# Stability and Bifurcation Analysis of an SIR Epidemic Model with Vaccination

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**Abstract- Mathematical modeling provides a powerful framework for understanding the spread of infectious diseases and evaluating control strategies. In this study, a susceptible–infected–recovered (SIR) epidemic model incorporating vaccination is proposed and analyzed. The model is formulated as a system of nonlinear ordinary differential equations. The basic reproduction number $R_0$is derived to characterize the threshold behavior of disease transmission. Stability analysis is performed to investigate the local and global dynamics of the equilibrium points. Bifurcation analysis is carried out to study qualitative changes in the system near critical parameter values. Sensitivity analysis is used to determine the relative importance of model parameters. Numerical simulations based on the fourth-order Runge–Kutta method are presented to validate the analytical results. The results demonstrate that vaccination significantly reduces the infected population and plays a crucial role in preventing epidemic outbreaks.**

**Keywords- SIR model; infectious disease; vaccination; stability analysis; bifurcation; sensitivity analysis; numerical simulation**

## I. INTRODUCTION

Infectious diseases remain one of the major global challenges to public health systems. Epidemics such as influenza, tuberculosis, HIV/AIDS, malaria, and more recently COVID-19 have highlighted the urgent need for effective tools to understand disease transmission and control mechanisms [1]. The rapid spread of infectious diseases often leads to severe social, economic, and healthcare impacts, making epidemic prediction and prevention a priority for policymakers and researchers.

Mathematical modeling has emerged as an important approach for studying the dynamics of infectious diseases [2]. Mathematical models provide simplified but systematic representations of biological processes, allowing researchers to analyze how diseases spread within populations and how interventions such as vaccination and treatment influence disease dynamics [3].

Among various modeling approaches, compartmental models are widely used in epidemiology [4]. These models divide the population into distinct classes according to disease status and describe transitions between classes using differential equations. The classical susceptible–infected–recovered (SIR) model is one of the most fundamental compartmental models and has been extensively studied in the literature [5].

Over time, the SIR model has been extended to incorporate additional biological features such as exposed classes, temporary immunity, treatment, vaccination, age structure, and spatial diffusion [6,7]. In particular, vaccination has received significant attention as it is one of the most effective strategies for controlling infectious diseases [8]. Vaccination reduces the number of susceptible individuals and thereby limits the transmission of infection.

A key concept in mathematical epidemiology is the basic reproduction number $R_0$, which represents the average number of secondary infections generated by a single infected individual in a fully susceptible population [9]. The value of $R_0$determines whether a disease can invade and persist in a population. If $R_0 < 1$, the disease dies out, whereas if $R_0 > 1$, the disease becomes endemic [10].

Stability and bifurcation analyses are important tools in nonlinear dynamical systems and play a central role in epidemic modeling [11]. Stability analysis helps determine the long-term behavior of equilibrium points, while bifurcation analysis identifies critical thresholds at which qualitative changes in system dynamics occur [12].

The main objective of this study is to formulate an SIR epidemic model with vaccination and to analyze its stability, bifurcation, and sensitivity properties. Numerical simulations are also performed to support the theoretical results and to provide insights into the

effectiveness of vaccination as a disease control strategy.

## II. MATHEMATICAL PRELIMINARIES

This section presents the basic mathematical concepts and definitions required for the theoretical analysis of the proposed epidemic model. These preliminaries provide the necessary background for stability and bifurcation analysis of nonlinear dynamical systems [11,12].

### 2.1 Basic Concepts of Dynamical Systems

A dynamical system is a mathematical formulation that describes how the state of a system evolves over time according to a fixed rule [13]. In continuous-time epidemiological models, dynamical systems are typically represented using systems of ordinary differential equations of the form:

$$\frac{dx}{dt} = f(x)$$

where $x \in \mathbb{R}^n$is the state vector and $f(x)$is a continuously differentiable vector field.

In epidemic modeling, the state variables usually represent population compartments such as susceptible, infected, and recovered individuals. The trajectories of the system describe how these populations evolve over time.

### 2.2 Stability Theory of Nonlinear Systems

Let $x^*$be an equilibrium point of the dynamical system $\frac{dx}{dt} = f(x)$. The equilibrium point is said to be locally asymptotically stable if all solutions starting sufficiently close to $x^*$converge to $x^*$as time tends to infinity [14].

