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Mathematical Model for the Study of Human Papillomavirus Infection Towards Cervical Cancer Treatments with Clinical Intervention

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ABSTRACT

This study develops an extended deterministic compartmental model for HPV transmission and cervical cancer progression by incorporating vaccination, severe cervical cancer, hospitalization, and clinical treatment, including surgery, chemotherapy, and radiation therapy. The model describes transmission between female and male populations and the progression of HPV infection through precancerous and cancerous stages to treatment and recovery. The disease-free and endemic equilibria are derived, and the basic reproduction number is obtained using the next-generation matrix approach. Local stability of the disease-free equilibrium is established in terms of the reproduction number, while the endemic equilibrium is investigated using the Routh–Hurwitz criterion and eigenvalue analysis. For the parameter set considered, the stability analysis further indicates that the endemic equilibrium is locally asymptotically stable. Numerical simulations are performed in MATLAB using parameter values obtained from the literature and assumed clinical-intervention rates. The results show that vaccination reduces HPV infection, while the combined implementation of vaccination, hospitalization, and treatment produces a greater reduction in infection, cancer progression and increases recovery.

1. Introduction

Human papillomavirus (HPV) infection is a major cause of cervical cancer, particularly in populations where vaccination and access to clinical care remain limited. In this study, we extend the compartmental HPV transmission model previously developed by Mumtaz *et al.* (2024) by incorporating additional compartments representing hospitalization and medical treatments such as surgery, chemotherapy, and radiation therapy. The model further integrates vaccination as a crucial preventive strategy alongside clinical interventions targeting advanced stages of cervical cancer. This extension captures the full dynamics of HPV infection and cervical cancer progression, accounting for

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unequal male and female recruitment and natural death rates, and reflects realistic healthcare pathways for infected individuals.

The model structure considers vaccination as a primary public health intervention aimed at reducing the risk of HPV acquisition, while hospitalization and specific treatment compartments are introduced to reflect the progression of severe cervical cancer cases and the medical processes involved in recovery. Unlike the prior work of Mumtaz *et al.* (2024), this model explicitly tracks severe cancerous infections, hospitalization, and treatment outcomes.

Furthermore, three new compartments are incorporated: Severe Cancerous Females (females whose cervical cancer has progressed to a critical stage requiring urgent medical attention), Hospitalized Females (females admitted for advanced care), and Treated Females (females undergoing chemotherapy, surgery, or radiation therapy). These modifications allow for a more detailed analysis of how medical interventions influence the spread, control, and eventual eradication of HPV infections and cervical cancer within a population. High vaccination coverage, especially before the onset of sexual activity, is critical for achieving herd immunity and substantially lowering HPV prevalence. Studies by Brisson *et al.* (2016) highlight the effectiveness of HPV vaccination programs in reducing both HPV transmission and the incidence of cervical cancer. However, achieving optimal coverage levels remains a challenge in many regions due to socioeconomic factors, vaccine hesitancy, and limited healthcare access. As noted by Drolet *et al.* (2019), while high-income countries have seen significant reductions in HPV infections and related cancers due to extensive vaccination coverage, low- and middle-income countries—where the burden of cervical cancer is highest—continue to struggle with low vaccination rates. This disparity suggests the need for tailored strategies that consider local vaccination coverage, healthcare infrastructure, and public health campaigns to maximize vaccine uptake.

Models developed by Barnabas et al. (2006) and Canfell *et al.* (2011) show that combining vaccination with regular screening can provide significant additional reductions in cervical cancer incidence, particularly in older populations that are beyond the recommended age for vaccination. Optimal control theory, applied in works by Elbasha (2016) and Tewa *et al.* (2019), has been used to evaluate the most cost-effective strategies for HPV control. These studies demonstrate that higher initial investments in vaccination, coupled with sustained screening efforts, yield the greatest long-term benefits in terms of reducing both HPV infections and healthcare costs associated with cervical cancer treatment.

Research by Omame *et al.* (2022) calls for the development of more sophisticated models that not only capture the biological dynamics of HPV but also account for social, behavioral, and economic factors that influence the success of interventions. Existing literature provides a strong foundation for understanding HPV transmission dynamics and the role of vaccination in preventing cervical cancer. However, there remain critical gaps in the integration of sexual mixing patterns and vaccination coverage with clinical interventions.

2. Methodology

2.1 Model Description

The population of both susceptible female, S_f and susceptible male S_m changes due to the coming in of new recruited individuals at the rate π_f and π_m respectively. The later reduces to male infected class due to the rate, β_f and the former due to the rate, β_m. Vaccinated females also get infected at waning rate ω. Infected females moved to the Precancerous class at the rates δ. Individuals in the Precancerous class move to the Cancerous class at the rates θ. Cancerous females became Severe at the rate α while at this chronic situation, females were hospitalized at the rate τ and received treatment due to the rate ρ and finally recovered at the rate γ. Due to the fact that the disease is self-

treated before being chronic, infected and precancerous females may join the recovered compartment at the rates μ_f and ξ respectively. Infected males also recovered naturally at the rate μ_m, (See Fig. 1). The variables of the model is shown in Table 1, while Parameters of the model and their values are clearly displayed in Table 2.

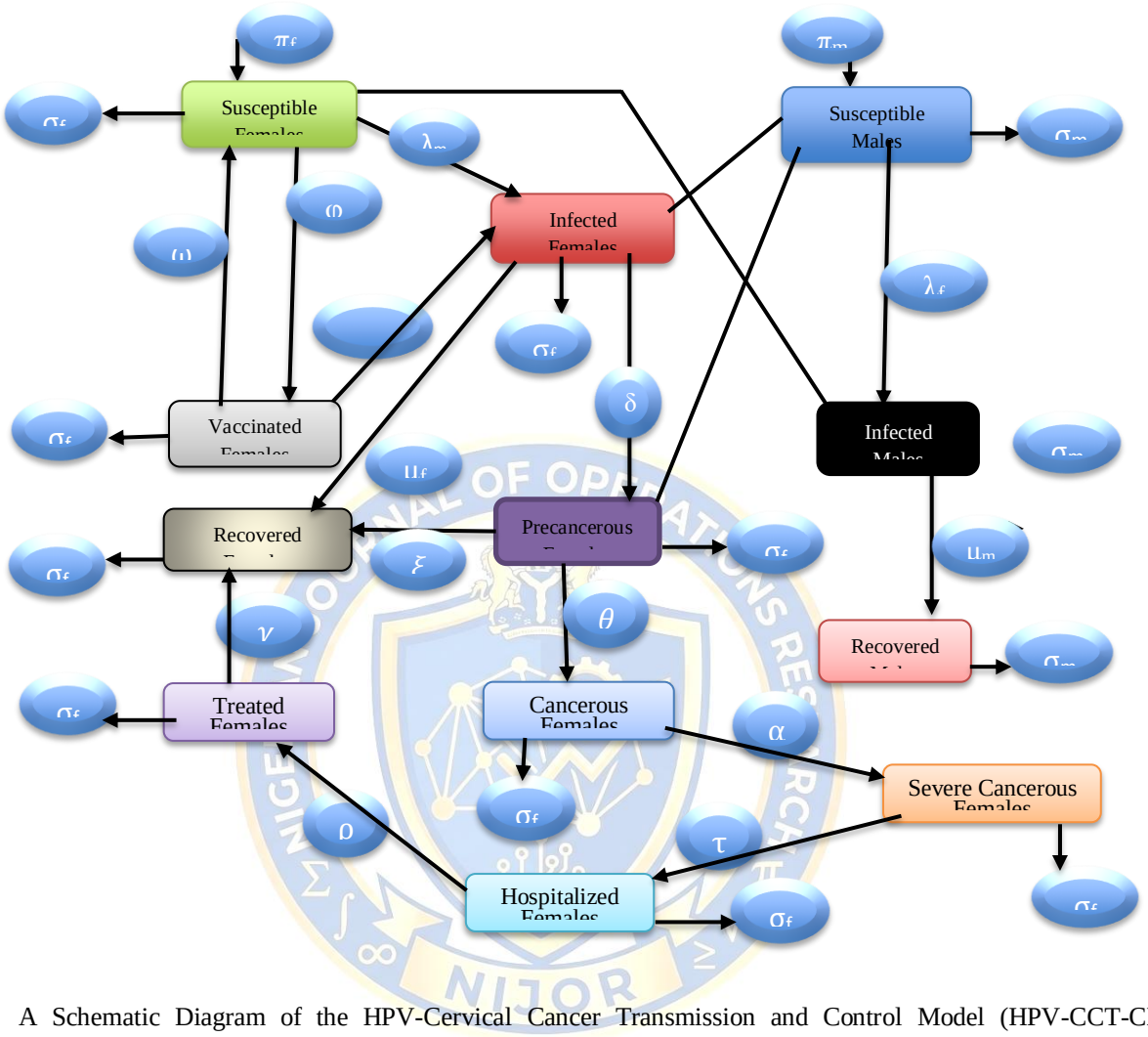


Fig. 1: A Schematic Diagram of the HPV-Cervical Cancer Transmission and Control Model (HPV-CCT-CM) Incorporating Vaccination, Hospitalization, and Treatment Interventions.

