In this study, we developed and analyzed a mathematical model for explaining the transmission dynamics of COVID-19 in India. The proposed $SI_uI_kR$ model is a modified version of the existing SIR model. Our model divides the infected class $I$ of SIR model into two classes: $I_u$ (unknown infected class) and $I_k$ (known infected class). In addition, we consider $R$ a recovered and reserved class, where susceptible people can hide them due to fear of the COVID-19 infection. Furthermore, a non-monotonic incidence function is deemed to incorporate the psychological effect of the novel coronavirus diseases on India’s community. The epidemiological threshold parameter, namely the basic reproduction number, has been formulated and presented graphically. With this threshold parameter, the local and global stability analysis of the disease-free equilibrium and the endemic proportion equilibrium based on disease persistence have been analyzed. Lastly, numerical results of long-run prediction using MATLAB show that the fate of this situation is very harmful if people are not following the guidelines issued by the authority.

**KEYWORDS**

basic reproduction number, epidemiological model, local and global stability, novel coronavirus, persistence

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**1 INTRODUCTION**

The first case of the coronavirus pandemic was reported on January 30, 2020 in India (Zhu et al., 2020). India’s response to COVID-19 has been graded, pro-active, and pre-emptive with high-level political commitment and a “whole government” approach to respond to the COVID-19 pandemic. Educational institutions, various Governments, and non-Government offices, and many commercial establishments have been shut down immediately. Government of India, exercise the Disaster Management Act, 2005, issued an order for State/UT’s prescribing lockdown for containment of COVID-19 pandemic in the country for 21 days with effect from March 25, 2020, and announced to maintain mandatory physical distancing in India. Later Government extend the lockdown period up to May 3, 2020 as the number of active cases increases daily. The most common symptoms are dry cough, fever, and tiredness, but some infected people may have aches and pains, running nose, nasal congestion, sore throat, vomiting, or diarrhea. These symptoms usually are severe and begin gradually. Some people become infected, but neither has symptoms nor feels ill. Disease recovery is high without requiring special treatment. The guidelines for preventing the spreading of COVID-19 are wearing a face mask, staying more than 3 ft away from a sick person, washing hands with soap, or using alcohol-based hand rub, and so forth.

During an epidemic, reported cases of coronavirus disease are rising worldwide day by day due to human-to-human transmission; the study for prevention and control of infectious COVID-19 disease is essential. The modernized mathematical model is necessary to give a deeper understanding and perception of disease transmission mechanisms and find how to control the spread of the COVID-19 disease. Xiao and Ruan (2007) studied an epidemic model with a non-monotonic incidence rate, which describes the psychological effect of certain serious diseases on the community when the number of infections is getting larger. Xu and Ma (2009) investigated a SIR epidemic
model with nonlinear incidence rate and time delay. Yang et al. (2010) formulated a SIR model with vaccination and varying population. Sun and Hsieh (2010) investigated an susceptible exposed infected recovered (SEIR) model with varying population size and vaccination strategy. Zhou and Cui (2011) studied an SEIR epidemic model with a saturated recovery rate. Bai and Zhou (2012) proposed an SEIRS epidemic model with a general periodic vaccination strategy and seasonally varying contact rates. Khan et al. (2015) considered an SEIR model with nonlinear saturated incidence rate and temporary immunity. Elkhaiar and Kaddar (2017) studied the dynamics of an SEIR epidemic model with nonlinear treatment function that takes into account the limited availability of resources in the community. Wang et al. (2018) extended the incidence rate of an SEIR epidemic model with relapse and varying total population size to a general nonlinear form. Tiwari et al. (2017) investigated an SEIRS epidemic model with nonlinear saturated incidence rate. Lahrouz et al. (2012) studied the global dynamics of a SIRS epidemic model for infections with non-permanent acquired immunity. Tian and Wang (2011) discussed the global stability analysis for several deterministic cholera epidemic models. Samanta (2011) discussed the permanence and extinction of a non-autonomous HIV/AIDS epidemic model with distributed time delay. Cai et al. (2014) investigated an HIV/AIDS treatment model.

Gralinski and Menachery (2020) studied the return of novel coronavirus in 2019. Chen et al. (2020) developed a mathematical model for calculating the transmissibility of the novel coronavirus. Saldana et al. (2020) developed a compartmental epidemic model to study the transmission dynamics of the COVID-19 epidemic outbreak, with Mexico as a practical example. Silva et al. (2020) proposed a new SEIR agent-based COVID-19 model to simulate the pandemic dynamics using a society of agents emulating people, business, and government. Pal et al. (2020) proposed a COVID-19 model for stability analysis with five compartments. Lee et al. (2020) proposed a COVID-19 epidemic model for estimating the unidentified infected population in China. Maheshwari et al. (2020) forecasted the epidemic spread of COVID-19 in India using the ARIMA model. Zakharov et al. (2020) predicted the dynamics of the COVID-19 epidemic in real-time using the case-based rate reasoning model. Bonnas and Gianatti (2020) proposed a COVID-19 epidemic model where the population is partitioned into classes corresponding to ages. Roda et al. (2020) demonstrated the reasons for wide variations in numerous model predictions of the COVID-19 epidemic in China. Liu et al. (2020a) developed two differential equations models to account for the latency period of COVID-19 infection. Basnarkov (2021) studied a SEAIR epidemic spreading model of COVID-19. Yang and Wang (2020) proposed a mathematical model for the novel coronavirus epidemic in Wuhan, China. Wang, Lu, et al. (2020) performed the dynamical analysis of a COVID-19 epidemic model. Zlatev et al. (2020) developed a COVID-19 epidemics model spreading on the availability of tests for the disease. Xue et al. (2020) proposed a data-driven network model for the COVID-19 epidemics in Wuhan, Toronto, and Italy. Neves and Guerrero (2020) presented the A-SIR model to predict the evolution of the COVID-19 epidemic. Ndairou et al. (2020) proposed a mathematical model for COVID-19 epidemic with a case study of Wuhan.

Jiao and Huang (2020) proposed a SIHR COVID-19 epidemic model with effective control strategies. Zhao and Chen (2020) modeled the epidemic dynamics and control of the COVID-19 outbreak in China. Li et al. (2020) modeled the impact of mass influenza vaccination and public health interventions on COVID-19 epidemics. Pizzuti et al. (2020) investigated the prediction accuracy of the SIHR model on networks for Italy. Wang, Zheng, et al. (2020) used the logistic model and machine learning technics to predict the COVID-19 epidemics. Pongkitivanichkul et al. (2020) estimated the size of the COVID-19 epidemic outbreak. Liu et al. (2020b) predicted the cumulative number of cases for the COVID-19 epidemic in China. Zhu and Zhu (2020) devised a method to analyze the COVID-19 epidemic. Kantner and Koprucki (2020) computed a strategy for the case that a vaccine is never found and complete containment is impossible. Engbert et al. (2021) presented a Stochastic SEIR epidemic model for regional COVID-19 dynamics by sequential data assimilation. Several researcher investigated the dynamics of COVID-19 using fractional order models (Askar et al., 2021; Awais et al., 2020; Rezapour et al., 2020). Rihan et al. (2020) analyzed a stochastic SIRC epidemic model with time-delay for COVID-19. Bambusi and Ponno (2020) explained the linear behavior in COVID-19 epidemic as an effect of lockdown. Alberti and Faranda (2020) presented statistical predictions of COVID-19 infections by fitting asymptotic distributions to actual data. Abbasi et al. (2020) discussed the Optimal control for Impulsive SQEIR Epidemic model on COVID-19 epidemic. Lobato et al. (2020) identified an epidemiological model to simulate the COVID-19 epidemic. Khan and Atangana (2020) modeled the dynamics of novel coronavirus with fractional derivative. Alshammari and Khan (2021) analyzed the dynamics of modified SIR model with nonlinear incidence and recovery rates. Pal et al. (2021) presented a COVID-19 model with optimal treatment of infected individuals and the cost of necessary treatment. Khan et al. (2021) focused on the novel coronal virus model to understand its dynamics and possible control. Khajanchi and Sarkar (2020) developed a new compartment model that explains the transmission dynamics of COVID-19. Rai et al. (2021) studied the social media advertisements in combating the coronavirus pandemic in India. Tuncer (2020) explored globalization’s effect on the spread of fear across the world by focusing on the case of COVID-19. Adekola et al. (2020) examined various forms of mathematical models relevant to the containment, risk analysis, and features of COVID-19.