The local stability of an equilibrium point is commonly determined by analyzing the eigenvalues of the Jacobian matrix $J$, defined as:

$$J = \left[\frac{\partial f_i}{\partial x_j}\right]$$

evaluated at the equilibrium point. If all eigenvalues of $J$have negative real parts, then the equilibrium is locally asymptotically stable [15].

Stability analysis is widely used in epidemic modeling to determine whether a disease-free or endemic state will persist under small perturbations.

### 2.3 Bifurcation Theory: Basic Definitions

Bifurcation theory deals with qualitative changes in the behavior of a dynamical system as system parameters vary [12]. A bifurcation occurs when a small change in a parameter causes a sudden change in the number or stability of equilibrium points.

Common types of bifurcations observed in epidemic models include transcritical, saddle-node, and Hopf bifurcations [11]. In particular, transcritical bifurcation often arises in compartmental epidemic models when the basic reproduction number crosses unity.

Bifurcation analysis provides deeper insight into the global behavior of epidemic systems and helps identify critical thresholds for disease control.

### 2.4 Epidemiological Terminologies

Several epidemiological concepts are frequently used in mathematical modeling [2,9]. These include:

- Incidence: the rate at which new infections occur in a population.
- Prevalence: the total number of infected individuals at a given time.
- Transmission rate: the rate at which susceptible individuals become infected.
- Recovery rate: the rate at which infected individuals recover.
- Basic reproduction number ($R_0$): the average number of secondary infections caused by a single infected individual in a fully susceptible population.

These concepts form the basis for interpreting the mathematical results in biological and public health contexts.

## III. MODEL FORMULATION AND ASSUMPTIONS

This section presents the formulation of the SIR epidemic model with vaccination and describes the biological assumptions underlying the model structure [4,6].

### 3.1 Description of the Model Variables

Let the total population at time $t$be denoted by $N(t)$, which is divided into three epidemiological compartments:

$$N(t) = S(t) + I(t) + R(t)$$

where:

- $S(t)$represents the number of susceptible individuals,
- $I(t)$represents the number of infected individuals, and
- $R(t)$represents the number of recovered individuals.

This compartmental structure is widely used in classical epidemic modeling [5].

3.2 Model Parameters and Their Biological Meaning

The model parameters represent key biological processes governing disease transmission. These include:

- $\Lambda$: recruitment rate of individuals into the population,
- $\beta$: transmission rate of the disease,
- $\mu$: natural death rate,
- $\gamma$: recovery rate,
- $v$: vaccination rate.

These parameters are consistent with those used in standard epidemic models [3,7].

3.3 Assumptions of the Model

The following assumptions are made in formulating the model:

1. The population is homogeneous and well-mixed.
2. All individuals have equal probability of coming into contact with infected individuals.
3. Recovered individuals acquire permanent immunity.
4. Vaccinated individuals move directly from the susceptible class to the recovered class.
5. The disease does not cause disease-induced mortality.
6. Recruitment occurs only in the susceptible class.

These assumptions simplify the biological system and allow analytical treatment of the model [4,6,8].

3.4 Flow Diagram of the SIR Model with Vaccination

The model structure follows a standard SIR framework with vaccination. Susceptible individuals may become infected through contact with infected individuals or may move directly to the recovered class through vaccination. Infected individuals recover at a constant rate, and all compartments experience natural death.

This flow structure captures the essential mechanisms of disease transmission and control [5,8].

## IV. BASIC PROPERTIES OF THE MODEL

This section establishes the fundamental mathematical properties of the proposed model. These properties ensure that the model is well-posed, biologically meaningful, and suitable for further qualitative analysis [14,15].

4.1 Positivity of Solutions

For an epidemiological model to be biologically realistic, all state variables must remain non-negative for all time. Let the initial conditions satisfy:

$$S(0) > 0, I(0) > 0, R(0) > 0$$

From the first equation of the model,

$$\frac{dS}{dt} = \Lambda - \beta SI - \mu S - vS$$

when $S(t) = 0$, we obtain:

$$\frac{dS}{dt} = \Lambda > 0$$

which implies that $S(t)$cannot become negative. Similarly, from the second and third equations,

$$\frac{dI}{dt} = \beta SI - (\gamma + \mu)I$$
$$\frac{dR}{dt} = \gamma I + vS - \mu R$$

it follows that when $I(t) = 0$or $R(t) = 0$, the corresponding derivatives are non-negative. Therefore, all state variables remain non-negative for all $t > 0$.

