E_p(t) \geq E_{p_0} e^{-(\eta_p+\mu)t}$, $S_0 = e^{c_4}$and $e^{-(\eta_p+\mu)t} \geq 0$, for all $t \geq 0$.

Hence, it can be concluded that $E_p(t) \geq 0$.

Positivity of $I_p(t)$: From *Eq. (2)* we have:

$\frac{dI_p}{dt} = \eta_p E_p - (\alpha_p + \omega_p + \mu)I_p$, eliminating the positive terms $(\eta_p E_p)$we get,

$\Leftrightarrow \frac{dI_p}{dt} \geq -(\alpha_p + \omega_p + \mu)I_p$, using variables separable method we get,

$\Rightarrow \frac{dI_p}{I_p} \geq -(\alpha_p + \omega_p + \mu)dt$, integrating both side we can get,

$$\Rightarrow \int \frac{dI_p}{I_p} \geq -\int (\alpha_p + \omega_p + \mu)\, dt,$$

$$\Rightarrow \ln I_p \geq -(\alpha_p + \omega_p + \mu)t + c_5,$$

where c_5 is integration constant

$\Rightarrow I_p(t) \geq I_{p0} e^{-(\alpha_p+\omega_p+\mu)t}$, $I_{p0} = e^{c_5}$and $e^{-(\alpha_p+\omega_p+\mu)t} \geq 0$,for all $t \geq 0$.

Hence, it can be concluded that $I_p(t) \geq 0$.

Positivity of $C(t)$: From *Eq. (2)* we have:

$\frac{dC}{dt} = \alpha_p I_p - (\mu + \xi)C$, eliminating the positive terms $(\alpha_p I_p)$we get,

$\Leftrightarrow \frac{dC}{dt} \geq -(\mu + \xi)C$, using variables separable method we get,

$\Rightarrow \frac{dC}{C} \geq -(\mu + \xi)dt$, integrating both side we can get,

$$\Rightarrow \int \frac{dC}{C} \geq -\int (\mu + \xi)\, dt,$$

$$\Rightarrow \ln C \geq -(\mu + \xi)t + c_6,$$

where c_6 is integration constant

$\Rightarrow C(t) \geq C_0 e^{-(\mu+\xi)t}$, $C_0 = e^{c_6}$ and $e^{-(\mu+\xi)t} \geq 0$, for all $t \geq 0$.

Hence, it can be concluded that $C(t) \geq 0$.

Positivity of $R_p(t)$: From *Eq. (2)* we have:

$\frac{dR_p}{dt} = \omega_p I_p - (\chi_p + \mu)R_p$, eliminating the positive terms $(\omega_p I_p)$ we get,

$\Leftrightarrow \frac{dR_p}{dt} \geq -(\chi_p + \mu)R_p$, using variables separable method we get,

$\Rightarrow c_7 \frac{dR_p}{R_p} \geq -(\chi_p + \mu)dt$, integrating both side we can get,

$$\Rightarrow \int \frac{dR_p}{R_p} \geq -\int (\chi_p + \mu)\, dt,$$

$$\Rightarrow \ln R_p \geq -(\chi_p + \mu)t + c_7,$$

where is integration constant

$\Rightarrow R_p(t) \geq R_{p0} e^{-(\chi_p+\mu)t}$, $R_{p0} = e^{c_7}$ and $e^{-(\chi_p+\mu)t} \geq 0$, for all $t \geq 0$.

Hence, it can be concluded that $R_p(t) \geq 0$.

Therefore, the model variables $S(t)$, $E_p(t)$, $I_p(t)$, $C(t)$ and $R_p(t)$representing population sizes of various types of cells are positive quantities and will remain in $\mathbb{R}_+^5$ for all t.

3.4. Local Stability of the Disease-Free Equilibrium (DFE)

The disease free equilibrium of *Eq. (2)* is obtained by equating all equations of the model equation to zero and then letting $E_p = I_p = C = R_p = 0$. Then we obtain

$$E_1 = \left\{\left(\frac{\Pi}{\mu}\right), \quad 0, \quad 0, \quad 0, \quad 0\right\}.$$

The linear stability of the DFE, E_1, can be established using the next generation operator method in Van den Driessche and Watmouth [23] on the *System (2)*. The matrice F s (for the new infection terms) and V (of the transition terms) are given, respectively by,

$$F = \begin{bmatrix} 0 & \beta_p & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix} \text{ and } V = \begin{bmatrix} \eta_p & 0 & 0 \\ -\eta_p & (\alpha_p + \omega_p + \mu) & 0 \\ 0 & -\alpha_p & \mu + \xi \end{bmatrix}.$$

The associated reproduction number, denoted by $\Re_p$ is then given by,

$$\Re_p = \frac{(\beta_p \eta_p)}{(\alpha_p + \omega_p + \mu)(\mu + \xi)}.$$

Further using theorem in Van den Driessche and Watmouth [23], the following result is established. The DFE is locally asymptotically stable if $\Re_p < 1$ and unstable is $\Re_p > 1$.

3.5. Stability Analysis of Endemic Equilibrium

Lemma 3. The HPV only model has a unique endemic equilibrium if and only if $\Re_p > 1$.

Proof. Let the endemic equilibrium point of the *Eq. (2)* be denoted by,

$$E_1^* = (S^*, \quad E_p^*, \quad I_p^*, \quad C^*, \quad R_p^*),$$

and consider the force of infection

$$\lambda_p^* = [\beta_p I^*]/[N]. \tag{5}$$

Solving the equations in *System (5)* by setting the right hand sides of equations equal to zero, gives,

$$S^* = [\Pi + \chi_p R_p^*]/[\lambda_p^* + \mu], \tag{6}$$

$$E_p^* = [\lambda_p^*(\Pi + \chi_p R_p^*)]/[(\lambda_p^* + \mu)(\eta_p + \mu)],$$

$$I_p^* = [\lambda_p^* \eta_p (\Pi + \chi_p R_p^*)]/[(\lambda_p^* + \mu)(\eta_p + \mu)(\alpha_p + \omega_p + \mu)],$$

$$C^* = [\lambda_p^* \eta_p \alpha_p (\Pi + \chi_p R_p^*)]/[(\lambda_p^* + \mu)(\eta_p + \mu)(\alpha_p + \omega_p + \mu)(\mu + \xi)]\, R_p^*$$
$$= [\omega_p \eta_p \Pi \lambda_p^*]/[(\lambda_p^* + \mu)(\eta_p^* + \mu)(\alpha_p + \omega_p + \mu)(\chi_p + \mu) - \omega_p \eta_p \lambda_p^* \chi_p].$$

Substituting *Eq. (6)* in *Eq. (5)* gives

$$(\eta_p + \mu)(\lambda_p^*)^2 + \lambda_p^* \mu \left[1 - \Re_p \left(\frac{\Pi + \chi_p + R_p^*}{\Pi}\right)\right] = 0. \tag{7}$$

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

$$D_1 \lambda_p^* + D_2 = 0. \tag{8}$$

Where $D_1 = (\eta_p + \mu)$and $D_2 = \mu \left[1 - \Re_p \left(\frac{\Pi + \chi_p + R_p^*}{\Pi}\right)\right]$.

It is clear that $D_1 > 0$ and $D_2 < 0$ when $\Re_p \left(\frac{\Pi+\chi_p+R_p^*}{\Pi}\right) > 1$. Thus the *Linear System (8)* has a unique positive solution, given by $\lambda_p^* = \frac{-D_2}{D_1}$ whenever $\Re_p > 1$.

Now, to show its local stability analysis, *Eq. (7)* gives a fixed point problem of the form

$$f(\lambda_p^*) = (\eta_p + \mu)(\lambda_p^*)^2 + \lambda_p^* \mu \left[1 - \Re_p \left(\frac{\Pi+\chi_p+R_p^*}{\Pi}\right)\right] = 0.$$

Then, derivatives of $f(\lambda_p^*)$ become

$$f'(\lambda_p^*) = \left[2(\eta_p + \mu)\lambda_p^*\right] + \mu \left[1 - \Re_p \left(\frac{\Pi + \chi_p + R_p^*}{\Pi}\right)\right].$$

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

$$f'(-D_2/D_1) = 3\mu \left[1 - \Re_p \left(\frac{\Pi + \chi_p + R_p^*}{\Pi}\right)\right],$$

$\Rightarrow |f'(\lambda_p^*)| < 1$ at $\lambda_p^* = -D_2/D_1$, whenever $\Re_p \left(\frac{\Pi+\chi_p+R_p^*}{\Pi}\right) > 1$.

