




A mathematical model for SARS-CoV-2 in variable-order fractional derivative

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Abstract A new coronavirus mathematical with hospitalization is considered with the consideration of the real cases from March 06, 2021 till the end of April 30, 2021. The essential mathematical results for the model are presented. We show the model stability when $\mathcal{R}_0 < 1$ in the absence of infection. We show that the system is stable locally asymptotically when $\mathcal{R}_0 < 1$ at infection free state. We also show that the system is globally asymptotically stable in the disease absence when $\mathcal{R}_0 < 1$. Data have been used to fit accurately to the model and found the estimated basic reproduction number to be $\mathcal{R}_0 = 1.2036$. Some graphical results for the effective parameters are drawn for the disease elimination. In addition, a variable-order model is introduced, and so as to handle the outbreak effectively and efficiently, a genetic algorithm is used to produce high-quality control. Numerical simulations clearly show that decision-makers may develop helpful and practical strategies to manage future waves by implementing optimum policies.

1 Introduction

The corona virus affected and effecting the populations throughout the world by providing severe infection and death. The early and effective strategy to overcome this infection needed to follow the rule and regulations suggested by the World health organization to prevent the people from further reinfection. It is well known that every researchers from their respective field of research provided great efforts for the elimination of this infection. Many countries were the infection provided many deaths with so many waves of infection. Pakistan is one of among those where there are some waves occurred for this COVID-19 infection from which the population suffered. It has been reported the number of reported cases and deaths in each wave and seems the increase in the cases. There has been reported the number of death percentage in wave 1 and 2 to be 1 %.

The formulation of mathematical models in epidemiology and engineering areas has proven his role to be important; see [1–3]. Many researchers in different per-

spective studied the coronavirus infection. While the mathematicians and biologists who worked on the modeling of the COVID-19 infection studied and formulated the mathematical models with real cases of different countries and presented about the peak of the infection and its eliminations of infection. In this regard, some mathematical models are highlighted here that formulated for this infection are [4–10]. The initial cases reported in China for the COVID-19 infection have been investigated in [4] through a mathematical model. The real cases from Spain and Italy are considered in the modeling of infection in the form of an SEIR model which has been studied in [5]. The COVID-19 infection dynamics and its prediction through a mathematical model of an SEIR have been investigated in [6]. The data from Italy are considered, and a mathematical model is formulated for the COVID-19 infection and its analysis has been considered in [7]. The impact of social distancing and other features that can be considered essential for the decrease in the COVID-19 infection has been studied by the authors in [8]. They formulated a mathematical model for the South African infected cases. A comparison study for the dynamics

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of coronavirus infection has been discussed in [9]. The number of real cases from Mexico population through a mathematical model is considered in [10]. The real infected cases from KSA are considered by the authors using mathematical modeling approach and obtained the results regarding the disease eliminations in the country [11]. The modeling and the contrail measure of infection of COVID-19 have been discussed in [12]. The disease eliminations and its control through optimal control theory are suggested by the authors in [13]. Addressing the model with lockdown measure for the COVID-19 infection is discussed in [14]. Some other interesting work related to the modeling of COVID-19 and related results regarding the disease are suggested in [15–17]. Moreover, the authors in [18–22] considered the COVID-19 infection models in fractional derivatives and some recommendations regarding the minimization of infection are given in the form of lockdown and control strategies. Moreover, the applications of fractional calculus and the numerical methods for the physical and biological problems have been discussed in [23–26, 29–39]. For example, the HIV infection model with antiviral drug therapy is considered in [23]. A fractional SEIR model using wavelet method has been proposed in [24]. Some biological models with analytical and numerical techniques are discussed in [25]. A fractional model in ABC operator in astrophysics is discussed in [26]. A recent study is conducted for the understanding of coronavirus infection and its controls [27]. A mathematical model in non-singular order to investigate the coronavirus infection is considered in [28]. Nonetheless, some studies show that in some conditions, time-varying fractional-order models are able to better demonstrate behavior of systems [40–47]. However, now, there are few studies on time-varying fraction diseases dynamics, and it demands more studies in this field. Motivated by this in the current research, we propose and study a variable-order fractional model of SARS-CoV-2 dynamic.