Hence, the solutions of the system are positive invariant in the region $\mathbb{R}^3_+$[15,16].

4.2 Boundedness of Solutions

To prove boundedness, we consider the total population:

$$N(t) = S(t) + I(t) + R(t)$$

Differentiating with respect to time:

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

The solution of this differential equation is:

$$N(t) = \frac{\Lambda}{\mu} + \left(N(0) - \frac{\Lambda}{\mu}\right) e^{-\mu t}$$

As $t \to \infty$, we obtain:

$$0 < N(t) \leq \frac{\Lambda}{\mu}$$

Therefore, the total population remains bounded for all time. This implies that each compartment $S(t)$, $I(t)$, and $R(t)$is also bounded [4,7].

4.3 Invariant Region

From the positivity and boundedness results, the biologically feasible region for the model is defined as:

$$\Omega = \left\{(S, I, R) \in \mathbb{R}_+^3 : N(t) \leq \frac{\Lambda}{\mu}\right\}$$

The region Ωis positively invariant, meaning that any solution starting in Ωremains in Ωfor all $t > 0$. Therefore, the proposed model is mathematically consistent and biologically meaningful within the region Ω[14,17].

## V. EQUILIBRIUM POINTS AND BASIC REPRODUCTION NUMBER

In this section, the equilibrium points of the system are determined and the basic reproduction number $R_0$is derived. These quantities play a central role in understanding the long-term behavior of the disease dynamics [2,9].

5.1 Disease-Free Equilibrium (DFE)

The disease-free equilibrium corresponds to the state in which no infected individuals are present in the population, that is, $I = 0$.

At equilibrium, the derivatives of all state variables are zero:

$$\frac{dS}{dt} = 0, \frac{dI}{dt} = 0, \frac{dR}{dt} = 0$$

Setting $I = 0$in the first equation gives:

$$\Lambda - \mu S - vS = 0$$

Solving for $S$, we obtain:

$$S = \frac{\Lambda}{\mu + v}$$

Hence, the disease-free equilibrium point is:

$$E_0 = \left(\frac{\Lambda}{\mu + v},\ 0,\ 0\right)$$

This equilibrium represents a situation where the disease is completely absent from the population [5,9].

5.2 Endemic Equilibrium (EE)

The endemic equilibrium represents a state in which the disease persists in the population with a positive number of infected individuals, that is, $I^* > 0$.

From the second equation of the model,

$$\beta S^* I^* - (\gamma + \mu) I^* = 0$$

Since $I^* \neq 0$, we obtain:

$$S^* = \frac{\gamma + \mu}{\beta}$$

Substituting this into the remaining equations and solving, the endemic equilibrium is given by:

$$E^* = (S^*, I^*, R^*)$$

where the explicit expressions exist only when $R_0 > 1$[10,18].

5.3 Derivation of the Basic Reproduction Number $R_0$

The basic reproduction number is derived using the next-generation matrix method [9].

The infected compartment equation is:

$$\frac{dI}{dt} = \beta SI - (\gamma + \mu) I$$

At the disease-free equilibrium, $S = \frac{\Lambda}{\mu + v}$. Substituting this into the infection term yields:

$$\frac{dI}{dt} = \beta \frac{\Lambda}{\mu + v} I - (\gamma + \mu) I$$

Thus, the basic reproduction number is:

$$R_0 = \frac{\beta \Lambda}{(\mu + v)(\gamma + \mu)}$$

This expression shows that increasing the vaccination rate $v$decreases $R_0$, thereby reducing disease transmission [9,20].

5.4 Epidemiological Interpretation of $R_0$

The basic reproduction number $R_0$represents the average number of secondary infections generated

by a single infected individual in a fully susceptible population [9].

- If $R_0 < 1$, the disease-free equilibrium is stable and the disease eventually dies out.
- If $R_0 > 1$, the endemic equilibrium exists and the disease persists in the population.