Table 1: The variables of the model

Variable	Description
$S_f(t)$	Susceptible females at time
$V_a(t)$	Vaccinated females at time
$I_f(t)$	Infected females at time
$P_r(t)$	Precancerous females at time
$C_n(t)$	Cancerous females at time
$T_r(t)$	Treated females at time
$R_f(t)$	Recovered females at time
$S_m(t)$	Susceptible males at time
$I_m(t)$	Infected males at time
$R_m(t)$	Recovered males at time

Table 2: Parameters of the model and their values

Description	Symbol	Value	Reference
Intrinsic growth rate of susceptible female (male) population	$\pi_f(\pi_m)$	10,000/year	Ref. 9
Contact Rate for female (male)	$\beta_f(\beta_m)$	0.5/contact	Ref. 9
Average number of female (male) sexual partners for male (females)	$d_f(d_m)$	2 contact/year	Ref. 9
Natural death rate for female (male)	$\sigma_f(\sigma_m)$	0.015/year	Ref. 9
Progression rate from infected to precancerous	δ	0.3/year	Ref. 9
Transition rate from precancerous to cancerous	θ	0.2/year	Ref. 9
Vaccinated rate	ϕ	0.6	Ref. 9
Efficacy rate of vaccine	ϵ	0.8	Ref. 9
Vaccine waning rate	ω	0.2	Ref. 9
Modification parameter	η	0.3	Ref. 9
Recovery rate of precancerous female	ξ	0.2	Ref. 9
Recovery rate of females (males) infected from HPV	$\mu_f(\mu_m)$	0.2(0.4)	Ref. 9
The rate at which cancerous individuals move to severe cancerous class	α	0.01	Assumed
The rate at which severe cancerous individuals move to hospitalized class	τ	0.22	Assumed
The rate at which hospitalized individuals move to treatment class	ρ	0.55	Assumed
The rate at which Treated individuals move to recovered class	γ	0.09	Assumed

2.2 Governing equations

$$
\begin{aligned}
\frac{dS_f}{dt} &= \pi_f + \omega V_a - \phi S_f - \lambda_m S_f - \sigma_f S_f \\
\frac{dV_a}{dt} &= \phi S_f - \omega V_a - \lambda_m(1-\varepsilon)V_a - \sigma_f V_a \\
\frac{dI_f}{dt} &= \lambda_m S_f + \lambda_m(1-\varepsilon)V_a - \delta I_f - \mu_f I_f - \sigma_f I_f \\
\frac{dP_r}{dt} &= \delta I_f - \theta P_r - \xi P_r - \sigma_f P_r \\
\frac{dC_n}{dt} &= \theta P_r - \alpha C_n - \sigma_f C_n \\
\frac{dS_c}{dt} &= \alpha C_n - \tau S_c - \sigma_f S_c \\
\frac{dH_p}{dt} &= \tau S_c - \rho H_p - \sigma_f H_p \\
\frac{dT_r}{dt} &= \rho H_p - \gamma T_r - \sigma_f T_r \\
\frac{dR_f}{dt} &= \mu_f I_f + \xi P_r + \gamma T_r - \sigma_f R_f \\
\frac{dS_m}{dt} &= \pi_m - \lambda_f S_m - \sigma_m S_m \\
\frac{dI_m}{dt} &= \lambda_f S_m - \mu_m I_m - \sigma_m I_m \\
\frac{dR_m}{dt} &= \mu_m I_m - \sigma_m R_m
\end{aligned}
\qquad (1)
$$

where the force of infection is defined as:

$$\lambda_f = \frac{d_m \beta_f (I_f + \eta P_r)}{N_f} \quad \text{and} \quad \lambda_m = \frac{d_f \beta_m I_m}{N_m}.$$

The parameters $d_m\beta_f$ and $d_f\beta_m$ in Eq.(1) are the effective contact rate for transfer of infection from female to male and male to female respectively, and $0 < \eta < 1$ is a modification parameter relative to precancerous humans.

3. Material and Methods

In this section, we adopt the model by (Mumtaz *et al.* 2024) to describe a deterministic modeling approach on HPV-Cervical Cancer Transmission and Control Model. The aim is to get a clear understanding of the mathematical model on the effect of the vaccine in the transmission of HPV. This model has been extended and modified as shown in Eq. (1) to include clinical intervention such as chemotherapy, surgery and Radiation therapy. There is no specific data collected primarily but the values of parameters were extracted as secondary data from the recent literatures and used for simulation analysis, (see Table 2). MATLAB software has been used for this simulation.

3.1 Model assumptions

1. There is vaccine available against the HPV infection.
2. The vaccine does not confer permanent immunity against the HPV infection.
3. Infectious individuals are assumed to transmit the infection at different constant rates.
4. The infectious individuals are assumed also to recover from the infection at different constant rates.
5. Recovery from the infection does not confer permanent immunity against the disease.
6. All individuals in the model suffer the effect of natural mortality at a uniform constant rate.

3.2 Equilibrium Points

The analysis of equilibrium points is fundamental to understanding the long-term behavior of the HPV-Cervical Cancer Transmission and Control Model (HPV-CC-TCM). Equilibrium points are achieved when the population within each compartment remains constant over time, indicating that the rates of inflow and outflow for all compartments are balanced (Arendt et al., 2012). The model focuses on two primary equilibrium points: the Disease-Free Equilibrium (DFE) and the Endemic Equilibrium (EE).

3.2.1 Disease-Free Equilibrium (DFE)

At the DFE, there are no infections in the population; hence, all compartments associated with infection are zero. The DFE is given explicitly in Eq.(2) as:

$$\left.\begin{aligned} S_f = \frac{\pi_f(\omega+\sigma_f)}{(\phi+\sigma_f)(\omega+\sigma_f)-\phi\omega}, V_a = \frac{\phi\pi_f}{(\phi+\sigma_f)(\omega+\sigma_f)-\phi\omega}, S_m = \frac{\pi_m}{\sigma_m}, \\ I_f = P_r = C_n = S_c = H_p = T_r = R_f = I_m = R_m = 0 \end{aligned}\right\} \quad (2)$$

3. 2.2 Model stability

At the steady stages we determine the model stability, since Eq. (3) holds well, that is;

$$\frac{dS_f}{dt}=\frac{dV_a}{dt}=\frac{dI_f}{dt}=\frac{dP_r}{dt}=\frac{dC_n}{dt}=\frac{dS_c}{dt}=\frac{dH_p}{dt}=\frac{dT_r}{dt}=\frac{dR_f}{dt}=\frac{dS_m}{dt}=\frac{dI_m}{dt}=\frac{dR_m}{dt}=0 \quad (3)$$

Now, to determine the stability of the model in Eq. (1), the following Lemma guides the study.

3.2.3 Force-of-infection derivatives

The force of infection is given by Eq.(4) as:

$$\lambda_f=\frac{d_m\beta_f(I_f+\eta P_r)}{N_f} \quad \text{and} \quad \lambda_m=\frac{d_f\beta_m I_m}{N_m} \quad (4)$$

Therefore,

$$\frac{\partial\lambda_f}{\partial I_f}=\frac{d_m\beta_f}{N_f},\ \frac{\partial\lambda_f}{\partial P_r}=\frac{\eta d_m\beta_f}{N_f} \text{ and } \frac{\partial\lambda_m}{\partial I_m}=\frac{\eta d_f\beta_m}{N_m}$$

All other derivatives of the force of infection with respect to the state variables are zero, apart from possible denominator effects. At the DFE, those denominator terms disappear because

$$I_f=P_r=I_m=0$$

This is exactly the coupling that we need to get the Jacobian for.

At the DFE, Eq. (5) hold true, that is,

$$I_f^*=P_r^*=C_n^*=S_c^*=H_p^*=T_r^*=R_f^*=I_m^*=R_m^*=0 \quad (5)$$

The non-infected equilibrium components are

$$S_f^*=\frac{\pi_f(\omega+\sigma_f)}{(\phi+\sigma_f)(\omega+\sigma_f)}$$

which simplifies to obtain Eq.(6) as

$$S_f^*=\frac{\pi_f}{(\phi+\sigma_f)} \quad (6)$$

$$V_a^*=\frac{\phi\pi_f}{(\phi+\sigma_f)(\omega+\sigma_f)}$$

$$S_m^*=\frac{\pi_m}{\sigma_m}$$

Thus, we finally obtain Eq. (7) as follows;

$$E_0=(S_f^*,V_a^*,0,0,0,0,0,0,0,S_m^*,0,0) \quad (7)$$

3.2. 4 Endemic Equilibrium (EE) points are:

$$S_f=\frac{\pi_f(\omega+\lambda_m(1-\varepsilon)+\sigma_f)}{(\phi+\lambda_m+\sigma_f)(\omega+\lambda_m(1-\varepsilon)+\sigma_f)-\phi\omega}$$

$$V_a=\frac{\phi\pi_f}{(\phi+\lambda_m+\sigma_f)(\omega+\lambda_m(1-\varepsilon)+\sigma_f)-\phi\omega}$$

$$I_f=\frac{\lambda_m\pi_f\{\omega+\sigma_f+(\lambda_m+\phi)(1-\varepsilon)\}}{\{(\phi+\lambda_m+\sigma_f)(\omega+\lambda_m(1-\varepsilon)+\sigma_f)-\phi\omega\}(\delta+\mu_f+\sigma_f)}$$

