Semptomatik ve Asemptomatik Bulaşmaların Etkisi ile COVID-19 Salgınının Matematiksel Modelinin Analizi

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Analyzing a Mathematical Model of the COVID-19 Pandemic with the Impact Symptomatic and Asymptomatic Transmissions

Article Info	ABSTRACT
Received: 09.05.2024 **Accepted:** 18.07.2024 **Published:** 31.12.2024 **Keywords:** COVID-19 Pandemic Model, Flip Bifurcation, Local Asymptotic Stability, SIR Model.	This study addresses the stability and flip bifurcation of a discrete-time SIR model expressing the COVID-19 pandemic. The model considers the effect of the vaccine, asymptomatic individuals, as well as symptomatic individuals in the transmission of the disease. Equilibrium solutions are obtained under certain parametric conditions. Then, the local stabilities of these equilibrium solutions are investigated. The existence of bifurcation is determined for the positive interior equilibrium solution.

INTRODUCTION

Modern epidemiological theory emerged in the first years of the 20th century. The first major theoretical contribution to epidemiological theory came from Hamer (1906), who proposed the idea that the rate of contact between susceptible and infectious individuals determines how quickly an epidemic spreads [1]. This concept as an important idea in mathematical epidemiology is proportional to the principle of "mass action" which posits the multiplication of the density of infectious individuals by the density of susceptible individuals to determine the rate of spread of a disease. Most deterministic and stochastic theories of disease dynamics are based on this simple suggestion. Afterwards, Kermack and McKendrick [2, 3, 4] published their theory predicting the number and distribution of infectious disease cases in a series of three papers in 1927, 1932, and 1933. These studies established fundamental steps for the application and development of epidemic models that describe infectious diseases. HIV/AIDS and Hepatitis B, as well as the Rubella, Zika, Ebola, Flu, SARS, MERS, and COVID-19 outbreaks, are a few examples of infectious diseases.

The novel coronavirus disease 2019 (COVID-19) outbreaks began in late December 2019 in Wuhan, China. COVID-19, a viral infection that has attracted worldwide attention for more than four years, is caused by the Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) [5, 6]. Unlike many other infectious diseases, COVID-19 is known to exhibit asymptomatic transmission as well as symptomatic transmission. Asymptomatic patients are defined as patients who show no signs of SARS-CoV-2 infection and can transmit the disease to other susceptible individuals [7]. Presymptomatic patients are cases that are defined as asymptomatic from diagnosis to isolation follow-up, and then, symptoms develop during their observation [8]. These patients can be evaluated in the asymptomatic class. Symptomatic patients are a group of patients who have symptoms at all stages of the diagnosis-treatment process. Therefore, unlike other infections, the R_0 (reproductive number of disease cases) value, representing the average number of secondary cases infected by a single infected person, is expected to be higher. The COVID-19 pandemic has affected most countries in the world, especially economically [9] and psychologically [10]. Since many infection cases emerged during the process of finding appropriate treatment methods against the disease or producing a vaccine, quarantine measures were taken to prevent the continuation of infection waves in the past. In the process, researchers, biologists, and medical experts have produced effective vaccines to control SARS-CoV-2 infections. Although many prevention mechanisms and other control measures have been established to reduce the spread of the disease, some deadly variants of the virus still threaten people's lives. In the literature, there are many studies with different perspectives describing the transmission of this virus [11, 12, 13, 14].

Creating useful models in many different fields or modifying existing models to reflect natural problems is effective in solving these problems [15, 16, 17, 18]. One of the best ways to understand the spread of an infection is to analyze mathematical models that have been developed so far.

We aim to develop a model for understanding the spread of COVID-19 infection cases. For this purpose, we characterize the transmission of the disease by the bilinear incidence rate which expresses contact between susceptible individuals and infected (symptomatic and asymptomatic (see [19])) individuals. We also take into account that there is currently no quarantine measure, and everyone can travel freely. We examine the transmission dynamics through the stability analysis and bifurcation theory of SARS-CoV-2 infections by including the vaccine in the model.

The dynamical behavior of the SIR epidemic model, which is an epidemic model of differential equations, was reported by Li and Wang [20] as follows

$$\dot{S} = A - dS - \lambda SI$$

$$\dot{I} = \lambda SI - (d + r)I$$

$$\dot{R} = rI - dR$$

where, $N_t = S_t + I_t + R_t$. S(t), I(t), R(t), and N(t) represent the numbers of susceptible, infectious, recovered, and total individuals at time t, respectively. A represents the population's recruitment rate, d stands for the population's natural death rate, r stands for the recovery rate of infectious individuals, and λ stands for the bilinear incidence rate.

In previous studies [21, 22], the authors studied the different dynamical behavior of the discrete-time model by implementing the forward Euler scheme to the model given in another study [20] and reducing it to two dimensions.