Therefore, reducing $R_0$below unity is a fundamental goal of public health interventions such as vaccination and treatment.

## VI. STABILITY ANALYSIS

This section investigates the stability of the disease-free and endemic equilibrium points of the proposed model using linear stability theory and Lyapunov function methods. Stability analysis is essential to determine whether the disease will die out or persist in the population over time [14,15].

### 6.1 Local Stability of the Disease-Free Equilibrium

To analyze the local stability of the disease-free equilibrium $E_0$, we compute the Jacobian matrix of the system. Let the system be written in vector form as:

$$\frac{dX}{dt} = F(X)$$

where $X = (S, I, R)^T$. The Jacobian matrix $J$is given by:

$$J = \begin{pmatrix} -\beta I - \mu - v & -\beta S & 0 \\ \beta I & \beta S - (\gamma + \mu) & 0 \\ v & \gamma & -\mu \end{pmatrix}$$

Evaluating the Jacobian at the disease-free equilibrium $E_0 = \left(\frac{\Lambda}{\mu+v}, 0, 0\right)$, we obtain:

$$J(E_0) = \begin{pmatrix} -(\mu + v) & -\beta\frac{\Lambda}{\mu + v} & 0 \\ 0 & \beta\frac{\Lambda}{\mu + v} - (\gamma + \mu) & 0 \\ v & \gamma & -\mu \end{pmatrix}$$

The eigenvalues of $J(E_0)$are:

$$\lambda_1 = -(\mu + v), \lambda_2 = \beta\frac{\Lambda}{\mu + v} - (\gamma + \mu), \lambda_3 = -\mu$$

Since $\lambda_1 < 0$and $\lambda_3 < 0$, the sign of $\lambda_2$determines the stability of the disease-free equilibrium. We note that:

$$\lambda_2 < 0 \text{if and only if} R_0 < 1$$

Therefore, the disease-free equilibrium $E_0$is locally asymptotically stable when $R_0 < 1$and unstable when $R_0 > 1$[14,18].

### 6.2 Local Stability of the Endemic Equilibrium

The local stability of the endemic equilibrium $E^*$is analyzed by evaluating the Jacobian matrix at $E^*$. Using standard eigenvalue analysis, it can be shown that all eigenvalues of the Jacobian matrix have negative real parts when $R_0 > 1$.

Hence, the endemic equilibrium is locally asymptotically stable whenever it exists, that is, for $R_0 > 1$[11,15].

This result implies that once the disease becomes established in the population, it will persist unless strong intervention strategies are implemented.

### 6.3 Global Stability Analysis (Lyapunov Function)

To investigate global stability, a suitable Lyapunov function $V$is constructed. Consider the Lyapunov function:

$$V = I$$

Taking the derivative of $V$along the trajectories of the system, we obtain:

$$\frac{dV}{dt} = \frac{dI}{dt} = \beta SI - (\gamma + \mu)I$$

At the disease-free equilibrium, substituting $S = \frac{\Lambda}{\mu+v}$, we have:

$$\frac{dV}{dt} = I\left(\beta\frac{\Lambda}{\mu + v} - (\gamma + \mu)\right)$$

Thus,

$$\frac{dV}{dt} \leq 0 \text{if} R_0 \leq 1$$

and $\frac{dV}{dt} = 0$if and only if $I = 0$.

By LaSalle's Invariance Principle, the disease-free equilibrium is globally asymptotically stable when $R_0 \leq 1$[16,19].

This result confirms that the disease will be eliminated from the population irrespective of initial conditions, provided that the basic reproduction number is less than or equal to unity.

## VII. BIFURCATION ANALYSIS

This section examines the qualitative behavior of the system near the critical threshold $R_0 = 1$. Bifurcation analysis provides insight into how small changes in system parameters can lead to significant changes in disease dynamics [11,12].

### 7.1 Bifurcation at $R_0 = 1$

Bifurcation occurs when a small variation in a parameter causes a qualitative change in the structure of equilibrium points. In the proposed model, the basic reproduction number $R_0$serves as the primary bifurcation parameter.

