Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

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Mathematical analysis of COVID-19 by using SIR model with convex incidence rate

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ABSTRACT

This paper is about a new COVID-19 SIR model containing three classes; Susceptible S(t), Infected I(t), and Recovered R(t) with the Convex incidence rate. Firstly, we present the subject model in the form of differential equations. Secondly, "the disease-free and endemic equilibrium" is calculated for the model. Also, the basic reproduction number R_0 is derived for the model. Furthermore, the Global Stability is calculated using the Lyapunov Function construction, while the Local Stability is determined using the Jacobian matrix. The numerical simulation is calculated using the Non-Standard Finite Difference (NFDS) scheme. In the numerical simulation, we prove our model using the data from Pakistan. "Simulation" means how S(t), I(t), and R(t) protection, exposure, and death rates affect people with the elapse of time.

Introduction

In December 2019, a new kind of virus named "corona" was reported to badly affect the Chinese city of Wuhan. The said virus and its resultant outbreak hit the city of Wuhan first and later affected almost the whole world. It took hundreds of thousands of lives worldwide. It is hard to take a single point of view on this virus's origin. It may be due to a seafood market exchange, or the people's migration from one place to another, or the transmission from animals to humans; It may also be due to human-to-human interactions. So far, the virus has devastated almost everything around the world. Social life, health, economy, education - generally, each segment of human life has been severely affected. Health researchers, governmental policymakers, and health care authorities are puzzled in combating the deadly outbreak. They all have their point of view on the situation. They are trying hard to, at least, minimize the number of deaths caused by the outbreak. The people infected in the coronavirus pandemic experience mild respiratory problems. Fever, dry cough, throat infection, and fatigue are the symptoms of this disease. People may also have the symptoms as follows; nasal infection, aches, and sore throat. Mathematical modeling plays an important role in describing the epidemic of infectious diseases. The purpose of mathematical modeling is to represent different types of a real-world situation in mathematical language. A number of mathematical model are studies in the pervious literature [1,2,8,10]. Also SARS-CoV-2 is study by many researchers in current research literature [9,11,12,14]. We will study SARS-CoV-2 by developing SEIR model later on in this work. Recently many authors have established numerious models for COVID-19 under different concept of fractional calculus. In this regards very useful models have been established, we refer some as [20–25]. To find out the different dynamics of a disease and therefore to overcome it at an early stage, mathematical modeling plays an important role there [26–28]. The area dedicated to the investigation of biological pandemic and also epidemic models for recent diseases SARS-CoV-2 of research. Numerous examples of mathematical models for this pandemic are found in the current study [16,17]. To understand the stability theory, existence theory, and theory of reform SARS-CoV-2 [6,7,13,19], can be model, and its outcome can be predicted. Plan of prevention is also possible. In addition, one can find a possible lock-down strategy. Especially impressed with the excellent features of the SEIR model using non-linear saturated incidence rates [3–6,8,15].

Model formulation

In this section of manuscript, we formulate our new model for *NCOVID* −19 in the form of following system (1). We take whole population N(t) into three classes S(t), I(t) and R(t), which represent Susceptible, Infected and Recovered compartment in the form of differential equations given below (1),

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$$\frac{dS(t)}{dt} = b - k(1 - \alpha S(t)I(t)) - \alpha k\beta S(t)I(t) - \mu S(t)$$
$$\frac{dI(t)}{dt} = k(1 - \alpha S(t)I(t)) + \alpha k\beta S(t)I(t) - (d_0 + \gamma + \mu)I(t) \quad (1)$$
$$\frac{dR(t)}{dt} = \gamma I(t) - \mu R(t).$$

For above system (1) is presented in the form of flow chart as.