While creating our model, we were also inspired by the model given in the study they took as reference [20]. In this model, we included the vaccine to see the effect of the vaccine. So, we can reach the following equations:

$$\dot{S} = A - dS - \lambda SI - vS$$

$$\dot{I} = \lambda SI - (d + r)I$$

$$\dot{R} = rI - dR + vS$$

where, $N_t = S_t + I_t + R_t$.

The following discrete-time SIR epidemic model is produced using the forward Euler scheme with $\frac{dS}{dt} \approx \frac{S_{t+1} - S_t}{h}$, $\frac{dI}{dt} \approx \frac{I_{t+1} - I_t}{h}$, $\frac{dR}{dt} \approx \frac{R_{t+1} - R_t}{h}$, and by replacing t (continuous time) with n=0,1,2,… (discrete-time)

$$S_{n+1} = S_n + h(A - (d + v)S_n - \lambda S_n I_n)$$

$$I_{n+1} = I_n + h(\lambda S_n I_n - (d + r)I_n)$$

$$R_{n+1} = R_n + h(rI_n - dR_n + vS_n)$$

where, $N_{n+1} = hA + (1 - hd)N_n$, $N_n = S_n + I_n + R_n$. The step size is denoted by h, A, d, λ, and r are used as stated in the aforementioned study [20]. Assumptions include that all parameters are positive, S(0) > 0, I(0) ≥ 0, and R(0) ≥ 0. Here, the third equation in model is the linear equation for Rn, while the previous two equations concern (S_n, I_n) and do not include Rn. As a result, the dynamical behaviors of model and the subsequent model are interchangeable,

$$S_{n+1} = S_n + h(A - (d + v)S_n - \lambda S_n I_n)$$

$$I_{n+1} = I_n + h(\lambda S_n I_n - (d + r)I_n)$$

which only consists of S_n and I_n.

In this study, we examine the next discrete-time SIR epidemic model which describes the interaction between susceptible individuals and infected (symptomatic and asymptomatic) individuals by including the vaccine v in this model:

$$\begin{aligned} x_{n+1} &= x_n + h(A - (d + v)x_n - \gamma x_n y_n) \\ y_{n+1} &= y_n + h(\gamma x_n y_n - (d + r)y_n) \end{aligned} \tag{1}$$

where, $S_{n \to} x_n$ and $I_{n \to} y_n$ denote the numbers of susceptible individuals and infected individuals, respectively, and the parameters $A, d, r, v, \gamma, and\ h$ are all positive parameters. In this model, $\lambda \to \gamma$ represents the bilinear incidence rate, and γ is the sum of $\beta + \xi$. The parameters β and ξ describe the

rate at which COVID-19 infections spread from asymptomatic and symptomatic infected individuals to susceptible individuals, respectively. Here, A denotes the recruitment rate of the population (or immigration), v is the vaccination rate, r refers to the recovery rate in infective individuals, d is the natural death rate within the population, and this death rate is an equal rate in each compartment in the model.

The paper is organized in the following manner: In Section 2, we explore the existence and local asymptotic stability of the fixed (equilibrium) points of the system (1) in $\mathbb{R}_+^2$. Section 3 delves into the dynamics of the system (1) experiencing a flip bifurcation, with A selected as the bifurcation parameter. The final section comprises discussions and results.

EXISTENCE AND STABILITY ANALYSES OF FIXED POINTS OF THE SYSTEM

This section presents an analysis of the existence and local stability of fixed points in the system (1) within $\mathbb{R}_+^2$. The local stability of fixed points in discrete-time systems is governed by the magnitudes of the eigenvalues of the Jacobian matrix.

To maintain solutions within the closed first quadrant, we can employ the following assessment: Let

$$f_{n+1}(x_n, y_n) = x_n + h(A - (d + v)x_n - \gamma x_n y_n)$$

$$g_{n+1}(x_n, y_n) = y_n + h(\gamma x_n y_n - (d + r)y_n)$$

such that $x_0 > 0$ and $y_0 > 0$. It is clear that if $y_n > 0$; and $x_n > \frac{h(d+r)-1}{h\gamma}$, $h(d + r) > 1$, then $g_{n+1}(x_n, y_n) \geq 0$ for $n = 0,1,2,...$. The set of (x_n, y_n) that makes $f_{n+1}(x_n, y_n) \geq 0$ can be represented as

$$\Omega = \left\{(x_n, y_n): 0 \leq y_n \leq \frac{1 - h(d + v)}{h\gamma}, h(d + v) < 1, x_n > 0\right\}.$$