In this work, a new mathematical model in the presence of hospitalization class is considered to better understand the COVID-19 infection in the presence of hospitalization and then using the concept of variable fractional order to study its dynamics. First, we will study the model in integer order and study the detailed mathematical results, and then, we extend the proposed model to have the results for the variable fractional-order model. We discuss in details the formulation of the model in Sect. 2. The stability results and the model endemic equilibria have been shown in Sect. 3. Estimations of the model parameters and its numerical results are discussed briefly in Sect. 4 and 5, respectively. In Sect. 6, using the approach of variable order and its related results are discussed. All the results are summarized and concluded in Sect. 7.

2 Model formulation

Due to the COVID infection and its emerging in the society that producing many cases again and again

in the society and creates a lot of difficulties for the humans as well as the government. Therefore, the eradications of the infections and to prevent the populations further, government present policies in light to World health organization. Therefore, here, our aims by formulating a novel mathematical model in the presence of hospitalization infection to understand in an effective way the dynamics of the COVID-19 infection with real cases reported from Pakistan. We denote the population of humans by $N(t)$ and split into it further into six compartments: The susceptible $S(t)$, exposed $E(t)$, infected with visible symptoms $I(t)$, infected with no visible symptoms $A(t)$, the individuals that are hospitalized/quarantined $H(t)$ and those recovered from infection is $R(t)$. We present the model below in the form of differential equations based on the above discussions

$$\begin{cases} \frac{dS}{dt} = \Pi - \rho(I + \sigma A)\frac{S}{N} - \omega S, \\ \frac{dE}{dt} = \rho(I + \sigma A)\frac{S}{N} - (\psi + \omega + \omega_0)E, \\ \frac{dI}{dt} = \psi(1 - \tau)E - (\omega + \omega_1 + \gamma_1 + \nu)I, \\ \frac{dA}{dt} = \psi\tau E - (\omega + \omega_2 + \gamma_2)A, \\ \frac{dH}{dt} = \nu I - \gamma_3 H - \omega_3 H - \omega H, \\ \frac{dR}{dt} = \gamma_1 I + \gamma_2 A + \gamma_3 H - \omega R, \end{cases} \quad (1)$$

subject to the initial conditions that are non-negative. The parameters given in the model (1) are defined as: The populations of healthy people that are susceptible to get corona virus infection are generated through the birth rate Π , while the natural death rate for each compartment in the model is shown by ω . The contact rate that generates the infection is given by ρ , while the infection that generated through the individuals with no clinical symptoms is given by the parameter σ . The death due to disease in the compartments of E , I , A , and H is shown by ω_0 , ω_1 , ω_2 , and ω_3 . The parameters ψ and τ distribute the infection in symptomatic and asymptomatic. The infected people are hospitalized at the rate ν . The recovery rate from the infected, infected with no clinical symptoms, and hospitalized people is shown by γ_i for $i = 1, 2, 3$, respectively. We write the model (2) in the absence of the last equation, given by

$$\begin{cases} \frac{dS}{dt} = \Pi - \rho(I + \sigma A)\frac{S}{N} - \omega S, \\ \frac{dE}{dt} = \rho(I + \sigma A)\frac{S}{N} - (\psi + \omega + \omega_0)E, \\ \frac{dI}{dt} = \psi(1 - \tau)E - (\omega + \omega_1 + \gamma_1 + \nu)I, \\ \frac{dA}{dt} = \psi\tau E - (\omega + \omega_2 + \gamma_2)A, \\ \frac{dH}{dt} = \nu I - (\gamma_3 + \omega_3 + \omega)H. \end{cases} \quad (2)$$