When $R_0 < 1$, the disease-free equilibrium $E_0$is stable and no endemic equilibrium exists. When $R_0 > 1$, the disease-free equilibrium becomes unstable and a positive endemic equilibrium emerges. This transition indicates the presence of a bifurcation at the critical threshold $R_0 = 1$.

7.2 Forward and Backward Bifurcation

A forward (supercritical) bifurcation occurs when the endemic equilibrium appears only for $R_0 > 1$. In such cases, reducing $R_0$below unity is sufficient to eradicate the disease.

A backward (subcritical) bifurcation occurs when a stable endemic equilibrium exists even when $R_0 < 1$. This phenomenon complicates disease control, as reducing $R_0$below one may not guarantee elimination of the disease [13,21].

For the proposed SIR model with vaccination, the system exhibits a forward bifurcation, indicating that disease elimination can be achieved by reducing $R_0$below unity.

7.3 Center Manifold Analysis

To rigorously determine the nature of the bifurcation, center manifold theory is applied near the critical point $R_0 = 1$. Using standard results from bifurcation theory, it can be shown that the bifurcation coefficient associated with the endemic equilibrium is positive.

This confirms that the system undergoes a forward transcritical bifurcation at $R_0 = 1$[11,12].

7.4 Biological Interpretation of Bifurcation Results

The bifurcation results have important biological implications. The presence of a forward bifurcation implies that public health interventions such as vaccination and reduction of contact rates are sufficient to eliminate the disease. Increasing vaccination coverage directly reduces $R_0$, thereby shifting the system from an endemic state to a disease-free state.

## VIII. SENSITIVITY ANALYSIS

Sensitivity analysis is used to quantify how variations in model parameters influence the basic reproduction number $R_0$. This analysis helps identify the most influential parameters in disease transmission and control [21,22].

8.1 Sensitivity Indices of Model Parameters

The normalized forward sensitivity index of $R_0$with respect to a parameter $p$is defined as:

$$\Upsilon_p^{R_0} = \frac{\partial R_0}{\partial p} \cdot \frac{p}{R_0}$$

Using the expression:

$$R_0 = \frac{\beta\Lambda}{(\mu + v)(\gamma + \mu)}$$

the sensitivity indices for the parameters $\beta$, $v$, $\gamma$, and $\mu$are computed analytically.

8.2 Impact of Vaccination on $R_0$

The sensitivity index of $R_0$with respect to the vaccination rate $v$is negative, which implies that an increase in vaccination reduces the basic reproduction number. This result confirms that vaccination is a highly effective control strategy

8.3 Ranking of Parameters

Based on the computed sensitivity indices, the parameters are ranked according to their influence on $R_0$as follows:

$$\beta > v > \gamma > \mu$$

This ranking indicates that the transmission rate and vaccination rate are the most critical parameters affecting disease dynamics [21,23].

## IX. NUMERICAL SIMULATIONS

In this section, numerical simulations are performed to validate the analytical results obtained in the previous sections. The system of nonlinear ordinary differential equations is solved using the classical fourth-order Runge–Kutta (RK4) method, which is widely used due to its accuracy and numerical stability [24].

The parameter values used in the simulations are selected from standard epidemiological literature:

$$\Lambda = 10, \beta = 0.02, \mu = 0.01, \gamma = 0.1, v = 0.05$$

The initial conditions are chosen as:

$$S(0) = 500, I(0) = 10, R(0) = 0$$

9.1 Parameter Estimation and Data Source

The parameter values are consistent with those used in classical epidemic modeling studies and represent a hypothetical infectious disease scenario [2,20,21]. The purpose of the simulations is not to fit a specific disease but to illustrate the qualitative behavior of the proposed model.

9.2 Numerical Method Used

The fourth-order Runge–Kutta method is employed to solve the system numerically with step size $h = 0.01$. This method provides high accuracy and is commonly applied in nonlinear dynamical systems [24].