From an ecological standpoint, for $(x_n, y_n) \in \Omega$, if $(f_{n+1}(x_n, y_n), g_{n+1}(x_n, y_n)) \notin \Omega$, then a population collapse is implied. The two-dimensional discrete-time dynamical system is

$$\begin{aligned} x_{n+1} &= f(x_n, y_n), \\ y_{n+1} &= g(x_n, y_n), \quad n = 0,1,2,\ldots, \end{aligned} \tag{2}$$

and the functions $f: I \times J \to I$ and $g: I \times J \to J$ are continuously differentiable, where I and J are real number intervals. Moreover, a solution $\{(x_n, y_n)\}_{n=0}^{\infty}$ of system (2) is uniquely defined by initial conditions $(x_0, y_0) \in I \times J$. A fixed point $(\overline{x}, \overline{y})$ of (2) satisfies

$$\overline{x} = f(\overline{x}, \overline{y}),$$

$$\overline{y} = g(\overline{x}, \overline{y}).$$

Let $(\overline{x}, \overline{y})$ be a fixed point of the map $F(x, y) = (f(x, y), g(x, y))$, where the functions f and g are continuously differentiable at $(\overline{x}, \overline{y})$. The linearized system of (2) around $(\overline{x}, \overline{y})$ is represented by $X_{n+1} = F(X_n) = J_F X_n$, where $\boldsymbol{X_n} = \begin{pmatrix} x_n \\ y_n \end{pmatrix}$, and J_F denotes a Jacobian matrix of system (2) around $(\overline{x}, \overline{y})$.

The Jacobian matrix J of system (2) computed for $(\overline{x}, \overline{y})$ is determined by

$$\boldsymbol{J_{(\overline{x},\overline{y})}} = \begin{pmatrix} a_{11} & a_{12} \\ a_{21} & a_{22} \end{pmatrix}$$

and the characteristic equation of matrix $\boldsymbol{J_{(\overline{x},\overline{y})}}$ can be given as

$$F(\lambda) = \lambda^2 - trJ_{(\overline{x},\overline{y})}\lambda + \det J_{(\overline{x},\overline{y})} = 0.$$

Assume that λ_1 and λ_2 be two roots of $F(\lambda) = 0$. Then, the fixed point $(\overline{x}, \overline{y})$ is locally asymptotically stable, if $|\lambda_1| < 1$ and $|\lambda_2| < 1$, and it is called a sink point. Otherwise, $(\overline{x}, \overline{y})$ is always unstable, and it is known as source (repeller) point. The fixed point $(\overline{x}, \overline{y})$ is called a saddle point if $|\lambda_1| < 1$ and $|\lambda_2| > 1$ (or $|\lambda_1| > 1$ and $|\lambda_2| < 1$). If $|\lambda_1| = 1$ or $|\lambda_2| = 1$, then $(\overline{x}, \overline{y})$ is known as a non-hyperbolic point. Here, we say that if $F(1) > 0, F(-1) > 0$ and $C < 1$, then the fixed point is defined as a sink point. Consequently, it is locally asymptotically stable.

Existence Analyses of Fixed Points of the System

By investigating the existence of all accessible fixed points of the epidemic system (1), we derive the following lemma.

Lemma 1 *System (1) exhibits the following cases*

(i) System (1) possesses an exclusion fixed point $E_1 = (\frac{A}{d+v}, 0)$ for all positive parameters,

(ii) If $A > \frac{(d+r)(d+v)}{\gamma}$, then system (1) possesses a unique positive interior fixed point $E_2 = (\frac{d+r}{\gamma}, \frac{-d^2-dr-dv-rv+A\gamma}{(d+r)\gamma})$.

Local Stability Analysis of the Exclusion Fixed Point of the System

Now, we perform local asymptotic stability analysis of the fixed point $E_1 = (\frac{A}{d+v}, 0)$ by using the Jocabian matrix. For $E_1 = (\frac{A}{d+v}, 0)$, the Jacobian matrix for system (1) is found as:

$$J_{E_1} = \begin{pmatrix} 1 - dh - hv & -\frac{Ah\gamma}{d+v} \\ 0 & 1 - dh - hr + \frac{Ah\gamma}{d+v} \end{pmatrix} \tag{3}$$

So, the eigenvalues are $\lambda_1 = 1 - dh - hv$ and $\lambda_2 = 1 - dh - hr + \frac{Ah\gamma}{d+v}$. The following lemma outlines the criteria for the local asymptotic stability of the exclusion fixed point. E_1.

Lemma 2 *Assume that* $A < \frac{(d+r)(d+v)}{\gamma}$. *For the fixed point* E_1 *of system (1),* the statements listed below are valid:

(i) *It behaves as a sink if any of the following terms hold:*

(i.1) $r \le v$ and $h < \frac{2}{(d+v)}$.

(i.2) $r > v$ and $h \le \frac{2}{(d+r)}$.

(i.3) $A > \frac{(-2+h(d+r))(d+v)}{h\gamma}, r > v$ and $\frac{2}{(d+r)} < h < \frac{2}{(d+v)}$.