We have the total dynamics for the system (2) shown by

$$\frac{dN}{dt} = \Pi - \omega N - \omega_0 E - \omega_1 I - \omega_2 A - \omega_3 H \leq \Pi - \omega N. \quad (3)$$

Thus

$$\frac{dN}{dt} \leq \Pi - \omega N, \tag{4}$$

and further

$$N(t) \leq \frac{\Pi}{\omega} \text{ whenever } t \longrightarrow \infty. \tag{5}$$

We consider the region given below for the system (2)

$$\Gamma = \left\{ (S, E, I, A, H) \in \mathbb{R}_+^5 : N(t) \leq \frac{\Pi}{\omega} \right\}, \tag{6}$$

which is feasible biologically and all the solutions contained in it.

2.1 Equilibria

The equilibria for the system (2) in case if there is no infection in the population denoted by E_0 are shown below

$$D_0 = (S^0, 0, 0, 0, 0) = \left(\frac{\Pi}{\omega}, 0, 0, 0, 0 \right).$$

Next, we compute the basic reproduction number \mathcal{R}_0 , using analysis given in [48], and present the results given by

$$F = \begin{pmatrix} 0 & \rho & \tau\rho & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}, \quad V = \begin{pmatrix} l_1 & 0 & 0 & 0 \\ -\psi(1-\tau) & l_2 & 0 & 0 \\ -\psi\tau & 0 & l_3 & 0 \\ 0 & -\nu & 0 & l_4 \end{pmatrix}, \tag{7}$$

where $l_1 = (\psi + \omega + \omega_0)$, $l_2 = (\omega + \omega_1 + \gamma_1 + \nu)$, $l_3 = (\omega + \omega_2 + \gamma_2)$, and $l_4 = (\gamma_3 + \omega_3 + \omega)$. The following expression is the required basic reproduction number for our considered system and is given by

$$\mathcal{R}_0 = \frac{l_2\rho\sigma\tau\psi + l_3\rho(1-\tau)\psi}{l_1l_2l_3}.$$

3 Stability results

In the following, the stability analysis for the considered system (2) at the disease-free equilibrium E_0 is carried out.

Theorem 1 *The system (2) at the disease-free case E_0 is locally asymptotically stable whenever $\mathcal{R}_0 < 1$.*

Proof Computing the Jacobian at the disease-free case E_0 is given by

$$J(E_0) = \begin{pmatrix} -\omega & 0 & -\rho & -\rho\sigma & 0 \\ 0 & -l_1 & \rho & \rho\sigma & 0 \\ 0 & (1-\tau)\psi & -l_2 & 0 & 0 \\ 0 & \tau\psi & 0 & -l_3 & 0 \\ 0 & 0 & \nu & 0 & -l_4 \end{pmatrix}.$$

We get easily the two roots $-\omega$ and $-l_4$. The remaining eigenvalues containing negative real parts can be determined through the equations given by

$$\lambda^3 + f_1\lambda^2 + f_2\lambda + f_3 = 0, \tag{8}$$

where

$$f_1 = l_1 + l_2 + l_3,$$

$$f_2 = l_2l_3 + l_1(l_2 + l_3) + \rho\psi(-\sigma\tau + \tau - 1),$$

$$f_3 = l_1l_2l_3(1 - \mathcal{R}_0).$$

It can be observed that f_i for $i = 1, 2, 3$ are positive whenever $\mathcal{R}_0 < 1$, and furthermore, it can be obtained easily the conditions of Routh–Hurwitz criteria, $f_i > 0$ and $f_1f_2 - f_3 > 0$, for $i = 1, 2, 3$. Therefore, it can be concluded that the system given in (2) at E_0 when $\mathcal{R}_0 < 1$ is locally asymptotically stable. \square

We state and prove the following theorem to show that the system (2) at E_0 is globally asymptotically stable.