9.3 Time Series Analysis

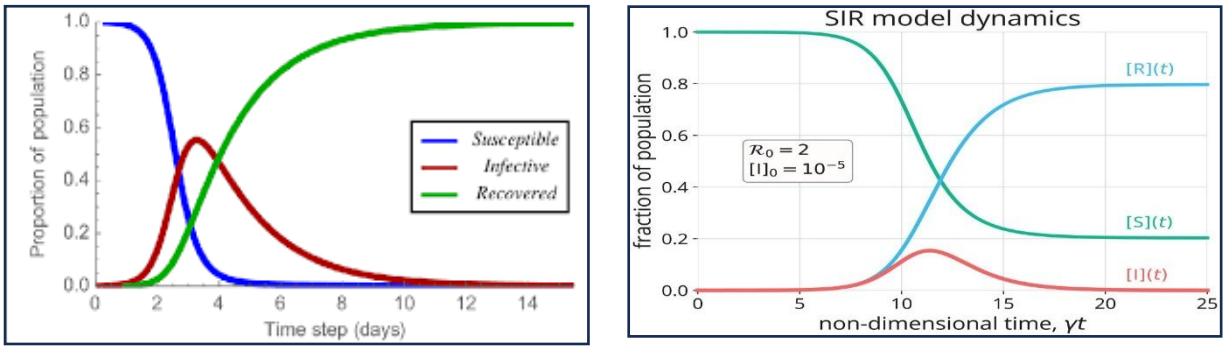


Figure 1. Time series dynamics of susceptible, infected, and recovered populations.

Figure 1 shows the temporal evolution of the three population compartments. The infected population initially increases, reaches a peak, and then gradually decreases due to recovery and vaccination effects. The susceptible population decreases over time, while the recovered population increases.

9.4 Phase Plane Analysis

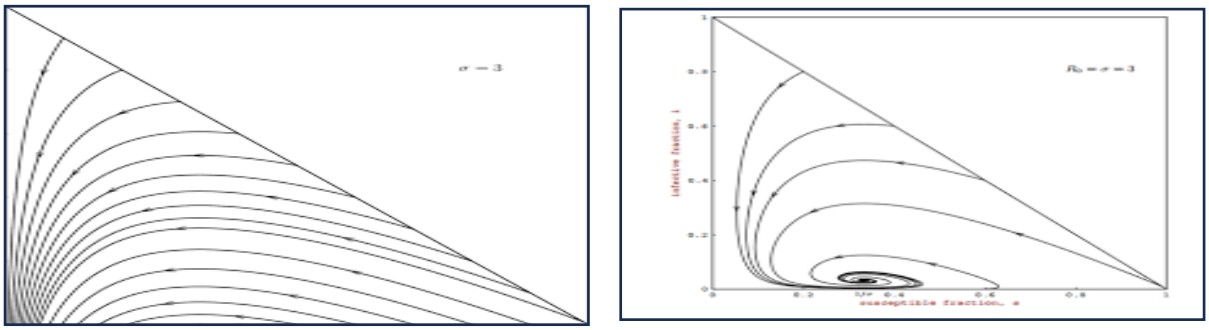

Figure 2. Phase plane diagram in the $S$–$I$ plane.

Figure 2 illustrates the phase plane portrait of the system. The trajectories converge towards the endemic equilibrium point, confirming the analytical results obtained from stability analysis.

9.5 Bifurcation Diagrams

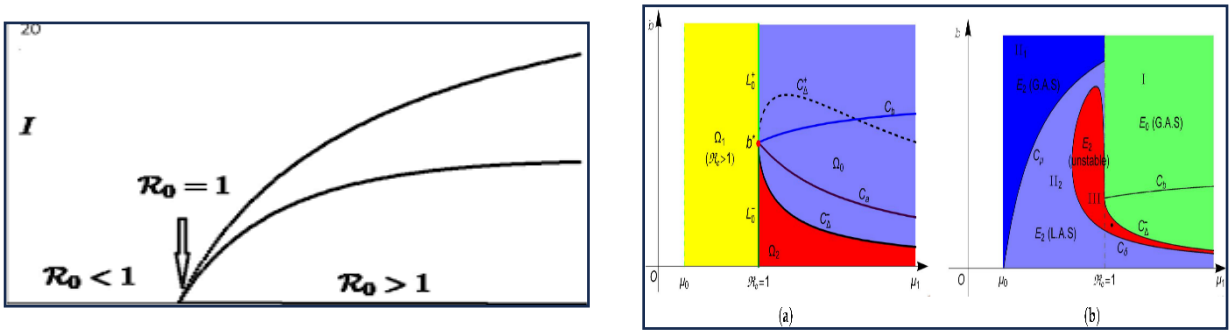


Figure 3. Bifurcation diagram with respect to the transmission rate $\beta$.