(i.4) $A > \frac{(-2+h(d+r))(d+v)}{h\gamma}$ and $h < \frac{2}{(d+v)}$.

(ii) *It is a source point if one the following terms is satisfied:*

(ii.1) $A < \frac{(-2+h(d+r))(d+v)}{h\gamma}, r \le v$ and $h > \frac{2}{(d+r)}$.

(ii.2) $A < \frac{(-2+h(d+r))(d+v)}{h\gamma}, r > v$ and $h > \frac{2}{(d+v)}$.

(iii) *It is a saddle point if one of the following terms is satisfied:*

(iii.1) $A < \frac{(-2+h(d+r))(d+v)}{h\gamma}, r > v$ and $\frac{2}{(d+r)} < h < \frac{2}{(d+v)}$

(iii.2) $A > \frac{(-2+h(d+r))(d+v)}{h\gamma}, r < v$ and $h > \frac{2}{(d+r)}$

(iii.3) $A > \frac{(-2+h(d+r))(d+v)}{h\gamma}, r \geq v$ and $h > \frac{2}{(d+v)}$.

for all $d, h, v, r, A, \gamma \in \mathbb{R}_+$.

Moreover, it behaves as a non-hyperbolic point if any of the conditions $h = \frac{2}{(d+v)}, A = \frac{(d+r)(d+v)}{\gamma}$, or $A = \frac{(-2+h(d+r))(d+v)}{h\gamma}$ is satisfied.

Local Stability Analysis of the Positive Interior Fixed Point

Here, we present the locally asymptotic stability analysis of the interior positive fixed point:

$$E_2 = (\overline{x}, \overline{y}) = (\frac{d+r}{\gamma}, \frac{-d^2-dr-dv-rv+A\gamma}{(d+r)\gamma}) \tag{1}$$

The Jacobian matrix of system (1) is

$$J_{E_2} = \begin{pmatrix} \dfrac{d+r-Ah\gamma}{d+r} & -h(d+r) \\ -\dfrac{h(d^2+rv+d(r+v)-A\gamma)}{(d+r)} & 1 \end{pmatrix}$$

evaluated at E_2. The characteristic polynomial is obtained via the Jacobian matrix as follows:

$$F(\lambda) = \lambda^2 + [-2 + \frac{Ah\gamma}{d+r}]\lambda + [\frac{(-d-r)(-1+h^2(d+r)(d+v)) + Ah(-1+h(d+r))\gamma}{d+cd^2}].$$

Subsequently, we derive the following Lemma by employing the characteristic polynomial of J_{E_2}.

***Lemma 3 A**. Let* $A > \frac{(d+r)(d+v)}{\gamma}$. *For a unique positive interior fixed point* (E_2), *the statements listed below are true:*

 (i) *It behaves as a sink if any of the following terms hold:*

(i.1) $A < \frac{(d+r)(-4+h^2(d+r)(d+v))}{h\gamma(-2+h(d+r))}, h \leq \frac{1}{d+r}$ and $v < \frac{4}{h^2(d+r)} - d$.

(i.2) $A < \min\{\frac{h(d+r)^2(d+v)}{(-1+h(d+r))\gamma}, \frac{(d+r)(-4+h^2(d+r)(d+v))}{h\gamma(-2+h(d+r))}\}, \frac{1}{d+r} < h < \frac{2}{d+r}$ and $v < \frac{4}{h^2(d+r)} - d$.

(i.3) $A > \frac{(d+r)(-4+h^2(d+r)(d+v))}{h\gamma(-2+h(d+r))}, \frac{2}{d+r} < h < 2\sqrt{\frac{1}{d(d+r)}}$ and $v > \frac{4}{h^2(d+r)} - d$.

(ii) *It behaves as a source point if any of the following terms hold:*

(ii.1) $\frac{h(d+r)^2(d+v)}{(-1+h(d+r))\gamma} < A < \frac{(d+r)(-4+h^2(d+r)(d+v))}{h\gamma(-2+h(d+r))}, \frac{1}{d+r} < h < \frac{2}{d+r}$ and $v < \frac{4}{h^2(d+r)} - d$.

(ii.2) $A > \max\{\frac{h(d+r)^2(d+v)}{(-1+h(d+r))\gamma}, \frac{(d+r)(-4+h^2(d+r)(d+v))}{h\gamma(-2+h(d+r))}\}, \frac{2}{d+r} < h < 2\sqrt{\frac{1}{d(d+r)}}$ and $v > \frac{4}{h^2(d+r)} - d$.

(iii) *It behaves as a saddle point if any of the following terms hold:*

(iii.1) $A < \frac{(d+r)(-4+h^2(d+r)(d+v))}{h\gamma(-2+h(d+r))}, \frac{2}{d+r} < h < 2\sqrt{\frac{1}{d(d+r)}}$ and $v > \frac{4}{h^2(d+r)} - d$.

