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RESEARCH

Stability and Bifurcations in a Discrete-Time Epidemic Model with Vaccination and Vital Dynamics

Mahmood Parsamanesh[1,2], Majid Erfanian[1,2*] and Saeed Mehrshad[1]

Abstract

Background: The spread of infectious diseases is such important that changes the demography of the population. Therefore, prevention and intervention measures are essential to control and eliminate the disease. Among the drug and non-drug interventions, vaccination is a powerful strategy to preserve the population from infection. Mathematical models are useful to study the behavior of an infection when it enters a population and investigate under which conditions it will be wiped out or continued.

Results: A discrete-time SIS epidemic model is introduced that includes a vaccination program. Some basic properties of this model are obtained; such as the equilibria and the basic reproduction number $\mathcal{R}_0$. Then the stability of the equilibria is given in terms of $\mathcal{R}_0$, and moreover, the bifurcations of the model are studied. By applying the forward Euler method on the continuous version of model, a discretized model is obtained and analyzed.

Conclusion: It is proved that the disease-free equilibrium and endemic equilibrium are stable if $\mathcal{R}_0 < 1$ and $\mathcal{R}_0 > 1$, respectively. The system has a transcritical bifurcation when $\mathcal{R}_0 = 1$ and it might also have period-doubling bifurcation. The sufficient conditions for the stability of equilibria in the discretized model are established. The numerical discussions verify the theoretical results.

Keywords: SIS epidemic model; discrete-time system; stability; Lyapunov exponent; bifurcation

1 Background

The spread of infectious diseases in populations and how to control and eliminate them from the population are important and necessary subjects. Mathematical models are introduced to study what happens when an infection enters in a population, and under which conditions the disease will be wiped out from population or persists in population. The literature about mathematical epidemic models that have been constructed and analyzed for various types of diseases, is very rich; see, for example, [1, 2]. Among these models, the susceptible-infected-susceptible (SIS) epidemic models are one of the well-known types of epidemic models. For the purpose of considering the effect of vaccination as an efficient strategy to control and eliminate infections, it is possible to add a compartment for the vaccinated individuals to the SIS model and obtain the SIS epidemic model with vaccination, namely SIVS epidemic model [8, 14]. These models may be deterministic [4] or stochastic [5], with constant [11] or variable [14] population size, and with standard [10] or bilinear [4, 5] incidence rate. In this paper, we consider a discrete-time SIVS epidemic model with standard incidence. The organization of the paper reads as follows: In the next section the model is introduced, and equilibria of the model and its basic reproduction number are obtained. Sections 3 and 4 are devoted to studying the stability of the equilibria and bifurcations of the model, respectively. In section 5, by using the forward Euler method, a discrete-time model is obtained from a continuous version of the model and stability of its equilibria is analyzed. After a numerical discussion in section 6, we summarize the results.

2 The model

Suppose that the individuals in a population are partitioned into susceptible individuals, infected individuals, and vaccinated individuals. Also, consider Δt as the appropriate time increment such that

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the changes in the model may take place at times $0, \Delta t, 2\Delta t, 3\Delta t, \ldots$. The number of total individuals at time $t = n\Delta t$, for some n, is denoted by N_t and numbers of individuals in other compartments in the same time are as S_t, I_t, and V_t. All possible changes in the model and transmissions between its sub-populations together with their transmission rates have been shown in Figure 1. Here, all parameters are assumed to be nonnegative, and moreover N and μ are positive. Also, μ is the natural death rate, β is the contact rate, γ is the cure rate, ϵ is the rate of losing immunity, while q and p are the vaccination rate in newcomers and susceptible individuals, respectively.

The model can be illustrated by the following system of difference equations:

$$\begin{aligned} I_{t+1} &= \beta S_t I_t/N_t + [1-(\mu+\gamma)]I_t, \\ S_{t+1} &= (1-q)\mu N_t \\ &\quad - \beta S_t I_t/N_t + [1-(\mu+p)]S_t + \gamma I_t + \epsilon V_t, \\ V_{t+1} &= q\mu N_t + pS_t + [1-(\mu+\epsilon)]V_t. \end{aligned} \tag{1}$$

The susceptible individuals become infected at standard incidence rate $\beta S_t I_t/N_t$. Moreover, summing equations in system (1), we see that $N_{t+1} = N_t$, and then the population size will remain a constant value. Thus, by letting $V_t = N - S_t - I_t$, the corresponding difference equation is deleted and the following system of two difference equations is obtained:

$$\begin{aligned} I_{t+1} &= \beta S_t I_t/N + [1-(\mu+\gamma)]I_t, \\ S_{t+1} &= [(1-q)\mu+\epsilon]N - \beta S_t I_t/N + [1-(\mu+p \\ &\quad +\epsilon)]S_t + (\gamma-\epsilon)I_t. \end{aligned} \tag{2}$$

System (2) is considered under the following conditions, which are sufficient but not necessary for nonnegativity of solutions.

$$\begin{aligned} &\mu + p + \epsilon + \beta < 1, \\ &\mu + \gamma < 1. \end{aligned} \tag{3}$$

The equilibria of the model are solutions of the following system:

$$\begin{aligned} &\bar{I}\Big[\beta\bar{S}/N - (\mu+\gamma)\Big] = 0, \\ &[(1-q)\mu+\epsilon]N - \beta\bar{S}\bar{I}/N \\ &-(\mu+p+\epsilon)\bar{S} + (\gamma-\epsilon)\bar{I} = 0. \end{aligned}$$

From the first equation, we must have either $\bar{I} = 0$ or $\beta\bar{S}/N - (\mu+\gamma) = 0$. When $\bar{I} = 0$, the equilibrium is named *the disease-free equilibrium* and is written as

$$Q^0 = (I^0, S^0) = \Big(0, \frac{[(1-q)\mu+\epsilon]N}{\mu+p+\epsilon}\Big),$$

while if $\beta\bar{S}/N - (\mu+\gamma) = 0$, we obtain

$$\bar{I} = \frac{[(1-q)\mu+\epsilon]N - \frac{(\mu+p+\epsilon)(\mu+\gamma)N}{\beta}}{(\mu+\epsilon)}.$$