$$P_r = \frac{\delta\lambda_m\pi_f\{\omega+\sigma_f+(\lambda_m+\phi)(1-\varepsilon)\}}{\{(\phi+\lambda_m+\sigma_f)(\omega+\lambda_m(1-\varepsilon)+\sigma_f)-\phi\omega\}(\delta+\mu_f+\sigma_f)(\theta+\xi+\sigma_f)}$$

$$C_n = \frac{\theta\delta\lambda_m\pi_f\{\omega+\sigma_f+(\lambda_m+\phi)(1-\varepsilon)\}}{(\rho+\sigma_f)\{(\phi+\lambda_m+\sigma_f)(\omega+\lambda_m(1-\varepsilon)+\sigma_f)-\phi\omega\}(\delta+\mu_f+\sigma_f)(\theta+\xi+\sigma_f)}$$

$$S_c^* = \frac{\{\omega+\sigma_f+(\lambda_m+\phi)(1-\varepsilon)\}\{\theta\delta\lambda_m\pi_f(\alpha+\sigma_f)+\alpha\theta\delta\lambda_m\pi_f\}}{(\tau+\sigma_f)\{(\phi+\lambda_m+\sigma_f)(\omega+\lambda_m(1-\varepsilon)+\sigma_f)-\phi\omega\}(\delta+\mu_f+\sigma_f)(\theta+\xi+\sigma_f)}$$

$$H_p^* = \frac{\tau\{\omega+\sigma_f+(\lambda_m+\phi)(1-\varepsilon)\}\{\theta\delta\lambda_m\pi_f(\alpha+\sigma_f)+\alpha\theta\delta\lambda_m\pi_f\}}{(\tau+\sigma_f)(\rho+\sigma_f)\{(\phi+\lambda_m+\sigma_f)(\omega+\lambda_m(1-\varepsilon)+\sigma_f)-\phi\omega\}(\delta+\mu_f+\sigma_f)(\theta+\xi+\sigma_f)}$$

$$T_r^* = \frac{\rho\tau\{\omega+\sigma_f+(\lambda_m+\phi)(1-\varepsilon)\}\{\phi\delta\lambda_m\pi_f(\alpha+\sigma_f)+\alpha\theta\delta\lambda_m\pi_f\}}{(\gamma+\sigma_f)(\tau+\sigma_f)(\rho+\sigma_f)\{(\phi+\lambda_m+\sigma_f)(\omega+\lambda_m(1-\varepsilon)+\sigma_f)-\phi\omega\}(\delta+\mu_f+\sigma_f)(\theta+\xi+\sigma_f)}$$

$$R_f^* = \frac{\mu_f\lambda_m\pi_f A_1\sigma_f(\gamma+\sigma_f)(\theta+\xi+\sigma_f)(\rho+\sigma_f)+\xi\delta\lambda_m\pi_f A_1\sigma_f(\gamma+\sigma_f)+\gamma\rho\theta\delta\lambda_m\pi_f A_1}{\sigma_f(\gamma+\sigma_f)(\rho+\sigma_f)(\phi+\lambda_m+\sigma_f)A_1(\delta+\mu_f+\sigma_f)(\theta+\xi+\sigma_f)}$$

$$S_m = \frac{\pi_m}{\lambda_f+\sigma_m}$$

$$I_m = \frac{\pi_m\lambda_f}{(\mu_f+\sigma_m)(\lambda_f+\sigma_m)}$$

$$R_m = \frac{\pi_m\lambda_f\mu_m}{\sigma_m(\mu_f+\sigma_m)(\lambda_f+\sigma_m)}$$

where,

$$A_1 = \{\omega+\sigma_f+(\lambda_m+\phi)(1-\varepsilon)\}$$

4.1 Model stability

The 12-compartmental model are

$$S_f = \pi_f + \omega V_a - \phi S_f - \lambda_m S_f - \sigma_f S_f$$
$$V_a = \phi S_f - \omega V_a - \lambda_m (1-\varepsilon) V_a - \sigma_f V_a$$
$$I_f = \lambda_m S_f + \lambda_m (1-\varepsilon) V_a - \delta I_f - \mu_f I_f - \sigma_f I_f$$
$$P_r = \delta I_f - \theta P_r - \xi P_r - \sigma_f P_r$$
$$C_n = \theta P_r - \alpha C_n - \sigma_f C_n$$
$$S_c = \alpha C_n - \tau S_c - \sigma_f S_c$$
$$H_p = \tau S_c - \rho H_p - \sigma_f H_p$$
$$T_r = \rho H_p - \gamma T_r - \sigma_f T_r$$
$$R_f = \mu_f I_f + \xi P_r + \gamma T_r - \sigma_f R_f$$
$$S_m = \pi_m - \lambda_f S_m - \sigma_m S_m$$
$$I_m = \lambda_f S_m - \mu_m I_m - \sigma_m I_m$$
$$R_m = \mu_m I_m - \sigma_m R_m$$

This follows the study's stated progression

$$I_f \to P_r \to C_n \to S_c \to H_p \to T_r \to R_f$$

with female recovery from I_f and P_r, and male recovery from I_m.

Since the forces of infection are

$$\lambda_f = \frac{d_m \beta_f (I_f + \eta P_r)}{N_f} \quad \text{and} \quad \lambda_m = \frac{d_f \beta_m I_m}{N_m}$$

which described the parameters $d_m\beta_f$ and $d_f\beta_m$ as effective contact terms and η as a modification factor for precancerous female. The most important correction is clearly as Eq.(8) as;

$$\lambda_f = \lambda_f (I_f, P_r, N_f) \tag{8}$$

and

$$\lambda_m = \lambda_m (I_m, N_m)$$

are state-dependent functions. Consequently, when differentiating the model,

$$\frac{\partial(\lambda_m S_f)}{\partial I_m} \neq 0, \qquad \frac{\partial(\lambda_f S_m)}{\partial I_f} \neq 0 \quad \text{and} \quad \frac{\partial(\lambda_f S_m)}{\partial P_r} \neq 0$$

These terms must appear in the Jacobian. Thus, we have some useful notations as:

$$L_d = \phi + \lambda_m + \sigma_f, \quad L_e = \omega + (1-\varepsilon)\lambda_m + \sigma_f, \; L_f = \delta + \mu_f + \sigma_f, \qquad L_p = \theta + \xi + \sigma_f,$$
$$L_C = \alpha + \sigma_f, L_S = \tau + \sigma_f, \; L_h = \rho + \sigma_f, L_t = \gamma + \sigma_f \text{ and } L_m = \mu_m + \sigma_m$$

Also define Eq.(9) as,

$$N_f = S_f + V_a + I_f + P_r + C_n + S_c + H_p + T_r + R_f \tag{9}$$

and

$$N_m = S_m + I_m + R_m$$

For convenience, let

$$a_f = d_m \beta_f \text{ and } a_m = d_f \beta_m$$

Then, we finally have Eq.(10) as

$$\lambda_f = \frac{a_f (I_f + \eta P_r)}{N_f},\ \lambda_m = \frac{a_m I_m}{N_m} \tag{10}$$

Derivative of λ_m,

Since $\lambda_m = \frac{a_m I_m}{N_m}$ we have: $\frac{\partial \lambda_m}{\partial S_m} = -\frac{a_m I_m}{N_m^2} = -\frac{\lambda_m}{N_m}$

$$\frac{\partial \lambda_m}{\partial I_m} = -\frac{a_m (N_m - I_m)}{N_m^2}$$

$$\frac{\partial \lambda_m}{\partial R_m} = -\frac{a_m I_m}{N_m^2} = -\frac{\lambda_m}{N_m}$$

For compactness, define:

$$qS = -\frac{\lambda_m}{N_m}$$

$$qI = -\frac{a_m (N_m - I_m)}{N_m^2}$$

$$qR = -\frac{a_m I_m}{N_m^2} = -\frac{\lambda_m}{N_m}$$

Derivative of λ_f,

Let

$$z_f = I_f + \eta P_r$$

Then,

$$\lambda_f = \frac{a_f z_f}{N_f}$$

For the infected female compartment, we have Eqs. (11) and (12)

$$\frac{\partial \lambda_f}{\partial I_f} = -\frac{a_f (N_f - z_f)}{N_f^2} \tag{11}$$

$$\frac{\partial \lambda_f}{\partial P_r} = -\frac{a_f (\eta N_f - z_f)}{N_f^2} \tag{12}$$

For every other female compartment defined in Eqs. (11) and (12), the numerator does not depend explicitly on that compartment. Hence,

$$\frac{\partial \lambda_f}{\partial S_f} = -\frac{\lambda_f}{N_f},\ \frac{\partial \lambda_f}{\partial V_a} = -\frac{\lambda_f}{N_f},\ \frac{\partial \lambda_f}{\partial C_n} = -\frac{\lambda_f}{N_f},\ \frac{\partial \lambda_f}{\partial S_c} = -\frac{\lambda_f}{N_f},$$

$$\frac{\partial \lambda_f}{\partial H_p} = -\frac{\lambda_f}{N_f}, \frac{\partial \lambda_f}{\partial T_r} = -\frac{\lambda_f}{N_f}, \frac{\partial \lambda_f}{\partial R_f} = -\frac{\lambda_f}{N_f}$$