This paper determines the fate of coronavirus infective individuals introduced into the population in India. The dynamics of the nonlinear system have been considered in the study with reinfection turned off. The basic reproduction number (BRN) $R_0$ is estimated and analyzed as a threshold parameter for the stability analysis of the disease-free equilibrium (DFE) and endemic equilibrium. The uniform persistence of the disease near the threshold parameter is also determined.

2 | FORMULATION OF COVID-19 MATHEMATICAL MODEL

The proposed COVID-19 model involves a specific postulate considered for developing mathematical modeling in the Indian perspective.
Hypothetically, we imagine unknown infected peoples are spreading the diseases. Known infected peoples are isolated, so they are not able to spread the diseases. In the model, susceptible individuals enter into the unknown infected population by adequate personal contact with the unknown infected individuals given by non-monotonic incidence function $\frac{\alpha S_I}{1 + \delta I}$. Here, $\alpha S_I$ describes the infection force of the disease and $\frac{1}{1 + \delta I}$ measures the infection effect from the behavioral change of the susceptible individuals when the number of infectious individuals increases. Some susceptible class individuals move to the reserved area, which is considered a safe zone during the pandemic. The known infected individuals entered the recovered class after recovered from the COVID-19. Here in this model, we consider the recovered class and the reserved class as the same and denote the density at time $t$ by $R(t)$. The model of the study has been taken in the following form

\[
\begin{align*}
\dot{S} &= \Lambda - \frac{\alpha S_I}{1 + \delta I} - r_1 S - d_1 S \\
\dot{I}_u &= \frac{\alpha S_I}{1 + \delta I} - \beta I_u - d_1 I_u \\
\dot{I}_k &= \beta I_u - r_2 I_k - d_2 I_k \\
\dot{R} &= r_1 S + r_2 I_k - d_1 R
\end{align*}
\]  

The above model is defined on the set $D = \{(S, I_u, I_k, R) \in \mathbb{R}_+^4 : S > 0, I_u \geq 0, I_k \geq 0, R \geq 0\}$ subject to initial conditions

\[S(0) > 0, I_u(0) \geq 0, I_k(0) \geq 0, R(0) \geq 0,\]

where $S(t), I_u(t), I_k(t)$ and $R(t)$ are the densities at the time $t$ of susceptible population, unknown infected population (incubate the illness but do not have any symptoms and not identified), known infected population (in the isolated ward), and recovered or isolated population, respectively, and the parameters $\Lambda$, $\alpha$, $\beta$, $\delta$, $r_1$, $r_2$, and $d_i (i = 1, 2)$ are all positive. Here, $W(t) = S(t) + I_u(t) + I_k(t) + R(t)$ is defined as the total number of population under risk at the time $t$ (Figure 1).

The biological meanings of the model parameters are listed below:

- $\Lambda$: The recruitment rate at which new individuals enter the Indian population.
- $\alpha$: The homogeneous transmission coefficient from the susceptible population ($S$) to the unknown infected population ($I_u$). The rate of transmission of infection is given by $\frac{\alpha S_I}{1 + \delta I}$.
- $\beta$: The transmission coefficient from the known infected population ($I_k$) to the known infected population (treatment population) ($I_k$).
- $r_1$: The transmission coefficient from the susceptible population ($S$) to the recovered or isolated population ($R$).
- $r_2$: The transmission coefficient from the known infected population (treatment population) ($I_k$) to the recovered population or isolated population ($R$).
- $d_1$: The natural death rate.
- $d_2$: The death rate of the known infected class ($I_k$).

The above mathematical model involves certain assumptions which is stated below:

i. The susceptible population $S$ are those people who are not yet infected by the COVID-19 disease but may be infected when contacted with the unknown infected individuals ($I_u$). One section of this susceptible population move directly to the reserved compartment which is also same as the recovered compartment ($R$).

ii. The unknown infected population ($I_u$) is composed of individuals who have COVID-19 infection without symptoms. These individuals are capable of infecting anyone who comes in contact with them.

iii. The known infected population ($I_k$) is composed of individuals who have COVID-19 disease with symptoms and undergo best available treatment in isolation ward. The individuals in this compartment undergo the supportive care treatment or treatment to support the vital organs of the body. These individuals do not spread the COVID-19 disease as they are in isolation.

iv. The recovered population and reserved population together named as ($R$) is composed of two kinds of individuals namely the individuals who are recovered from the COVID-19 disease after the best available treatment in the treatment compartment ($I_k$) and those individuals who move to the reserved or safer areas from the susceptible compartment ($S$).

3 | ANALYSIS OF THE MODEL AND BASIC PROPERTIES

3.1 | Non-negativity of solutions

Theorem 1. Every solution of the system (1) with initial conditions (2) are non-negative for every $t \geq 0$.
Proof. The right hand side of the dynamical system (1) is completely continuous and locally Lipschitzian on $C^1$ and hence the solution $(S(t), I_u(t), I_k(t), R(t))$ of the system (1) with the initial conditions (2) exists and is unique on the interval $[0,\infty)$ with $0 < t \leq \infty$. From the first equation of the system (1) with initial condition $S(0) > 0$, we get

$$\frac{dS}{dt} > - \left( \frac{\alpha I_u}{1 + \delta d_0} + r_1 + d_1 \right) S$$

and hence

$$S(t) > S(0)e^{-\int_0^t \frac{\alpha I_u}{1 + \delta d_0} dx} > 0$$

where

$$\phi(I_u) = \frac{\alpha I_u}{1 + \delta d_0} + r_1 + d_1$$

Integrating the second equation of the system (1) with initial condition $I_u(0) \geq 0$, the solution can be written in the form as

$$I_u(t) = I_u(0)e^{\int_0^t \frac{\alpha S}{1 + \delta d_0} dx} \geq 0$$

where

$$\psi(S, I_u) = -\left( \frac{\alpha S}{1 + \delta d_0} - (\beta + d_1) \right)$$

From the third and fourth equations of the system (1) with initial conditions $I_k(0) \geq 0$ and $R(0) \geq 0$, we have

$$\frac{dI_k}{dt} = \beta I_u - (r_2 + d_2)I_k \geq -(r_2 + d_2)I_k$$

and hence

$$I_k(t) \geq I_k(0)e^{-(r_2 + d_2)t} \geq 0$$

and

$$\frac{dR}{dt} = r_1 S + r_2 I_k - d_1 R - d_1 R$$

and hence

$$R(t) > R(0)e^{-d_1 t} \geq 0$$

which yields $0 < W(t) \leq \frac{\Lambda}{a}$ as $t \to \infty$. Thus, all solutions of the COVID-19 system (1) which initiate in $\mathbb{R}_+^4$ are uniformly bounded and confined to the region $\Delta$, where $\Delta = \{ (S, I_u, I_k, R) \in \mathbb{R}_+^4 : 0 < W(t) \leq \frac{\Lambda}{a} \}$. Hence the feasible region $\Delta$ with initial conditions (2) is positively invariant under the flow induced by the system (1) in $\mathbb{R}_+^4$.