This equilibrium in which $\bar{I} \neq 0$, is called *the endemic equilibrium* and is written as

$$Q^* = (I^*, S^*) = \Big(\frac{[(1-q)\mu+\epsilon]\beta N - (\mu+p+\epsilon)(\mu+\gamma)N}{\beta(\mu+\epsilon)}, \frac{(\mu+\gamma)N}{\beta}\Big).$$

Notice that $I^* > 0$ if and only if $[(1-q)\mu+\epsilon]\beta - (\mu+p+\epsilon)(\mu+\gamma) > 0$ if and only if

$$\mathcal{R}_0 = \frac{\beta[(1-q)\mu+\epsilon]}{(\mu+p+\epsilon)(\mu+\gamma)} > 1.$$

The quantity $\mathcal{R}_0$ is referred to as *the basic reproduction number* of model (2) and is interpreted as the number of individuals who become infected by entering one infected individual into a fully susceptible population; see [6]. We see that $\mathcal{R}_0$ is independent from the total population size N. Also

$$S^0 = \frac{(\mu+\gamma)N}{\beta}(\mathcal{R}_0)$$

and

$$I^* = \frac{(\mu+p+\epsilon)(\mu+\gamma)N}{(\mu+\epsilon)\beta}(\mathcal{R}_0 - 1).$$

Therefore, we can state the following lemma about the existence of equilibria of the model.

Lemma 2.1 *For SIVS epidemic model* (2)*, the disease-free equilibrium Q^0 always exists and the endemic equilibrium Q^* also exists if $\mathcal{R}_0 > 1$.*

3 Stability of the equilibria

We study stability of the system at an equilibrium by considering eigenvalues of the corresponding Jacobian matrix at that equilibrium. When eigenvalues are less than one, the system is stable.

Theorem 3.1 *The disease-free equilibrium is stable if and only if $\mathcal{R}_0 < 1$.*

proof:
The Jacobian matrix of model (2) at (I, S) is

$$J(I,S) = \begin{pmatrix} 1-(\mu+\gamma)+\beta S/N & \beta I/N \\ -\beta S/N+(\gamma-\epsilon) & 1-(\mu+p+\epsilon)-\beta I/N \end{pmatrix}. \quad (4)$$

Therefore, the Jacobian matrix at Q^0 is given by

$$J(Q^0) = \begin{pmatrix} 1-(\mu+\gamma)+(\mu+\gamma)\mathcal{R}_0 & 0 \\ -(\mu+\gamma)\mathcal{R}_0+(\gamma-\epsilon) & 1-(\mu+p+\epsilon) \end{pmatrix}.$$

The eigenvalues of $J(Q^0)$ are $\lambda_1 = 1-(\mu+\gamma)+(\mu+\gamma)\mathcal{R}_0$ and $\lambda_2 = 1-(\mu+p+\epsilon)$. obviously, $|\lambda_2| < 1$ by assumptions (3) and $|\lambda_1| < 1$ if and only if $\mathcal{R}_0 < 1$. Thus we have the following result.

Theorem 3.2 *When $\mathcal{R}_0 > 1$, the endemic equilibrium Q^* is stable and otherwise is unstable.*
proof:
On the other hand, at Q^*, we have $\beta S^*/N = (\mu+\gamma)$ and so

$$J^* = J(Q^*) = \begin{pmatrix} 1 & \beta I^*/N \\ -(\mu+\epsilon) & 1-(\mu+p+\epsilon)-\beta I^*/N \end{pmatrix}.$$

Thus we get

$$tr(J^*) = 2-(\mu+p+\epsilon)-\beta I^*/N,$$
$$det(J^*) = 1-(\mu+p+\epsilon)-\beta I^*/N+(\mu+\epsilon)\beta I^*/N,$$

and by assuming

$$b_1 = (\mu+p+\epsilon)+\beta I^*/N,$$
$$b_2 = (\mu+\epsilon)\beta I^*/N,$$

we can rewrite them as

$$tr(J^*) = 2-b_1,$$
$$det(J^*) = 1-b_1+b_2.$$

The characteristic equation of J^* is of the form $P(\lambda) = \lambda^2 - tr(J^*)\lambda + det(J^*)$ and according to *the Jury conditions*, all eigenvalues of J^* are from module less than one if and only if (see [3])

$$|tr(J^*)| < 1+det(J^*) < 2. \quad (5)$$

First, $1+det(J^*) < 2$ holds if and only if $-b_1+b_2 < 0$. Besides, $\beta I^*/N > (\mu+\epsilon)\beta I^*/N$ and so $(\mu+p+\epsilon)+\beta I^*/N > (\mu+\epsilon)\beta I^*/N$, that is, $b_1 > b_2$ and thus the condition $1+det(J^*) < 2$ holds.
Second, for $tr(J^*) > 0$ we must show that $tr(J^*) < 1+det(J^*)$, which holds since it is equivalent to $b_2 > 0$. If $tr(J^*) < 0$, then we have to prove $-tr(J^*) < 1+det(J^*)$, which holds if and only if $4-2b_1+b_2 > 0$. Indeed

$$\begin{aligned} 4-2b_1+b_2 &= 4+(\mu+\epsilon)\beta I^*/N \\ &\quad -2[(\mu+p+\epsilon)+\beta I^*/N] \\ &> 2+(\mu+\epsilon)\beta I^*/N-2\beta I^*/N \\ &> (\mu+\epsilon)\beta I^*/N > 0, \end{aligned}$$

since $\mu+p+\epsilon < 1$ and $\beta I^*/N < 1$. Therefore, when $\mathcal{R}_0 > 1$, the Jury conditions are satisfied and the following theorem has been proved.