In Table 1, we describe parameters used in system (1). In system (1), add all equations, implies

$$\frac{dN(t)}{dt} = -(\mu N(t) + d_0 I(t) - b). \quad (2)$$

Here $N(t)$ represent whole population as $N(t) = S(t) + I(t) + R(t)$. We get

$$0 \leqslant \lim_{t\to\infty} sup N(t) \leqslant N_0.$$

With

$$\lim_{t\to\infty} sup N(t) = N_0.$$

If and only if

$$\lim_{t\to\infty} sup I(t) = 0.$$

From the 1^{st} equation of the system (1), it show

$$0 \leqslant \lim_{t\to\infty} sup S(t) \leqslant S_0.$$

Which implies that if $N > N_0$, where $\frac{dN(t)}{dt} < 0$. We can get

$$\Omega = (S(t), I(t), R(t)) \in \mathbf{R}^4_+ : S(t) + I(t) + R(t) \leqslant N_0, S \leqslant S_0.$$

Equilibria

For the system (1), we suppose the existence of equilibrium. Disease free equilibrium is exist for some values of the variables used in (1), which is denoted by $E_0 = (S^0, 0, 0)$.

$$E_0 = (S^0, 0, 0) = \left(\frac{b}{\mu}, 0, 0\right).$$

Endemic equilibria

$$S^*(t) = \frac{(\mu + d_0 + \gamma)I^*(t) - b}{\mu}$$
$$I^*(t) = \frac{k\mu}{k\alpha(1-\beta)(\mu + d_0 + \gamma - b)I^*(t) + \mu(\mu + d_0 + \gamma)}$$
$$R^*(t) = \frac{\gamma}{\mu} I^*(t).$$

Expression for R_0 The basic reproductive number

In epidemiology there R_0 is most important parameter, which give us idea about how the disease is flow in the whole population. From R_0, we look how the disease id spread in population and we can control it from this. The method of finding R_0 is below let $X = (S(t), I(t))$, then from system (1),

$$\frac{dX}{dt} = \mathscr{F} - \mathscr{V},$$

where

$$\mathscr{F} = \begin{pmatrix} k(1 - \alpha I(t)S(t)) + \alpha k\beta I(t)S(t) \\ 0 \end{pmatrix}$$

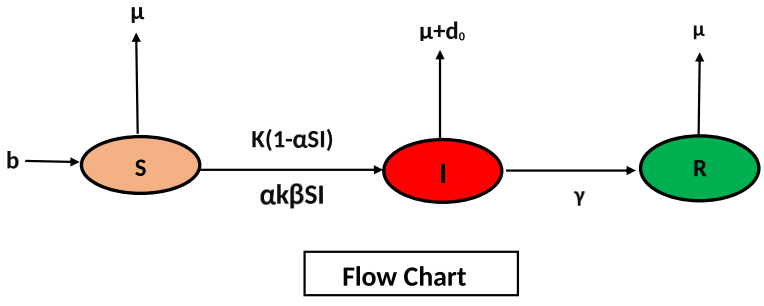
and

$$\mathscr{V} = \begin{pmatrix} b - S(t) \\ (d_0 + \gamma + \mu)I(t) \end{pmatrix}$$

Jacobian of $\mathscr{F}$ is

$$F = \begin{pmatrix} -k\alpha S^0 + k\alpha\beta S^0 & 0 \\ 0 & 0 \end{pmatrix}$$

Table 1
Physical Interpretation of parameters of the system.



Parameters	The physical Description
$S(t)$	Susceptible compartment
$I(t)$	Infected compartment
$R(t)$	Recovered compartment
d_0	Death due to corona
μ	Natural death
b	Birth rate
β	Protection rate
k	Constant rate
α	Isolation rate
γ	Recovery rate

and Jacobian of $\mathscr{V}$ is

$$V = \begin{pmatrix} -\mu & 0 \\ 0 & d_0+\gamma+\mu \end{pmatrix}.$$

Hence

$$V^{-1} = \frac{1}{-\mu(\gamma+d_0+\mu)} \begin{pmatrix} \mu+d_0+\gamma & 0 \\ 0 & -\mu \end{pmatrix}.$$

