A discrete-time epidemic model for the analysis of transmission of COVID19 based upon data of epidemiological parameters

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Abstract The forecasting of the nature and dynamics of emerging coronavirus (COVID-19) pandemic has gained a great concern for health care organizations and governments. The efforts aim to to suppress the rapid and global spread of its tentacles and also control the infection with the limited available resources. The aim of this work is to employ real data set to propose and analyze a compartmental discrete time COVID-19 pandemic model with non-linear incidence and hence predict and control its outbreak through dynamical research. The Basic Reproduction Number ($R_0$) is calculated analytically to study the disease-free steady state ($R_0 < 1$), and also the permanency case ($R_0 > 1$) of the disease. Numerical results show that the transmission rates $\alpha (> 0)$ and $\beta (> 0)$ are quite effective in reducing the COVID-19 infections in India or any country. The fitting and predictive capability of the proposed discrete-time system are presented for relishing the effect of disease through stability analysis using real data sets.

1 Introduction

Today, the daily life of the human population starts with the concern of fighting against the pandemic COVID-19 outbreak cited by Choi et al. [9] and Gralinski and Menachery [17]. It is reported that COVID-19 virus can transmit from infected individual to susceptible one through a direct contact with respiratory droplets caused by coughing or sneezing. Although coronavirus can survive on surfaces for several hours, it is found that conventional disinfectants can eliminate it. The ways and mechanisms by which COVID-19 affects people gains a lot of attentions, see for example Huang et al. [21], Cheng and Shan [8], Gralinski and Menachery [17], Chen et al. [7]. It has been observed that older people and individuals having chronic medical conditions are more risk of developing severe symptoms when infected by the COVID-19. Although, there are relatively fewer cases of COVID-19 among children, individuals of any age can get infected by the virus.

The main aim of the proposed discrete-time model is to realize the effect of disease due to coronavirus and find all the characteristics which are liable for this outbreak of respiratory illness. The discrete time models provide more appropriate tools for describing processes having different scales of time or which evolve over non-overlapping intervals. In addition, employing discrete models results in a significant reduction in computational complexity of the associated continuous time models. Thus, mathematical modeling and study of nonlinear maps can be advantageously [2,4,13]. The non-linear incidence rate are used in epidemic models to provide more accurate modeling of the disease spread rate [15,24,26,28]. Wesley et al. [27] presented a discrete-time rodent-hantavirus model structured by infection and developmental stages. The differences between the dynamics of the male and female rodents in deterministic and stochastic versions of the model are investigated using numerical simulations. Hernandez et al. [19] studied the epidemic maps when arbitrary stage distributions were considered and also the potential applications to disease control were investigated. The analytical and numerical results of this model clarified the inconsistencies in forecasting which arise due to the employment of specific parametric distributions. The
quarantine or isolation, among other control measures, are utilized to control the reproduction number and drive the final epidemic size to a predetermined value. Biswas et al. [5] presented an SEIR Model and studied control the infectious Diseases with constraints. Different models for the COVID-19 pandemic have been proposed and analyzed in literature. Huang and Qiao [20] presented the characteristics of the epidemic dynamics through data-driven time-dependent transmission rate for the COVID-19. The paper discusses the equilibrium points of the proposed discrete-time model of COVID-19 and their stability analysis. The basic reproduction number (\(R_0\)) for the proposed discrete-time COVID-19 model is obtained using the next-generation matrix method. The values of parameters in the model are estimated by fitting realistic data sets. The numerical analysis with a brief discussion and conclusion have been presented incorporating spreading and transmission dynamics of COVID-19.