(iii.2) $A > \frac{(d+r)(-4+h^2(d+r)(d+v))}{h\gamma(-2+h(d+r))}, h < \frac{2}{d+r}$ and $v < \frac{4}{h^2(d+r)} - d$.

Moreover, it behaves as a non-hyperbolic point if any of the conditions $A = \frac{(d+r)(-4+h^2(d+r)(d+v))}{h\gamma(-2+h(d+r))}$ or $A = \frac{(d+r)(d+v)}{\gamma}$ is satisfied.

Example 4 *Taking into account the parameter values $d = 1.95, r = 0.24, \gamma = 2.949$, and $h = 0.5, v = 0.449$, and the initial conditions $x_0 = 0.4, y_0 = 0.8$, we write the following system*

$$x_{n+1} = x_n + 0.5(A - 2.399x_n - 2.949x_ny_n)$$
$$y_{n+1} = y_n + 0.5(2.949x_ny_n - 2.19y_n)$$

(5)

For $A = 4.3$ and $A = 4.5$, the fixed point is locally asymptotically stable and unstable, respectively. Computations yield the fixed points $(\bar{x}, \bar{y}) = (0.742625, 1.14977)$ for $A = 4.3$ and $(\bar{x}, \bar{y}) = (0.742625, 1.2413)$ for $A = 4.5$.
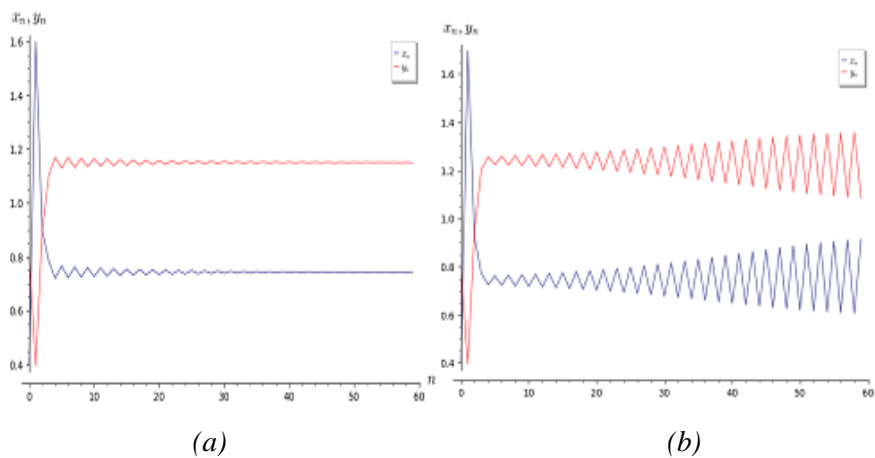

(a) *(b)*

Figure 1

Time series plots of system (1) with the parameter values $d = 1.95, r = 0.24, \gamma = 2.949, h = 0.5, v = 0.449$ (a) $A = 4.3$ (stable) *(b) $A = 4.5$* (unstable).

ANALYSIS OF FLIP BIFURCATION

In this section, we discuss the proposition that the positive interior fixed point E_2 of system (1) undergoes flip bifurcation by using bifurcation theory [23]. Bifurcation point is a value that causes a change in the nature of the model's equilibrium solutions as the model passes through this point. Flip bifurcation involves the situation where the system switches to a new behavior with a period twice that of the original system. A is selected as the bifurcation parameter to get the conditions of flip bifurcation. Assume that λ_1 and λ_2 be two roots of $F(\lambda) = 0$. If $F(-1) = 0$ and $-trJ \neq 0,2$, then the E_2 is a flip bifurcation point. Considering the characteristic polynomial of J_{E_2}, we can see that $-trJ = 2 - \frac{Ah\gamma}{d+r}$. The conditions determining a flip bifurcation occurring at E_2 are determined as follows: If

$$A = A_F = \frac{(d + r)(-4 + h^2(d + r)(d + v))}{h(-2 + h(d + r))\gamma}$$

such that $h(d + r) \neq 2$, then $\lambda_1 = -1$ and $\lambda_2 = \frac{(2+h(d+r)(-3+h(d+v)))}{(2-h(d+r))}$ with

$$|\lambda_2| \neq 1$$

(6)

The following set can be used to express these conditions:

$$FB_{E_2} = \left\{ A, d, r, \gamma, h, v \epsilon \mathbb{R}^+ : A_F = \frac{(d+r)(-4 + h^2(d+r)(d+v))}{h(-2 + h(d+r))\gamma}, h(d+r) \neq 2, \frac{Ah\gamma}{d+r} \neq 2,4, |\lambda_2| \neq 1 \right\}.$$