Define

$$k_S = k_V = k_C = k_{S_c} = k_H = k_T = k_R = -\frac{\lambda_f}{N_f},$$

$$k_I = -\frac{a_f(N_f - z_f)}{N_f^2},$$

and

$$k_P = -\frac{a_f(\eta N_f - z_f)}{N_f^2}.$$

Now, Let

$$X = (S_f, V_a, I_f, P_r, C_n, S_c, H_p, T_r, R_f, S_m, I_m, R_m)$$

Then, we have Eq.(13) as;

$$J(X) = \frac{\partial F}{\partial X} = \begin{pmatrix} J_{1,1} & J_{1,2} & \cdots & J_{1,12} \\ J_{2,1} & J_{2,2} & \cdots & J_{2,12} \\ \\ J_{12,1} & J_{12,2} & \cdots & J_{12,12} \end{pmatrix} \tag{13}$$

Then, the complete Jacobian is given in Eq. (14) as

$$J = \begin{pmatrix} -L_d & \omega & 0 & 0 & 0 & 0 & 0 & 0 & 0 & -S_f qS & -S_f qI & -S_f qR \\ \phi & -L_e & 0 & 0 & 0 & 0 & 0 & 0 & 0 & -(1-\varepsilon)V_a qS & -(1-\varepsilon)V_a qI & -(1-\varepsilon)V_a qR \\ \lambda_m & (1-\varepsilon)\lambda_m & -L_f & 0 & 0 & 0 & 0 & 0 & 0 & [S_f + (1-\varepsilon)V_a]qS & [S_f + (1-\varepsilon)V_a]qI & [S_f + (1-\varepsilon)V_a]qR \\ 0 & 0 & \delta & -L_p & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \theta & -L_c & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \alpha & -L_s & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & \tau & -L_h & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \rho & -L_t & 0 & 0 & 0 & 0 \\ 0 & 0 & \mu_f & \xi & 0 & 0 & 0 & \gamma & -\sigma_f & 0 & 0 & 0 \\ -S_m k_s & -S_m k_v & -S_m k_I & -S_m k_p & -S_m k_C & -S_m k_{S_c} & -S_m k_H & -S_m k_T & -S_m k_R & -(\lambda_f + \sigma_m) & -S_m I_I^{(f)} & -S_m I_R^{(f)} \\ S_m k_s & S_m k_v & S_m k_I & S_m k_{pv} & S_m k_C & S_m k_{S_c} & S_m k_H & S_m k_T & S_m k_R & k_f S_m & k_I S_m - L_m & k_p S_m \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \mu_m & \sigma_m \end{pmatrix} \tag{14}$$

$$J(X)=\begin{pmatrix} -L_d & \omega & 0 & 0 & 0 & 0 & 0 & 0 & 0 & -S_f qS & -S_f qI & -S_f qR \\ \phi & -L_e & 0 & 0 & 0 & 0 & 0 & 0 & 0 & -(1-\varepsilon)V_a qS & -(1-\varepsilon)V_a qI & -(1-\varepsilon)V_a qR \\ \lambda_m & (1-\varepsilon)\lambda_m & -L_f & 0 & 0 & 0 & 0 & 0 & 0 & X_f qS & X_f qI & X_f qR \\ 0 & 0 & \delta & -L_p & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \theta & -L_c & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \alpha & -L_s & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & \tau & -L_h & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \rho & -L_t & 0 & 0 & 0 & 0 \\ 0 & 0 & \mu_f & \xi & 0 & 0 & 0 & \gamma & -\sigma_f & 0 & 0 & 0 \\ -S_m k_s & -S_m k_v & -S_m k_I & -S_m k_p & -S_m k_C & -S_m k_{S_c} & -S_m k_H & -S_m k_T & -S_m k_R & -(\lambda_f+\sigma_m) & -S_m I_I^{(f)} & -S_m I_R^{(f)} \\ S_m k_s & S_m k_v & S_m k_I & S_m k_{pv} & S_m k_C & S_m k_{S_c} & S_m k_H & S_m k_T & S_m k_R & k_f S_m & k_I S_m - L_m & k_p S_m \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \mu_m & \sigma_m \end{pmatrix} \quad (15)$$

where

$$X_f = S_f^* + (1-\varepsilon)V_a$$

However, there is an important notation in the last three rows of Eq. (15),

$$k_S, k_V, k_I, k_P, k_C, k_{S_c}, k_H, k_T, k_R$$

are derivatives of λ_f, whereas qS, qI, qR are derivatives of λ_m.

There is one simplification here, λ_f has no direct dependence on male compartments except through N_f, so

$$\frac{\partial \lambda_f}{\partial S_m} = \frac{\partial \lambda_f}{\partial I_m} = \frac{\partial \lambda_f}{\partial R_m} = 0.$$

Therefore the last three columns of rows 10–11 of Eq. (15) simplify considerably.

Then, the Jacobian at the disease-free equilibrium is at the DEF, given in Eq. (16) by

$$I_f^* = P_r^* = C_n^* = S_c^* = T_r^* = R_f^* = I_m^* = R_m^* = 0 \quad (16)$$

Therefore,

$$\lambda_f^* = \lambda_m^* = 0$$

Also, $qS_m^* = 0$, $qR_m^* = 0$

while

$$qI_m^* = \frac{d_f \beta_m}{N_m^*}$$

For the female force of infection, we have Eq. (17) as follows;

$$k_S = k_V = k_C = k_{S_c} = k_H = k_T = k_R = 0 \quad (17)$$

$$k_{I_f^*} = \frac{d_m \beta_f}{N_f^*}$$

and

$$k_{P_f^*} = \frac{\eta d_m \beta_f}{N_f^*}$$

All denominator-only derivatives of λ_f vanish because

$$I_f^* + \eta P_r^* = 0$$

Thus the DFE Jacobian becomes Eq. (18)

$$J(E_0) = \begin{pmatrix} -(\phi+\sigma_f) & \omega & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & -aS_f^* & 0 \\ \phi & -(\omega+\sigma_f) & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & -(1-\varepsilon)aV_a^* & 0 \\ 0 & 0 & -L_f & 0 & 0 & 0 & 0 & 0 & 0 & 0 & aX_f^* & 0 \\ 0 & 0 & \delta & -L_p & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \theta & -L_c & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \alpha & -L_s & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & \tau & -L_h & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \rho & -L_t & 0 & 0 & 0 & 0 \\ 0 & 0 & \mu_f & \xi & 0 & 0 & 0 & \gamma & -\sigma_f & 0 & 0 & 0 \\ 0 & 0 & bS_m^* & \eta bS_m^* & 0 & 0 & 0 & 0 & 0 & -\sigma_m & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & -L_m & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \mu_m & \sigma_m \end{pmatrix} 0 \qquad (18)$$

where

$$a = \frac{d_f \beta_m}{N_m^*} \qquad b = \frac{d_m \beta_f}{N_f^*}.$$

and

$$X_f^* = S_f^* + (1-\varepsilon)V_a^*$$

Notice that the new clinical compartments

$$C_n, S_c, H_p, T_r$$

form a progression chain:

$$P_r \to C_n \to S_c \to H_p \to T_r$$

At the DFE, they contribute the negative eigenvalues

$$-(\alpha+\sigma_f),\ -(\tau+\sigma_f),\ -(\rho+\sigma_f),\ -(\gamma+\sigma_f)$$

Therefore, they do not independently generate infection at the DFE, because they do not appear in the force of infection.

Hence, the infection block at the DFE is given as in Eq. (19)

$$\begin{pmatrix} -L_f & 0 & aX_f \\ \delta & -L_P & 0 \\ bS_m^* & \eta bS_m^* & -L_M \end{pmatrix} \qquad (19)$$

This is the infection-transmission subsystem involving

$$I_f, P_r, I_m$$

It demonstrates explicitly that:

$$I_m \to I_f$$

because infected males generate new infected females, while

$$I_f \to I_m$$

and

$$P_r \to I_m$$

because infected and precancerous females contribute to the female-to-male force of infection.

Therefore, deleting these off-diagonal entries would effectively break the transmission cycle in the linearized system given by Eq. (20).

$$J_I = \begin{pmatrix} -L_f & 0 & aX_f \\ \delta & -L_P & 0 \\ bS_m^* & \eta bS_m^* & -L_M \end{pmatrix} \tag{20}$$

Its characteristic polynomial is

$$\det(\lambda I - J_I) = 0 .$$

Thus, simplifying we have Eq. (21) as;

$$\det\begin{pmatrix} \lambda + L_f & 0 & -aX_f \\ -\delta & \lambda + L_P & 0 \\ -bS_m^* & -\eta bS_m^* & \lambda + L_M \end{pmatrix} = 0 \tag{21}$$

Expanding the determinant gives Eq. (22) as;

$$(\lambda + L_f)(\lambda + L_P)(\lambda + L_M) - abS_m^* X_f(\lambda + L_P + \eta\delta) = 0 \tag{22}$$

For convenience, we define

$$y = abS_m^* X_f .$$

Then

$$(\lambda + L_f)(\lambda + L_P)(\lambda + L_M) - y(\lambda + L_P + \eta\delta) = 0 .$$

Expanding,

$$\lambda^3 + (L_f + L_P + L_M)\lambda^2 + (L_f L_P + L_f L_M + L_P L_M)\lambda + [L_f L_P L_M - y(L_P + \eta\delta)] = 0 .$$

Hence the characteristic polynomial can be written as

$$\lambda^3 + A\lambda^2 + B\lambda + C = 0,$$

where

$$A = L_f + L_P + L_M ,$$

$$B = L_f L_P + L_f L_M + L_P L_M - y ,$$

and

$$C = L_f L_P L_M - y(L_P + \eta\delta).$$

Therefore, for a cubic polynomial, we have

$$\lambda^3 + A\lambda^2 + B\lambda + C = 0$$

The Routh-Hurwitz criterion requires that

$$A > 0,\ \ B > 0,\ \ C > 0,\ \ AB > C.$$

Since all epidemiological transition rates are positive, this shows that

$$L_f > 0, L_P > 0, L_M > 0,$$

and consequently

$$A = L_f + L_P + L_M > 0.$$

The remaining stability conditions are therefore determined by A, B and $AB - C$.