## 2 Description of discrete-time COVID-19 model

In the past 50 years, many researchers have formulated a plethora of mathematical models of the spread of infectious diseases in human populations. After the eruption of COVID-19 disease in 2019, the study of coronavirus and its implications are an active field of research work nowadays. India is highly affected by COVID-19 pandemic and the number of active COVID-19 infections is increased continuously right now. In response to this severe status, the Indian government has undertaken several strategies to suppress spreading COVID-19 viruses such as lockdown and social distancing. In this section, a new discrete-time SEIR model for presenting COVID-19 situations in the Indian environment is formulated by promoting an alternating that induces various fundamental epidemiological properties of COVID-19. The proposed COVID-19 model describes the dynamics of four population groups which are categorized according to the state of each individual. More specifically, we consider susceptible (\(S(t)\)), infected individuals without any treatment (\(I(t)\)) which can spread the disease, infected individuals under isolation ward for treatment which are not spreading the disease (\(T(t)\)), and finally the population in a secure zone or recovered ones (\(R(t)\)). Assuming that total population size is \(N(t)\), hence we have \(N(t) = S(t) + I(t) + T(t) + R(t)\). To formulate a more realistic COVID-19 pandemic model, several demographic effects are included by assigning a specific value for natural death rate in each of the four populations categories, namely, \(d_1(>0)\) and employing another factor called \(d_2(>0)\) in \(T(t)\) individuals to represent the death rate due to the infection by COVID-19 virus. Moreover, it is assumed that new born individuals are introduced into the susceptible population at a rate \(\Lambda(>0)\) per unit time. A transition diagram of the proposed COVID-19 model is shown in Fig. 1.

### Rate of change of \((S(t))\): Susceptible individuals density is increased by new births at the rate \(\Lambda(>0)\), decreased by natural death \(d_1(>0)\), and it also decreases via the interaction with infectious individuals. For these, the transmission coefficient is \(\alpha\), and the parameter \(\delta\) is essential to control the susceptible individuals. This population also decreases due to fear and lockdown, which is acquired by the account of the population who are in the secure zone at a constant rate \(\gamma_1\). Consequently, the rate equation for \(S(t)\) can be formulated as: 
\[
\frac{dS(t)}{dt} = \Lambda - \frac{\alpha SI}{1 + \delta T} - \gamma_1 S - d_1 S.
\]

### Rate of change of the infected population without treatment \((I(t))\): The individual who is exposed as infected but not under treatment, and are not infectious for other non-infected individuals. This population increases by interaction with susceptible. The population decreases due to quarantine with the rate \(\beta\) (population is in the secure zone at the same rate) and due to the natural death rate \(d_1\) and is expressed by the equation:
\[
\frac{dI(t)}{dt} = \frac{\alpha SI}{1 + \delta T} - \beta I - d_1 I.
\]

### Rate of change of infected in an isolation ward for treatment not spreading the disease \((T(t))\): A proportion \(\beta\) of infected individuals without treatment transferred to this category after the clinical symptoms of COVID-19 are exposed. These individuals decrease by the rate \(\gamma_2\) by getting acquired into the account of the secure zone, the natural death rate, and a death factor caused by COVID-19. The expression for this population is:
\[
\frac{dT(t)}{dt} = \beta I - \gamma_2 T - d_1 T - d_2 T.
\]

### Rate of change of population in the secure zone \((R(t))\): The population increases from susceptible due to fear and lockdown with rate \(\gamma_1\), and infected individuals due to in isolation ward for treatment are recovered from the disease at rate \(\gamma_2\). A natural death rate \(d_1\) condenses these densities; therefore, the expression for this individual is:
\[
\frac{dR(t)}{dt} = \gamma_1 S + \gamma_2 T - d_1 R.
\]
From the above deliberations, the groups $S(t)$, $I(t)$, $T(t)$ and $R(t)$ denote the densities of the susceptible population (SP), the infected population which spread the disease (IP), infected in an isolated ward for treatment not spreading the disease (TP) and population is in a secure zone (RP), respectively, at time $t$. Therefore, $N(t) = S(t) + I(t) + T(t) + R(t)$ refers to the total size of the population at the time $t$. The proposed discrete-time COVID-19 system will discuss for the total human population ($N(t)$) along with the next initial densities:

\[ S(0) > 0, I(0) \geq 0, T(0) \geq 0 \text{ and } R(0) > 0 \quad (1) \]

Now, using the forward Euler method, we obtain $S_n$, $I_n$, $T_n$ and $R_n$, which are the densities of the populations in discrete-time $t$. The equations for the $(n+1)\text{th}$ generation of the populations can be obtained by replacing $t$ by $n$, and the proposed discrete-time COVID-19 model is given by:

\[
S_{n+1} = S_n + h[\frac{\alpha S_n I_n}{1 + \delta T_n} - \gamma_1 S_n - d_1 S_n] \\
I_{n+1} = I_n + h[\frac{\alpha S_n I_n}{1 + \delta T_n} - \beta I_n - d_1 I_n] \\
T_{n+1} = T_n + h[\beta I_n - \gamma_2 T_n - d_1 T_n - d_2 T_n] \\
R_{n+1} = R_n + h[\gamma_1 S_n + \gamma_2 T_n - d_1 R_n]. \quad (2)
\]