Therefore, the unique endemic equilibrium is locally asymptotically stable if $\Re_p > 1$.

4. Analysis HIV only Model

Here analysis of HIV only model is considered and model equation obtained from *Eq. (1)*. This is

$$\begin{aligned}
\frac{dS}{dt} &= \Pi - (\lambda_h + \mu)S, \qquad (9)\\
\frac{dE_h}{dt} &= \lambda_h S - (\eta_h + \mu)E_h,\\
\frac{dI_h}{dt} &= \eta_h E_h - (\alpha_h + \mu)I_h,\\
\frac{dA}{dt} &= \alpha_h I_h - (\mu + \xi)A.
\end{aligned}$$

The invariant region, existence of solution and uniqueness of solution is can be determined similar to Section 3.1, 3.2, and 3.3.

4.1. Local Stability of the Disease-Free Equilibrium (DFE)

The disease free equilibrium of *Eq. (9)* is obtained by setting the system of equations in *Model (9)* to zero. At disease free equilibrium there are no infection and recovery. Then we obtain

$$E_2 = \left\{\left(\frac{\Pi}{\mu}\right), \quad 0, \quad 0, \quad 0\right\}.$$

The stability analysis of the DFE, E_2, can be established using basic reproduction number. The concept of the next generation matrix would be employed in computing the basic reproduction number. Using theorem 2 in Van den Driessche and Watmouth [23] on the HIV model in *Eq. (9)*, the basic reproduction number of the HIV only model, denoted by $\Re_h$ is then given by

$$\Re_h = \frac{(\beta_h \eta_h)}{(\alpha_h + \mu)(\mu + \xi)}.$$

Further using theorem 2 in Van den Driessche and Watmouth [23], the following result is established. The DFE is locally asymptotically stable if $\Re_h < 1$ and unstable is $\Re_h > 1$.

4.2. Stability Analysis of Endemic Equilibrium

The endemic equilibrium points are computed by setting the system of differential equations in the HIV only *Model (9)* to zero. The endemic equilibrium points are as follows:

$$S^* = [\Pi]/[\lambda_h^* + \mu], \tag{10}$$

$$E_h^* = [\lambda_h^* \Pi]/[(\lambda_h^* + \mu)(\eta_h + \mu)],$$

$$I_h^* = [\lambda_h^* \eta_h \Pi]/[(\lambda_h^* + \mu)(\eta_h + \mu)(\alpha_h + \mu)],$$

$$A^* = [\lambda_h^* \eta_h \alpha_h \Pi]/[(\lambda_h^* + \mu)(\eta_h + \mu)(\alpha_h + \mu)(\mu + \xi)].$$

Lemma 4. The HIV only model has a unique endemic equilibrium if and only if $\Re_h > 1$.

Proof. Substituting *Eq. (10)* into force of infection, we can get

$$(\eta_h + \mu)(\lambda_h^*)^2 + \lambda_h^* \mu[1 - \Re_h] = 0. \tag{11}$$

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

$$D_1 \lambda_h^* + D_2 = 0. \tag{12}$$

Where $D_1 = (\eta_h + \mu)$ and $D_2 = \mu[1 - \Re_h]$.

It is clear that $D_1 > 0$ and $D_2 < 0$ when $\Re_h > 1$. Thus the *Linear System (12)* has a unique positive solution, given by $\lambda_h^* = \frac{-D_2}{D_1}$ whenever $\Re_h > 1$.

Now, to show its local stability analysis, *Eq. (11)* gives a fixed point problem of the form

$$f(\lambda_h^*) = (\eta_h + \mu)(\lambda_h^*)^2 + \lambda_h^* \mu[1 - \Re_h] = 0.$$

Then, derivatives of $f(\lambda_h^*)$ become

$$f'(\lambda_h^*) = [2(\eta_h + \mu)\lambda_h^*] + \mu[1 - \Re_h]].$$

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

$$f'(-D_2/D_1) = 3\mu[1 - \Re_h]],$$

$\Rightarrow |f'(\lambda_h^*)| < 1$ at $\lambda_h^* = -D_2/D_1$, whenever $\Re_h > 1$.

Therefore, the unique endemic equilibrium is locally asymptotically stable if $\Re_h > 1$.

5. Analysis HSV-II only Model

Here analysis of HSV-II only model is considered and model equation obtained from *Eq. (1)*. This is

$$\begin{aligned}
\frac{dS}{dt} &= \Pi + \chi_s R_s - (\lambda_s + \mu)S, \\
\frac{dE_s}{dt} &= \lambda_s S - (\eta_s + \mu)E_s, \\
\frac{dI_s}{dt} &= \eta_s E_h - (\alpha_s + \omega_s + \mu)I_s, \\
\frac{dH}{dt} &= \alpha_s I_s - (\mu + \xi)H, \\
\frac{dR_s}{dt} &= \omega_s I_s - (\chi_s + \mu)R_s.
\end{aligned} \tag{13}$$

The invariant region, existence of solution and uniqueness of solution is can be determined similar to Section 3.1, 3.2, and 3.3.

5.1. Local Stability of the Disease-Free Equilibrium (DFE)

The disease free equilibrium of *Eq. (13)* is obtained by setting the system of equations in *Model (13)* to zero. At disease free equilibrium there are no infection and recovery. Then we obtain;

$$E_3 = \left\{\left(\frac{\Pi}{\mu}\right), \quad 0, \quad 0, \quad 0, \quad 0\right\}.$$

The stability analysis of the DFE, E_3, can be established using basic reproduction number. The concept of the next generation matrix would be employed in computing the basic reproduction number. Using theorem 2 in Van den Driessche and Watmouth [23] on the HSV-II model in *Eq. (13)*, the basic reproduction number of the HSV-II only model, denoted by $\Re_s$ is then given by

$$\Re_s = \frac{(\beta_s \eta_s)}{(\alpha_s + \omega_s + \mu)(\mu + \xi)}.$$

Further using theorem 2 in Van den Driessche and Watmouth [23], the following result is established. The DFE is locally asymptotically stable if $\Re_s < 1$ and unstable is $\Re_s > 1$.

5.2. Stability Analysis of Endemic Equilibrium

The endemic equilibrium points are computed by setting the system of differential equations in the HSV-II only *Model (13)* to zero. The endemic equilibrium points are as follows

$$S^* = [\Pi + \chi_s R_s^*]/[\lambda_s^* + \mu], \tag{14}$$

$$E_s^* = [\lambda_s^*(\Pi + \chi_s R_s^*)]/[(\lambda_s^* + \mu)(\eta_s + \mu)],$$

$$I_s^* = [\lambda_s^* \eta_s(\Pi + \chi_s R_s^*)]/[(\lambda_s^* + \mu)(\eta_s + \mu)(\alpha_s + \omega_s + \mu)],$$

$$H^* = [\lambda_s^* \eta_s \alpha_s(\Pi + \chi_s R_s^*)]/[(\lambda_s^* + \mu)(\eta_s + \mu)(\alpha_s + \omega_s + \mu)(\mu + \xi)]\, R_s^*$$
$$= [\omega_s \eta_s \Pi \lambda_s^*]/[(\lambda_s^* + \mu)(\eta_s^* + \mu)(\alpha_s + \omega_s + \mu)(\chi_s + \mu) - \omega_s \eta_s \lambda_s^* \chi_s].$$

Lemma 5. The HSV-II only model has a unique endemic equilibrium if and only if $\Re_s > 1$.

Proof. Substituting *Eq. (10)* into force of infection, we can get

$$(\eta_s + \mu)(\lambda_s^*)^2 + \lambda_s^* \mu \left[1 - \Re_s \left(\frac{\Pi + \chi_s + R_s^*}{\Pi}\right)\right] = 0. \tag{15}$$

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

$$D_1 \lambda_s^* + D_2 = 0. \tag{16}$$

Where $D_1 = (\eta_s + \mu)$and $D_2 = \mu \left[1 - \Re_s \left(\frac{\Pi + \chi_s + R_s^*}{\Pi}\right)\right]$.

It is clear that $D_1 > 0$ and $D_2 < 0$ when $\Re_s \left(\frac{\Pi + \chi_s + R_s^*}{\Pi}\right) > 1$. Thus the *Linear System (16)* has a unique positive solution, given by $\lambda_s^* = \frac{-D_2}{D_1}$ whenever $\Re_s > 1$.