Theorem 2 *The system (2) at E_0 is locally asymptotically if $\mathcal{R}_0 \leq 1$.*

Proof Define the Lyapunov function given by

$$\mathcal{L}(t) = \xi_1E(t) + \xi_2I(t) + \xi_3A(t), \tag{9}$$

where $\xi_m > 0$ for $m = 1, 2, 3, 4$, that can be adjusted their values at later stage. Taking $\frac{d}{dt}$ of \mathcal{L} , we have

$$\mathcal{L}'(t) = \xi_1E' + \xi_2I' + \xi_3A'. \tag{10}$$

Using the equations from (2) and making some setting, we have

$$\begin{aligned} \mathcal{L}'(t) &= \xi_1\left[\rho(I + \sigma A)\frac{S}{N} - l_1E\right] \\ &\quad + \xi_2[\psi(1-\tau)E - l_2I] + \xi_3[\psi\tau E - l_3A], \\ &= [\xi_2\psi(1-\tau) + \xi_3\psi\tau - l_1\xi_1]E + [l_1\rho - l_2\xi_2]I \\ &\quad + [\xi_1\sigma\rho - l_3\xi_3]A. \end{aligned} \tag{11}$$

Let us consider the values for the constants ξ_1, ξ_2 , and ξ_3 . We choose as follows: $\xi_1 = l_2, \xi_3 = \rho$, and $\xi_3 = \rho\sigma l_2/l_3$. Then, we have the following results finally:

$$\mathcal{L}'(t) = -l_1 l_2 [1 - \mathcal{R}_0] E. \tag{12}$$

Here, $\mathcal{R}_0 < 1$, and so, we have $\mathcal{L}'(t)$ is negative and so the model (2) is globally asymptotically stable at E_0 . \square

3.1 Endemic equilibria

Here, we present and obtain the endemic equilibria of the system (2) by describing its endemic equilibrium by $E_1 = (S^*, E^*, I^*, A^*, H^*)$, and so, we have the below

$$\begin{cases} S^* = \frac{\Pi}{\lambda^* + \omega} \\ E^* = \frac{\lambda^* S^*}{l_1} \\ I^* = \frac{(1-\tau)\psi E^*}{l_2} \\ A^* = \frac{e\tau\psi}{l_3}, \\ R^* = \frac{\nu I^*}{l_4}. \end{cases}$$

Consider the above values in the following equation:

$$\lambda^* = \frac{\rho(I^* + \tau A^*)}{N^*}, \tag{13}$$

getting the following:

$$\Phi_1 I^* + \Phi_2 = 0,$$

where

$$\begin{aligned} \Phi_1 &= l_3(1 - \tau)\psi(l_4 + \nu) + l_2 l_4(l_3 + \tau\psi), \\ \Phi_2 &= l_1 l_2 l_3 l_4(1 - \mathcal{R}_0). \end{aligned}$$

We can see that $\Phi_1 > 0$, while Φ_2 can be positive depending on the value of \mathcal{R}_0 . When $\mathcal{R}_0 < 1$, so we getting $I^* = -\Phi_2/\Phi_1$, and thus, there is no equilibria. The requirements for the positive endemic equilibria are

to have $\mathcal{R}_0 > 1$, and hence, for the system (2), a unique positive endemic equilibrium exists.

4 Estimations of the parameters

To understand effectively the dynamics of an epidemic model, it is necessary or useful to have the real data to demonstrate the model parameters and to obtain reasonable results for the epidemic model. In this regard, we consider the cases from March 06, 2021, till April 30, 2021 for the finding of parameter values; we can refer the readers for the real data [49]. The population of Pakistan considered here is $N(0) = 220000000$, and we estimate the parameters Π and ω as follows: $\Pi \approx 8903$ per day using the expression $N(0) = \Pi/\omega$, and $\omega = 1/(67.7 \times 365)$, where $\omega = 1/(67.7)$ is the average life span in Pakistan. The parameters other than these can be obtained through the model data fitting. The data considered in this paper from March 06, 2021 to April 30, 2021. We use the curve fitting technique to get the values of the parameters, as shown in Table 1, and the possible fitting of the model to the data is shown in Fig. 1a with the estimated basic reproduction number $\mathcal{R}_0 \approx 1.2036$. Figure 1b describes the behavior of the model versus data for long time level. It follows from Fig. 1(a) that the model behaves good to the real cases. Thus, the model parameters considered in Table 1 are realistic and can better study the dynamics of the COVID-19 infection.