It is assumed that the total population size is constant, the system of equations can be reduced by one. In particular, the equation for $R$ can be ignored by substituting with $R_n = N - S_n - I_n - T_n$ in the system. Therefore, the proposed discrete-time COVID-19 system can be expressed as follows:

\[
S_{n+1} = S_n + h[\frac{\alpha S_n I_n}{1 + \delta T_n} - \gamma_1 S_n - d_1 S_n] \\
I_{n+1} = I_n + h[\frac{\alpha S_n I_n}{1 + \delta T_n} - \beta I_n - d_1 I_n] \\
T_{n+1} = T_n + h[\beta I_n - \gamma_2 T_n - d_1 T_n - d_2 T_n]. \quad (3)
\]

The model parameters are described below:

3 Equilibrium points and their stability analysis

3.1 Existence of equilibrium points

Fixed points of the discrete-time COVID-19 system (3) are obtained via solving the next equations:

\[
\Lambda - \frac{\alpha SI}{1 + \delta T} - \gamma_1 S - d_1 S = 0 \\
\frac{\alpha SI}{1 + \delta T} - \beta I - d_1 I = 0 \\
\beta I - \gamma_2 T - d_1 T - d_2 T = 0.
\]

We get the following two non-negative equilibrium points:

(i) The disease-free equilibrium (DFE) point $P_1 = \left( \frac{\Lambda}{\gamma_1 + d_1}, 0, 0 \right)$, (ii) The endemic equilibrium (EEP) $P_2 = \left( S^*, I^*, T^* \right)$, where $S^* = \frac{\Lambda - (\beta + d_1) I^*}{(\gamma_1 + d_1)}$, $T^* = \frac{\gamma_2 T^*}{(\beta + d_1)}$ and $I^* = \frac{\beta (\alpha - (\beta + d_1)(\gamma_1 + d_1))}{(\beta + d_1)(\alpha + (d_1 - d_2) S^*)}.$

3.2 Computations of basic reproduction number

The basic reproduction number ($R_0$) is one of the most crucial quantities in the analysis of epidemiological models. It enables making effective policies and strategies for control and prevention of diseases. Various approaches for continuous-time models in Castillo-Chavez et al. [6], De Camino-Beck et al. [12], Driessche [4] and see also De Jong et al. [13]).

A well-known technique to estimate $R_0$ is called next-generation matrix method. Let $X_0 = (x_1, x_2, \ldots, x_m)^T$ and $X_1 = (x_m+1, x_m+2, \ldots, x_n)^T$ where $x_1, x_2, \ldots, x_m$ refer to the infected state variables in the model whereas $x_m+1, x_m+2, \ldots, x_n$ denote the uninfected ones. Suppose that the epidemic model is written as

\[ X(n + 1) = G(X(n)), \quad n = 0, 1, 2, \ldots \]

where $G : \mathbb{R}^n_+ \to \mathbb{R}^n_+$ is a $C^1$ function. Assume also there is unique DFE point of the model where the Jacobian matrix $J$ has the following form:

\[ J = \begin{pmatrix} F + H & 0 \\ A & C \end{pmatrix}. \quad (5) \]

The following theorem (Theorem 2.1 in Allen and Driessche [4] and see also De Jong et al. [13]) explains how to compute $R_0$ and demonstrates stable conditions of DFE point.

Theorem 1 Let the system of difference equations (4) possesses single DFE point and the corresponding Jacobian matrix (5) involves non-negative matrices $F$ and $H$. Furthermore, suppose that $F + H$ is irreducible whereas matrices $C$ and $H$ are achieving $\rho(C), \rho(H) < 1$, therefore we get $R_0 = \rho(F(I - H)^{-1})$. Finally, the DFE point of the epidemic model is locally asymptotically stable if $R_0 < 1$ and unstable if $R_0 > 1$.