Using the transformation $u = x - \frac{d+r}{\gamma}$, $v = y - \frac{-d^2 - dr - dv - rv + A\gamma}{(d+r)\gamma}$, the fixed point E_2 is shifted to the origin. So, we obtain:

$$\begin{pmatrix} u \\ v \end{pmatrix} \rightarrow J_{E_2} \begin{pmatrix} u \\ v \end{pmatrix} + \begin{pmatrix} F_1(u,v) \\ F_2(u,v) \end{pmatrix} \tag{7}$$

where

$$F_1(u,v) = -h\gamma uv \quad \text{and} \quad F_2(u,v) = h\gamma uv \tag{8}$$

such that $\boldsymbol{U} = (u,v)^T$. From there, system (1) can be given as

$$(U_{n+1}) \rightarrow J_{E_2}(U_n) + \frac{1}{2}B(u_n, u_n) + \frac{1}{6}C(u_n, u_n, u_n) + O(\|U_n\|^4), \tag{9}$$

with the vector functions of $\boldsymbol{u}, \boldsymbol{v}, \boldsymbol{w} \ \epsilon \mathbb{R}^2$:

$$B(u,v) = \begin{pmatrix} B_1(u,v) \\ B_2(u,v) \end{pmatrix}$$

and

$$C(u,v,w) = \begin{pmatrix} C_1(u,v,w) \\ C_2(u,v,w) \end{pmatrix}.$$

These vectors are expressed by:

$$B_1(u,v) = \sum_{j,k=1}^{2} \frac{\partial^2 F_1}{\partial \xi_j \partial \xi_k}|_{\xi=0} u_j v_k = -h\gamma(u_2 v_1 + u_1 v_2)$$

$$B_2(u,v) = \sum_{j,k=1}^{2} \frac{\partial^2 F_2}{\partial \xi_j \partial \xi_k}|_{\xi=0} u_j v_k = h\gamma(u_2 v_1 + u_1 v_2)$$

$$C_1(u,v,w) = \sum_{j,k=1}^{2} \frac{\partial^3 F_1}{\partial \xi_j \partial \xi_k \xi_l}|_{\xi=0} u_j v_k w_l = 0$$

$$C_2(u,v,w) = \sum_{j,k=1}^{2} \frac{\partial^3 F_2}{\partial \xi_j \partial \xi_k \xi_l}|_{\xi=0} u_j v_k w_l = 0$$

and $A = A_F$. Let $\boldsymbol{q}, \boldsymbol{p} \in \mathbb{R}^2$ be eigenvectors of $\boldsymbol{J}_{E_2}(\boldsymbol{A}_F)$ and transposed matrix $\boldsymbol{J}_{E_2}^T(\boldsymbol{A}_F)$, respectively, for $\lambda_1(A_F) = -1$. Then, we have $J_{E_2}(A_F)q = -q$ and $J_{E_2}^T(A_F)p = -p$. These eigenvectors calculated in the Mathematica program are:

$$q \sim \left(\frac{(2 - h(d+r))}{(-2 + h(d+v))}, 1 \right)^T$$

and

$$p \sim \left(\frac{2}{(h(d+r))}, 1 \right)^T.$$

We utilize the standard scalar product in $\mathbb{R}^2$ to normalize $\boldsymbol{p}$ relative to $\boldsymbol{q}$, such that $< p, q >= p_1 q_1 + p_2 q_2$. So, we obtain:

$$p \sim \left(\frac{2(-2 + h(d + v)))}{(4 + h(d + r)(-4 + h(d + v)))}, \frac{h(d + r)(-2 + h(d + v))}{(4 + h(d + r)(-4 + h(d + v)))} \right)^T.$$

It is evident that $< p, q >= 1$. We must ascertain the sign of the coefficient $c(A_F)$ in the manner described below in order to establish the direction of the flip bifurcation:

$$c(A_F) = \frac{1}{6} < p, C(q, q, q) > - \frac{1}{2} < p, B(q, (J_{E_2} - I)^{-1} B(q, q) >. \tag{10}$$

The following theorem provides the outcome on flip bifurcation concerning the coefficient of the critical normal form.

Theorem 5 *If (6) holds true, with $c(A_F) \neq 0$, and the parameter A varies around A_F, then system (1) experiences a flip bifurcation at E_2. Additionally, if $c(A_F) > 0$ ($c(A_F) < 0$)), then the period 2 orbits emerging from E_2 are stable (unstable).*

The following Example 6 demonstrates the emergence of flip bifurcation according to our theoretical findings.