5 Numerical results

Here, we consider the system (2) with the consideration of the cases reported from March to the end of April in Pakistan to understand the parameters impact on the model. The cases consider here are in daily basis, so the time unit is to be *per day*. In numerical results, we consider the parameters values shown in Table 1. We

Table 1 Estimated parameters

Symbol	Definition	Value/per day	Source
Π	Recruitment rate	$\omega \times N(0)$	Estimated
ω	Natural death rate	$\frac{1}{67.7 \times 365}$	[50]
ρ	Disease contact rate	0.9549	[51]
σ	Disease contact of A	0.9635	[51]
ψ	Incubation period	0.7961	Fitted
ω_0	Disease death rate of exposed people	0.0126	[51]
ω_3	Death due to infection at H	0.04	Fitted
τ	Progress to asymptomatic infection	0.9635	Fitted
ω_1	Death due to infection at I	0.0010	[51]
γ_1	Recovery of symptomatic people	0.1456	[51]
ω_2	Disease death of asymptomatic people	0.0069	[51]
γ_2	Recovery of asymptomatic people	0.8666	[51]
ν	Hospitalization rate of symptomatic people	0.021	Fitted

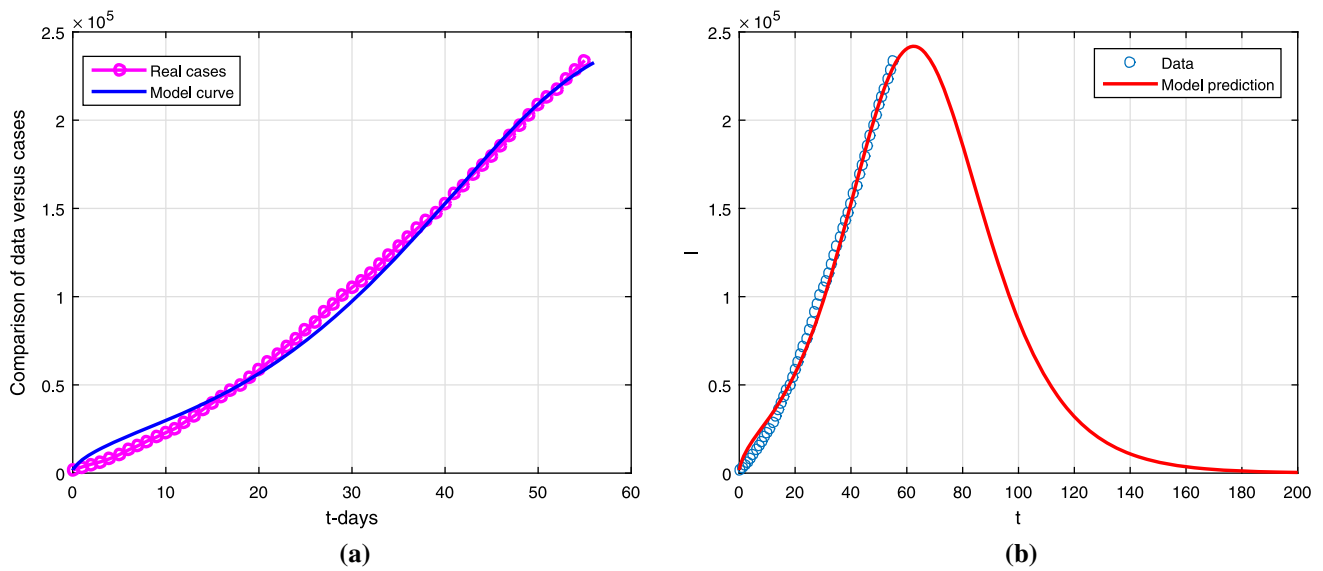


Fig. 1 a Reported cases versus model prediction. b Long time behavior of model versus cases