Now, to show its local stability analysis, *Eq. (15)* gives a fixed point problem of the form

$$f(\lambda_s^*) = (\eta_s + \mu)(\lambda_s^*)^2 + \lambda_s^*\mu\left[1 - \Re_s\left(\frac{\Pi + \chi_s + R_s^*}{\Pi}\right)\right] = 0.$$

Then, derivatives of $f(\lambda_s^*)$ become

$$f'(\lambda_s^*) = [2(\eta_s + \mu)\lambda_s^*] + \mu\left[1 - \Re_s\left(\frac{\Pi + \chi_s + R_s^*}{\Pi}\right)\right].$$

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

$$f'(-D_2/D_1) = 3\mu\left[1 - \Re_s\left(\frac{\Pi + \chi_s + R_s^*}{\Pi}\right)\right].$$

$\Rightarrow |f'(\lambda_s^*)| < 1$ at $\lambda_s^* = -D_2/D_1$, whenever $\Re_s\left(\frac{\Pi+\chi_s+R_s^*}{\Pi}\right) > 1$.

Therefore, the unique endemic equilibrium is locally asymptotically stable if $\Re_s > 1$.

6. Analysis HPV-HIV only Coinfection Model

Here analysis of HPV-HIV only coinfection model is considered and model equation obtained from *Eq. (1)*. This is

$$\frac{dS}{dt} = \Pi - (\lambda_{ph} + \mu)S, \tag{17}$$

$$\frac{dE_{ph}}{dt} = \lambda_{ph}S - (\eta_{ph} + \mu)E_{ph},$$

$$\frac{dI_{ph}}{dt} = \eta_{ph}E_{ph} - (\alpha_{ph} + \mu)I_{ph},$$

$$\frac{dCA}{dt} = \alpha_{ph}I_{ph} - (\mu + \xi)CA.$$

The invariant region, existence of solution and uniqueness of solution is can be determined similar to section 3.1, 3.2, and 3.3.

6.1. Local Stability of the Disease-Free Equilibrium (DFE)

The disease free equilibrium of *Eq. (17)* is obtained by setting the system of equations in *Model (17)* to zero. At disease free equilibrium there are no infection and recovery. Then we obtain

$$E_4 = \left\{\left(\frac{\Pi}{\mu}\right), \quad 0, \quad 0, \quad 0\right\}.$$

The stability analysis of the DFE, E_4, can be established using basic reproduction number. The concept of the next generation matrix would be employed in computing the basic reproduction number. Using theorem 2 in Van den Driessche and Watmouth [23] on the HPV-HIV coinfection model in *Eq. (17)*,

the basic reproduction number of the HPV-HIV only coinfection model, denoted by $\mathfrak{R}_{ph}$ is then given by

$$\mathfrak{R}_{\mathrm{ph}} = \frac{(\beta_{\mathrm{ph}}\eta_{\mathrm{ph}})}{(\alpha_{\mathrm{ph}} + \mu)(\mu + \xi)}.$$

Further using theorem 2 in Van den Driessche and Watmouth [23], the following result is established. The DFE is locally asymptotically stable if $\mathfrak{R}_{ph} < 1$ and unstable is $\mathfrak{R}_{ph} > 1$.

6.2. Stability Analysis of Endemic Equilibrium

The endemic equilibrium points are computed by setting the system of differential equations in the HPV-HIV only *Coinfection Model (17)* to zero. The endemic equilibrium points are as follows;

$$S^* = [\Pi]/[\lambda_{ph}^* + \mu], \tag{18}$$

$$E_{ph}^* = [\lambda_{ph}^*\Pi]/[(\lambda_{ph}^* + \mu)(\eta_{ph} + \mu)],$$

$$I_{ph}^* = [\lambda_{ph}^*\eta_{ph}\Pi]/[(\lambda_{ph}^* + \mu)(\eta_{ph} + \mu)(\alpha_{ph} + \mu)],$$

$$CA^* = [\lambda_{ph}^*\eta_{ph}\alpha_{ph}\Pi]/[(\lambda_{ph}^* + \mu)(\eta_{ph} + \mu)(\alpha_{ph} + \mu)(\mu + \xi)].$$

Lemma 6. The HPV-HIV only coinfection model has a unique endemic equilibrium if and only if $\mathfrak{R}_{ph} > 1$.

Proof. Substituting *Eq. (18)* into force of infection, we can get

$$(\eta_{\mathrm{ph}} + \mu)(\lambda_{\mathrm{ph}}^*)^2 + \lambda_{\mathrm{ph}}^*\mu[1 - \mathfrak{R}_{\mathrm{ph}}] = 0. \tag{19}$$

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

$$\mathrm{D}_1\lambda_{\mathrm{ph}}^* + \mathrm{D}_2 = 0. \tag{20}$$

Where $D_1 = (\eta_{ph} + \mu)$ eand $D_2 = \mu[1 - \mathfrak{R}_{ph}]$.

It is clear that $D_1 > 0$ and $D_2 < 0$ when $\mathfrak{R}_{ph} > 1$. Thus the *Linear System (20)* has a unique positive solution, given by $\lambda_{ph}^* = \frac{-D_2}{D_1}$ whenever $\mathfrak{R}_{ph} > 1$.

Now, to show its local stability analysis, *Eq. (19)* gives a fixed point problem of the form

$$f(\lambda_{ph}^*) = (\eta_{ph} + \mu)(\lambda_{ph}^*)^2 + \lambda_{ph}^* \mu[1 - \Re_{ph}] = 0.$$

Then, derivatives of $f(\lambda_{ph}^*)$ become

$$f'(\lambda_{ph}^*) = [2(\eta_{ph} + \mu)\lambda_{ph}^*] + \mu[1 - \Re_{ph}].$$

Evaluating $f'(\lambda_{ph}^*)$ at $\lambda_{ph}^* = -D_2/D_1$ gives

$f'(-D_2/D_1) = 3\,\mu[1 - \Re_{ph}] \Rightarrow |f'(\lambda_{ph}^*)| < 1$ at $\lambda_{ph}^* = -D_2/D_1$, whenever $\Re_{ph} > 1$.

Therefore, the unique endemic equilibrium is locally asymptotically stable if $\Re_{ph} > 1$.

7. Analysis HPV-HSV-II only Coinfection Model

Here analysis of HPV-HSV-II only coinfection model is considered and model equation obtained from *Eq. (1)*. This is

$$\frac{dS}{dt} = \Pi - (\lambda_{ps} + \mu)S, \tag{21}$$

$$\frac{dE_{ps}}{dt} = \lambda_{ps}S - (\eta_{ps} + \mu)E_{ps},$$

$$\frac{dI_{ps}}{dt} = \eta_{ps}E_{ps} - (\alpha_{ps} + \mu)I_{ps},$$

$$\frac{dCH}{dt} = \alpha_{ps}I_{ps} - (\mu + \xi)CH.$$

The invariant region, existence of solution and uniqueness of solution is can be determined similar to Section 3.1, 3.2, and 3.3.

7.1. Local Stability of the Disease-Free Equilibrium (DFE)

The disease free equilibrium of *Eq. (21)* is obtained by setting the system of equations in *Model (21)* to zero. At disease free equilibrium there are no infection and recovery. Then we obtain;

$$E_5 = \left\{\left(\frac{\Pi}{\mu}\right), \quad 0, \quad 0, \quad 0\right\}.$$

The stability analysis of the DFE, E_5, can be established using basic reproduction number. The concept of the next generation matrix would be employed in computing the basic reproduction number. Using theorem 2 in Van den Driessche and Watmouth [23] on the HPV-HSV-II coinfection model in *Eq. (21)*, the basic reproduction number of the HPV-HSV-II only coinfection model, denoted by $\Re_{ps}$ is then given by

$$\Re_{ps} = \frac{(\beta_{ps}\eta_{ps})}{(\alpha_{ps} + \mu)(\mu + \xi)}.$$

Further using theorem 2 in Van den Driessche and Watmouth [23], the following result is established. The DFE is locally asymptotically stable if $\Re_{ps} < 1$ and unstable is $\Re_{ps} > 1$.

7.2. Stability Analysis of Endemic Equilibrium

The endemic equilibrium points are computed by setting the system of differential equations in the HPV-HSV-II only *Coinfection Model (21)* to zero. The endemic equilibrium points are as follows;

$$S^* = [\Pi]/[\lambda_{ps}^* + \mu], \tag{22}$$

$$E_{ps}^* = [\lambda_{ps}^* \Pi]/[(\lambda_{ps}^* + \mu)(\eta_{ps} + \mu)],$$

$$I_{ps}^* = [\lambda_{ps}^* \eta_{ps} \Pi]/[(\lambda_{ps}^* + \mu)(\eta_{ps} + \mu)(\alpha_{ps} + \mu)],$$

$$CH^* = [\lambda_{ps}^* \eta_{ps} \alpha_{ps} \Pi]/[(\lambda_{ps}^* + \mu)(\eta_{ps} + \mu)(\alpha_{ps} + \mu)(\mu + \xi)].$$

Lemma 7. The HPV-HSV-II only coinfection model has a unique endemic equilibrium if and only if $\Re_{ps} > 1$.