We have

$$FV^{-1} = \begin{pmatrix} k\alpha(\beta-1)S^0 & 0 \\ 0 & 0 \end{pmatrix}.$$

From this, we get R_0 is

$$R_0 = \frac{k\alpha(1-\beta)b}{\mu^2}. \tag{3}$$

To computes the basic reproduction number we obtained $R_0 = 0.7831$ from the parameters used in Table 2 [18], which show that the COVID-19 that occurred in Pakistan is well controlled by Pakistan government. We have the following theorem on the basis of (3).

Theorem 1. *(i) If $R_0 \leq 1$ there is no positive equilibrium of system.*

(ii) If $R_0 > 1$ there is a unique positive equilibrium $E^* = (S^*(t), I^*(t), R^*(t))$ of the model (1), called the endemic equilibrium.

Local Stability

We reduced our model (1) for local stability. Furthermore, to obtained the result which show "disease free and endemic equilibrium". For system (1). We reduced and get

$$\begin{aligned} \frac{dS(t)}{dt} &= b - k(1-\alpha S(t)I(t)) - \alpha k\beta S(t)I(t) - \mu S(t) \\ \frac{dI(t)}{dt} &= k(1-\alpha S(t)I(t)) + \alpha k\beta S(t)I(t) - (\mu+d_0+\gamma)I(t). \end{aligned} \tag{4}$$

Subject to initial condition

$$S(0) = S_0 \geqslant 0, I(0) = I_0 \geqslant 0.$$

For local stability, we have the following theorem.

Theorem 2. *If $R_0 < 1$, then the system (4) is locally asymptotically stable at the disease free equilibrium E^0.'*

Proof. At E^0 the jacobian matrix is given by

$$J^0 = \begin{pmatrix} -\mu & \dfrac{k\alpha(1-\beta)b}{\mu} \\ 0 & R_0 - 1 \end{pmatrix}.$$

The auxiliary equation of J^0 is given by

$$\lambda^3 + \lambda^2 a_1 + \lambda a_2 + a_3 = 0,$$

where

$$\begin{aligned} a_1 &= (\mu+\beta)(\mu+\alpha) + (\mu+d_0+\gamma)(1-R_0) > 0 \\ a_2 &= (\mu+\beta)(\mu+\beta)[1+(\mu+\gamma+d_0)(1-R_0)] > 0 \\ a_3 &= (\mu+\beta)(\mu+\alpha)(\mu+\gamma+d_0)(1-R_0) > 0. \end{aligned}$$

We have

$$\begin{aligned} a_1a_2 - a_3 &= (\mu+\beta)(\mu+\alpha)\big((\mu+\gamma+d_0)^2 + (\mu+\beta)(\mu+\alpha)[(d_0+\gamma+\mu)+1]\big)(1-R_0) \\ &> 0. \end{aligned} \tag{5}$$

The Routh-Hurtwriz criteria is satisfied as $a_1 > 0, a_2 > 0, a_3 > 0$ and $a_1r_2 - r_3 > 0$ if $R_0 < 1$. which show the system (1) is locally asymptotically stable at E^0. Furthermore, at E^* the system (4) is locally asymptotically stability analogous to $R^0 > 1$. We are going to prove it in the next theorem.