Example 6 *Taking into account the parameter values $d = 1.95, r = 0.24, \gamma = 2.949, h = 0.5,$ and $v = 0.449$, we write the following system:*

$$\begin{aligned} x_{n+1} &= x_n + 0.5(4.40905 - 2.399x_n - 2.949x_n y_n) \\ y_{n+1} &= y_n + 0.5(2.949x_n y_n - 2.19y_n) \end{aligned} \tag{11}$$

and $A_F = 4.40905$ is a flip bifurcation point. Computation yields $(\overline{x}, \overline{y}) = (0.742625, 1.19977)$. The Jacobian matrix is $J = \begin{bmatrix} -1.96856 & -1.095 \\ 1.76906 & 1 \end{bmatrix}$. The eigenvalues are $\lambda_1 = -1$ and $\lambda_2 = 0.031439$ such that $|\lambda_2| \neq 1$. The flip bifurcation diagram is displayed in Figure 2 with the initial conditions $x_0 = 0.4$ and $y_0 = 0.8$. System (1) experiences a flip bifurcation at E_2 as the parameter varies within a small vicinity of A_F. This indicates that the fixed point E_2 is stable for $A < 4.40905$, becomes unstable at $A = 4.40905$, and exhibits period-doubling phenomena for $A > 4.40905$. After the required computations are completed, we obtain:

$$F_1(u, v) = -1.4745uv \tag{12}$$

$$F_2(u, v) = 1.4745uv \tag{13}$$

$$B_1(u, v) = -1.4745(u_2 v_1 + u_1 v_2)$$

$$B_2(u, v) = 1.4745(u_2 v_1 + u_1 v_2)$$

$$C_1(u, v, w) = C_2(u, v, w) = 0$$

and

$$p \sim (1.82648, 1)^T, q \sim (-1.13054, 1)^T.$$

We obtain $c(A_F) = 2.41377 > 0$. Bifurcating from E, the period-2 orbits exhibit stability.

DISCUSSIONS AND CONCLUSIONS

This article focuses on analyzing the dynamical behavior of a discrete-time epidemic system (1). We find that system (1) has fixed points $E_1 = (\overline{x}, 0) = (\frac{A}{d+v}, 0)$ and $E_2 = (\overline{x}, \overline{y}) = (\frac{d+r}{\gamma}, \frac{-d^2 - dr - dv - rv + A\gamma}{(d+r)\gamma})$. It can be seen that system (1) possesses a unique positive interior fixed point E_2 with $A > \frac{(d+r)(d+v)}{\gamma}$. We examine the local asymptotic stability conditions of these fixed points using the linearization method. Additionally, we demonstrate that system (1) undergoes flip bifurcation at

$E_2 = (\bar{x}, \bar{y})$. To examine flip bifurcation, the recruitment rate A is taken as the bifurcation parameter. Applying mathematical techniques from bifurcation theory, we demonstrate that system (1) experiences flip bifurcation under the condition $A = A_F = \frac{(d+r)(-4+h^2(d+r)(d+v))}{h(-2+h(d+r))\gamma}$, $h(d+r) \neq 2$. The dynamical characteristics of system (1) are illustrated in some figures. By choosing the value A as the bifurcation parameter, the effects of the recruitment rate on susceptible individuals are observed in the absence of vaccination or when the presence of asymptomatic individuals is ignored. Here, the Figures are displayed using SageMath programming [24]. The situation and interpretations of the system dynamics for some parameter values are briefly summarized:
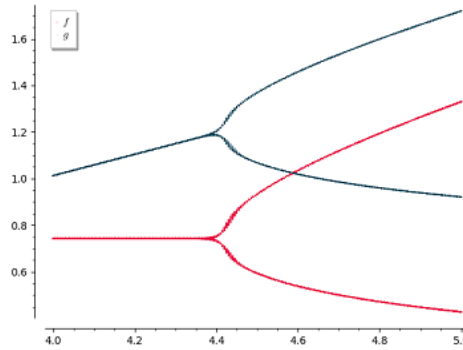

Figure 2.
Bifurcation diagram of the epidemic system (11) with the parameter values $A \in (4,5)$, $d = 1.95$, $r = 0.24$, $\gamma = 2.949$, $h = 0.5$, and $v = 0.449$.

Let us consider system (1) without vaccination. Considering the values in Example 4 without vaccination, we have the following system for $A = 4.3$:

$$x_{n+1} = x_n + 0.5(4.3 - 1.95x_n - 2.949x_ny_n)$$
$$y_{n+1} = y + 0.5(2.949x_ny_n - 2.19y_n). \tag{14}$$

Computation yields $(\bar{x}, \bar{y}) = (0.742625, 1.30223)$. Although vaccination causes a decrease in the number of infected individuals, it gives us the result that the population depending on the number of infected and susceptible individuals reaches a constant value in a longer time. Consequently, it is seen that the system approaches a steady state more quickly when vaccination is not included (Figures 1-(a) and 3-(a)).