Proof. Substituting *Eq. (22)* into force of infection, we can get

$$(\eta_{ps} + \mu)(\lambda_{ps}^*)^2 + \lambda_{ps}^* \mu[1 - \Re_{ps}] = 0. \tag{23}$$

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

$$D_1 \lambda_{ps}^* + D_2 = 0. \tag{24}$$

Where $D_1 = (\eta_{ps} + \mu)$ and $D_2 = \mu[1 - \Re_{ps}]$.

It is clear that $D_1 > 0$ and $D_2 < 0$ when $\Re_{ps} > 1$. Thus the *Linear System (24)* has a unique positive solution, given by $\lambda_{ps}^* = \frac{-D_2}{D_1}$ whenever $\Re_{ps} > 1$.

Now, to show its local stability analysis, *Eq. (23)* gives a fixed point problem of the form

$$f(\lambda_{ps}^*) = (\eta_{ps} + \mu)(\lambda_{ps}^*)^2 + \lambda_{ps}^* \mu[1 - \Re_{ps}] = 0.$$

Then, derivatives of $f(\lambda_{ps}^*)$ become

$$f'(\lambda_{ps}^*) = [2(\eta_{ps} + \mu)\lambda_{ps}^*] + \mu[1 - \Re_{ps}]].$$

Evaluating $f'(\lambda_{ps}^*)$ at $\lambda_{ps}^* = -D_2/D_1$ gives

$$f'(-D_2/D_1) = 3\mu[1 - \Re_{ps}]],$$

$\Rightarrow |f'(\lambda_{ps}^*)| < 1$ at $\lambda_{ps}^* = -D_2/D_1$, whenever $\Re_{ps} > 1$.

Therefore, the unique endemic equilibrium is locally asymptotically stable if $\Re_{ps} > 1$.

8. Analysis HIV-HSV-II only Coinfection Model

Here analysis of HIV-HSV-II only coinfection model is considered and model equation obtained from *Eq. (1)*. This is

$$\frac{dS}{dt} = \Pi - (\lambda_{hs} + \mu)S, \tag{25}$$

$$\frac{dE_{hs}}{dt} = \lambda_{hs}S - (\eta_{hs} + \mu)E_{hs},$$

$$\frac{dI_{hs}}{dt} = \eta_{hs}E_{hs} - (\alpha_{hs} + \mu)I_{hs},$$

$$\frac{dAH}{dt} = \alpha_{hs}I_{hs} - (\mu + \xi)AH.$$

The invariant region, existence of solution and uniqueness of solution is can be determined similar to Section 3.1, 3.2, and 3.3.

8.1. Local Stability of the Disease-Free Equilibrium (DFE)

The disease free equilibrium of *Eq. (25)* is obtained by setting the system of equations in *Model (25)* to zero. At disease free equilibrium there are no infection and recovery. Then we obtain

$$E_6 = \left\{\left(\frac{\Pi}{\mu}\right), \quad 0, \quad 0, \quad 0\right\}.$$

The stability analysis of the DFE, E_6, can be established using basic reproduction number. The concept of the next generation matrix would be employed in computing the basic reproduction number. Using theorem 2 in Van den Driessche and Watmouth [23] on the HIV-HSV-II coinfection model in *Eq. (25)*, the basic reproduction number of the HIV-HSV-II only coinfection model, denoted by $\Re_{hs}$ is then given by

$$\Re_{hs} = \frac{(\beta_{hs}\eta_{hs})}{(\alpha_{hs} + \mu)(\mu + \xi)}.$$

Further using theorem 2 in Van den Driessche and Watmouth [23], the following result is established. The DFE is locally asymptotically stable if $\Re_{hs} < 1$ and unstable is $\Re_{hs} > 1$.

8.2. Stability Analysis of Endemic Equilibrium

The endemic equilibrium points are computed by setting the system of differential equations in the HIV-HSV-II only *Coinfection Model (25)* to zero. The endemic equilibrium points are as follows

$$S^* = [\Pi]/[\lambda_{hs}^* + \mu], \tag{26}$$

$$E_{hs}^* = [\lambda_{hs}^* \Pi]/[(\lambda_{hs}^* + \mu)(\eta_{hs} + \mu)],$$

$$I_{hs}^* = [\lambda_{hs}^* \eta_{hs} \Pi]/[(\lambda_{hs}^* + \mu)(\eta_{hs} + \mu)(\alpha_{hs} + \mu)],$$

$$AH^* = [\lambda_{hs}^* \eta_{hs} \alpha_{hs} \Pi]/[(\lambda_{hs}^* + \mu)(\eta_{hs} + \mu)(\alpha_{hs} + \mu)(\mu + \xi)].$$

Lemma 7. The HIV-HSV-II only coinfection model has a unique endemic equilibrium if and only if $\Re_{hs} > 1$.

Proof. Substituting *Eq. (26)* into force of infection, we can get

$$(\eta_{hs} + \mu)(\lambda_{hs}^*)^2 + \lambda_{hs}^* \mu[1 - \Re_{hs}] = 0. \tag{27}$$

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

$$D_1 \lambda_{hs}^* + D_2 = 0. \tag{28}$$

Where $D_1 = (\eta_{hs} + \mu)$ and $D_2 = \mu[1 - \Re_{hs}]$.

It is clear that $D_1 > 0$ and $D_2 < 0$ when $\Re_{hs} > 1$. Thus the *Linear System (28)* has a unique positive solution, given by $\lambda_{hs}^* = \frac{-D_2}{D_1}$ whenever $\Re_{hs} > 1$.

Now, to show its local stability analysis, *Eq. (27)* gives a fixed point problem of the form

$$f(\lambda_{hs}^*) = (\eta_{hs} + \mu)(\lambda_{hs}^*)^2 + \lambda_{hs}^* \mu[1 - \Re_{hs}] = 0.$$

Then, derivatives of $f(\lambda_{hs}^*)$ become

$$f'(\lambda_{hs}^*) = [2(\eta_{hs} + \mu)\lambda_{hs}^*] + \mu[1 - \Re_{hs}]].$$

Evaluating $f'(\lambda_{hs}^*)$ at $\lambda_{hs}^* = -D_2/D_1$ gives

$$f'(-D_2/D_1) = 3\mu[1 - \Re_{hs}]],$$

$\Rightarrow |f'(\lambda_{hs}^*)| < 1$ at $\lambda_{hs}^* = -D_2/D_1$, whenever $\Re_{hs} > 1$.

Therefore, the unique endemic equilibrium is locally asymptotically stable if $\Re_{hs} > 1$.

9. Analysis HPV-HIV-HSV-II only Coinfection Model

Here analysis of HPV-HIV-HSV-II *Coinfection Model (1)* is considered. The invariant region, existence of solution and uniqueness of solution is can be determined similar to Section 3.1, 3.2, and 3.3.

9.1. Local Stability of the Disease-Free Equilibrium (DFE)

The disease free equilibrium of *Eq. (1)* is obtained by setting the system of equations in *Model (1)* to zero. At disease free equilibrium there are no infection and recovery. Then we obtain;

$$\mathrm{E}_7 = \left\{\left(\frac{\Pi}{\mu}\right), 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0\right\}.$$

The stability analysis of the DFE, E_7, can be established using basic reproduction number. The concept of the next generation matrix would be employed in computing the basic reproduction number. Using theorem 2 in Van den Driessche and Watmouth [23] on the HPV-HIV-HSV-II coinfection model in *Eq. (1)*, the basic reproduction number of the HPV-HIV-HSV-II only coinfection model, denoted by $\Re_{phs}$ is then given by

$$\Re_{\mathrm{phs}} = \max\{\Re_{\mathrm{p}}, \Re_{\mathrm{h}}, \Re_{\mathrm{s}}, \Re_{\mathrm{ph}}, \Re_{\mathrm{ps}}, \Re_{\mathrm{hs}}\}.$$