Theorem 3. *At E^*, if $R^0 > 1$ then system (4) is locally asymptotically stable.*

Proof. For system (4) jacobian matrix is

$$J_1 = \begin{pmatrix} \alpha kI^*(t) - \mu - \alpha k\beta I^*(t) & \alpha kS^*(t) - \alpha k\beta S^*(t) \\ -\alpha kI^*(t) + \alpha k\beta I^*(t) & -k\alpha S^*(t) + \alpha k\beta S^*(t) - (\mu+d_0+\gamma) \end{pmatrix}.$$

After some operations on matrix J_1, we get

$$M_1 = \begin{pmatrix} -\mu & -(\mu+d_0+\gamma) \\ -\alpha k(1-\beta)I^*(t) & -k\alpha(1+\beta)S^*(t) - (\mu+d_0+\gamma) \end{pmatrix}.$$

We calculate trace and determinant of M_1

$$tra(M_1) = -2\mu - k\alpha(\beta+1)S^*(t) - d_0 - \gamma < 0, \tag{6}$$

and

$$\det(M_1) = \mu[\alpha\beta(1+\beta) + d_0 + \mu + \gamma] + \alpha k(\mu+d_0+\gamma)(\beta+1) > 0. \tag{7}$$

The determinant of $J_1 > 0$. The real part at $E^*(t)$ "endemic equilibrium" of model (4) has negative. Thus, with condition $R_0 > 1$, we have that the endemic equilibrium E^* of system (4) is locally asymptotically stable.

Global stability

Here, we present Global stability for the system (1). For "global stability of disease-free and endemic equilibrium", we constructed a function known as Lyapunov function in the following theorem.

Theorem 4. *If $R_0 < 1$ then disease free equilibrium of the system (4) is globally asymptotically stable. Otherwise unstable.*

Proof. To prove this, we construct a Lyapunov function as following

$$\rho = c_1(S(t) - S_0) + c_3I(t), \tag{8}$$

such that $c_1, c_2, c_3 > 0$ are constants. With respect to time t taking derivative of (8) with, we have

$$\begin{aligned} \frac{d\rho}{dt} &= c_1(b - k(1-\alpha S(t)I(t))b - \alpha k\beta S(t)I(t) \\ &\quad - \mu S(t)) + c_2(k(1-\alpha S(t)I(t)) + \alpha k\beta S(t)I(t) - (\mu+d_0+\gamma)I(t)). \end{aligned}$$

We get

$$\begin{aligned} \frac{d\rho}{dt} &= c_1b + k(1-\alpha S(t)I(t))(c_2-c_1) + \alpha k\beta S(t)I(t)(c_2-c_1) + c_1\mu S(t) \\ &\quad - c_2\mu I(t) - c_1d_0I(t) - c_2\gamma I(t). \end{aligned}$$

Let assume $c_1 = c_2 = c_3 = 1$, we get finally

$$\frac{d\rho}{dt} = -(\mu N(t) - b) - (d_0+\gamma)I(t) < 0.$$

Hence "globally asymptotically stable" for system (1) with $R_0 < 1$ has reached. Further, We are going to prove a theorem for "global stability of the endemic equilibrium" of model (1).

Table 2
Description of parameters and their values [18].

Parameters	Physical description	Numerical value
$S(t)$	Susceptible compartment	220 in millions
$I(t)$	Infected compartment	0 in million
$R(t)$	Recovered compartment	0 in million
d_0	Death due to corona	0.02
μ	Natural death	0.0062
b	Birth rate	10.7
β	Protection rate	0.009, 0.0009
k	Constant rate	0.00761
α	Isolation rate	0.009, 0.0009
γ	Recovery rate	0.0003

Theorem 5. *The endemic equilibrium E^* of model (1) is stable globally asymptotically if $R_0 > 1$.*

Proof. By constructing Lyapunov function, we prove the above result

$$\omega = (\mu+\beta)(S(t) - S^*(t)) + (\mu+\beta)I(t). \tag{9}$$

Taking derivative with respect to time (9), we get

$$\frac{d\omega}{dt} = (\mu+\beta)S'(t) + (\mu+\beta)I'(t).$$

Putting the values from (1)

$$\frac{d\omega}{dt} = (\mu+\beta)(b - k(1-\alpha S(t)I(t)) - \alpha k\beta S(t)I(t) - \mu S(t))$$
$$+ (\mu+\beta)(k(1-\alpha S(t)I(t)) + \alpha k\beta S(t)I(t) - (\mu + d_0 + \gamma)I^*(t)).$$

After some arrangement we get

$$\frac{d\omega}{dt} = -(\mu+\beta)(\mu S(t) + (\mu + d_0 + \gamma)I^*(t)) < 0.$$

Thus $\frac{d\omega}{dt} < 0$, the "endemic equilibrium" E^* of the model (1) is " globally asymptotically stable", show that $R_0 > 1$.