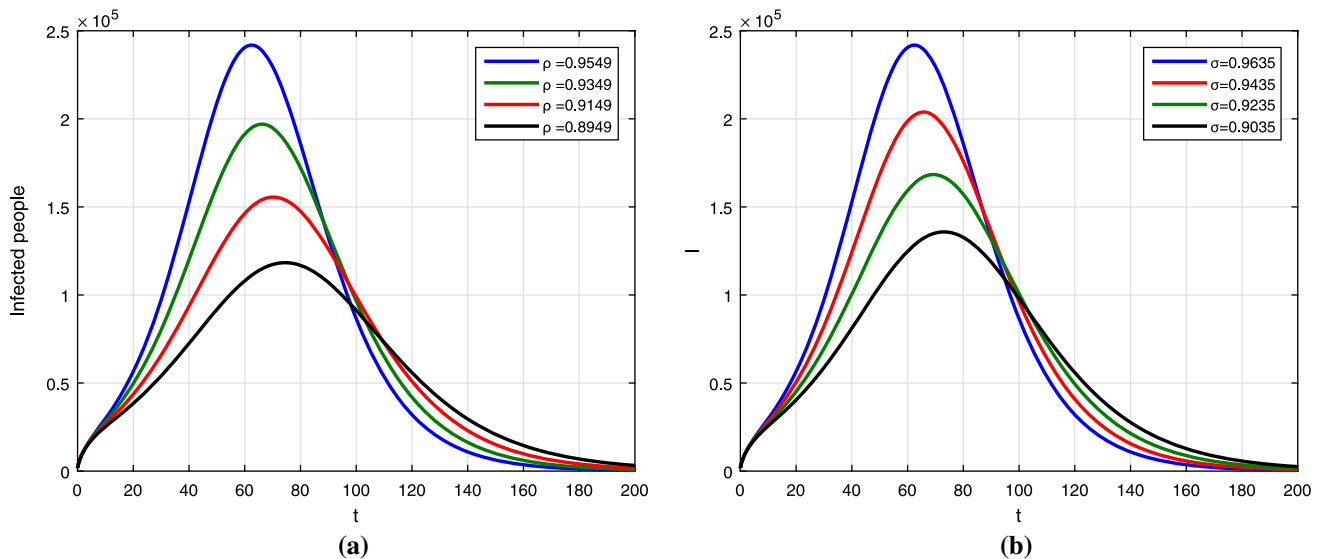


Fig. 2 a ρ with different values; b σ with different values

estimate the initial values of the model (2) is as follows: $S(0) = 219698286$, $E(0) = 300000$, $I(0) = 1714$, while assuming that there is no recovery from the infection yet and so $R(0) = 0$, and no enough information about the asymptomatic and hospitalized data, so we consider $A(0) = H(0) = 0$. We consider the disease contact rate ρ and σ with different values on the dynamics of infected people shown in Fig. 2. In Fig. 2a, we see when decreasing the value of ρ , the number of infected people decreases faster. It can be concluded that the prevention from the infection using the instructions suggested by World Health organization should follow to decrease the disease burden from the populations. Washing hands, social distances, using masks, avoid gathering, self-quarantine, and restrictions to home can better reduce the infection. In Fig. 2b, one can see that

the infection decreases when decreasing the value of σ . The parameter σ that denotes the contacts of healthy people with asymptomatic infected people (individuals do not show clinical symptoms) can decrease the infection risk in the population. It should be noted that asymptomatic infected does not show visible disease symptoms and can increase the infection. It is documented that the number of infected individuals due to COVID-19 has a high percentage of infection due to asymptomatic infection. Therefore, it is important for the government to make increase the testing facility to identify the number of asymptomatic infected people. The impact of the parameters ψ , τ and ν has been shown graphically in Fig. 3. Decreasing the values of these parameters, we have a decrease in the number of infected people.