4 Bifurcations of the model

In a discrete-time system, bifurcations occur at the equilibria of the understudy system when there exist some eigenvalues of the Jacobian matrix with module one. Indeed, for an eigenvalue λ, if $\lambda = 1$, then a *transcritical bifurcation* occurs and when $\lambda = -1$, a *period-doubling bifurcation* occurs; see [1, 3]. While a *Neimark–Sacker bifurcation*, which is the same as the *Hopf bifurcation* in continuous systems [9], occurs if there is a complex pair of conjugate eigenvalues with module one, $|\lambda| = 1$.
As we saw, the eigenvalues of $J(Q^0)$ are $\lambda_1 = 1-(\mu+\gamma)+(\mu+\gamma)\mathcal{R}_0$ and $\lambda_2 = 1-(\mu+p+\epsilon)$. Also, $\lambda_1 = 1$ if and only if $\mathcal{R}_0 = 1$ and thus a transcritical bifurcation occurs at Q^0 when $\mathcal{R}_0 = 1$. On the other hand, $\lambda_1 = -1$ if and only if $\mathcal{R}_0 = 1-\frac{2}{\mu+\gamma}$, but this is impossible because $\mu+\gamma < 1$ and $\mathcal{R}_0$ becomes a negative value. This shows that a period-doubling bifurcation does not occur at Q^0. In addition, the eigenvalues of $J(Q^0)$ are both real, and therefore a Neimark-Sacker bifurcation does not take place, too. Thus we can state the following.

Theorem 4.1 *At disease-free equilibrium Q^0 of SIVS epidemic model* (2)*, transcritical bifurcation happens if $\mathcal{R}_0 = 1$ while a period-doubling bifurcation and a Neimark-Sacker bifurcation do not take place.*

Now, we consider bifurcations at the endemic state. The following theorem is devoted for this purpose.

Theorem 4.2 *At endemic equilibrium Q^* for SIVS model* (2)*,*
I) transcritical bifurcation happens if $\mathcal{R}_0 = 1$,
II) a period-doubling bifurcation does not occur,
III) a Neimark-Sacker bifurcation cannot be appeared.
proof:
We have $\lambda = 1$ is an eigenvalue of Jacobian matrix

$J(Q^*)$ if it is a root of the corresponding characteristic equation, $1 - tr(J^*) + det(J^*) = 0$. This holds if and only if $b_2 = 0$, if and only if $\beta I^*/N = 0$, if and only if $\mathcal{R}_0 = 1$, since

$$\beta I^*/N = \frac{(\mu + p + \epsilon)(\mu + \gamma)}{(\mu + \epsilon)}(\mathcal{R}_0 - 1).$$

However, $\lambda = -1$ is an eigenvalue of $J(Q^*)$ if $P(-1) = 0$. This is satisfied if and only if $4 - 2b_1 + b_2 = 0$ that can be written as

$$4 - 2(\mu + p + \epsilon) - \beta I^*/N[2 - (\mu + \epsilon)] = 0,$$

or equivalently

$$2[2 - (\mu + p + \epsilon)] - \beta I^*/N[2 - (\mu + \epsilon)] = 0. \quad (6)$$

Now, notice that as we concluded previously, $P(-1) > 0$ when $\mathcal{R}_0 > 1$. Also, $\mathcal{R}_0 = 1$ implies $\beta I^*/N = 0$ and this results in $2 - (\mu + p + \epsilon) = 0$ which is impossible. These discussions state that a period-doubling bifurcation does not happen at Q^*.
If we write the characteristic equation of J^* as $P(\lambda) = \lambda^2 + a_1\lambda + a_2$, we see that

$$\begin{aligned} a_1^2 - 4a_2 &= (-2 + b_1)^2 - 4(1 - b_1 + b_2) \\ &= b_1^2 - 4b_2 \\ &= (\mu + p + \epsilon)^2 + 2(\mu + p + \epsilon)\beta I^*/N \\ &+ (\beta I^*/N)^2 - 4(\mu + \epsilon)\beta I^*/N \\ &> (\mu + p + \epsilon)^2 - 2(\mu + p + \epsilon)\beta I^*/N \\ &+ (\beta I^*/N)^2 = [(\mu + p + \epsilon) + \beta I^*/N]^2 > 0. \end{aligned}$$

Hence, the roots of $P(\lambda)$ are both real and thus a Neimark-Sacker bifurcation cannot be appeared at Q^*.
Remark 4.1 *If we omit the restriction $\beta < 1$ from the system and allow β to take values greater than or equal to one, then from* (6)*, we get*

$$\beta I^*/N = \frac{2[2 - (\mu + p + \epsilon)]}{2 - (\mu + \epsilon)}.$$

Thus a period-doubling bifurcation occurs at Q^* for $\beta \geq 1$ if

$$\mathcal{R}_0 = 1 + \Big(\frac{2[2 - (\mu + p + \epsilon)]}{2 - (\mu + \epsilon)}\Big)\Big(\frac{\mu + \epsilon}{(\mu + p + \epsilon)(\mu + \gamma)}\Big).$$

5 The model obtained by the forward Euler discretization

The model described in Figure 1 can be stated as a continuous-time model by the following system of ordinary differential equations (see [12, 13]):

$$\begin{aligned} \dot{I} &= \beta SI/N - (\mu + \gamma)I, \\ \dot{S} &= (1 - q)\mu N - \beta SI/N - (\mu + p)S + \gamma I + \epsilon V, \\ \dot{V} &= q\mu N + pS - (\mu + \epsilon)V. \end{aligned} \quad (7)$$

We see that $\dot{N} = dN/dt = 0$ and therefore the population size is constant. Similar to the discrete-time model, we get the following two-dimensional system by substituting $V = N - S - I$ and omitting variable V from the system:

$$\begin{aligned} \dot{I} &= \beta SI/N - (\mu + \gamma)I, \\ \dot{S} &= [(1 - q)\mu + \epsilon]N - \beta SI/N - (\mu + p + \epsilon)]S + (\gamma - \epsilon)I. \end{aligned} \quad (8)$$

Now in this section, we discretize and analyze model (8) by using the forward Euler method. Substituting $\dot{S} = (S_{t+1} - S_t)/\Delta$ and $\dot{I} = (I_{t+1} - I_t)/\Delta$, where Δ is the fixed step size of the discretization, we obtain the discrete version of model as follows:

$$\begin{aligned} I_{t+1} &= I_t + \Delta\Big(\beta S_t I_t/N - (\mu + \gamma)I_t\Big), \\ S_{t+1} &= S_t + \Delta\Big([(1 - q)\mu + \epsilon]N - \beta S_t I_t/N \\ &\quad - (\mu + p + \epsilon)S_t + (\gamma - \epsilon)I_t\Big). \end{aligned} \quad (9)$$

It can be seen that the equilibria of this model and the corresponding basic reproduction number are similar to model (2). The disease-free equilibrium of discretized model, Q_d^0, always exists while, its endemic equilibrium, Q_d^*, exists only when $\mathcal{R}_0 > 1$.