Where

$$\Re_{\mathrm{p}} = \frac{(\beta_{\mathrm{p}}\eta_{\mathrm{p}})}{(\alpha_{\mathrm{p}}+\omega_{\mathrm{p}}+\mu)(\mu+\xi)}, \qquad \Re_{\mathrm{ph}} = \frac{(\beta_{\mathrm{ph}}\eta_{\mathrm{ph}})}{(\alpha_{\mathrm{ph}}+\mu)(\mu+\xi)},$$

$$\Re_{\mathrm{h}} = \frac{(\beta_{\mathrm{h}}\eta_{\mathrm{h}})}{(\alpha_{\mathrm{h}}+\mu)(\mu+\xi)}, \qquad \Re_{\mathrm{ps}} = \frac{(\beta_{\mathrm{ps}}\eta_{\mathrm{ps}})}{(\alpha_{\mathrm{ps}}+\mu)(\mu+\xi)},$$

$$\Re_{\mathrm{s}} = \frac{(\beta_{\mathrm{s}}\eta_{\mathrm{s}})}{(\alpha_{\mathrm{s}}+\omega_{\mathrm{s}}+\mu)(\mu+\xi)}, \qquad \Re_{\mathrm{hs}} = \frac{(\beta_{\mathrm{hs}}\eta_{\mathrm{hs}})}{(\alpha_{\mathrm{hs}}+\mu)(\mu+\xi)}.$$

Further using theorem 2 in Van den Driessche and Watmouth [23], the following result is established. The DFE is locally asymptotically stable if $\Re_{phs} < 1$ and unstable is $\Re_{phs} > 1$.

10. Numerical Simulation

In this section, numerical simulation study of model *Eqs. (1), (2), (9), (13), (17), (21)* and *(25)* are carried out using the software MATLAB R 2015b with ODE45 solver. To conduct the study, a set of physically meaningful values are assigned to the model parameters. These values are either taken from literature or assumed on the basis of reality. Using the parameter values given in *Table 2* and the initial conditions $S(0) = 600,\ E_p(0) = 170,\ E_{ph}(0) = 250,\ E_{ps}(0) = 200, E_h(0) = 200,\ E_{hs}(0) = 240,\ E_s(0) = 250,\ I_p(0) = 140,\ I_{ph}(0) = 140,\ I_{ps}(0) = 140,\ I_h(0) = 160,\ I_{hs}(0) = 180, I_s(0) = 160,\ A(0) = 40,\ C(0) = 60,\ CA(0) = 40,\ AH(0) = 50,\ CH(0) = 50,\ H(0) = 50\ , ACH(0) = 30, R_p = 120, R_s = 130$ in the model

Eqs. (1), (2), (9), (13), (17), (21) and *(25)* a simulation study is conducted and the results are given in the following Figures.

Table 2. *Parameter values used in simulations.*

Parameter	Value	Source	Parameter	Value	Source
Π	*0.004*	*[18]*	π	*0.01*	*assumed*
β_s	*0.0018*	*assumed*	ψ	*0.3*	*assumed*
β_h	*0.042*	*assumed*	δ	*0.12*	*assumed*
β_p	*0.042*	*assumed*	γ	*0.14*	*assumed*
β_{ph}	*0.019*	*assumed*	ν_{19}	*0.02*	*assumed*
β_{ps}	*0.03*	*assumed*	ν_1	*0.04*	*assumed*
β_{hs}	*0.02*	*assumed*	ν_2	*0.02*	*assumed*
χ_p	*0.045*	*assumed*	ν_{20}	*0.03*	*assumed*
χ_s	*0.045*	*assumed*	ν_3	*0.04*	*assumed*
η_s	*0.02*	*assumed*	ν_4	*0.05*	*assumed*
η_h	*0.02*	*assumed*	ν_{15}	*0.02*	*assumed*
η_p	*0.02*	*assumed*	ν_6	*0.03*	*assumed*
η_{ph}	*0.02*	*assumed*	ν_7	*0.04*	*assumed*
η_{ps}	*0.02*	*assumed*	ν_{16}	*0.03*	*assumed*
η_{hs}	*0.02*	*assumed*	ν_8	*0.02*	*assumed*
α_s	*0.03*	*assumed*	ν_9	*0.02*	*assumed*
α_h	*0.03*	*assumed*	ν_{10}	*0.03*	*assumed*
α_p	*0.03*	*assumed*	ν_{17}	*0.04*	*assumed*
α_{ph}	*0.03*	*assumed*	ν_{11}	*0.05*	*assumed*
α_{ps}	*0.03*	*assumed*	ν_{18}	*0.02*	*assumed*
α_{hs}	*0.03*	*assumed*	ν_{12}	*0.03*	*assumed*
ω_p	*0.035*	*assumed*	ν_{13}	*0.04*	*assumed*
ω_s	*0.045*	*assumed*	φ	*0.1*	*assumed*
ξ	*0.0001*	*[18]*	θ	*0.2*	*assumed*

In *Fig. 2* we observe that all the solutions converge towards the equilibrium point. This was obtained when $\Re_p < 1$. At disease free equilibrium point, all infection solutions converge to zero while the susceptible individuals decreases and then remains constant. Cervical cancer cannot be cured that is why susceptible individuals remain constant. This indicates that the disease free equilibrium point is locally asymptotically stable.

Fig. 3 illustrate that all the solutions converge towards the equilibrium point. This was obtained when $\Re_h < 1$. At disease free equilibrium point, all infection solutions converge to zero while the susceptible individuals decreases and then remains constant. AID cannot be cured that is why susceptible individuals remain constant. This indicates that the disease free equilibrium point is locally asymptotically stable. *Fig. 4* show that all the solutions converge towards the equilibrium point. This was obtained when $\Re_s < 1$. At disease free equilibrium point, all infection solutions converge to zero while the susceptible individuals decreases and then remains constant. This indicates that the disease free equilibrium point is locally asymptotically stable.