For the our model (3), the $J$ matrix computed at $(E, I, S) = (0, 0, S_0)$ where $S_0 = \frac{\Lambda}{\gamma_1 + d_1}$ is given by...
\[ J = \begin{bmatrix} h \alpha S_0 - h (\beta + d_1) + 1 & -h (\gamma_2 + d_1 + d_2) + 1 & 0 \\ -h (\gamma_1 + d_1 + 1) & 0 & 0 \\ -h \alpha S_0 & 0 & -h (\gamma_1 + d_1 + 1) \end{bmatrix}. \]

The other sub-matrices are extracted as
\[ F = \begin{bmatrix} h \alpha S_0 & 0 \\ 0 & 0 \end{bmatrix} \text{ and } H = \begin{bmatrix} h (\beta + d_1) + 1 & 0 \\ 0 & h (\gamma_2 + d_1 + d_2) + 1 \end{bmatrix}. \]

Now \( \rho (H) = \max \{ -h (\beta + d_1) + 1, -h (\gamma_2 + d_1 + d_2) + 1 \} \), and
\[ (I - H)^{-1} = \begin{bmatrix} h (\beta + d_1) & h (\gamma_2 + d_1 + d_2) \\ -h \beta & h (\gamma_2 + d_1 + d_2) \end{bmatrix}^{-1} = \begin{bmatrix} \frac{1}{h (\beta + d_1)} & 0 \\ 0 & \frac{1}{h (\gamma_2 + d_1 + d_2)} \end{bmatrix}. \]

Therefore, the next-generation matrix for the proposed discrete-time COVID-19 system (3) is obtained as follows:
\[ F (I - H)^{-1} = \begin{bmatrix} h \alpha S_0 & 0 \\ 0 & 0 \end{bmatrix} \begin{bmatrix} \frac{1}{h (\beta + d_1)} & 0 \\ 0 & \frac{1}{h (\gamma_2 + d_1 + d_2)} \end{bmatrix} = \begin{bmatrix} \frac{\alpha h S_0}{(\gamma_1 + d_1)(\beta + d_1)} & 0 \\ 0 & 0 \end{bmatrix}. \]

As \( R_0 = \rho \left( F (I - H)^{-1} \right) \), i.e. it is the the spectral radius of the matrix \( F (I - H)^{-1} \). Then, it can be obtained for the proposed model (3) in the form \( R_0 = \frac{\alpha h S_0}{(\gamma_1 + d_1)(\beta + d_1)} \). Since all the parameters are positive, the model (3) has a unique EEP since \( R_0 = \frac{\alpha h S_0}{(\gamma_1 + d_1)(\beta + d_1)} > 1 \). It can be shown that DFE point \( P_1 = \left( \frac{\alpha h S_0}{\gamma_1 + d_1}, 0, 0 \right) \) is locally asymptotically stable for \( R_0 < 1 \), and unstable for \( R_0 > 1 \).

### 3.3 Local stability analysis

The local behavior of the discrete-time pandemic model (3) is presented for each equilibrium point by evaluation of Jacobian matrix at each fixed point of the model. More specifically, the Jacobian Matrix \( J \) of the COVID-19 model (3) is given by

\[ J (P_1) = \begin{bmatrix} 1 - h (\gamma_1 + d_1) & 0 & 0 \\ h (\gamma_2 + d_1 + d_2) & 1 + h \left[ \frac{\alpha h S_0}{(\gamma_1 + d_1) - (\beta + d_1)} \right] & 0 \\ 0 & 0 & 1 - h (\gamma_2 + d_1 + d_2) \end{bmatrix}. \]

Theorem 2 Consider the polynomial equation \( \lambda^3 + C_1 \lambda^2 + C_2 \lambda + C_3 = 0 \), where \( C_1, C_2 \) and \( C_3 \) are real numbers. Then, the necessary and sufficient conditions that the roots of the equation lie within the open disk \( |\lambda| < 1 \) are: \( 1 + C_1 + C_2 + C_3 > 0, 1 - C_1 + C_2 - C_3 > 0, |C_3| < 1 \) and \( 1 - C_2^2 > |C_2 - C_3 C_1| \).

Theorem 3 The equilibrium point \( P_1 = \left( \frac{\lambda}{\gamma_1 + d_1}, 0, 0 \right) \) of the COVID-19 model (3) is locally asymptotically stable at \( R_0 < 1 \) while it is unstable at \( R_0 > 1 \).
The transmission rate from IP to TP is 0.05, from TP to RP is 0.005, the natural death rate of population is 0.00002, and the death rate of population caused by COVID-19 is 0.00197.