Theorem 5.1 *When $\mathcal{R}_0 < 1$, the disease-free equilibrium of model* (9) *is stable if $\Delta < 2/\min\{(\mu + p + \epsilon), (\mu + \gamma)(1 - \mathcal{R}_0)\}$.*
Proof:
The the Jacobian matrix of the model at (I, S) is given by

$$J(I, S) = \quad (10)$$
$$\begin{pmatrix} 1 + \Delta(\beta S/N - (\mu + \gamma)) & \Delta\beta I/N \\ \Delta(-\beta S/N + (\gamma - \epsilon)) & 1 - \Delta((\mu + p + \epsilon) + \beta I/N) \end{pmatrix}.$$

and at the disease-free equilibrium, it is

$$J(Q_d^0) =$$
$$\begin{pmatrix} 1 + \Delta((\mu + \gamma)\mathcal{R}_0 - (\mu + \gamma)) & 0 \\ \Delta(-(\mu + \gamma)\mathcal{R}_0 + (\gamma - \epsilon)) & 1 - \Delta(\mu + p + \epsilon) \end{pmatrix}.$$

Thus the eigenvalues of $J(Q_d^0)$ are $\lambda_1 = 1 + \Delta(\mu + \gamma)(\mathcal{R}_0 - 1)$ and $\lambda_2 = 1 - \Delta(\mu + p + \epsilon)$. Therefore, $|\lambda_1| < 1$ if and only if $\Delta < \frac{2}{(\mu+\gamma)(1-\mathcal{R}_0)}$, and $|\lambda_2| < 1$ if and only if $\Delta < \frac{2}{(\mu+p+\epsilon)}$.

Theorem 5.2 *When $\mathcal{R}_0 < 1$, the endemic equilibrium of model* (9) *is stable if $\Delta < \Delta^*$, where Δ^* is the least root of $b_2x^2 - 2b_1x + 4$, in which $b_1 = (\mu + p + \epsilon) + \beta I^*/N$ and $b_2 = (\mu + \epsilon)\beta I^*/N$.*

Proof:

The the Jacobian matrix at endemic equilibrium is

$$J_d^* = J(Q_d^*) = \begin{pmatrix} 1 & \Delta\beta I^*/N \\ -\Delta(\mu+\epsilon) & 1 - \Delta((\mu + p + \epsilon) - \beta I^*/N) \end{pmatrix}.$$

According to Jury conditions (Schur–Cohn criterion), the matrix J_d^* is stable (i.e., the roots of its characteristic equation $P_d(\lambda) = \lambda^2 + a_1\lambda + a_2$ lie inside the unit disk) if and only if the following conditions hold (see [7]):

(i) $1 - a_2 > 0$,
(ii) $P(1) = 1 + a_1 + a_2 > 0$,
(iii) $P(-1) = 1 - a_1 + a_2 > 0$.

Here, $a_1 = -tr(J_d^*)$ and $a_2 = det(J_d^*)$. We see, $tr(J_d^*) = 2 - \Delta b_1$ and $det(J_d^*) = 1 - \Delta b_1 + \Delta^2 b_2$. Thus condition (i) holds if and only if $\Delta b_1 - \Delta^2 b_2 > 0$, or equivalently $\Delta < \frac{b_1}{b_2}$. Condition (ii), $P(1) = 1 - tr(J_d^*) + det(J_d^*) > 0$, holds if and only if $b_2\Delta^2 > 0$, which holds because $b_2 = (\mu+\epsilon)\beta I^*/N > 0$. Condition (iii), $P(-1) = 1 + tr(J_d^*) + det(J_d^*) > 0$, holds if and only if $b_2\Delta^2 - 2b_1\Delta + 4 > 0$. Since

$$\begin{aligned} b_1^2 - 4b_2 &= ((\mu + p + \epsilon) + \beta I^*/N)^2 - 4(\mu + \epsilon)\beta I^*/N \\ &= ((\mu + \epsilon) - \beta I^*/N)^2 \\ &\quad + p(p + 2(\mu + \epsilon) + 2\beta I^*/N) > 0, \end{aligned}$$

thus $b_2\Delta^2 - 2b_1\Delta + 4 > 0$ has two roots of the form $\frac{b_1 \pm \sqrt{b_1^2 - 4b_2}}{b_2}$. Now, if we denote two roots as r_1 and r_2 (suppose $r_1 < r_2$), then $P(-1)$ is positive when $\Delta < r_1$ or $\Delta > r_2$, since $b_2 > 0$. Moreover, we can easily see that $b_1 - \sqrt{b_1^2 - 4b_2} > 0$, and thus $r_1 > 0$. Therefore we can state, conditions (i)–(iii) hold if $\Delta < r_1$, because we also have $r_1 < \frac{b_1}{b_2}$.

Remark 5.1 *Model* (2) *was formulated straightly by considering a population and its transmissions. Also, the model can be concluded from discretized model* (9) *for $\Delta = 1$ and assumptions* (3).