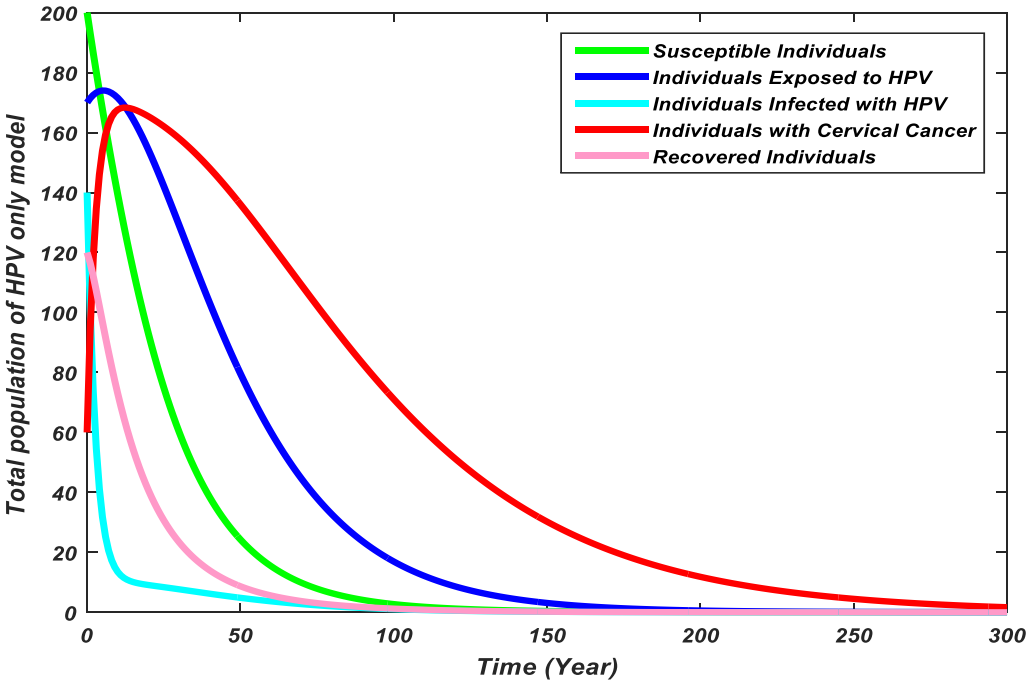

Fig. 2. *Dynamics of HPV model.*

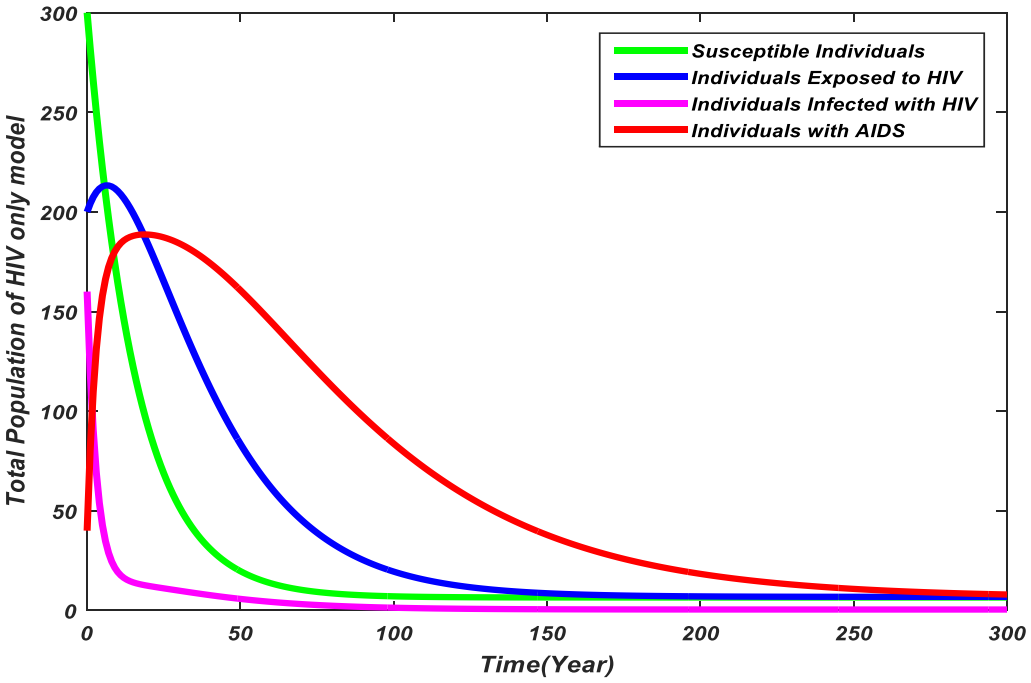

Fig. 3. *Dynamics of HIV model.*

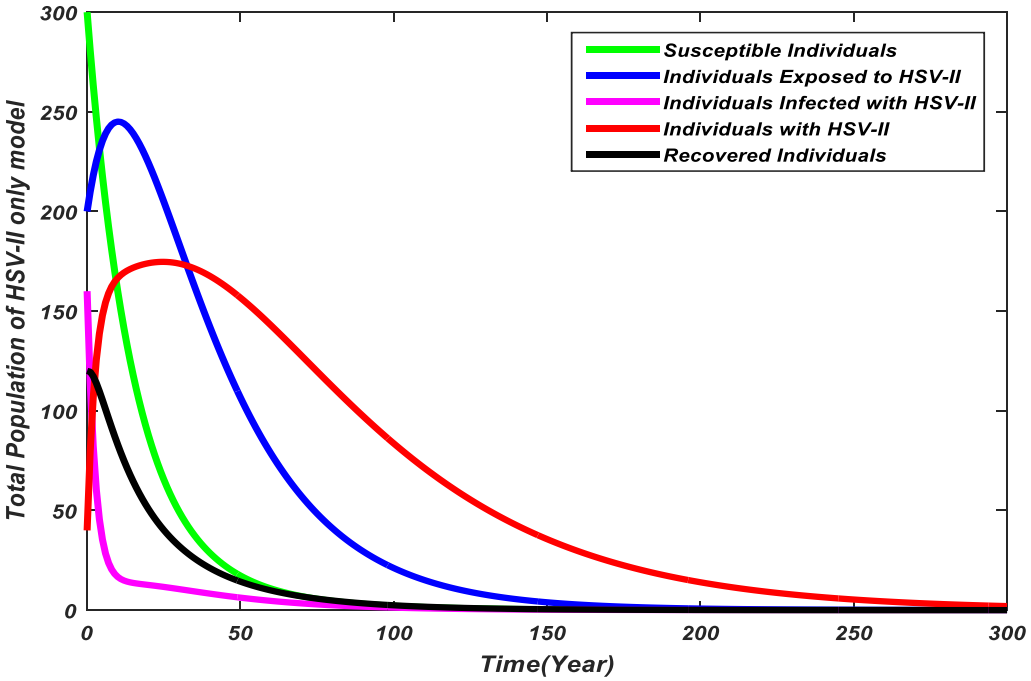

Fig. 4. *Dynamics of HSV-II.*

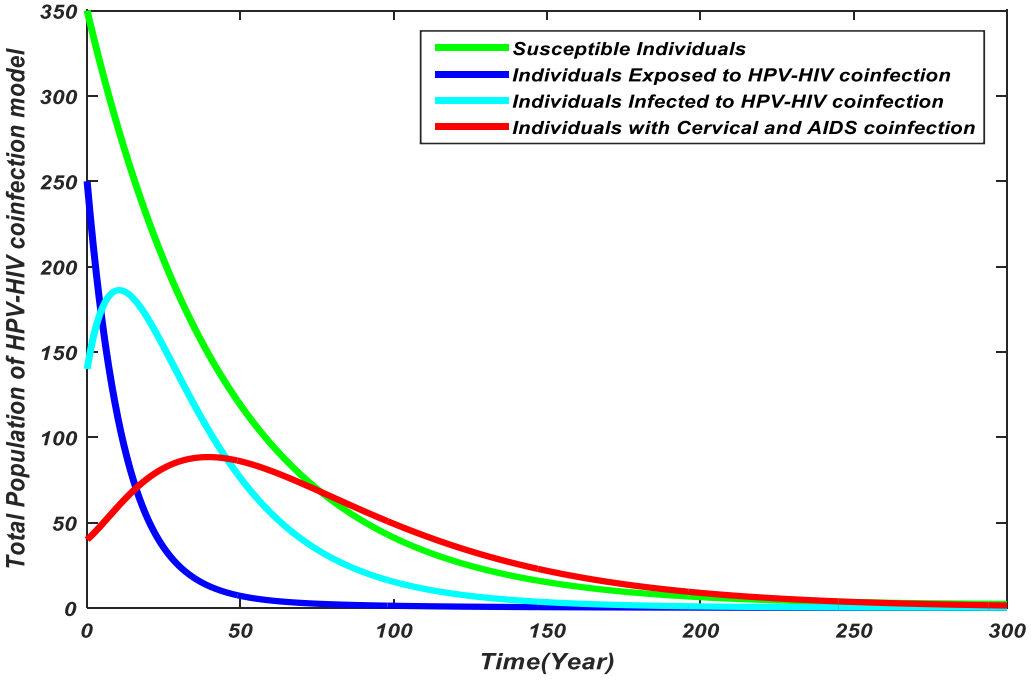

Fig. 5. *Dynamics of HPV-HIV coinfection.*

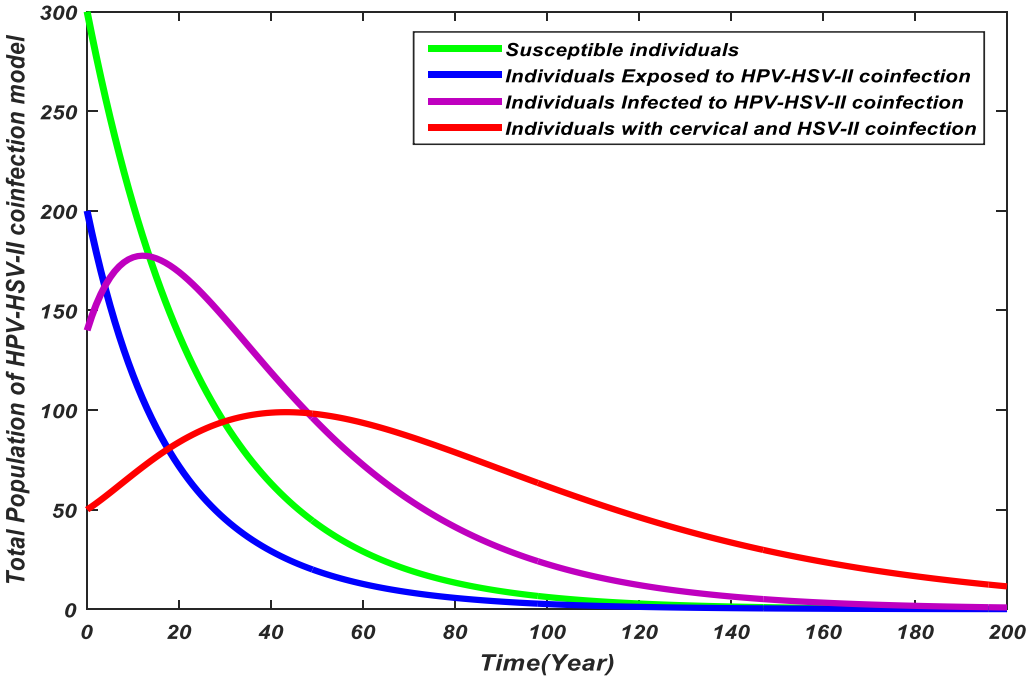