3.2 Boundedness of the system and invariant region

Theorem 2. All solutions of system (1) which lies in $\mathbb{R}_+^4$ are uniformly bounded and are confined to the invariant region $\Delta$ defined by $\Delta = \{ (S, I_u, I_k, R) \in \mathbb{R}_+^4 : 0 < W(t) \leq \frac{\Lambda}{a} \}$ as $t \to \infty$, where $a = \min\{d_1, d_2\}$.

Proof. Let us assume that $(S(t), I_u(t), I_k(t), R(t))$ is a solution of (1). Since,

$$W(t) = S(t) + I_u(t) + I_k(t) + R(t)$$

The time derivative of Equation (3) is

$$\frac{dW(t)}{dt} = \Lambda - (d_1 S + d_1 I_u + d_2 I_k + d_1 R)$$

For each $a > 0$, we get

$$\frac{dW}{dt} + aW = \Lambda - (d_1 - a)S - (d_1 - a)I_u - (d_2 - a)I_k - (d_1 - a)R$$

Assuming $a = \min\{d_1, d_2\}$, we get

$$\frac{dW}{dt} + aW \leq \Lambda$$

Applying the theory of differential inequality (Birkhoff & Rota, 1989), we find that

$$0 < W(S, I_u, I_k, R) \leq \frac{\Lambda}{a}(1 - e^{-at}) + W(S(0), I_u(0), I_k(0), R(0))e^{-at}$$

which yields $0 < W \leq \frac{\Lambda}{a}$ as $t \to \infty$. Thus, all solutions of the COVID-19 system (1) which initiate in $\mathbb{R}_+^4$ are uniformly bounded and confined to the region $\Delta$, where $\Delta = \{ (S, I_u, I_k, R) \in \mathbb{R}_+^4 : 0 < W(t) \leq \frac{\Lambda}{a} \}$. Hence the feasible region $\Delta$ with initial conditions (2) is positively invariant under the flow induced by the system (1) in $\mathbb{R}_+^4$.

Remark. All solutions of system (1) have non-negative components, given non-negative initial values in $\Delta$ and stay in $\Delta$ for $t \geq 0$ and globally attracting in $\mathbb{R}_+^4$ with respect to the system (1). Therefore, we restrict our attention to the dynamics of the system (1) in $\Delta$. Thus the system (1) with initial conditions (2) defined on $\Delta = \{ (S, I_u, I_k, R) \in \mathbb{R}_+^4 : 0 < W(t) \leq \frac{\Lambda}{a} \}$ is well-posed mathematically and epidemiologically and it is sufficient to
study the dynamics of the dynamical system (1) with initial conditions (2) defined on $\Delta$.

### 3.3 Equilibrium of system

To evaluate the equilibrium points of the system (1), we have to study the zero growth isolines and the point of interaction. The possible steady-state boundary equilibrium point is $P_0(S_0,0,0,R_0)$, where $S_0 = \frac{1}{r_1+\delta_1}$ and $R_0 = \frac{r_1}{r_1+\delta_1}\alpha$. Since the last equation of system (1) does not depend on other equations, we simply study the reduced system

$$\begin{align*}
\dot{S} &= \Lambda - Sg(l_u) - r_1S - d_1S \\
\dot{l}_u &= Sg(l_u) - \beta l_u - d_1 l_u \\
\dot{I}_u &= \beta l_u - r_2 I_u - d_2 I_u
\end{align*}$$

(4)

where $g(l_u) = \frac{\delta_1}{1+\delta_1}$ is increasing when $l_u$ is small and decreasing when $l_u$ is large. The DFE point becomes $P_0(S_0,0,0)\text{, where } S_0 = \frac{1}{r_1+\delta_1}, P_0 \in \Delta_{\Lambda}$ and $\Delta_{\Lambda} = \{(S,l_u,I_u) \in \mathbb{R}^3_+ : 0 < S + l_u + I_u \leq \frac{\Lambda}{r_1+\delta_1}\}$, where $\Lambda = \min(d_1,d_2)$. The endemic equilibrium point of the system (4) is $P^*(S',l'_u,I'_u)$, where $S' = \frac{(1+\delta_1)(\beta+d_1)}{\alpha} l'_u$, $l'_u = \frac{\beta}{r_2+\delta_2} I'_u$, and $I'_u = \frac{\delta_2}{\beta+\delta_2} S'$. The endemic equilibrium point exists if $S' > 0, l'_u > 0, I'_u > 0$.

### 4 DFE AND STABILITY ANALYSIS

To eradicate the disease from a varying size population, the more stringent way requires that the total number of the virus-infected population $(l_u(t) + I_u(t)) \to 0$, while a weaker requirement is that proportion sum of the same tends to zero (Busenberg et al., 1991). Thus we need to find the conditions for the existence and stability of the DFE $P_0\left(\frac{1}{r_1+\delta_1},0,0\right)$ and the endemic equilibrium $P^*(S',l'_u,I'_u)$. Therefore, $P_0\left(\frac{1}{r_1+\delta_1},0,0\right)$ is the DFE of (4), which exists for all positive parameters.

| **Table 1** Parameters with their real field value |
|-----------------------------------------------|
| **Parameters** | **Value** | **Reference** |
| $\Lambda$ | $4 \times 10^4$ | Estimated |
| $\alpha$ | $25 \times 10^{-11}$ | Estimated |
| $\delta$ | $9 \times 10^{-10}$ | Assumed |
| $\beta$ | $4 \times 10^{-2}$ | Estimated |
| $r_1$ | $5 \times 10^{-4}$ | Assumed |
| $r_2$ | $6 \times 10^{-4}$ | Estimated |
| $d_1$ | $2 \times 10^{-5}$ | Estimated |
| $d_2$ | $199 \times 10^{-5}$ | Estimated |

### 4.1 The basic reproduction number

The BRN is the average number of secondary infections generated by a single infection and is one of the most vital threshold quantities which mathematically represent the spreading of the virus infection.

The Jacobian matrix of system (4) at an arbitrary point $P(S,l_u,I_u)$ becomes

$$J(P) = \begin{pmatrix}
-\alpha l_u & -\alpha S(1-\delta_u^2) & 0 \\
\alpha l_u & \alpha S(1-\delta_u^2) & (\beta+d_1) \\
0 & \beta & -(r_2+d_2)
\end{pmatrix}$$

(5)

The stability of $P_0$ is equivalent to all the eigenvalues of the characteristic equation of $J(P)$ at $P = P_0$ being with negative real parts, which can be assured by the BRN ($R_0$) obtained by the next-generation matrix method (Van den Driessche & Watmough, 2002), where $R_0$ is the epidemiological threshold parameter.