Table 1 Explanation of parameters with their real-life value

| Parameters | Meaning | Value | Reference |
|------------|---------|-------|-----------|
| $\Lambda$  | Recruitment rate of new individuals enter population | 40000 | Estimated |
| $\alpha$   | The transmission rate from SP to IP | $3.7 \times 10^{-9}$ | Estimated |
| $\beta$    | The transmission rate from IP to TP | 0.05 | Estimated |
| $\delta$   | Parameter measures psychological/inhibitory effect | 0.00042 | Assumed |
| $\gamma_1$ | The transmission rate from SP to RP | 0.0005 | Assumed |
| $\gamma_2$ | The transmission rate from TP to RP | 0.005 | Estimated |
| $d_1$      | Natural death rate of population | 0.00002 | Estimated |
| $d_2$      | Death rate of population caused by COVID-19 | 0.00197 | Estimated |

The three eigenvalues of $J(P_1)$ are $w_1 = 1 - h (\gamma_1 + d_1).$ if
\[
0 < w_2 = 1 + h \left( \frac{a_\Lambda}{(\gamma_1 + d_1)} - (\beta + d_1) \right), \quad w_3 = 1 - h (\gamma_2 + d_1 + d_2) < 1. \]
Therefore, the disease-free equilibrium $P_1$ is locally asymptotically stable if $w_2 = 1 + h \left( \frac{a_\Lambda}{(\gamma_1 + d_1)} - (\beta + d_1) \right) < 1,$ i.e., $R_0 = \frac{a_\Lambda}{(\gamma_1 + d_1)}(\beta + d_1) < 1$ and it is unstable for $R_0 > 1.$

Theorem 4 The fixed point $P_3 = (S^*, I^*, T^*)$ of the proposed map is locally asymptotically stable if $I + C_1 + C_2 + C_3 > 0,$ $1 - C_1 + C_2 - C_3 > 0,$ $|C_3| < 1,$ and $1 - C_3 > |C_2 - C_3 C_1|.$

Proof The $J(P_2)$ matrix for the COVID-19 map (3) is expressed as
\[
J(P_2) = \begin{bmatrix}
b_{11} & b_{12} & b_{13} \\
b_{21} & b_{22} & b_{23} \\
b_{31} & b_{32} & b_{33} \\
\end{bmatrix}
\]
Now, the characteristic equation of $J(P_2)$ is $\lambda^3 + C_1 \lambda^2 + C_2 \lambda + C_3 = 0,$ where $C_1 = -[b_{11} + b_{22} + b_{33}], \quad C_2 = [b_{12} b_{21} + b_{13} b_{31} + b_{23} b_{32} - b_{21} b_{32} - b_{12} b_{31} - b_{13} b_{21}], \quad C_3 = [b_{11} b_{23} b_{32} + b_{12} b_{21} b_{33} - b_{13} b_{22} + b_{21} b_{32} - b_{13} b_{21} b_{32}].$
Therefore, by Jury condition, the fixed point $P_2 = (S^*, I^*, T^*)$ is known to be locally asymptotically stable if $I + C_1 + C_2 + C_3 > 0,$ $1 - C_1 + C_2 - C_3 > 0,$ $|C_3| < 1,$ and $1 - C_3 > |C_2 - C_3 C_1|.$

4 Control strategies of COVID-19 with respect to $R_0$
This section presents a sensitivity analysis of model parameters to limit COVID-19 cases of India. More specifically, we investigate the most influential parameters in the model on the value of $R_0$ via employing a quantity known as the normalized forward sensitivity indices for the key parameters. The effects of the parameters $\alpha, \beta, \gamma_1$ and $d_1$ are considered in the analysis. The values of estimated parameters given in Table 1 are used along with the initial values $S(0) = 8 \times 10^8,$ $I(0) = 1400,$ $T(0) = 256,$ $t = 30,$ $h = 1$ from 21st March 2020 to 16th April 2020. The definition of the normalized forward sensitivity index of $f$ to a parameter $\kappa$ is mathematically expressed as:
\[
X_f^{\kappa} = \frac{\partial f}{\partial \kappa} \times \frac{\kappa}{f}.
\]

5 Numerical analysis
In this section numerical simulation experiments and comparisons with real data in India are carried out. The following data have been collected from the reports of Ministry of Health and Family Welfare, Government of India in 2020.