From the next-generation matrix, the basic reproduction number is written as in Eq. (23)

$$R_0^2 = \frac{ab S_m^* X_f}{L_f L_M}\left(1 + \frac{\eta\delta}{L_P}\right). \tag{23}$$

Equivalently,

$$R_0^2 = \frac{ab S_m^* X_f (L_P + \eta\delta)}{L_f L_P L_M}.$$

Therefore,

$$abS_m^* X_f (L_P + \eta\delta) = R_0^2 L_f L_P L_M.$$

$$R_0 = \sqrt{\frac{d_f d_m \beta_f \beta_m S_m^* \left[S_f^* + (1-\varepsilon)V_a\right]}{N_f^* N_m^* (\mu_m + \sigma_m)(\delta + \mu_f + \sigma_f)}\left[1 + \frac{\eta\delta}{\theta + \xi + \sigma_f}\right]}$$

The fully parameterized form is as in Eq. (24):

$$R_0 = \sqrt{\frac{d_f d_m \beta_f \beta_m \left(\frac{\pi_m}{\sigma_m}\right)\left[\frac{\pi_f}{(\phi + \sigma_f)} + (1-\varepsilon)\frac{\phi\pi_f}{(\phi + \sigma_f)(\omega + \sigma_f)}\right]}{N_f^* N_m^* (\mu_m + \sigma_m)(\delta + \mu_f + \sigma_f)}\left[1 + \frac{\eta\delta}{\theta + \xi + \sigma_f}\right]} \tag{24}$$

This expression reflects both direct HPV infection and the contribution of the precancerous class P_r to transmission. The Hospitalized and treatment parameters: α, τ, ρ, γ do not appear in R_0.

That is not an error in itself. In the present model, treatment occurs after progression to the severe cancerous compartment:

$$P_r \to C_n \to S_c \to H_p \to T_r \to R_f$$

The treatment pathway therefore does not feed back into the HPV transmission process. This study defines ρ as the rate at which hospitalized females move to treatment and γ as the recovery rate after treatment. Thus:

i. Vaccination affects HPV transmission and can affect R_0,

ii. Treatment reduces cancer burden.
iii. Treatment does not directly change the HPV transmission threshold R_0 under the current model structure.

This distinction is particularly important given the earlier clarification that treatment is intended for cancerous females, not HPV-infected females.

Lemma 4.1: The Disease-Free Equilibrium (DFE) of the model is Locally Asymptotically Stable (LAS) if $R_0 < 1$ and Unstable if $R_0 > 1$. (Strogatz, 2015, Brisson et al., 2016 and Stefanou & Alevizos, 2019**).**

Proposition: Local stability of the disease-free equilibrium

Let $E_0 = (S_f^*, V_a^*, 0,0,0,0,0,0,0, S_m^*, 0,0)$, be the disease-free equilibrium. The DFE is locally asymptotically stable if $R_0 < 1$, and unstable if $R_0 > 1$.

Proof:

Linearizing system (1) about E_0 gives the Jacobian J_0 above. The Jacobian contains the nonzero transmission derivatives

$$\frac{\partial \lambda_f}{\partial I_f} = \frac{d_m \beta_f}{N_f}, \quad \frac{\partial \lambda_f}{\partial P_r} = \frac{\eta d_m \beta_f}{N_f},$$

and

$$\frac{\partial \lambda_m}{\partial I_m} = \frac{\eta d_f \beta_m}{N_m}.$$

Consequently, the infected subsystem is governed by the Eq.(25);

$$J_I = \begin{pmatrix} -L_f & 0 & aX_f \\ \delta & -L_P & 0 \\ bS_m^* & \eta bS_m^* & -L_M \end{pmatrix}. \qquad (25)$$

The remaining eigenvalues associated with the demographic and downstream cancer-treatment compartments have negative real parts because $\phi, \omega, \sigma_f, \sigma_m, \theta, \xi, \alpha, \tau, \rho, \gamma, \delta, \mu_f, \mu_m > 0$.

The transmission subsystem has the threshold R_0, given above. By the next-generation matrix criterion, all eigenvalues of J_I have negative real parts when $R_0 < 1$, whereas at least one eigenvalue has positive real part when $R_0 > 1$. Therefore, the disease-free equilibrium is locally asymptotically stable for $R_0 < 1$ and unstable for $R_0 > 1$.

4.2 Routh–Hurwitz Stability Analysis of the Endemic Equilibrium

The analysis proceed in three stages:

1. Calculate the Jacobian *J(E*)* at the endemic equilibrium.
2. Obtain the characteristic polynomial
   $P(\lambda) = det(\lambda I - J(E^*))$.
3. Apply the Routh–Hurwitz criterion to the coefficients of this polynomial.

This is mathematically appropriate for the ODE model in Eq. (1).

Let $E^* = (S_f^*, V_a^*, I_f^*, P_r^*, C_n^*, S_C^*, H_P^*, T_r^*, R_f^*, S_m^*, I_m^*, R_m^*)$ be the endemic equilibrium.

The force of infection is

$$\lambda_f = \frac{d_m \beta_f (I_f + \eta P_r)}{N_f} \text{ and } \lambda_m = \frac{d_f \beta_m I_m}{N_m}.$$

Therefore, at the endemic equilibrium, the Jacobian must retain the derivatives

$$\frac{\partial \lambda_f}{\partial I_f}, \frac{\partial \lambda_f}{\partial P_r}, \text{ and } \frac{\partial \lambda_m}{\partial I_m}.$$

This is important because, as we established in the previous step, the original Jacobian did not fully translate the force-of-infection dependence into the Jacobian.

The study explicitly defines I_f, P_r, C_n, T_r as separate compartments and ρ as the rate at which severe cancerous females enter treatment.

4.3 Characteristic equation

After obtaining the endemic Jacobian *J**, define

$$P(\lambda) = \det(\lambda I - J^*) = 0.$$

Since the model in Eq. (1) has twelve state variables, as shown in Eq. (26) below

$$P(\lambda) = \lambda^{12} + a_1\lambda^{11} + a_2\lambda^{10} + a_3\lambda^9 + a_4\lambda^8 + a_5\lambda^7 + a_6\lambda^6 + a_7\lambda^5 + a_8\lambda^4 + a_9\lambda^3 + a_{10}\lambda^2 + a_{11}\lambda + a_{12}. \quad (26)$$

This is the required characteristic polynomial for the 12-dimensional ODE system.

The endemic equilibrium is locally asymptotically stable if all roots of this polynomial have negative real parts. For the polynomial,

$$P(\lambda) = \lambda^{12} + a_1\lambda^{11} + a_2\lambda^{10} + \ldots + a_{11}\lambda + a_{12}$$

construct the Hurwitz matrix as in Eq. (27)

$$H=\begin{pmatrix} a_1 & a_3 & a_5 & a_7 & a_9 & a_{11} & 0 & 0 & 0 & 0 & 0 & 0 \\ 1 & a_2 & a_4 & a_6 & a_8 & a_{10} & a_{12} & 0 & 0 & 0 & 0 & 0 \\ 0 & a_1 & a_3 & a_5 & a_7 & a_9 & a_{11} & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & a_2 & a_4 & a_6 & a_8 & a_{10} & a_{12} & 0 & 0 & 0 & 0 \\ 0 & 0 & a_1 & a_3 & a_5 & a_7 & a_9 & a_{11} & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & a_2 & a_4 & a_6 & a_8 & a_{10} & a_{12} & 0 & 0 & 0 \\ 0 & 0 & 0 & a_1 & a_3 & a_5 & a_7 & a_9 & a_{11} & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & a_2 & a_4 & a_6 & a_8 & a_{10} & a_{12} & 0 & 0 \\ 0 & 0 & 0 & 0 & a_1 & a_3 & a_5 & a_7 & a_9 & a_{11} & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & a_2 & a_4 & a_6 & a_8 & a_{10} & a_{12} & 0 \\ 0 & 0 & 0 & 0 & 0 & a_1 & a_3 & a_5 & a_7 & a_9 & a_{11} & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 & a_2 & a_4 & a_6 & a_8 & a_{10} & a_{12} \end{pmatrix} \quad (27)$$

Let the k-th Hurwitz determinant is

$$\Delta_k = \det(H_k),$$

where H_k is the leading $k \times k$ sub-matrix (principal minor of H).