Let $x = (l_u,I_u,R,S)^T$. Then the system (1) can be written as

**Figure 2** Change of $R_0$ with respect to $\alpha$
\[ \frac{dx}{dt} = \mathcal{F}(x) - \mathcal{V}(x), \]

where \( \mathcal{F}(x) = \begin{pmatrix} \frac{a\Lambda}{1 + d_1} & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix} \) and

\[ \mathcal{V}(x) = \begin{pmatrix} (\beta + d_1)I_x \\ -\beta I_x + (r_2 + d_2)S \\ -r_1S - r_2I_x + d_1R \\ -\Lambda + \frac{a\Lambda}{1 + d_1} + (r_1 + d_1)S \end{pmatrix}. \]

The Jacobian matrices of \( \mathcal{F}(x) \) and \( \mathcal{V}(x) \) at the DFE \( P_0 \) are given by

\[ D\mathcal{F}(P_0) = \begin{pmatrix} \frac{a\Lambda}{r_1 + d_1} & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix} \text{ and } D\mathcal{V}(P_0) = \begin{pmatrix} \beta + d_1 & 0 & 0 & 0 \\ 0 & r_2 + d_2 & 0 & 0 \\ 0 & -r_1 & d_1 & -r_1 \\ \Lambda & 0 & 0 & r_1 + d_1 \end{pmatrix}. \]

From the above two matrices we get the matrices \( F \) and \( V \) as below

\[ F = \begin{pmatrix} \frac{\Lambda \alpha}{r_1 + d_1} & 0 \\ 0 & 0 \end{pmatrix} \text{ and } V = \begin{pmatrix} \beta + d_1 & 0 \\ -\beta & r_2 + d_2 \end{pmatrix}. \]

The next generation matrix for the system (1) is \( FV^{-1} = \begin{pmatrix} \frac{\Lambda \alpha}{r_1 + d_1} & \frac{\Lambda \alpha}{r_1 + d_1} \\ 0 & 0 \end{pmatrix}. \)

The spectral radius of the matrix \( FV^{-1} \) is \( \rho(FV^{-1}) \) which is the BRN \( R_0 = \rho(FV^{-1}) = \frac{\alpha\Lambda}{(r_1 + d_1)(\beta + d_1)}. \) Now, it has been observed that \( \frac{dR_0}{da} = \frac{\Lambda}{(r_1 + d_1)(\beta + d_1)} > 0. \) From this observation, it is obvious that if the transmission coefficient \( \alpha \) from the susceptible population (S) to unknown infected population (I) decreases, then the BRN \( R_0 \) also decreases and therefore reduces the burden on the infection. Otherwise, if \( \alpha \) increases, then \( R_0 \) would also increase and thus, the transmission of virus infection will also rise; therefore, the scenario will be very harmful to society.

Now, the BRN \( R_0 \) has been presented graphically in Figure 2 with respect to related estimated or hypothetical parameter values given in Table 1. From Figure 2, it is observed that as the value of \( \alpha \) increases, \( R_0 \) also increases simultaneously and become greater than unity after a certain value of \( \alpha \). Therefore, it is said that up to a certain value of \( \alpha \), the DFE point is stable (Theorem 3) and beyond that value of \( \alpha \), the endemic equilibrium point is stable (Theorem 6).

### 4.2 Local stability of the DFE

This section will discuss the parameter restrictions of the local stability of DFE.

**Theorem 3.** The disease free equilibrium \( P_0 \left( \frac{\alpha\Lambda}{r_1 + d_1}, 0, 0 \right) \) of the system (4) is locally asymptotically stable if \( R_0 < 1 \). Whereas, it is unstable if \( R_0 > 1 \).

**Proof.** The variational matrix of the system (4) at \( P_0 \left( \frac{\alpha\Lambda}{r_1 + d_1}, 0, 0 \right) \) is given by

\[
J(P_0) = \begin{pmatrix}
-r_1 - d_1 & -\frac{a\Lambda}{(r_1 + d_1)} & 0 \\
0 & \frac{a\Lambda}{(r_1 + d_1)} - (\beta + d_1) & 0 \\
0 & \beta & -(r_2 + d_2)
\end{pmatrix}
\]

The eigen values of the characteristic equation of \( J(P_0) \) are

\[ \lambda_1 = -(r_1 + d_1) < 0, \lambda_2 = \frac{a\Lambda}{(r_1 + d_1)} - (\beta + d_1), \lambda_3 = -(r_2 + d_2) < 0. \]

For stability, all eigen values must be negative. So, \( \lambda_2 < 0 \) gives

\[ \frac{a\Lambda}{r_1 + d_1} - (\beta + d_1) < 0 \Rightarrow \frac{a\Lambda}{(r_1 + d_1)(\beta + d_1)} < 1 \Rightarrow R_0 < 1. \]

Hence, the DFE is locally asymptotically stable if \( R_0 < 1. \)

### 4.3 Global stability of the DFE

In this section, we will discuss the parameter restrictions of the global stability of DFE.

**Theorem 4.** When \( R_0 < 1 \), the disease free equilibrium \( P_0 \left( \frac{\alpha\Lambda}{r_1 + d_1}, 0, 0 \right) \) is globally asymptotically stable in \( \Delta_1 \).

**Proof.** To prove the global stability of DFE \( P_0 \) when \( R_0 < 1 \), we choose a suitable Lyapunov function \( L(S, I_x, I) = (S - S_0 - S_0\ln \frac{S}{S_0}) + I + \alpha I \). Differentiating \( L(S, I_x, I) \) along (4), we obtain that

\[ L(S, I_x, I) = \text{ is the singleton set} \]

We observe that \( \frac{dL}{dt} = 0 \) if and only if \( S = S_0, I_x = 0, I = 0 \). Therefore, the maximum invariant set in \( (S, I_x, I) \in \Delta_1 : L(S, I_x, I) = 0 \) is the singleton set \( P_0 \), when \( R_0 < 1 \). By using Lasalle’s invariance principle
TABLE 2  COVID-19 active cases in India from 25th March to 20th April, 2020

| Date     | Active cases |
|----------|--------------|
| 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         |

| Date     | Active cases |
|----------|--------------|
| 3/4      | 2283         |
| 4/4      | 2757         |
| 5/4      | 3244         |
| 6/4      | 3835         |
| 7/4      | 4271         |
| 8/4      | 4642         |
| 9/4      | 5181         |
| 10/4     | 5867         |
| 11/4     | 6401         |

| Date     | Active cases |
|----------|--------------|
| 12/4     | 7165         |
| 13/4     | 7942         |
| 14/4     | 9252         |
| 15/4     | 10250        |
| 16/4     | 10823        |
| 17/4     | 11619        |
| 18/4     | 11808        |
| 19/4     | 13094        |
| 20/4     | 14634        |

\[
\frac{dL}{dt} = S \left(1 - \frac{S_0}{S} \right) L_0 + \alpha d_1 L_0
\]

\[
= \left(\Lambda - \frac{\alpha S L_0}{1 + \alpha d_1^2} - (r_1 + d_1)S\right) \left(1 - \frac{S_0}{S} \right) L_0 + \alpha \left(\frac{S L_0}{1 + \alpha d_1^2} - (r_2 + d_2)\right) L_0 + a_1 \beta L_0 - (r_2 + d_2) L_0
\]

\[
= (r_1 + d_1)S \left(1 - \frac{S_0}{S} \right) L_0 + \alpha \left(\frac{S L_0}{1 + \alpha d_1^2} - (r_2 + d_2)\right) L_0 + a_1 \beta L_0 - (r_2 + d_2) L_0
\]

\[
\leq 0 \text{ if } 0 < a_1 \leq \frac{1 - \rho_{\infty}(\beta + d_1)}{\beta} \text{ which is possible, as } \rho_{\infty} > 1
\]

(LaSalle, 1976), the DFE \( P_0 \) is globally asymptotically stable in \( \Delta_1 \), when \( \rho_{\infty} < 1 \).