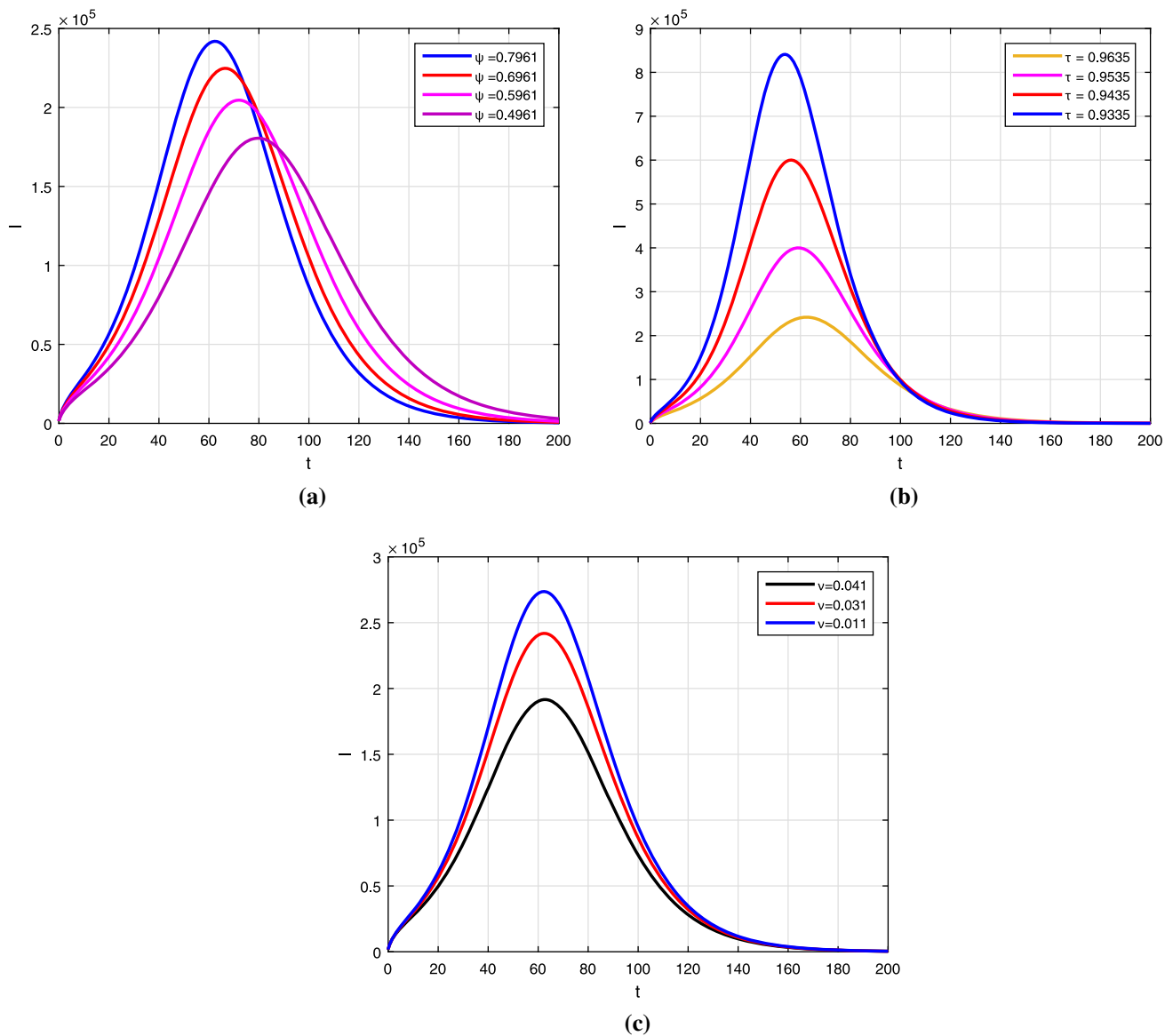


Fig. 3 **a** ψ with different values, **b** τ with different values, and **c** τ with different values