Figures 4, 6, 7 and 8 are obtained according to the parameter given in Table 1 and Table 2. The values of the parameters are set based on the following real data of India. After lockdown in India, the spread of the COVID is recorded as follows (source: ICMR and WHO):
Table 3  COVID-19 cases in India from 21st March to 16th April

| Date | Active cases |
|------|--------------|
| 21/3 | 256          |
| 22/3 | 326          |
| 23/3 | 431          |
| 24/3 | 469          |
| 25/3 | 551          |
| 26/3 | 629          |
| 27/3 | 741          |
| 28/3 | 810          |
| 29/3 | 902          |
| 30/3 | 1122         |
| 31/3 | 1263         |
| 1/4  | 1641         |
| 2/4  | 1863         |
| 3/4  | 2283         |

Table 4  Change $R_0$ in different level of $\alpha$

| $\alpha$ | $R_0$ |
|----------|-------|
| $1.7 \times 10^{-10}$ | 0.2614 |
| $3.7 \times 10^{-10}$ | 0.5690 |
| $5.7 \times 10^{-10}$ | 0.8766 |
| $6.6 \times 10^{-10}$ | 1.0149 |

In the proposed model (2), it is known that the most effective parameter in controlling $R_0$ is $\alpha$. Our goal now is to illustrate computationally how effective $\alpha$ to spread the disease COVID-19 form human to the human population. For our support, we have given Table 3 as follows:

Table 3 represents the value of $R_0$ at different levels of $\alpha$. We see that $R_0$ increases if the value of $\alpha$ is increasing. That is why $\alpha$ is most sensitive with respect to our model. So for a better understanding of the situation, we attain the plot of $R_0$ versus $\alpha$.

The $R_0$ is more effective when the value of $\alpha < 6.6 \times 10^{-10}$, i.e., the DFE point of system (3) is stable but when the value of $\alpha \geq 6.6 \times 10^{-10}$ then $R_0 > 1$, i.e., the DFE point of the model is unstable, and then the situation is more dangerous to our human life. So our aim, in every situation, is to reduce the value of $\alpha$. That is why we maintain the policy of lockdown, usage of hand sanitizer, social distancing, mask, etc.

From Fig. 2A, we see that if $\alpha$ increases, the value of $R_0$ increases. So it is clear, that if we control the such disease transmission, i.e., $\alpha$, using some precaution such as lockdown, usage of hand sanitizer, social distancing, mask etc. then the disease rate automatically minimise otherwise it should be out of control. That is why $\alpha$ is most sensitive with respect to our model. Figure 2B tells that if $\beta$ increases, the value of $R_0$ decreases. These things are matching in our life, which means if the testing rate ($\beta$) of COVID-19 patient increases, the spread of this virus decreases, i.e., $R_0 < 1$. For that reason, the Indian Government has taken the initiative in every state to increase the rate of testing as much as possible.

From Fig. 3A, it is demonstrated that when $\alpha$ and $\beta$ eventually decreases, the value of $R_0$ decreases too. In Fig. 3B, the contour plots for $R_0$ as a function parameters $\alpha$ and $\beta$ are visualized to further explore the effects of the control parameters on $R_0$ values and the dynamics of the proposed model.

The real data regarding COVID-19 pandemic in India are plotted. From Fig. 4, it is noticed that infected patients increase day by day due to the value of disease transmission ($\alpha$) also increases.

The 27 days of actual epidemic data in India are presented in Fig. 4 as illustration for the critical period of initialization of COVID-19 epidemic spread. After this period, the influences of emergent governmental response and different measures taken out on active cases of coronavirus infections in India are depicted in Fig. 5. The real data presented in Fig. 6 show the evolution of number of COVID-19 infections throughout the first wave of epidemic spread in India (about 367 days). It is observed that, the number of active cases greatly reduced after sufficient long time

![Fig. 2](image_url)  The figure shows the variations of $R_0$ with respect to A $\alpha$ and B $\beta$
complying with numerical simulation results in Figs. 7 and 8. However, the emergence of mutated versions of coronavirus with highly infection rates causes the subsequent waves of COVID-19 epidemic. This point will be investigated in a separate future work. Figure 6 indicates that if the infection rate increases, the number of infections increases too. The spread of COVID-19 can condense, if the control measures, i.e., social distancing, disease transmission, etc. increases while if they are maintained efficiently, the subsequent outbreaks of COVID-19 can be controlled.