5  | DISEASE PERSISTENCE

5.1  | Uniformly persistence

In this subsection, an effort is made to understand the uniform persistence of the dynamical system (4) for the threshold parameter by applying the acyclicity theorem (Sun & Hsieh, 2010).

**Definition 1.** The system (4) is said to be uniformly persistent (Butler et al., 1986) if there exists a constant \( \sigma > 0 \) such that all solutions \( (S(t), L_0(t), L_0(t)) \) with positive initial \( S(0), L_0(0), L_0(0) \) satisfy the following inequality

\[
\min \left\{ \limsup_{t \to \infty} S(t), \liminf_{t \to \infty} S(t), \liminf_{t \to \infty} L_0(t) \right\} \geq \sigma
\]

Let \( X \) be a locally compact metric space with metric \( d \), and let \( \Gamma \) is a closed non-empty subset of \( X \) with the boundary \( \partial \Gamma \) and interior \( \Gamma^0 \). Clearly, \( \partial \Gamma \) is a closed subset of \( \Gamma \) and let \( \Phi \) be a dynamical system on \( \Gamma \). Then set \( Y \) in \( X \) is said to be invariant if \( \Phi(Y, t) = Y \).

**Theorem 5.** Suppose the conditions H1 and H2 holds true for the dynamical system \( \Phi \),

- **H1:** The system \( \Phi \) has a global attractor.
- **H2:** If \( M = \{ M_1, M_2, ..., M_n \} \) of disjoint, compact and isolated invariant sets in \( \partial \Gamma \) such that
  - i. There are no subsets of \( M \) which form a cycle on \( \partial \Gamma \);
  - ii. \( \bigcup \omega(x) \subset \bigcup_{i=1}^{n} M_i \), where \( \omega(x) \) is the omega limit set of \( X \)
  - iii. Every set \( M_i \) is isolated in \( \Gamma \), \( 1 \leq i \leq n \);
  - iv. \( W^s(M_i) \cap \Gamma^0 = \emptyset \) for \( 1 \leq i \leq n \), where \( W^s(M_i) \) is a stable manifold of \( M_i \).
Then the dynamical system $\Phi_t$ is uniformly persistent with respect to $\Gamma^0$.

Proof. For the modified COVID-19 system (4), we assume that

$$\Gamma = \Delta_S = \{(S, I_u, I_k) \in \mathbb{R}_+^3 : 0 < S + I_u + I_k < \frac{\Lambda}{\alpha}\}, \quad \Gamma^0 = \{(S, I_u, I_k) \in \mathbb{R}_+^3 : I_u, I_k > 0\} \quad \text{and} \quad \partial \Gamma = \Gamma \setminus \Gamma^0.$$  

Clearly, $M_j = \partial \Gamma$. On $\partial \Gamma$, the system (4) reduces to

$$\frac{dS}{dt} = \Lambda - (r_1 + d_2)S,$$

in which $S(t) \to \frac{\Lambda}{(r_1 + d_2)}$ as $t \to \infty$. So it is concluded that $M = \{P_0\}$ and $\omega(x) = \{P_0\}$ for all $x \in M_j$ which proves (i) and (ii) of H2. From Theorem 3 the DFE $P_0$ is unstable when $R_0 > 1$ and also $W^s(M) = \partial \Gamma$ which indicates that (iii) and (iv) of H2 are satisfied. Since all system (4) solutions are uniformly bounded, a global attractor exists and hence H1 holds true for the

**FIGURE 3**  Time series plot of $S$ (a), $I_u$ (b), $I_k$ (c) when $R_0 < 1$ for different initial conditions using parameter values from Table 1

**FIGURE 4**  Time series plot of $S$ (a), $I_u$ (b), $I_k$ (c) when $R_0 > 1$ for different initial conditions with parameter values from Table 1 with $\alpha = 2 \times 10^{-9}$
Hence the system (4) is uniformly persistent with respect to $\Gamma^0$, when $\Re_0 > 1$.

6 | ENDEMIC EQUILIBRIUM AND STABILITY ANALYSIS

From Theorem 4, it is already observed that DFE is globally asymptotically stable when $\Re_0 < 1$ which implies that there is no endemic equilibrium when $\Re_0 < 1$. To analyze the existence of nontrivial interior equilibrium of system (4), it should satisfy the following conditions:

$$\frac{dS}{dt} = \frac{dl_u}{dt} = \frac{dl_k}{dt} = 0$$

(8)

with $S, l_u, l_k > 0$ and the above Equations (9) leads to the following solutions as $S^* = \frac{(1+\delta\alpha)}{\alpha}$, $l_u^* = \frac{\beta}{\gamma_1 + \delta\alpha} l_u^*$, and $l_k^* = \frac{\lambda - (\gamma_1 + \delta\alpha)}{\gamma_0} S^*$. Clearly $S^* = \frac{(1+\delta\alpha)\beta}{\alpha} > 0$ but $l_u^* = \frac{\lambda - (\gamma_1 + \delta\alpha)}{\gamma_0} S^* \leq \frac{(1+\delta\alpha)\beta}{\alpha} (\Re_0 - 1)$ and $l_k^* = \frac{\beta}{\gamma_1 + \delta\alpha} l_u^* \leq \frac{(1+\delta\alpha)\beta}{\gamma_1 + \delta\alpha} (\Re_0 - 1)$ are positive if $\Re_0 > 1$. Hence the nontrivial interior equilibrium $P^*$ of system (4) exists if $\Re_0 > 1$.

6.1 | Local stability analysis of the endemic equilibrium

Theorem 6. The endemic equilibrium $P^*$ of the system (4) is locally asymptotically stable in $\Delta_1$ if $\Re_0 > 1$. 

FIGURE 5 | Time history of the unknown infected population ($l_u$) and known infected population ($l_k$) for $\alpha = 15 \times 10^{-11}$; $\alpha = 25 \times 10^{-11}$, and $\alpha = 35 \times 10^{-11}$

FIGURE 6 | Time history of the unknown infected population ($l_u$) and known infected population ($l_k$) for $\alpha = 13 \times 10^{-11}$; $\alpha = 23 \times 10^{-11}$, and $\alpha = 33 \times 10^{-11}$
Proof. The variational matrix of the system (4) at 
$P^* (S^*, \text{I}_u^*, \text{I}_k^*)/C_0/C_1$ is

$$J(P^*) = \begin{pmatrix} a_{11} & a_{12} & 0 \\ a_{21} & a_{22} & 0 \\ 0 & a_{32} & a_{33} \end{pmatrix}$$

where

$$a_{11} = -\frac{a_1}{1 + \delta_u^2} - (r_1 + d_1), a_{12} = \frac{a_S}{1 + \delta_u^2} \left( 1 - \delta_u^2 \right), a_{21} = \frac{a_1}{1 + \delta_u^2},$$

$$a_{22} = \frac{a_S}{1 + \delta_u^2} \left( 1 - \delta_u^2 \right), a_{32} = \beta, a_{33} = -(r_2 + d_2).$$

The characteristic equation of $J(P^*)$ is

$$(a_{33} - \lambda)(\lambda^2 + B_1\lambda + B_2) = 0 \quad (9)$$

where $B_1 = -(a_{11} + a_{22})$ and $B_2 = a_{11}a_{22} - a_{21}a_{12}$. One of the eigenvalues of $J(P^*)$ from the Equation (10) is $a_{33}$ which is negative. The Routh–Hurwitz conditions state that the quadratic equation $\lambda^2 + B_1\lambda + B_2 = 0$ has negative roots or complex conjugates with negative real part if and only if $B_1 > 0$ and $B_2 > 0$. But after simplification, we get

$$B_1 = \frac{(r_1 + d_1) + a_1u + a_2u(r_1 + 3d_1 + 2\beta)\delta}{1 + \delta_u^2},$$

$$B_2 = \frac{l_u(\beta + d_1)(a + 2u(r_1 + d_1)\delta)}{1 + \delta_u^2}.$$

Obviously $B_i > 0$ for $i = 1, 2$. Hence, the positive equilibrium point $P^* (S^*, \text{I}_u^*, \text{I}_k^*)/C_0/C_1$ is locally asymptotically stable if $R_0 > 1$. 