6 Numerical discussions

In this section, we consider numerically theoretical results obtained in the paper. For this purpose assume that the parameters in the model are as $q = 0.4$, $p = 0.2$, $\gamma = 0.15$, $\mu = 0.1$, and $\epsilon = 0.25$. Moreover, consider units of time and population as one day and one million individuals, respectively. Let the number of initial individuals in each sub-populations be as $I_0 = 0.4$, $S_0 = 0.8$, and $V_0 = 0.5$. We take the contact rate β as the bifurcation parameter and get the bifurcation diagram as it is shown in Figure 2. We see that at $\beta = 0.443$, the dynamic of the system changes: The disease-free equilibrium that was stable for values $\beta < 0.443$ becomes unstable and instead the endemic equilibrium becomes stable. Indeed, at $\beta = 0.4435$, we have $\mathcal{R}_0 = 1$ and a transcritical bifurcation occurs. Moreover, it is seen that at $\beta = 2.428$, the endemic equilibrium becomes unstable and a period-doubling bifurcation happens and after that the system remains unstable. This value for β also is obtained according to Remark 4.1 as $\beta = 2.4279$. Figure 3 shows the Lyapunov exponents of the Jacobian matrix for the same values of β. Here also it is observable that for values $\beta = 0.443, 2.428$ and 3.235, the Lyapunov exponent is positive as seen in the bifurcation diagram. Figure 4 presents solutions of the system for various values of β and behavior of the solutions is the same as we expect from the bifurcation diagram and the Lyapunov exponents. For $\beta = 0.4$, we have $\mathcal{R}_0 = 0.9018 < 1$ and as we expect from Theorem 3.1, the disease will vanish. While, for values $\beta = 0.55$, $\beta = 2.45$, and $\beta = 2.5$, we have $\mathcal{R}_0 = 1.2400$, $\mathcal{R}_0 = 5.5236$, and $\mathcal{R}_0 = 5.6364$, respectively, that all are greater than one and according to Theorem 3.2, the infection remains at a positive level. In addition, Figure 5 displays some parts of solutions of infected population I_t for different values of β. It is observable that the behavior of solutions corresponds with those are in the bifurcation diagram. The effect of the discretization of continuous-time model (8) by applying the forward Euler method has been considered in Figure 6. The bifurcation diagram shows the dynamics of infected population in discretized model (9) when the step size Δ varies. The contact rate has been supposed as $\beta = 2.7$ and other parameters are the same as preceding simulations. As it was established in Theorem 5.2, the endemic equilibrium Q_d^* is stable for $\Delta < \Delta^* = 0.8946$ while for greater values of Δ, the endemic equilibrium becomes unstable.

7 Summary

In this paper, we introduced and studied an SIS epidemic model that includes a vaccination program. The equilibria of the model were detected: The disease-free equilibrium Q^0 in which the infection will be extinct, and the endemic equilibrium Q^* in which the disease will persist in population. It was proved that under

some assumptions on parameters for positivity of solutions, Q^0 and Q^* are stable if $\mathcal{R}_0 < 1$ and $\mathcal{R}_0 > 1$, respectively. Furthermore, the bifurcations of the model were investigated and it was proved that when $\mathcal{R}_0 = 1$ system has a transcritical bifurcation and although the Neimark–Sacker bifurcation does not appear, it may have a period-doubling bifurcation if we ignore the restriction $\beta < 1$. To study the discretization of the continuous version of the model, we applied the forward Euler method and analyzed the effect of step size of the discretization on dynamics of model. We established the sufficient condition for stability of disease-free equilibrium Q_d^0 and endemic equilibrium Q_d^* in discretized model. Finally, we examine the results obtained in the paper in numerical example by considering the bifurcation diagram, the Lyapunov exponents of the Jacobian matrix, and graphs of solutions for values of β and Δ. It was observed that the numerical discussions verify the theoretical results.

Abbreviations:
SIS: susceptible-infected-susceptible; SIVS: susceptible-infected-susceptible epidemic model with vaccination;

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Author's contributions
MP and ME conceived the method. MP, ME and SM drafted the manuscript. Also, MP, ME and SM read and approved the final manuscript.