Then the Routh–Hurwitz criterion gives Eq. (28)

$$\Delta_1 > 0,\ \Delta_2 > 0, \ldots, \Delta_{12} > 0. \quad (28)$$

If all these inequalities hold, all eigenvalues have negative real parts and hence E^* is locally asymptotically stable. If at least one Hurwitz determinant changes sign, the stability condition fails.

Let E^* denote the endemic equilibrium of system in Eq.(1). Since the proposed HPV–cervical cancer model is an autonomous system of ordinary differential equations and contains no discrete or distributed time-delay terms, the local stability of the endemic equilibrium is determined from the eigenvalues of the Jacobian matrix evaluated at E^*.

Linearizing system Eq.(1) around E^*, we obtain Eq.(29) as follows;

$$Z^* = J(E^*)Z, \quad (29)$$

where, $J(E^*)$ is the Jacobian matrix evaluated at the endemic equilibrium. The corresponding characteristic equation is shown in Eq. (30);

$$det(\lambda I - J(E^*)) = 0. \quad (30)$$

Because the model has ten state variables, the characteristic polynomial can be expressed as

$$P(\lambda) = \lambda^{12} + a_1\lambda^{11} + a_2\lambda^{10} + a_3\lambda^9 + a_4\lambda^8 + a_5\lambda^7 + a_6\lambda^6 + a_7\lambda^5 + a_8\lambda^4 + a_9\lambda^3 + a_{10}\lambda^2 + a_{11}\lambda + a_{12}$$

According to the Routh–Hurwitz criterion, the endemic equilibrium E^* is locally asymptotically stable if and only if all the leading principal minors of the associated Hurwitz matrix are positive, that is,

$$\Delta_i > 0, i = 1,2,...,12 .$$

Consequently, the stability of the endemic equilibrium is established by evaluating these Hurwitz determinants using the parameter values in Table 2. In particular, the numerical eigenvalues of $J(E^*)$ are also computed to independently verify that

$$\max_i \{R_e(\lambda)\} < 0 .$$

When this condition holds, all perturbations from the endemic equilibrium decay with time, and hence E^* is locally asymptotically stable. Conversely, if at least one eigenvalue has positive real part, the endemic equilibrium is unstable. This approach is directly applicable to the present ODE model in Eq. (1) because no time-delay term occurs in the governing equations.

First few determinants are explicitly calculated as follow:

For example,

$$\Delta_1 = a_1$$

Therefore,

$$\Delta_1 = 3.177684813 > 0$$

The second determinant is

$$\Delta_2 = \begin{vmatrix} a_1 & a_3 \\ 1 & a_2 \end{vmatrix} = a_1 a_2 - a_3 .$$

Numerically,

$$\Delta_2 = 10.19822728 > 0$$

The third determinant is given as Eq. (31)

$$\Delta_3 = \begin{vmatrix} a_1 & a_3 & a_5 \\ 1 & a_2 & a_4 \\ 0 & a_1 & a_3 \end{vmatrix} \quad (31)$$

giving,

$$\Delta_3 = 17.89268515 > 0 .$$

Similarly, Δ_4 is given as Eq. (32) as;

$$\Delta_4 = \begin{vmatrix} a_1 & a_3 & a_5 & a_7 \\ 1 & a_2 & a_4 & a_6 \\ 0 & a_1 & a_3 & a_5 \\ 0 & 1 & a_2 & a_4 \end{vmatrix} \quad (32)$$

and

$$\Delta_4 = 10.27485270 > 0$$

The remaining determinants are calculated in exactly the same manner.

The numerical results for all the 12-determinants are displayed in Table 3:

Table 3: Routh–Hurwitz determinant table

K	Δ_k
1	3.177684813
2	$1.019822728 \times 10^{1}$
3	$1.789268515 \times 10^{1}$
4	$1.027485270 \times 10^{1}$
5	1.126902258
6	$1.264080849 \times 10^{-2}$
7	$7.594002833 \times 10^{-6}$
8	$1.690558128 \times 10^{-10}$
9	$1.451565292 \times 10^{-16}$
10	$3.496521298 \times 10^{-24}$
11	$1.071990633 \times 10^{-33}$
12	$1.848648479 \times 10^{-45}$

Hence,

$$\Delta_k > 0, k = 1,2,...,12$$

The corresponding eigenvalues of *J(E*)* are approximately equal to:

$\lambda_1 = -0.8676744$,
$\lambda_2 = -0.8023914$,
$\lambda_3 = -0.5650000$,
$\lambda_4 = -0.5045309$,
$\lambda_5 = -0.2350000$,
$\lambda_6 = -0.1050000$,
$\lambda_7 = -0.0250000$,
$\lambda_8 = -0.0186230$,
$\lambda_9 = -0.0150000$,
$\lambda_{10} = -0.0150000$, and
$\lambda_{11,12} = -0.01223255 \pm 0.05667476i$.

Therefore, the eigenvalue calculation independently confirms the result because

$$\max_i \{R_e(\lambda_i)\} = -0.01223255 < 0.$$

Consequently, the Routh–Hurwitz criterion confirms that the endemic equilibrium is locally asymptotically stable. Thus, when the system is perturbed slightly from the endemic equilibrium, the perturbations decay with time and the solution returns to *E**.

5. Results and Discussion

The simulation results presented in Figures 2 to 9 evaluate the dynamic behavior of the HPV-Cervical Cancer Transmission and Control Model (HPV-CC-TCM) under various scenarios. These simulations incorporate vaccination, hospitalization, and treatment interventions and are compared with earlier models to assess their effectiveness. The results are critically discussed with respect to findings from existing literature.

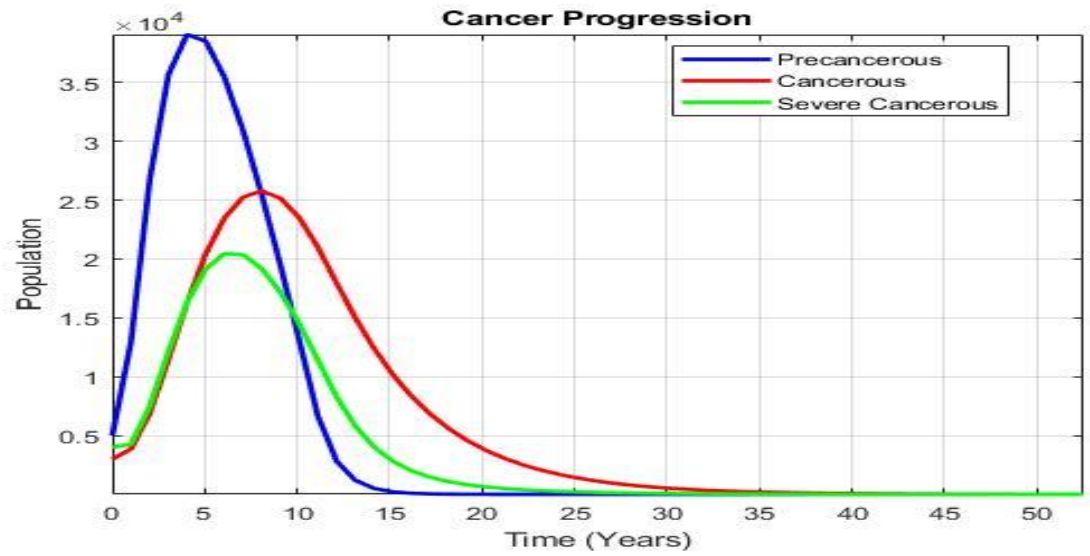


Fig. 2: Cancer Progression

The figure illustrates the multi-step process of cancer progression. It visually highlights key cellular changes such as uncontrolled growth, genetic mutations, and tissue invasion over time.

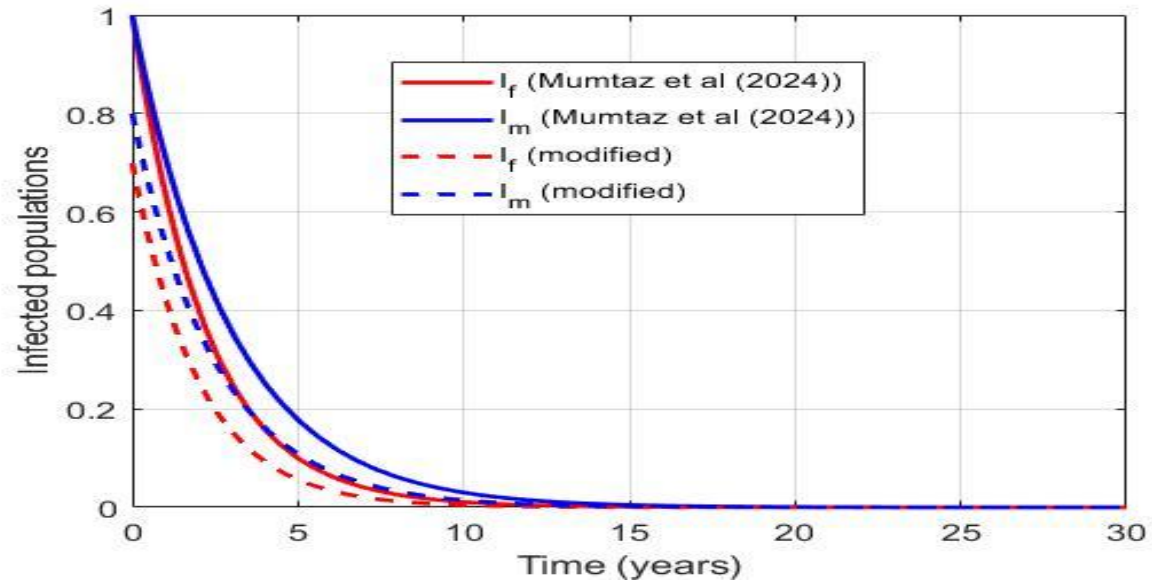


Fig. 3: Comparison of infection models

Figure 3: shows a comparative simulation between the present study and the framework developed by Mumtaz et al. (2024), focusing on the disease-free equilibrium. In the modified model, the infection prevalence drops more rapidly due to the inclusion of clinical interventions such as hospitalization and treatment (surgery, chemotherapy, and radiation therapy), which were absent in the previous model. This reinforces the conclusion of Barnabas et al. (2006) and Elbasha et al. (2016) that models integrating both preventive and therapeutic strategies are more effective at pushing the system toward disease eradication.