\section*{Figure 7} Time history of the unknown infected population ($I_u$) and known infected population ($I_k$) for $\alpha = 23 \times 10^{-11}$ and $\alpha = 25 \times 10^{-11}$

\section*{Figure 8} Long run prediction of the unknown infected population ($I_u$) and known infected population ($I_k$) for $\alpha = 23 \times 10^{-11}$ and $\alpha = 25 \times 10^{-11}$.
6.2 Global stability analysis of the endemic equilibrium

To investigate the globally stability of the endemic equilibrium of system (4) when $\mathcal{R}_0 > 1$, we apply here a geometric approach (Li & Muldowney, 1996). We begin the preliminary discussion on the geometric approach by formulating the local version of the $C^1$ closing lemma of Pugh (Hirsch, 1991). Consider the differential equation

$$\dot{y} = f(y)$$

(10)

where $f : G \to \mathbb{R}^n$, $G \subset \mathbb{R}^n$ open set, simply connected and $f \in C^1(G \to \mathbb{R}^n)$.

Let $A(y)$ be an $\binom{n}{2} \times \binom{n}{2}$ matrix valued function which is $C^1$ in $G$ and $Q = A_\varepsilon A^{-1} + A J^2 A^{-1}$, where $A_\varepsilon$ is the matrix obtained by replacing each entry $a_{ij}$ in $A$ by its directional derivative in the direction of $f \frac{\partial f}{\partial x}$. Let $J^R$ be the second additive compound matrix of $J(P)$ and $\mu$ be the Lozinskii measure (Coppel, 1965) with respect to a vector norm $|\cdot|$ on $\mathbb{R}^n$ defined as $\mu(Q) = \lim_{h \to 0} \frac{\mu_h Q - 1}{h}$, $I$ is the unit matrix.

The following quantity $q_2 = \limsup_{t \to \infty} \sup_{y_0 \in \kappa} \mu(Q_{yp}(t))$ is well defined. If there exists a compact absorbing set $\kappa \subset G$ and the system (11) has a unique equilibrium $\bar{y}$ in $G$, then the unique equilibrium $\bar{y}$ of (11) is globally asymptotically stable in $G$ if $q_2 < 0$.

**Theorem 7.** Assume that $\mathcal{R}_0 > 1$. Then there exist $\beta > 0$ such that the unique endemic equilibrium $P^*$ is globally asymptotically stable in the interior of $\Delta_1$ when $\beta \geq \beta_0$.

**Proof.** To prove this result, we find the second additive compound matrix $J^R$ from the Jacobian matrix $J(P)$ of (5) for the reduced system (4) at $P^*$ in the following form:
\[ f^{(2)} = \begin{pmatrix}
A_{11} & 0 & 0 \\
\alpha S (1 - \delta_0^2) & A_{22} - \frac{\alpha S (1 - \delta_0^2)}{(1 + \delta_0^2)^2} & 0 \\
0 & \frac{\alpha u}{1 + \delta_0^2} & A_{33}
\end{pmatrix}
\]

\[ (11) \]

where

\[ A_{11} = -\frac{\alpha u}{1 + \delta_0^2} + \frac{\alpha S (1 - \delta_0^2)}{(1 + \delta_0^2)^2} - (r_1 + \beta + 2d_1) \]

\[ A_{22} = -\frac{\alpha u}{1 + \delta_0^2} - (r_1 + d_1 + r_2 + d_2) \]

\[ A_{33} = \frac{\alpha S (1 - \delta_0^2)}{(1 + \delta_0^2)^2} - (\beta + d_1 + r_2 + d_2) \]

and the matrix function \( A = A(S, l_u, l_k) \) is defined by \( A = \text{diag}\left(\frac{1}{l_u}, \frac{1}{l_k} \right) \) with \( A^{-1} = \text{diag}\left(1, l_u, l_k \right) \). Then \( A_l A^{-1} = \text{diag}\left(\frac{\alpha u}{l_u}, \frac{\alpha S (1 - \delta_0^2)}{(1 + \delta_0^2)^2}, l_k \right) \). Therefore, the matrix \( Q \) can be written in the following block form as

\[ Q = \begin{pmatrix}
Q_{11} & Q_{12} \\
Q_{21} & Q_{22}
\end{pmatrix}
\]

where \( Q_{11} = A_{11}, Q_{12} = (0, 0)^T, Q_{21} = \left(\frac{l_u}{l_k}, \frac{l_k}{l_u} + A_{33}\right) \) and

\[ Q_{22} = \begin{pmatrix}
\frac{\alpha u}{1 + \delta_0^2} & \frac{l_u}{l_k} + A_{22} - \frac{\alpha S (1 - \delta_0^2)}{(1 + \delta_0^2)^2} & 0 \\
\frac{l_u}{l_k} & \frac{l_k}{l_u} + A_{33}
\end{pmatrix}
\]

The vector norm \( |\cdot| \) of the vector \((U_1, U_2, U_3)\) in \( \mathbb{R}^3 \) can be defined as \(|(U_1, U_2, U_3)| = \text{sup}(|U_1|, |U_2| + |U_3|)\). Suppose \( \mu \) be the Lozinskii measure with the above defined norm, so as described in (Martin, 1974) and it follows the condition as \( \mu(Q) \leq \text{sup}(f_1, f_2) \), where \( f_1 = \mu_1(Q_{11}) + |Q_{12}|, f_2 = \mu_1(Q_{22}) + |Q_{21}|, |Q_{22}|, \) and \( |Q_{21}| \) are the matrix norm with respect to the \( L^1 \) vector norm. If \( \mu_1 \) denotes the Lozinskii measure with respect to \( L^1 \) norm. Using the second equation of system (4), we have

\[ f_1 = \frac{l_u}{l_k} - \frac{\alpha u}{1 + \delta_0^2} + \frac{\alpha S (1 - \delta_0^2)}{(1 + \delta_0^2)^2} - (r_1 + d_1) \leq \frac{l_u}{l_k} - (r_1 + d_1) \]

FIGURE 11 Day wise infected, recovered, and deceased population from 1st to 20th March 2020 in India
Using the third equation of system (4), we have

\[ f_2 = \frac{l_0}{l_0} - \frac{l_0}{\beta} - (r_2 + d_2) + \sup \left\{ -(r_1 + d_1), -\frac{\alpha S_0}{\left(1 + \delta_u^2\right)^2} - (\beta + d_1) + \frac{-\alpha S_0}{\left(1 + \delta_u^2\right)^2} \right\} + \frac{l_0}{\beta} \]

\[ = \frac{l_0}{l_0} + \sup \left\{ -(r_1 + d_1), -\frac{\alpha S_0}{\left(1 + \delta_u^2\right)^2} - (\beta + d_1) + \frac{-\alpha S_0}{\left(1 + \delta_u^2\right)^2} \right\} \]

which implies that \( \beta_2 < 0 \). Thus, the endemic equilibrium \( P^* \) of the reduced system (4) is globally asymptotically stable, when \( \text{RI}_0 > 1 \).

