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

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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 \( \Delta t \) as the appropriate time increment such that...
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 $\mu$ are positive. Also, $\mu$ is the natural death rate, $\beta$ is the contact rate, $\gamma$ is the cure rate, $\epsilon$ 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:

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

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:

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

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

\[
\begin{align*}
\mu + p + \epsilon + \beta &< 1, \\
\mu + \gamma &< 1.
\end{align*}
\]

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

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

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

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

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

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

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

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

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

\[
R_0 = \frac{\beta(1-q)\mu + \epsilon}{(\mu + p + \epsilon)(\mu + \gamma)} > 1.
\]

The quantity $R_0$ 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 $R_0$ is independent from the total population size $N$. Also

\[
S^0 = \frac{(\mu + \gamma)N}{\beta} R_0
\]

and

\[
I^* = \frac{(\mu + p + \epsilon)(\mu + \gamma)N}{(\mu + \epsilon)R_0 - 1}.
\]

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 $R_0 > 1$.

### 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 $R_0 < 1$. 


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

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

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

\[
J(Q^0) = \begin{pmatrix}
1 - (\mu + \gamma) + (\mu + \gamma) R_0 & 0 \\
-(\mu + \gamma) R_0 + (\gamma - \epsilon) & 1 - (\mu + p + \epsilon)
\end{pmatrix}.
\]

The eigenvalues of \(J(Q^0)\) are \(\lambda_1 = 1 - (\mu + \gamma) + (\mu + \gamma) R_0\) and \(\lambda_2 = 1 - (\mu + p + \epsilon)\). Obviously, \(|\lambda_2| < 1\) by assumptions (3) and \(|\lambda_1| < 1\) if and only if only if \(R_0 < 1\). Thus we have the following result.

**Theorem 3.2** When \(R_0 > 1\), 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

\[
\text{tr}(J^*) = 2 - (\mu + p + \epsilon) - \beta I^*/N,
\]

\[
\text{det}(J^*) = 1 - (\mu + p + \epsilon) - \beta I^*/N + (\mu + \epsilon)\beta I^*/N,
\]

and by assuming

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

\[
b_2 = (\mu + \epsilon)\beta I^*/N,
\]

we can rewrite them as

\[
\text{tr}(J^*) = 2 - b_1,
\]

\[
\text{det}(J^*) = 1 - b_1 + b_2.
\]

The characteristic equation of \(J^*\) is of the form

\[
P(\lambda) = \lambda^2 - \text{tr}(J^*) \lambda + \text{det}(J^*)
\]

and according to the Jury conditions, all eigenvalues of \(J^*\) are from module less than one if and only if (see [3])

\[
|\text{tr}(J^*)| < 1 + \text{det}(J^*) < 2.
\]

First, \(1 + \text{det}(J^*) < 2\) 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 \(1 + \text{det}(J^*) < 2\) holds.

Second, for \(\text{tr}(J^*) > 0\) we must show that \(\text{tr}(J^*) < 1 + \text{det}(J^*)\), which holds since it is equivalent to \(b_2 > 0\).
If \(\text{tr}(J^*) < 0\), then we have to prove \(-\text{tr}(J^*) < 1 + \text{det}(J^*)\), which holds if and only if \(4 - 2b_1 + b_2 > 0\). Indeed

\[
4 - 2b_1 + b_2 = 4 + (\mu + \epsilon)\beta I^*/N - 2[(\mu + p + \epsilon) + \beta I^*/N] > 2 + (\mu + \epsilon)\beta I^*/N - 2\beta I^*/N > (\mu + \epsilon)\beta I^*/N > 0,
\]

since \(\mu + p + \epsilon < 1\) and \(\beta I^*/N < 1\). Therefore, when \(R_0 > 1\), the Jury conditions are satisfied and the following theorem has been proved.

**Theorem 4.1** At disease-free equilibrium \(Q^0\) of SIVS epidemic model (2), transcritical bifurcation happens if \(R_0 = 1\) 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 \(R_0 = 1\),
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...
\[ J(Q^*) \text{ if it is a root of the corresponding characteristic equation, } 1 - \text{tr}(J^*) + \det(J^*) = 0. \] This holds if and only if \( b_2 = 0 \), if and only if \( \beta I^*/N = 0 \), if and only if \( R_0 = 1 \), since

\[
\beta I^*/N = \frac{(\mu + p + \epsilon)(\mu + \gamma)}{(\mu + \epsilon)}(R_0 - 1).
\]

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

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

Now, notice that as we concluded previously, \( P(-1) = 0 \) when \( R_0 > 1 \). Also, \( R_0 = 1 \) 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

\[
a_1^2 - 4a_2 = (-2 + b_1)^2 - 4(1 - b_1 + b_2)
\]

\[
= b_1^2 - 4b_2
\]

\[
= (\mu + p + \epsilon)^2 + 2(\mu + p + \epsilon)\beta I^*/N
\]

\[
+ (\beta I^*/N)^2 - 4(\mu + \epsilon)\beta I^*/N
\]

\[
> (\mu + p + \epsilon)^2 - 2(\mu + p + \epsilon)\beta I^*/N
\]

\[
+ (\beta I^*/N)^2 = [(\mu + p + \epsilon) + \beta I^*/N]^2 > 0.
\]

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 \( \beta \) 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

\[
R_0 = 1 + \left( \frac{2[2 - (\mu + p + \epsilon)]}{2 - (\mu + \epsilon)} \right) \left( \frac{\mu + \epsilon}{(\mu + p + \epsilon)(\mu + \gamma)} \right).
\]