Numerical results and discussion

In this part of our manuscript, we calculated numerical simulation for model (1) with values used on Table 2. We take data from 1 February 2020 to 20*th* September corresponding to different compartments involve in the system (1) from Pakistan. Here, we use (NSFD) Non-standard Finite Difference scheme [13,15,19] to rewrite the system is

$$\frac{dS(t)}{dt} = b - k(1-\alpha S(t)I(t)) - \alpha k\beta S(t)I(t) - \mu S(t). \tag{10}$$

Which is decomposed in Nonstandard Finite Difference scheme as

$$\frac{S_{j+1} - S_j}{h} = b - k(1-\alpha S_j(t)I_j(t)) - \alpha k\beta S_j(t)I_j(t) - \mu S_j(t). \tag{11}$$

Just like above Eq. (11), we can write the system (1) in Non-Standard Finite Difference Scheme as

$$\begin{aligned} S_{j+1} &= S_j + h\big(b - k(1-\alpha S_j(t)I_j(t)) - \alpha k\beta S_j(t)I_j(t) - \mu S_j(t)\big) \\ I_{j+1} &= I_j + h\big(k(1-\alpha S_j(t)I_j(t)) + \alpha k\beta S_j(t)I_j(t) - (d_0+\gamma+\mu)I_j(t)\big) \\ R_{j+1} &= R_j + h\big(\gamma I_j(t) - \mu R_j(t)\big). \end{aligned} \tag{12}$$

For the real data of Pakistan [18], we testified our model (1) taking the values of parameter of Table 2 from first February 2020 to 20th of September 2020. From Figs. 1–3, we see that as the susceptibility was decreasing the infection was increasing in first four months but in the month of July and August the infection rate became slow and finally in

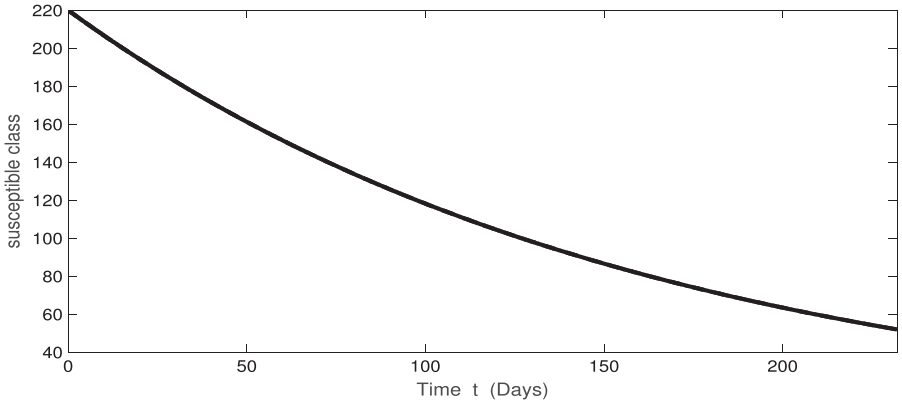


Fig. 1. Dynamical behavior in of susceptible population of the considered model.