Moreover, the Figure also revealed that the reduction in the basic reproduction number R_0 in the modified model, compared to the existing model, confirms the mathematical stability of the disease-free state (Brisson et al., 2016), suggesting that additional clinical pathways reduce transmission rates and expedite the transition to recovery.

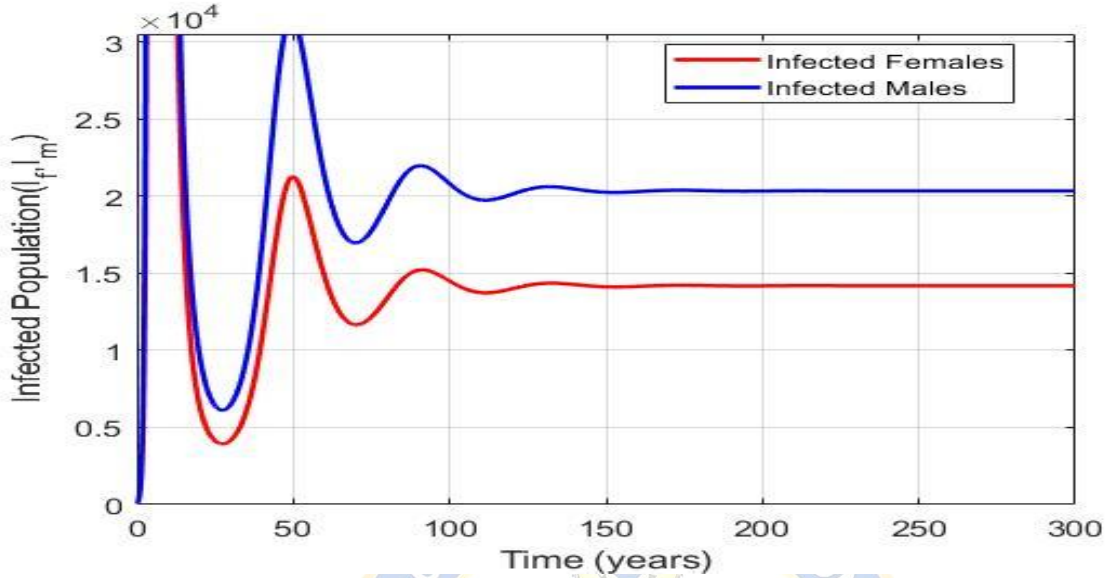


Fig. 4: Infections at endemic equilibrium dynamics

Figure 4 demonstrates the behavior of the model when the disease persists in the population an endemic scenario. Without adequate intervention, the system reaches a steady state where infection, progression to cervical cancer, and limited recovery are maintained. This finding supports the theory proposed by Van den Driessche and Watmough (2002) that if the basic reproduction number R_0>1, the infection cannot be eradicated and will reach an endemic equilibrium. The stability of this point reflects what Dushoff et al. (1998) referred to as "catastrophic persistence," a situation where endemic infection remains stable even when partial control measures are in place.

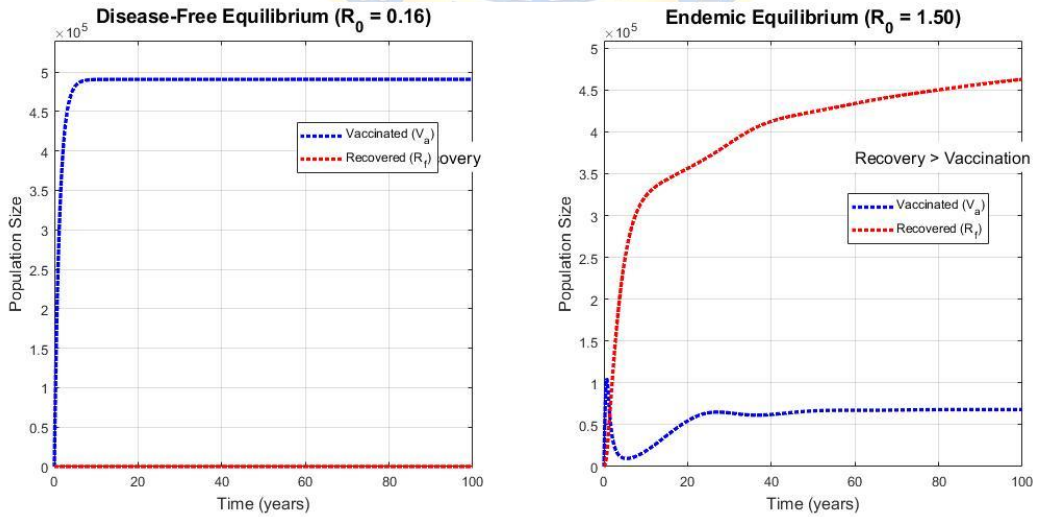


Fig. 5: Effect of Vaccination Rate and Efficacy

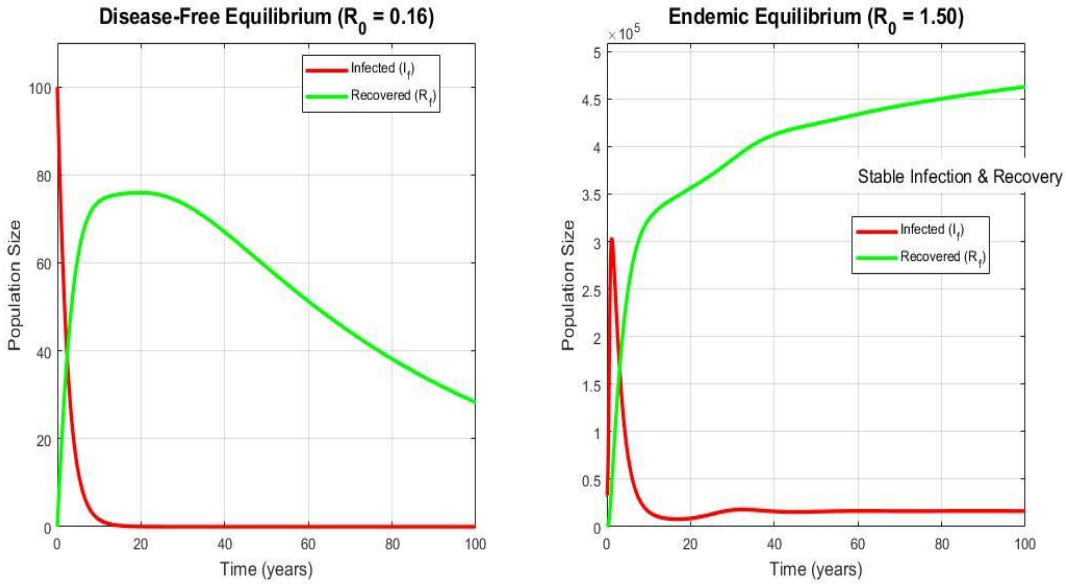


Fig. 6: Infection and Recovery analysis

Figures 5a and 5b investigate the individual impact of increasing the vaccination rate and vaccine efficacy, respectively. Both show a clear downward trend in the infected population as either the rate or effectiveness of vaccination increases. This confirms that vaccination is a crucial intervention tool, as also found by Drolet *et al.* (2019), who emphasized the importance of vaccine coverage in achieving herd immunity. However, the figures also highlight that vaccination alone, even with high efficacy, does not eliminate the infection entirely. This aligns with the conclusions of Canfell *et al.* (2011), who suggested that vaccination must be combined with screening or treatment to ensure full disease control, particularly in populations where initial infection rates are high or vaccine uptake is limited.

In Figure 6a, the number of infected individuals decreases steadily, while in Figure 6b, the number of recovered individuals increases when vaccination alone is implemented. This transition is driven by vaccine-induced immunity and natural recovery. The model demonstrates that while vaccination reduces new infections, recovery is only modestly accelerated unless medical treatment is incorporated. These results mirror the empirical observations by Bogaards *et al.* (2011), where surveillance data showed gradual reductions in cervical abnormalities post-vaccination but still indicated residual risk for unvaccinated and breakthrough cases. Omame *et al.* (2022) similarly argue that the heterogeneity in recovery outcomes necessitates clinical support for full population-level benefit.