Let us consider system (1) without vaccination and asymptomatic individuals. Considering the values in Example 4, we have the following system for $A = 4.3$:

$$x_{n+1} = x_n + 0.5(4.3 - 1.95x_n - 1.749x_n\,y_n)$$
$$y_{n+1} = y_n + 0.5(1.749x_n\,y_n - 2.19y_n). \tag{15}$$

Here, $\gamma = \beta + \xi$ such that $\beta = 1.2$ (asymptomatic individuals) and $\xi = 1.749$ (symptomatic individuals). Assuming that only symptomatic individuals spread the disease and that the vaccine is not available, the system appears to reach the equilibrium point $(\bar{x}, \bar{y}) = (1.25214, 0.848548)$ more quickly (Figures 3-(a) and 3-(b)).

Considering the parameter values $d = 1.95$, $r = 0.24$, $\gamma = 2.949$, $h = 0.5$, and $v = 0$, we compute the flip bifurcation point $A = 4.81249$ for the system *(14)*. For the same parameter values, $A = 4.40905$ is the bifurcation value of the vaccine-effective system *(11)*. As a result, the system without the vaccine effect reaches the flip bifurcation point later. In other words, the system remains stable for longer (Figure 3-(c)). In this system, flip bifurcation occurs at a higher immigration rate.

If the parameter values $d = 1.95$, $r = 0.24$, $\gamma = 1.749$, $h = 0.5$, and $v = 0$ are considered, we

reach the flip bifurcation point $A = 8.11438$ for the system *(15)*. When the impact of asymptomatic individuals on the system is ignored, the system can maintain its stability for a long time even if there is no vaccine (Figure 3-(d)).
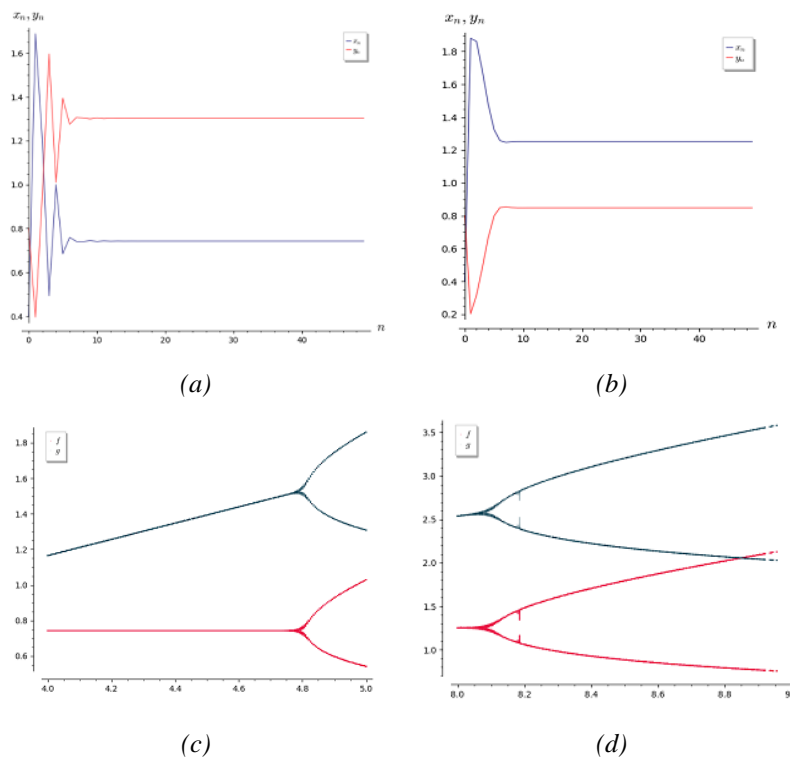

Figure 3

Time series plots of system (1) with the parameter values $d = 1.95, r = 0.24$, and $h = 0.5$, (a) system (14) $A = 4.3, \gamma = 2.949, v = 0$ (b) system (15) $A = 4.3, \gamma = 1.749, v = 0$ (c) $A \in (4,5), \gamma = 2.949, v = 0$ (d) $A \in (4,5), \gamma = 1.749, v = 0$.

We would especially like to emphasize that the study involved theoretically obtaining the stability and bifurcation conditions of the model. The theoretical results were confirmed by selecting appropriate parameter values that met the obtained conditions. Since we included the vaccine effect as well as the effect of asymptomatic individuals in the model, the parameters were diversified specifically for this study. In our future studies, diagrams for the course of this disease will be obtained using real disease data for COVID-19, and they will be compared to the results obtained in this paper.

Ethical Statement
This work is an original research article designed and developed by the author.
Author Contributions Research Design (CRediT 1) Ö.A.G. (%100)
Data Collection (CRediT 2) Ö.A.G. (%100)
Research - Data Analysis - Validation (CRediT 3-4-6-11) Ö.A.G. (%100)
Writing the Article (CRediT 12-13) Ö.A.G. (%100)
Revision and Improvement of the Text (CRediT 14) Ö.A.G. (%100)

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Data availability
Data sharing is not applicable to this article as no datasets were generated or analyzed during the current study.

Conflict of interest

The author declare that she has no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Sustainable Development Goals (SDG)

3 Health and Quality Life

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