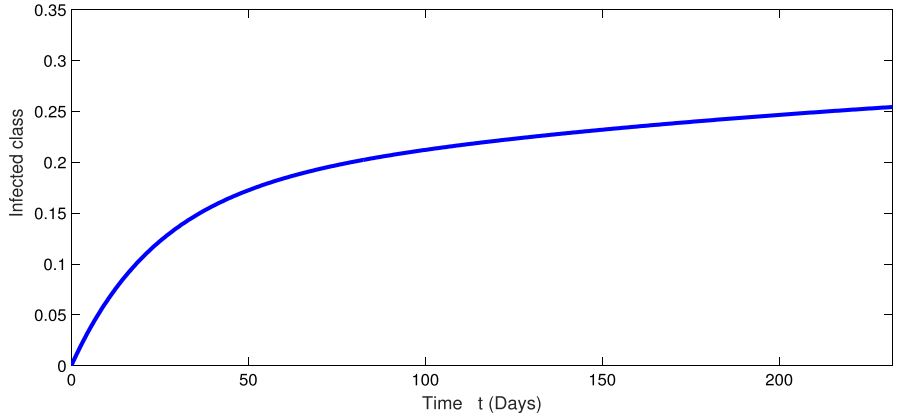


Fig. 2. Dynamical behavior of infected population of the considered model.

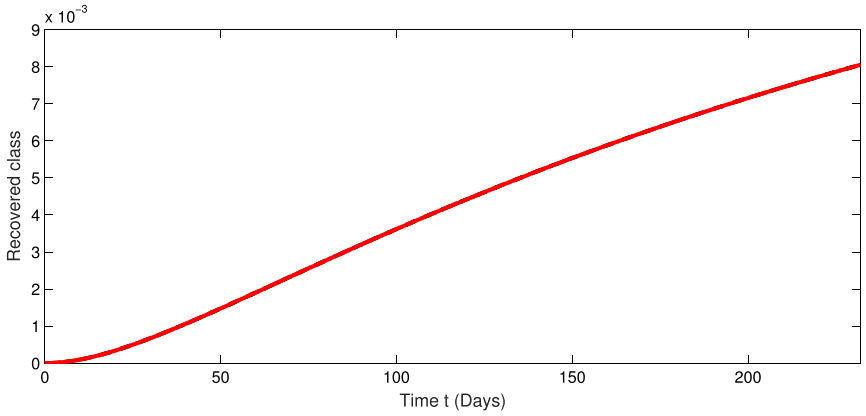


Fig. 3. Dynamical behavior of recovered population of the considered model.

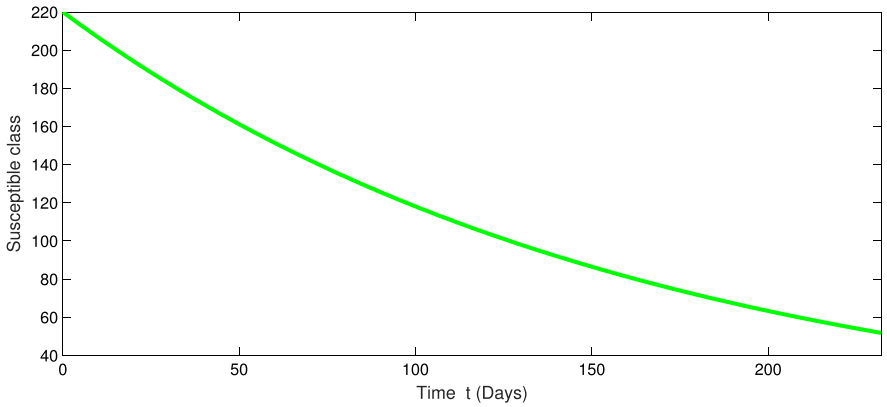


Fig. 4. Dynamical behavior in of susceptible population of the considered model.