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Figures

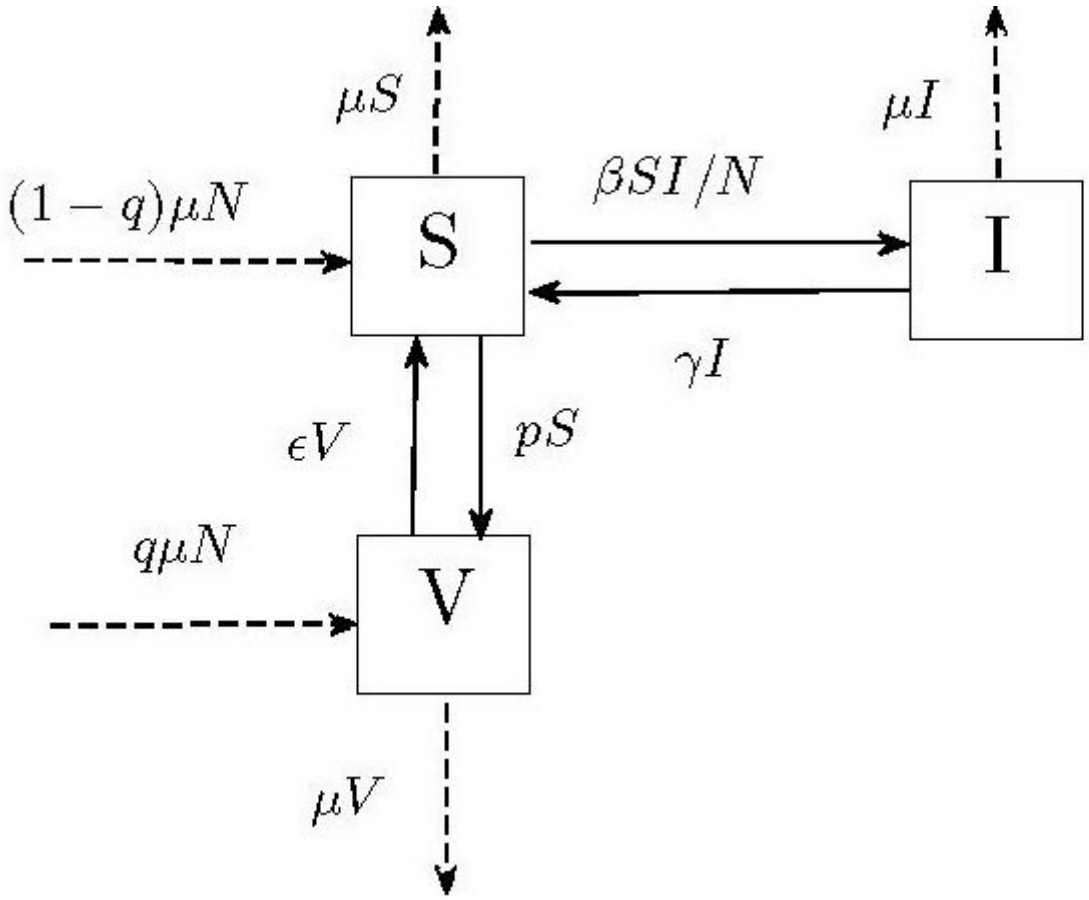

Figure 1

Flow diagram of the model together with transmission rates.

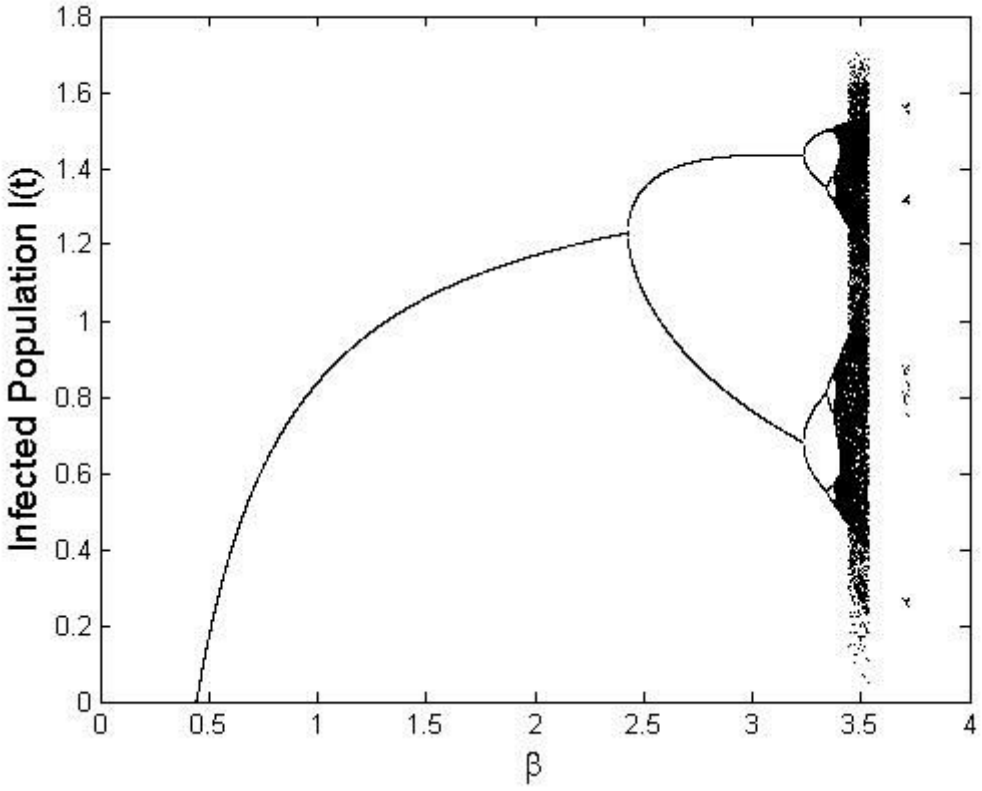

Figure 2

Bifurcation diagram for It in terms of β ∈ [0, 4].

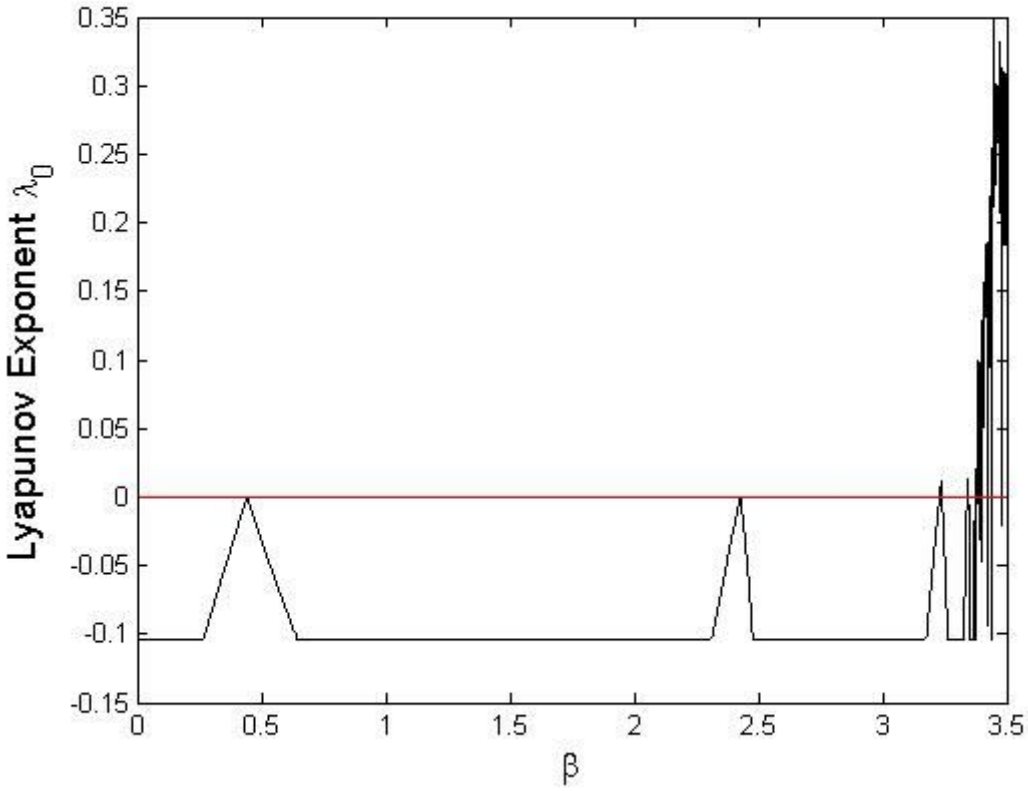

Figure 3

Lyapunov exponents of the Jacobian matrix in terms of β ∈ [0, 4].