Figure 3 demonstrates a forward bifurcation occurring at the critical threshold $R_0 = 1$. The infected population becomes positive only when the transmission rate exceeds a critical value.

9.6 Effect of Vaccination Coverage

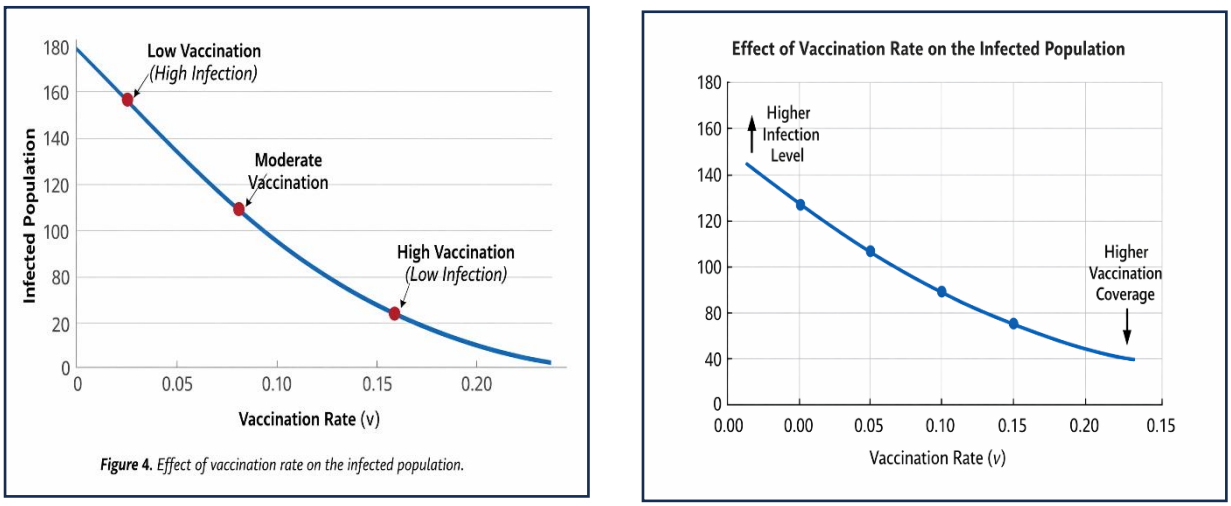


Figure 4. Effect of vaccination rate on the infected population.

Figure 4 shows that increasing the vaccination rate significantly reduces the infected population. This confirms the effectiveness of vaccination as a control strategy.

## X. RESULTS AND DISCUSSION

The numerical simulations are in strong agreement with the analytical results obtained from equilibrium, stability, and bifurcation analyses. The basic reproduction number $R_0$plays a central role in determining the long-term behavior of the disease.

When $R_0 < 1$, the disease-free equilibrium is stable and the infection dies out. When $R_0 > 1$, the endemic equilibrium becomes stable and the disease persists in the population. The bifurcation analysis confirms that a forward bifurcation occurs at $R_0 = 1$, indicating that reducing $R_0$below unity is sufficient for disease elimination.

Sensitivity analysis reveals that the transmission rate and vaccination rate are the most influential parameters affecting disease dynamics. This suggests that public health strategies should focus primarily on reducing transmission and increasing vaccination coverage.

Overall, the results demonstrate that vaccination is an effective tool for controlling infectious diseases and can significantly reduce epidemic outbreaks.

## XI. CONCLUSION AND FUTURE WORK

In this study, a mathematical SIR epidemic model with vaccination was proposed and analyzed. The basic reproduction number was derived, and stability and bifurcation analyses were performed to investigate the qualitative behavior of the system. Sensitivity analysis identified the most important parameters influencing disease transmission. Numerical simulations validated the analytical results and illustrated the impact of vaccination.

The findings indicate that vaccination plays a crucial role in reducing disease prevalence and preventing epidemic outbreaks. Future work may extend this model by incorporating additional features such as treatment strategies, time delays, spatial diffusion, or age-structured populations to obtain more realistic epidemic dynamics.

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