Figure 7 shows that after sufficiently long time, the COVID-19 epidemic will vanish. Prevention (i.e., lockdown, social distancing, wash hand regularly, mask) strategies are required to minimize the effect of COVID-19 cases, but it did not diminish the virus. Prevention may be a solution to lessen the outbreak of COVID-19, but the alternate requirement of vaccines and medical treatment is required to avoid the harmfulness of COVID-19 virus worldwide.

Figure 8 shows that the proposed discrete-time pandemic model curve for $T$ is a best-fitted curve for real data of COVID-19 cases in India. For the given data set, it is found that $R_0 = 1.025 > 1$, therefore, there may be a need of strategic action by India on the control policy of COVID-19, which will be able to fight the dangerous situation and prevent the community from COVID-19 in the near future.
Fig. 5 Evolution of active cases of COVID-19 infections during the first wave of coronavirus disease in India

Fig. 6 Time history of disease for different value of $\alpha$

6 Conclusions and observations

This study aims at providing a framework and a guide for addressing the issues of the prevention, early detection, and control of COVID-19 pandemic. Based on the available information by the WHO about COVID-19, including its symptoms, complications, transmission procedure, and how to prevent the transmission, we have proposed and analyzed a compartmental discrete-time COVID-19 epidemic model. The more realistic non-linear incidence rate is employed due to its significance [24,26,28]. The basic reproduction number is calculated for the present COVID-19 model both analytically and numerically using the actual database of COVID-19 spread in India. It is demonstrated that for $R_0 < 1$, the proposed model has globally asymptotically stable disease free fixed point.

Regarding the analysis of parameter $\alpha$, it is shown that this parameter is a critical parameter in the discrete-time system (2) along with $\beta$ and they play critical role in reducing COVID-19 active cases in India, which may extend the study for any other country. From Fig. 2, it is depicted that when the value of infection transmission rate $\alpha$ from SP to IP is less than $6.5 \times 10^{-10}$, the basic reproduction number is less than one and therefore the disease free equilibrium point is asymptotically stable. Similarly, when the value of infection transmission rate $\beta$ from IP to SP is greater than 0.029, the disease free equilibrium point is asymptotically stable and the spread of the disease will die out eventually. The control of these parameters can be achieved via using some precaution such as lockdown, usage of hand sanitizer, social distancing, mask etc. Figure 4 illustrates that real data of COVID-19
spread in India leads to give an approximate value of $37 \times 10^{-11}$ to parameter $\alpha$ while the value of $\beta$ is estimated to be 0.05. This means that a governmental efforts should be directed towards decreasing the value of $\beta$ by appropriate measures.

Moreover, from Fig. 6, we see that if the value of disease transmission rate ($\alpha$) is increased, the number of infections increases due to the effect of COVID-19 from long term prediction. It is demonstrated that if $\alpha$ and $\beta$ are not controlled, then the situation may take the worst form in the future. So far, to reduce the effect of the coronavirus pandemic, the Indian government has taken some meaningful strategies like as reducing the contacts between infected individuals, increasing the effective health care products, maintain the social distancing and washing hands regularly for at least 20 s, etc.

More interestingly, the results also reveal that COVID-19 can exhibit oscillatory behavior in future. However, the social distancing measures, efficiency in quarantine, and isolation can control it. Finally, to suppress or minimize the harmful effect of dangerous coronavirus, the most and effective responsibility should be taken by the public of India, and strong cooperation should be rendered to the local administration and Governments. The future work may consider the influences of recent coronavirus mutations such as Delta and Omicron on the dynamics of COVID-19 pandemic. The different cases where the present vaccines can either resist against these virus variants of concern or fail to protect humans against them can be also investigated.

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Declarations

Conflict of interest The authors declare that they have no competition of interests.

Ethical approval This paper does not involve any studies carried out with human participants or on animals.

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