Fig. 6. *Dynamics of HPV-HSV-II coinfection.*

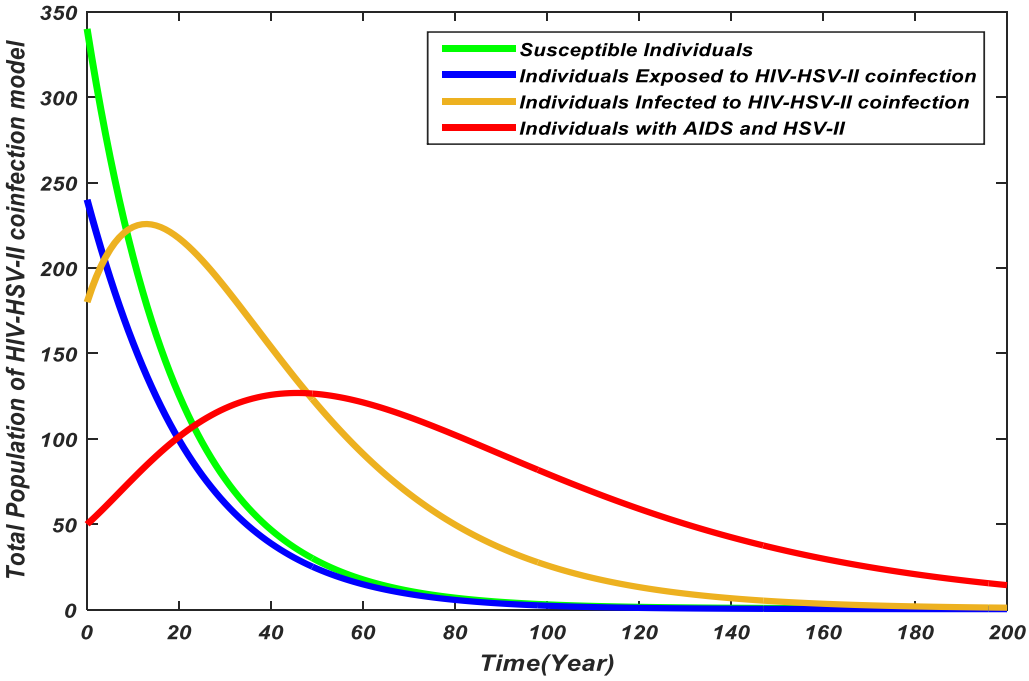

Fig. 7. *Dynamics of HIV-HSV-II coinfection.*

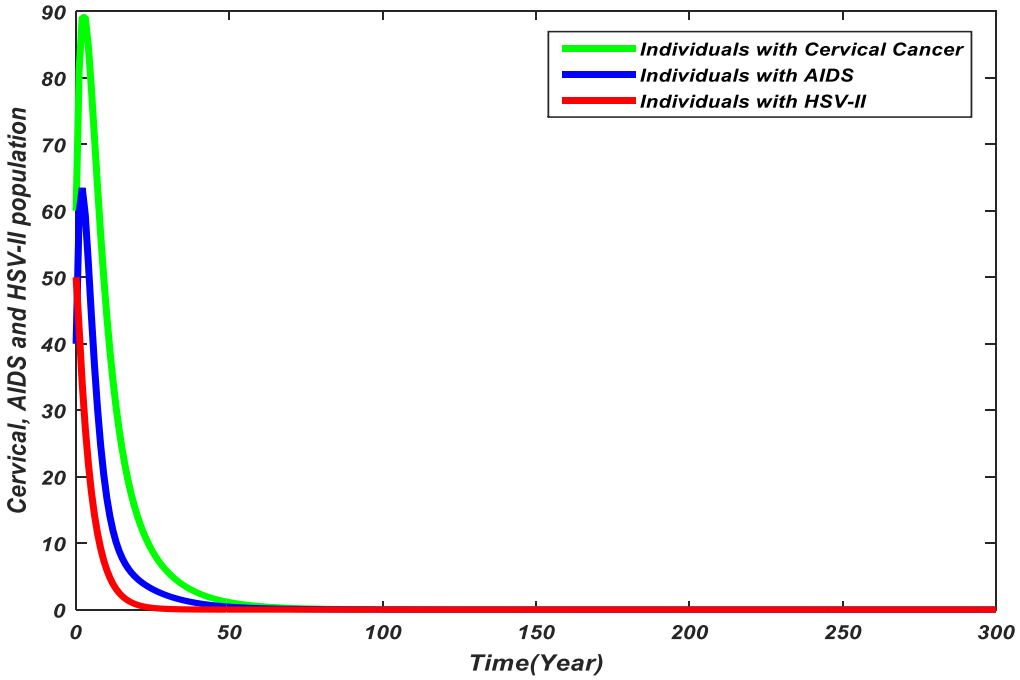

Fig. 8. *Dynamics of cervical cancer, AIDS and HSV-II.*

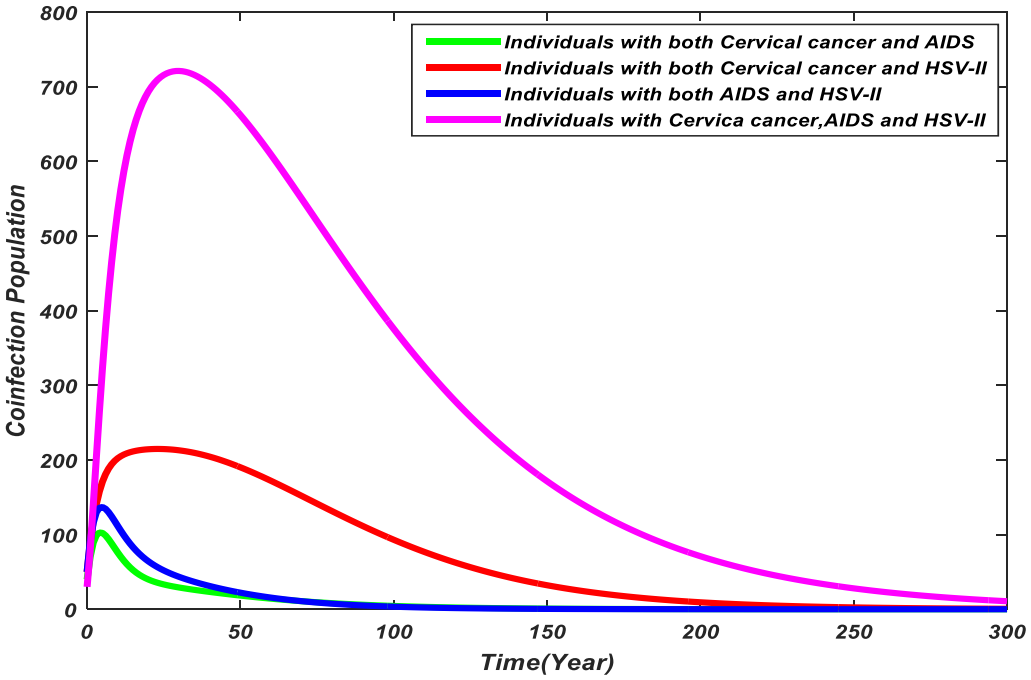

Fig. 9. *Dynamics of co-infectious.*

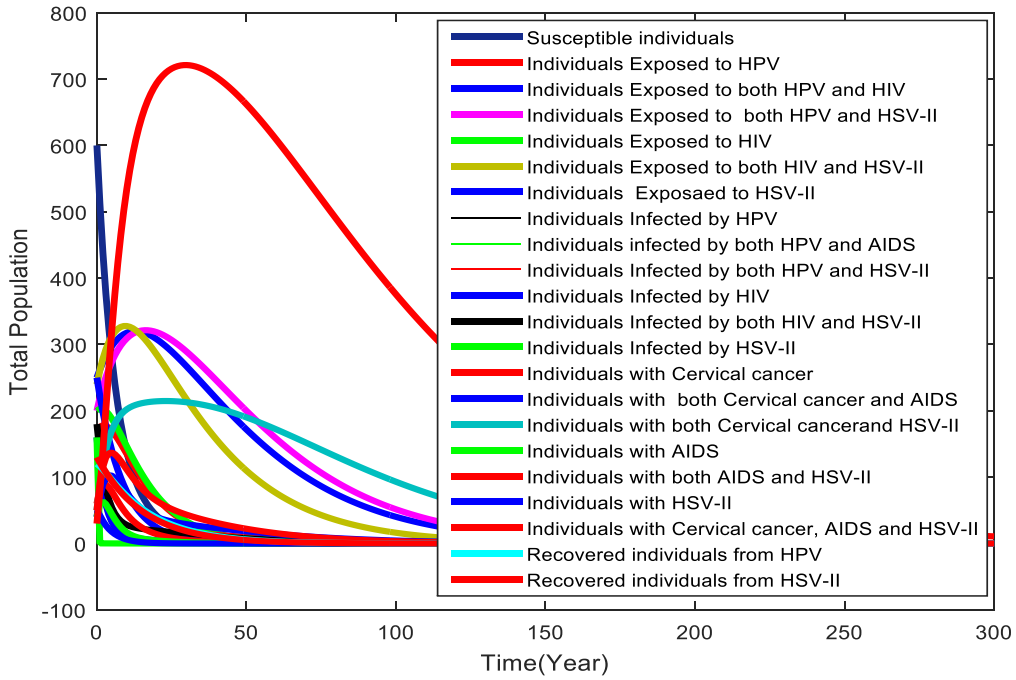

Fig. 10. *Dynamics of total population*.