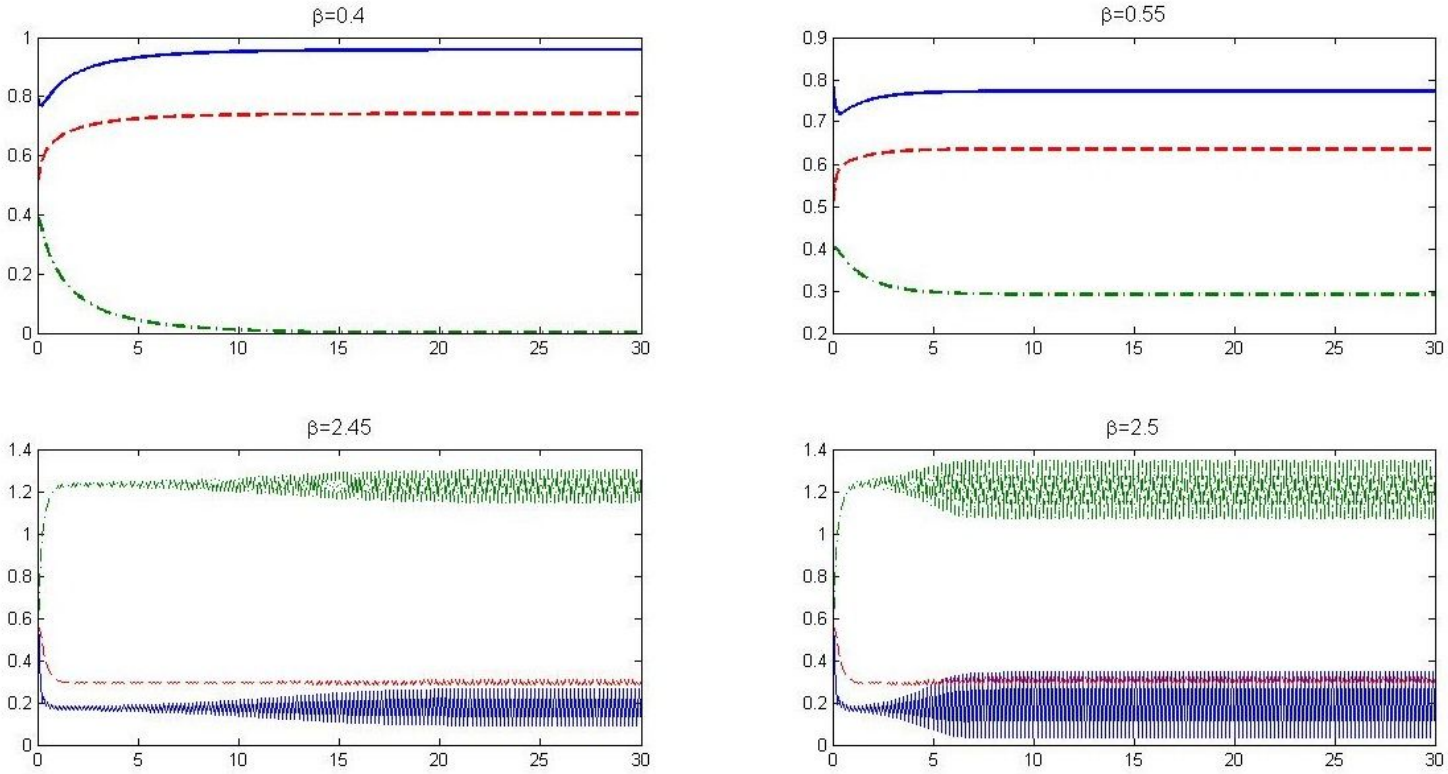

Figure 4

Solutions of the model for various values of β, I(t):'-.' GREEN, S(t):'-' BLUE, V(t):'- -' RED.