7 | DISCUSSION AND SIMULATIONS

In this section, firstly we consider the case when the BRN \( \text{RI}_0 = 0.4805 < 1 \) by utilizing the parameter values as in Table 1. For different initial conditions, the dynamics of the system (4) is represented in Figure 3. These figures illustrate that the susceptible population (S) persists and tends to \( S_0 = 7.6231 \times 10^7 \) as \( t \to \infty \) and the unknown infected population (Iu) tends to zero as \( t \to \infty \), that is, the system (4) approaches the DFE \( P_0 \left( 7.6231 \times 10^7, 0, 0 \right) \). This numerical simulation supports the result stated in Theorem 4. Next, we consider the case when \( \text{RI}_0 = 3.8442 > 1 \) by utilizing the values of parameter from Table 1 with \( \alpha = 2 \times 10^{-9} \). For various initial conditions, the dynamics of the system (4) is represented in Figure 4. These figures illustrate that the susceptible population (S), the unknown infected population (Iu) and the known infected population (Ik) all persist, that is, the system (4) tends to endemic equilibrium \( P^* \left( 7.27579 \times 10^7, 5.4120 \times 10^4, 8.35830 \times 10^5 \right) \). To determine the outbreak of infected individuals of COVID-19 disease in the Indian population, we present the numerical simulation of the proposed dynamical system (1), using MATLAB for simulation experiments, based on the SARS-CoV-2 virus-infected cases in the time frame in India. Here, we employ the nonlinear least-squares curve fitting method with the help of “fminsearch” function from the MATLAB Optimization Toolbox to obtain the best-fit parameters for INDIA. The procedure looks for the set of initial guesses and pre-estimated parameters for the model whose solutions best fit or pass through all the data points by reducing the sum of the square difference between the observed data and the model solution, that is, if a theoretical model \( t \to P_0(t, q_1, q_2, \ldots, q_n) \) is attained and depend on a few unknown parameters \( q_1, q_2, \ldots, q_n \) and a sequence of actual data points \((t_0, y_0), (t_1, y_1)\) is also at hand then the aim is to obtain values of the parameters so that the error \( E \) calculated can attain a minimum, where \( E = \sqrt{\sum_{t=0}^{\infty} (P(t, q_1, q_2, \ldots, q_n) - y_i)^2} \).

For simulation, we assume the initial values are \( S(0) = 8 \times 10^8 \), \( I_u(0) = 2 \times 10^3 \), \( I_k(0) = 5.51 \times 10^5 \) from March 25 to April 14, 2020 and \( S(0) = 8 \times 10^8 \), \( I_u(0) = 1.9 \times 10^4 \), \( I_k(0) = 1.0250 \times 10^5 \) from April 15 to April 20, 2020.

Figures 5–8 are drawn based on the parameter values (shown in Table 1). The values of the parameters are fixed based on the following real-time data of India, as shown in Table 2, the spread of the COVID-19 disease during the lockdown period is recorded as follows (MoHFW, 2021).

Figure 5 has been drawn for the unknown infected population \( (I_u) \) and known infected population \( (I_k) \) for \( a = 15 \times 10^{-11} \); \( a = 25 \times 10^{-11} \); and \( a = 35 \times 10^{-11} \); for the specified period from March 25 to April 14, 2020 during the first lockdown. This figure is fascinating because it is observed that for \( a = 25 \times 10^{-11} \), the known infected population curve of our proposed system fits to the curve of the real confirmed infected individuals in India during the above said period.

Figure 6 shows the time history of the unknown infected population \( (I_u) \) and known infected population \( (I_k) \) for \( a = 13 \times 10^{-11} \); \( a = 23 \times 10^{-11} \); and \( a = 33 \times 10^{-11} \) for the period from April 15 to April 20, 2020 during the second lockdown situation. Figure 10 is very interesting because it is observed that for \( a = 23 \times 10^{-11} \), the known infected population curve of our proposed COVID-19 system fits to the curve of the real confirmed infected individuals in India during the above said period.
Figure 7 shows that the time history of the unknown infected ($I_u$) and known infected ($I_k$) populations of the proposed system corresponding to $\alpha = 23 \times 10^{-11}$ and $\alpha = 25 \times 10^{-11}$ fits to the curve of the real confirmed infected individuals in India during the lockdown period from March 25 to April 20, 2020.

It is also clear that $\alpha$ as a representative of lack of following the good practices such as proper hand wash, sanitizing the places, nasal, and oral covering with a mask, social distancing has an effect in the proposed coronavirus model and an increase in $\alpha$ means many individuals are not following the good practices as said above and as a result, many individuals get infected and move to the unknown infected population ($I_u$). Long run prediction of the time history of the known infected population ($I_k$) for $\alpha = 23 \times 10^{-11}$ and $\alpha = 25 \times 10^{-11}$ is drawn in Figure 8, which shows that the disease gets diminished may be due to the availability of a Vaccine.

From Figure 8, it is observed that the active cases will decrease and the COVID-19 disease will persist in the society for a long period. Furthermore, it is noticed that the COVID-19 disease diminishes after a long period if people do not strictly follow the government guidelines and vaccination is not found at the earliest as we have considered that geographical and climatic factors do not have any impact on this virus infection.

From Figure 9, it is noticed that if $\beta$ increases, which is a representative of the identification process of the infected individuals, then the unknown infected population reduces and hence we can identify the individuals for quarantine. Thus, the lockdown period can be reduced and people can come back to a normal situation.

Figure 10 shows that if the recovery rate $r_2$ increases, which representing the quality of treatment and cooperation of the patient to the treatment, then the known infected population ($I_k$) tends to zero in the long run. Hence, the rapid spread of COVID-19 disease is reduced drastically.

Figure 11 represents the graphical representation of the day-wise increase of infected, recovered, and deceased population from March 1 to March 20, 2020 in India (COVID19 tracker, 2021). It is observed that active infected cases start to increase from the third week of March because many have already been infected, failed to be in isolation, not strictly adhering to the rules imposed by the Government and ICMR at the time of the second week of March, and hence the active cases increases but in control during the first lockdown stage. It is also observed that the day-wise recovered cases are also increasing and day-wise deceased cases are very low. From the above discussions, it can be said that SARS-COV-2 is threatening to the society, but not deadly dangerous until now in Indian perspective.

8 | CONCLUSION

The proposed model has determined the outbreak of COVID-19 disease in the Indian population. The BRN $R_0$ is the threshold limit that determines the dynamical proliferation. The reproduction number $R_0$ decreases if the transmission coefficient $\alpha$ decreases. If $\alpha$ increases, then the transmission of COVID-19 disease increases and is very harmful to society. The system has a unique DFE $P_0$, which is globally stable if $R_0 < 1$ which symbolizes that the disease diminishes eventually. When $R_0 > 1$, the system is uniformly persistent under some conditions, a unique endemic equilibrium is globally stable. The study shows that the infected population who incubate the illness of our proposed system fits well to the real confirmed infected individuals in India during the lockdown period.