Furthermore, *Fig. 5* describe that all the solutions converge towards the equilibrium point. At disease free equilibrium point, all infection solutions converge to zero while the susceptible individuals decreases and then remains constant. AIDS with Cervical cancer cannot be cured that is why susceptible individuals remain constant. This indicates that the disease free equilibrium point is locally asymptotically stable. Also, in *Fig. 6* we observe that all the solutions converge towards the equilibrium point. At disease free equilibrium point, all infection solutions converge to zero while the susceptible individuals decreases and then remains constant. Cervical cancer with HSV-II cannot be cured that is why susceptible individuals remain constant. This indicates that the disease free equilibrium point is locally asymptotically stable. Similarly *Fig. 7* show that all solution converges to disease free equilibrium.

Moreover, *Fig. 8* illustrate that cervical cancer affects people more than AIDS and HSV-II, but AIDS affects people more than HSV-II. Also, *Fig. 9* describe that the coinfection of three diseases (i.e. Cervical cancer, AIDS and HSV-II) affects people more than coinfection of two diseases (i.e. Cervical cancer-AIDS, Cervical cancer-HSV-II, AIDS-HSV-II coinfection). Finally, *Fig. 10* show that at disease free equilibrium all solution converges to zero. This indicates that the disease free equilibrium point is locally asymptotically stable.

11. Discussions and Conclusions

In this paper, we developed a deterministic model for the transmission dynamics of HPV, HIV and HSV-II coinfection. The qualitative analysis of the model shows that there exists a domain where the model is epidemiologically and mathematically well-posed. The stability analysis of the model was investigated using the basic reproduction number that governs the disease transmission. The HPV only model, HIV only model, HSV-II only model, HPV-HIV only coinfection model, HPV-HSV-II only coinfection model, HIV-HSV-II only coinfection model, and HPV-HIV-HSV-II only coinfection model, has a locally stable disease free equilibrium whenever the associated reproduction number is

less than unity. Also, the model has a unique endemic equilibrium whenever the basic reproduction number is less great unity. Furthermore, numerical simulation shows that at disease free equilibrium point, all infection solutions converge to zero. This was obtained when the associated reproduction number is less than unity. This indicates that the disease free equilibrium point is locally asymptotically stable.

Data Availability

The data used in this paper is freely accessible for the user.

Conflicts of Interest

The authors state that there are no conflicts of interest concerning to the publication of this article.

Reference

[1] Shahzad, N., Farooq, R., Aslam, B., & Umer, M. (2017). Microbicides for the Prevention of HPV, HIV-1, and HSV-2: Sexually Transmitted Viral Infections. In *Fundamentals of sexually transmitted infections*. DOI: 10.5772/intechopen.68927

[2] Bergot, A. S., Kassianos, A., Frazer, I. H., & Mittal, D. (2011). New approaches to immunotherapy for HPV associated cancers. *Cancers*, *3*(3), 3461-3495.

[3] Lowy, D. R., & Schiller, J. T. (2006). Prophylactic human papillomavirus vaccines. *The journal of clinical investigation*, *116*(5), 1167-1173.

[4] World Health Organization. (2017). *WHO list of priority medical devices for cancer management*. World Health Organization.

[5] Wodarz, D. (2007). *Killer cell dynamics mathematical and computational approaches to immunology*. Springer.

[6] Nowak, M., & May, R. M. (2000). *Virus dynamics: mathematical principles of immunology and virology: mathematical principles of immunology and virology*. Oxford University Press, UK.

[7] UNAIDS data 2019. (2019). Retrieved from https://www.unaids.org/en/resources/documents/2019/2019-UNAIDS-data

[8] CDC. (2001). *Genital herpes information*. Retrieved July 15, 2020, from www.cdc.gov/std/Herpes/default.htm

[9] *WHO guidelines for the treatment of genital herpes simplex virus*. (2016). World Health Organization. Retrieved from file:///C:/Users/jpour/Downloads/9789241549875-eng.pdf

[10] Taira, A. V., Neukermans, C. P., & Sanders, G. D. (2004). Evaluating human papillomavirus vaccination programs. *Emerging infectious diseases*, *10*(11), 1915-1923.

[11] Ribassin-Majed, L., Lounes, R., & Clémençon, S. (2012). Efficacy of vaccination against HPV infections to prevent cervical cancer in France: present assessment and pathways to improve vaccination policies. *PloS one*, *7*(3), e32251.

[12] Gurmu, E. D., & Koya, P. R. (2019). Sensitivity analysis and modeling the impact of screening on the transmission dynamics of human papilloma virus (HPV). *American journal of applied mathematics*, *7*(3), 70-79. Doi: 10.11648/j.ajam.20190703.11

[13] Okosun, K. O., Makinde, O. D., & Takaidza, I. (2013). Impact of optimal control on the treatment of HIV/AIDS and screening of unaware infectives. *Applied mathematical modelling*, *37*(6), 3802-3820.

[14] Silva, C. J., & Torres, D. F. (2017). Modeling and optimal control of HIV/AIDS prevention through PrEP. *Discrete and continuous dynamical systems series S*, *11*(9), 119-141. 10.3934/dcdss.2018008

[15] Gurmu, E. D., Bole, B. K., & Koya, P. R. (2020). Mathematical Modelling of HIV/AIDS Transmission Dynamics with Drug Resistance Compartment. *American journal of applied mathematics*, *8*(1), 34-45.

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

[17] Mhlanga, A., Bhunu, C. P., & Mushayabasa, S. (2015, November). A computational study of HSV-2 with poor treatment adherence. *Abstract and applied analysis* (Vol. 2015). https://doi.org/10.1155/2015/850670

[18] Gurmu, E. D., Bole, B. K., & Koya, P. R. (2020). Mathematical model for co-infection of HPV with cervical cancer and HIV with AIDS diseases. *Int. J. Sci. Res. in mathematical and statistical sciences*, *7*(2), 107-121.

[19] Sanga, G. G., Makinde, O. D., Massawe, E. S., & Namkinga, L. (2017). Modeling co-dynamics of Cervical cancer and HIV diseases. *Global journal of pure and applied mathematics*, *13*(6), 2057-2078.

[20] Gurmu, E. D., Bole, B. K., & Koya, P. R. (2020). A Mathematical model for co-infection of HPV and HSV-II with drug resistance compartment. *Int. J. Sci. Res. in mathematical and statistical sciences*, *7*(2), 34-46.

[21] Hühns, M., Simm, G., Erbersdobler, A., & Zimpfer, A. (2015). HPV infection, but not EBV or HHV-8 infection, is associated with salivary gland tumours. *BioMed research international*. https://doi.org/10.1155/2015/829349

[22] Mhlanga, A. (2018). A theoretical model for the transmission dynamics of HIV/HSV-2 co-infection in the presence of poor HSV-2 treatment adherence. *Applied mathematics and nonlinear sciences*, *3*(2), 603-626.

[23] Van den Driessche, P., & Watmough, J. (2002). Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission. *Mathematical biosciences*, *180*(1-2), 29-48.

[24] Weinstein, S. J., Holland, M. S., Rogers, K. E., & Barlow, N. S. (2020). Analytic solution of the SEIR epidemic model via asymptotic approximant. *Physica D: nonlinear phenomena*, *411*, 132633. https://doi.org/10.1016/j.physd.2020.132633