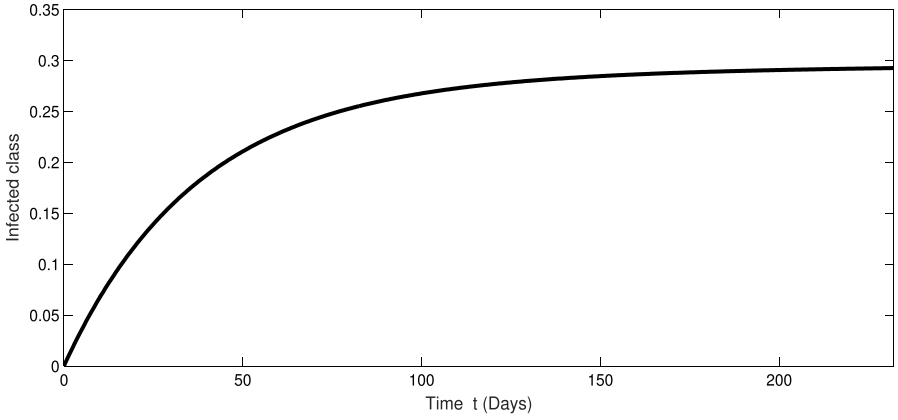


Fig. 5. Dynamical behavior of infected population of the considered model.

the last it was nearly become stable. Also during this time the recovery rate was rapid from the infection as in Fig. 3. The concerned simulation was performed for taking the protection parameter $\alpha = \beta = 0.009$. Now by deceasing the protection and isolation rate further up to $\alpha = 0.0009, \beta = 0.0009$. We plot the results in the given Figs. 4–6. We see that the infection rate became slow on reducing the protection and isolation rate. Therefore the recovery is also become slow. From these simulation we observed that protection and isolation rate play significant roles in controlling the infection from further spreading in the community. see Fig. 2,.

Conclusion

Conclusion of the numerical results shows the projection of model (1). The output derived from the NCOVID-19 display convex incidence rate. The current manuscript declared the high contiguous rate from infected population to susceptible population. To overcome the pandemic the migration should be strictly prohibited for the sake of saving humanity. Also the immigration of exposed population to infected community increased the infection. Isolation of infected one is the best option to secured the healthy community. It is necessary to judge the spread and model with various parameters for proper supervision. The proper treatment of this pandemic is to keep infected away from

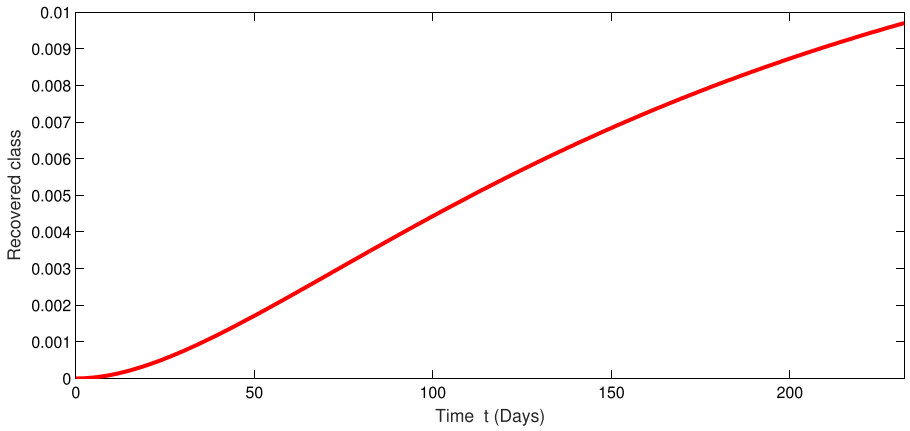


Fig. 6. Dynamical behavior of recovered population of the considered model.

healthy people. High internal defense system aids to get healthy soon while the low internal defense system need more attention. This is the only solution to overcome recent outbreak within a short period. The current discussion demonstrate the quick transfer of NCOVID-19. The COVID-19 shared the same properties like SARS having mortality rate of 2 percent. There is no vaccine available in the current time but to isolate was the best option. Also social distancing is the best way to control this deadly various.

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Availability of Data

This is not applicable in this research work.

Declaration of Competing Interest

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

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