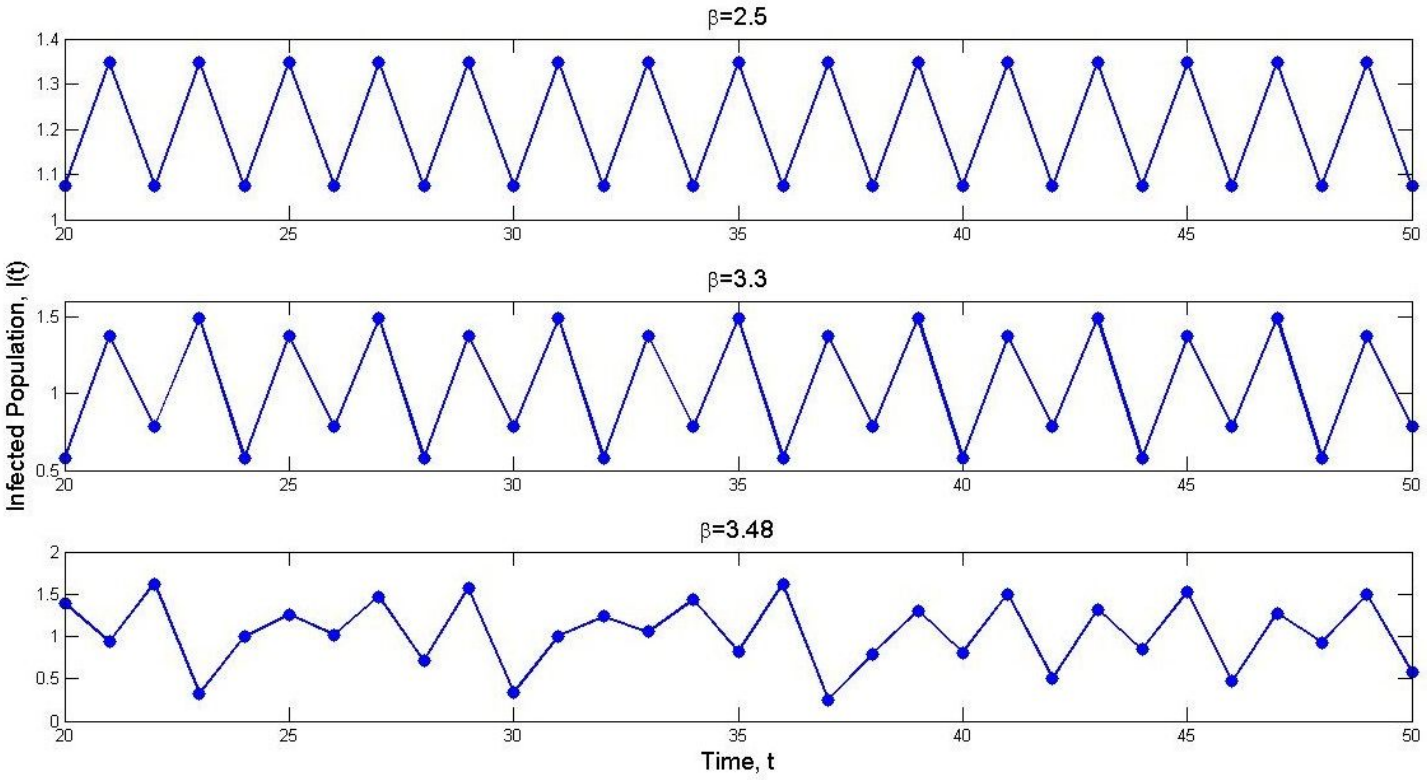

Figure 5

Partial solutions of infected population It for values β = 2.5, 3.3 and 3.48.

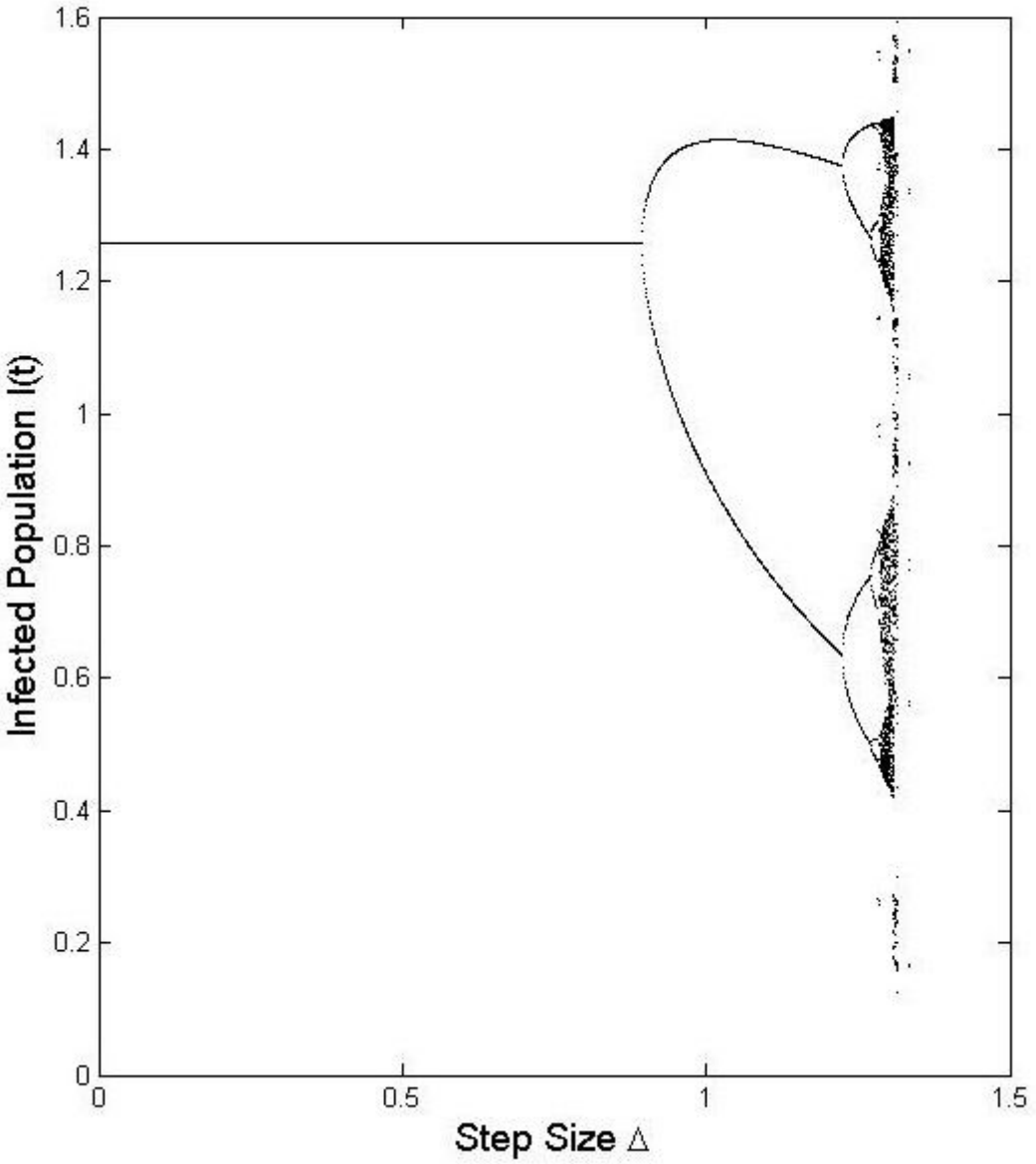

Figure 6

Bifurcation diagram for It in terms of Δ in model (9).