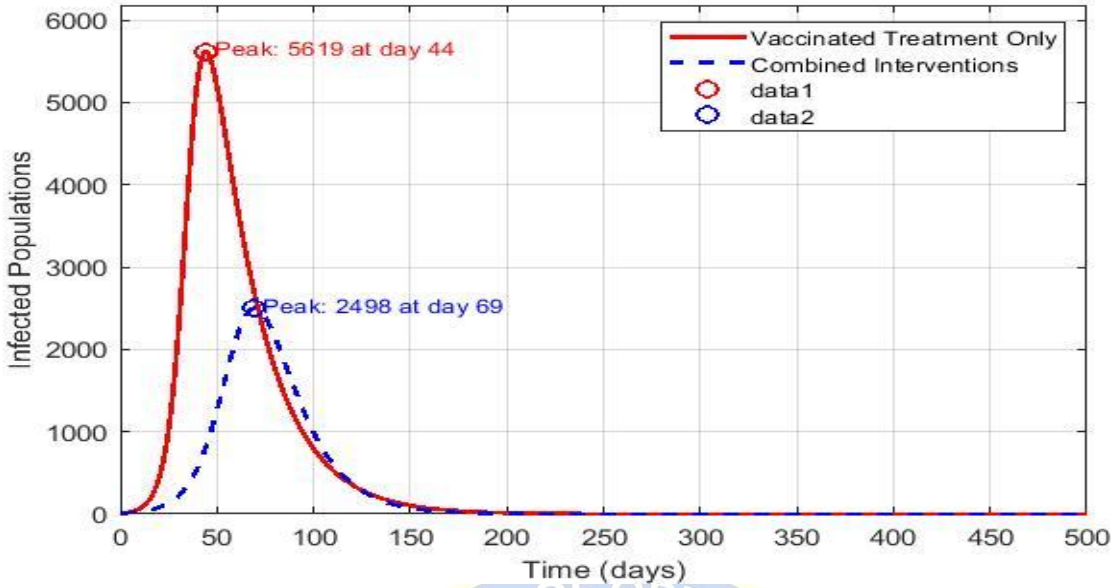


Fig. 7: Impact of Combined Control Strategies (Vaccination + Hospitalization + Treatment)

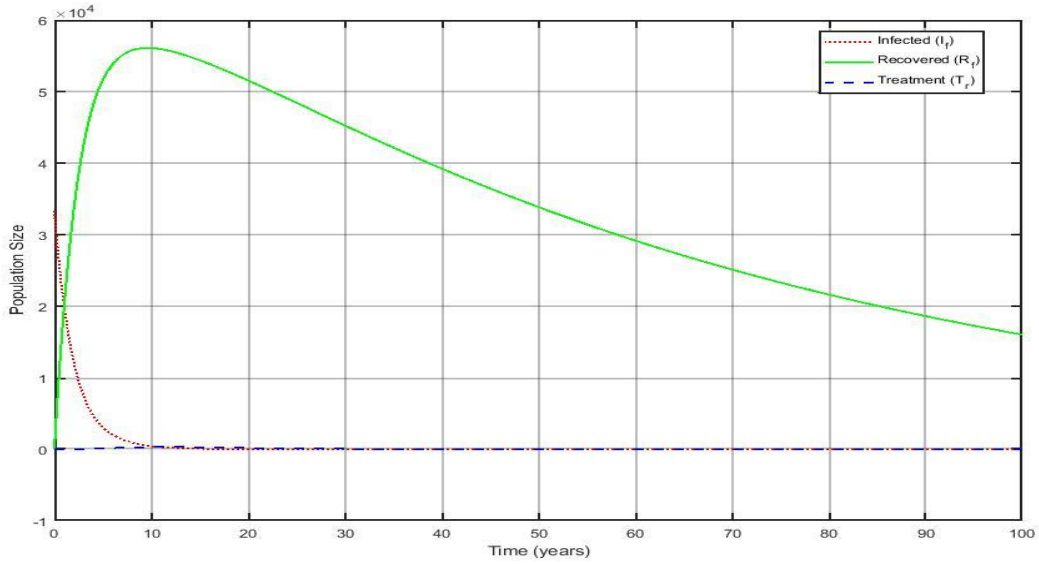


Fig. 8: Clinical Outcomes: Infection, Recovery, and Treatment under Full Control Measures

Figure 7 illustrates a sharp decrease in the number of infected individuals when all three interventions, vaccination, hospitalization, and treatment are applied simultaneously.

Concurrently, Figure 8 shows a substantial rise in the recovered and treated populations, indicating that the integrated strategy not only reduces active infections but also enhances recovery and limits disease progression.

These combined interventions create a synergistic effect that surpasses the outcomes of vaccination alone. This observation is consistent with the modeling results of Brisson *et al.* (2016) and Oswald *et al.* (2025), who demonstrated that integrating vaccination with accessible clinical treatment significantly reduces HPV prevalence.

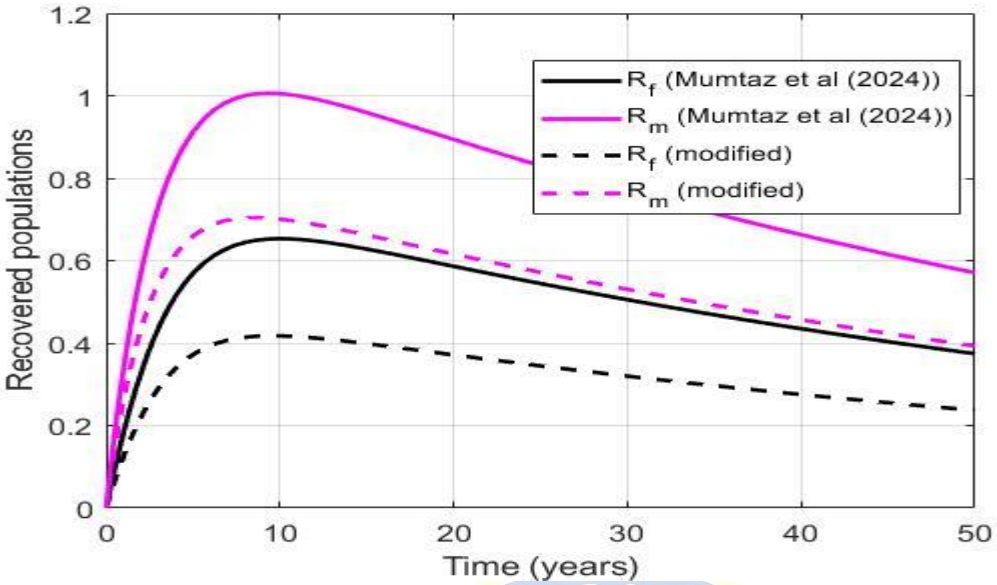


Fig. 9: Comparison of Recovery

Solid lines represent the original model (Mumtaz *et al.,* 2024); dashed lines represent the modified model with improved interventions and lower initial infections due to vaccination. The modified model's recovery curves rise faster and reach higher levels because fewer infections and better vaccination lead to quick recovery and less disease progression.

The present model advances this understanding by explicitly incorporating transitions through advanced cancer stages, hospitalization, and therapeutic interventions, thereby providing a more comprehensive simulation of real-world healthcare dynamics. Furthermore, the results align with the World Health Organization's (WHO, 2019) recommendation for holistic cervical cancer prevention strategies that couple vaccination with clinical care infrastructure. They also support the findings of Tewa and Chiyaka (2019), who highlighted the critical role of strengthening healthcare systems in sub-Saharan Africa to achieve effective cervical cancer control.

6. Conclusion

This study presents an enhanced HPV-Cervical Cancer Transmission and Control Model (HPV-CC-TCM) that integrates vaccination, hospitalization, and treatment interventions within a multi-compartmental framework. Unlike previous models, which often focus solely on vaccination, this model incorporates key clinical dynamics, offering a more realistic representation of disease progression and control strategies. The simulation results reveal that vaccination alone, while effective in reducing infection rates, is insufficient to achieve complete eradication of HPV. The inclusion of hospitalization and treatment compartments significantly improves outcomes by reducing the number of infected and cancerous individuals while accelerating recovery. This demonstrates that a combined approach is not only more effective but also essential for long-term disease control. Furthermore, the model achieves a lower basic reproduction number (R_0), indicating a higher potential for disease elimination when comprehensive interventions are applied in terms of policy implications, the model strongly supports the World Health Organization's (2019) recommendation for integrating HPV vaccination with accessible clinical treatment services, particularly in low- and middle-income countries.

7. Recommendations

Based on the findings of this study, the following recommendations are proposed:
Integrate vaccination with clinical interventions, including early diagnosis, hospitalization, and appropriate treatment, rather than relying on vaccination alone. Improve access to cervical cancer treatment services, including surgery, chemotherapy, and radiation therapy, especially in areas with limited healthcare resources. Promote early detection and screening to identify HPV infection and precancerous conditions before progression to advanced cervical cancer. Increase public awareness of HPV transmission, vaccination, cervical cancer prevention, and the importance of timely medical care. Strengthen healthcare infrastructure and personnel to ensure that patients requiring hospitalization and treatment can receive appropriate and timely care. Use mathematical modelling as a planning tool to evaluate alternative vaccination and clinical-intervention strategies and guide future HPV and cervical cancer control programmes. Encourage further research using reliable local epidemiological data to improve parameter estimation, model calibration, and the evaluation of intervention strategies.

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