By observing the time graph of the known infected class ($I_k$) for various values of $\alpha$, we conclude that if people do not strictly follow the guidelines and lockdown measures imposed by the Government of India to prevent the rapid spread of the infection, the situation will be out of control.

ACKNOWLEDGMENTS

We are grateful to the editor and anonymous referees for their careful reading, valuable comments, and helpful suggestions which have helped us to improve the presentation of this work significantly.

CONFLICT OF INTEREST

The authors declare no conflicts of interest.

AUTHOR CONTRIBUTIONS

Analysis and draft the paper: R. Prem Kumar and Sanjoy Basu. Collected the data, conceived and designed the analysis, perform the analysis tool for the paper: D. Ghosh and P. K. Santra. Supervised, designed the analysis and wrote the paper: G. S. Mahapatra.

DATA AVAILABILITY STATEMENT

Available at https://www.who.int, www.mohfw.gov.in, www.covid19india.org

CONSENT TO PARTICIPATE

This article does not contain any studies involving animals or human participants performed by any authors. Anyone can read material published in the Journal.

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We, the undersigned, give our consent for the publication of identifiable details, which can include figures and details within the text (“Material”) to be published in the above Journal and Article. Therefore, anyone can read material published in the Journal.

NOMENCLATURE

$D = \{ (S, I_u, I_k, R) \in \mathbb{R}_+^4 : 5 > 0, I_u \geq 0, I_k \geq 0, R \geq 0 \}$ is the set on which the dynamical system is defined

$\mathbb{R}_+^4$ 4-dimensional positive real space

$\mathbb{R}$ the set of all real numbers

$W(t)$ the total number of population at time $t$

$g(I_u)$ is the non-monotonic incidence function
\[ \psi(S, I_0) = \frac{dS}{1 + e^r} - (\beta + d) I_0 \] used for simplifying big expressions in Theorem 1

\[ \phi(I_0) = \frac{dI_0}{1 + e^r} + r + d I_0 \] used for simplifying big expressions in Theorem 1

\[ \Delta = \{ (S, I_0, R) \in \mathbb{R}^3_+ : 0 < W(t) \leq \frac{S}{4} \} \] which is positively invariant region in \( \mathbb{R}^3_+ \) for the system (1)

\[ \Delta_1 = \{ (S, I_0, R) \in \mathbb{R}^3_+ : 0 < S + I_0 + R \leq \frac{S}{4} \} \] which is positively invariant region in \( \mathbb{R}^3_+ \) for the reduced system (4)

\[ \rho_0 \] the disease free equilibrium of the reduced system (4)

\[ \rho^* \] the endemic equilibrium of the reduced system (4)

\[ S^*, I^*, R^* \] the coordinates of the endemic equilibrium point \( \rho^* \) of the reduced system (4)

\[ J(\rho_0) \] the Jacobian or variational matrix of the system (4) evaluated at the disease free equilibrium point \( \rho_0 \)

\[ J(\rho^*) \] the Jacobian or variational matrix of the system (4) evaluated at the endemic equilibrium point \( \rho^* \)

\[ R_0 \] basic reproduction number

\[ F, V, D(F(\rho_0)), DV(\rho_0), F, V \] these standard symbols are used in the calculation of the basic reproduction number \( R_0 \) as per the cited reference used for calculation

\[ \lambda_1, \lambda_2, \lambda_3 \] the eigen values of the characteristic equation of \( J(\rho_0) \)

\[ L(S, I_0, I_0) \] Lyapunov function chosen to prove the global stability of the disease free equilibrium

\[ a_1 \] the positive constant in Lyapunov function \( L(S, I_0, I_0) \)

\[ S(0), I(0), T(0) \] the initial conditions for the reduced system (4)

\[ d \] the metric for the metric space \( X \)

\[ \Gamma \] a closed non-empty subset of \( X \) used in the introduction of the uniform persistence theorem

\[ \partial \Gamma \] the boundary of \( \Gamma \)

\[ \Gamma^0 \] the interior of \( \Gamma \)

\[ \Phi \] it is a dynamical system

\[ Y \] \( Y \subset X \)

\[ \Phi(Y, t) \] the solution space of the dynamical system \( \Phi \)

\[ M_2 = \{ x \in \partial \Gamma : \Phi_t(x) \in \partial \Gamma, \forall \ t \geq 0 \} \]

\[ M = \{ M_1, M_2, M_3, \ldots, M_n \} \] is compact, pairwise disjoint, isolated invariant subsets in \( \partial \Gamma \)

\[ W^s(M_i) \] the stable manifold of \( M_i \)

\[ C^1 \] the class \( C^1 \) consists of all differentiable functions whose derivative is continuous. Those functions are called continuously differentiable functions

\[ \dot{y} = f(y) \] the dynamical system used in the introduction of the geometric approach method used to investigate the global stability of the endemic equilibrium

\[ G \subset \mathbb{R}^n \] is the domain of \( f \) used in the introduction of the geometric approach method used to investigate the global stability of the endemic equilibrium

\[ A(y) \] \( \left( \begin{array}{c} n \end{array} \right) \times \left( \begin{array}{c} n \end{array} \right) \) matrix valued function which is \( C^1 \) in \( G \)

\[ Q = A_1 A^{-1} + A^2 A^{-1}, \] which is used in accordance with the geometric approach method to investigate the global stability of the endemic equilibrium

\[ A_1 \] is the matrix obtained by replacing each entry of the matrix \( A \) by its directional derivative in the direction of \( f \)

\( J_2 | \) the second additive compound matrix obtained from the jacobian matrix \( J(\rho) \)

\[ \mu_1, \mu_2 \] Lozinskii measure with respect to \( L^1 \) norm

\( \mu(Q) = \lim_{t \to \infty} \sup \sup_{h \in \mathbb{R}} \frac{1}{h} \left\{ \sup_{y \in X} \left\| \frac{\partial}{\partial t} \left( Q(y(p, y_0)) \right) \right\| dp \right\}. \] This quantity is defined as per the Geometric approach method to investigate the global stability of the endemic equilibrium

\[ \kappa = \text{it is a compact absorbing set in the interior of } \Delta_2 \text{ which is absorbing for the reduced system (4)} \]

\[ G \subset \mathbb{R}^n \text{ is an open and simply connected set used in the introduction of \( \text{Geometric approach method} \)} \]

\[ \text{the unique endemic equilibrium in } G \text{ of the reduced system (4)} \]

\[ \text{the endemic equilibrium of the reduced system (4)} \]

\[ \text{the Lozinskii measure with respect to } L^1 \text{ norm} \]

\[ \text{the Lozinskii measure of the matrix } Q \text{ which is given by } \mu(Q) = \lim_{t \to \infty} \sup \sup_{h \in \mathbb{R}} \frac{1}{h} \left\{ \sup_{y \in X} \left\| \frac{\partial}{\partial t} \left( Q(y(p, y_0)) \right) \right\| dp \right\}. \] This quantity is defined as per the Geometric approach method to investigate the global stability of the endemic equilibrium

\[ \text{these symbols are used as per the Geometric approach to investigate the global stability of the endemic equilibrium} \]

\( \sigma \) used in the definition of uniform persistence

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How to cite this article: Prem Kumar, R., Basu, S., Ghosh, D., Santra, P. K., & Mahapatra, G. S. (2021). Dynamical analysis of novel COVID-19 epidemic model with non-monotonic incidence function. *Journal of Public Affairs*, e2754. [https://doi.org/10.1002/pa.2754](https://doi.org/10.1002/pa.2754)