**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]):

\[
\dot{I} = \beta SI/N - (\mu + \gamma)I,
\]

\[
\dot{S} = (1 - q)\mu N - \beta SI/N - (\mu + p)S + \gamma I + \epsilon V, \tag{7}
\]

\[
\dot{V} = q\mu N + pS - (\mu + \epsilon)V.
\]

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:

\[
\dot{I} = \beta SI/N - (\mu + \gamma)I,
\]

\[
\dot{S} = [(1 - q)\mu N - \beta SI/N - (\mu + p)S + \gamma I + \epsilon V, \tag{8}
\]

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 \( \Delta \) is the fixed step size of the discretization, we obtain the discrete version of model as follows:

\[
I_{t+1} = I_t + \Delta \left( \beta S_t I_t/N - (\mu + \gamma)I_t \right),
\]

\[
S_{t+1} = S_t + \Delta \left[ ((1 - q)\mu N - \beta S_t I_t/N - (\mu + p)S_t + \gamma I_t + \epsilon V, \tag{9}
\right.

\]

\[
- (\mu + p + \epsilon)S_t + (\gamma - \epsilon)I_t \right).
\]

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, \( Q^*_0 \), always exists while, its endemic equilibrium, \( Q^*_e \), exists only when \( R_0 > 1 \).

**Theorem 5.1** When \( R_0 < 1 \), the disease-free equilibrium of model (9) is stable if \( \Delta < 2/min\{(\mu + p + \epsilon), (\mu + \gamma)(1 - R_0)\} \).

**Proof:**

The the Jacobian matrix of the model at \((I, S)\) is given by

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

and at the disease-free equilibrium, it is

\[
J(Q^*_0) = \begin{pmatrix}
1 + \Delta((\mu + \gamma)R_0 - (\mu + \gamma)) & 0 \\
\Delta(-\mu + (\mu + \gamma)R_0 + (\gamma - \epsilon)) & 1 - \Delta((\mu + p + \epsilon) + \beta I/N)\end{pmatrix}.
\]
Thus the eigenvalues of $J(Q^*_1)$ are $\lambda_1 = 1 + \Delta (\mu + \gamma)(R_0 - 1)$ and $\lambda_2 = 1 - \Delta (\mu + \gamma)(1 - R_0)$. Therefore, $|\lambda_1| < 1$ if and only if $\Delta < \frac{1}{2}(\mu + \gamma)(1 - R_0)$, and $|\lambda_2| < 1$ if and only if $\Delta < \frac{1}{2}(\mu + \gamma)(1 - R_0)$.

**Theorem 5.2** When $R_0 < 1$, the endemic equilibrium of model (9) is stable if $\Delta < \Delta^*$, where $\Delta^*$ is the least root of $b_2x^2 - 2b_1x + 4$, in which $b_1 = (\mu + p + \epsilon) + \beta I^*/N$ and $b_2 = (\mu + p)\beta I^*/N$.

**Proof:**

The Jacobian matrix at endemic equilibrium is

$$J_* = J(Q^*_1) = \begin{pmatrix} 1 & \Delta \beta I^*/N \\ -\Delta (\mu + \epsilon) & 1 - \Delta((\mu + p + \epsilon) - \beta I^*/N) \end{pmatrix}.$$

According to Jury conditions (Schur–Cohn criterion), the matrix $J_*$ 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, $a_1 = -tr(J_*)$ and $a_2 = det(J_*)$. We see, $tr(J_*) = 2 - \Delta b_1$ and $det(J_*) = 1 - \Delta b_1 + \Delta^2 b_2$.

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), $P(1) = 1 - tr(J_*) + det(J_*) > 0$, holds if and only if $b_2 \Delta > 0$, which holds because $b_2 = (\mu + p + \epsilon)\beta I^*/N > 0$. Condition (iii), $P(-1) = 1 + tr(J_*) + det(J_*) > 0$, holds if and only if $b_2 \Delta^2 - 2b_2 \Delta + 4 > 0$. Since $b_2 = (\mu + p + \epsilon) + \beta I^*/N$ and $\beta I^*/N > 0$,

thus $b_2 \Delta^2 - 2b_2 \Delta + 4 > 0$ has two roots of the form $\frac{b_1 \pm \sqrt{b_1^2 - 4b_2}}{2b_2}$. 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 straightforwardly 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 $\beta$ 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 $R_0 = 1$ 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 $\beta$ 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 $\beta$. 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 $\beta$ 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 $R_0 = 0.9018 < 1$ 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 $R_0 = 1.2400, R_0 = 5.5236$, and $R_0 = 5.6364$, 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 $I_1$ for different values of $\beta$. 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 $\Delta$ 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 $Q^*_1$ is stable for $\Delta < \Delta^* = 0.8946$ while for greater values of $\Delta$, 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 $R_0 < 1$ and $R_0 > 1$, respectively. Furthermore, the bifurcations of the model were investigated and it was proved that when $R_0 = 1$, the 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 $Q^0$ and endemic equilibrium $Q^*$ 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 $\beta$ and $\Delta$. It was observed that the numerical discussions verify the theoretical results.

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

Ethics approval and consent to participate
- Not applicable.

Consent for publication
- Not applicable.

Availability of data and materials
- Please contact author for data requests.

Competing interests
- The authors declare that they have no competing interests.

Funding
- No funding was obtained for this study

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.

Acknowledgements
- We thank the reviewers’ valuable comments for improving the quality of this work.

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