6 Variable-order fractional model of SARS-CoV-2 dynamic

It has been shown in the literature that fractional calculus is able to produce more accurate results in modeling natural systems and processes. As a result, in this part, we present a novel variable-order fractional model of SARS-CoV-2 dynamics in Pakistan. Also, we consider an additional component, namely, hospitalized people (H). The fractional model with variable order is given as follows:

$$\begin{aligned}
 {}_0^c D_t^{q(t)} S &= \Pi - \rho(I + \sigma A) \frac{S}{N} - \omega S \\
 {}_0^c D_t^{q(t)} E &= \rho(I + \sigma A) \frac{S}{N} - (\psi + \omega + \omega_0) E \\
 {}_0^c D_t^{q(t)} I &= \psi(1 - \tau) E - (\omega + \omega_1 + \gamma_1 + \nu) I \quad (14)
 \end{aligned}$$

$$\begin{aligned}
 {}_0^c D_t^{q(t)} A &= \psi \tau E - (\omega + \omega_2 + \gamma_2) A \\
 {}_0^c D_t^{q(t)} H &= \nu I - (\gamma_3 + \omega_3 + \omega) H \\
 {}_0^c D_t^{q(t)} H &= \gamma_1 I + \gamma_2 A + \gamma_3 H - \omega R.
 \end{aligned}$$

γ_H is the recovery rate of quarantined infected individuals and δ_I is the rate of symptomatic infected individual's transition to the quarantined infected component. Also, $q(t)$ indicates the time-varying fractional-order derivative. In this study, the Caputo fractional derivative based on the predictor–corrector method is applied for numerical calculations of the fractional model. It is one of the most widely used methods for analyzing fractional differential equations in a chaotic manner (see [52, 53] for more details on the predictor–corrector method). To investigate the effects of the time-varying fractional derivative, we present the results of the model with two different fractional derivatives. Figure 4 shows

Fig. 4 The number of individuals when $q_1(t) = 0.9$ and $q(t) = 0.9 + \frac{0.1}{1+exp(-t)}$

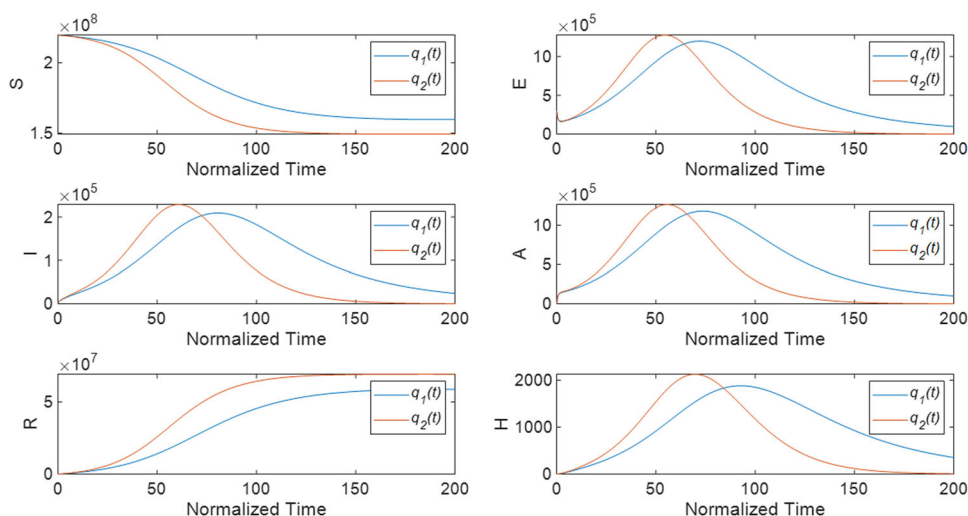


Table 2 Parameters of genetic algorithm

Parameter	Value
Crossover fraction	0.75
Population size	90
Selection function	Tournament
Mutation function	Constraint-dependent
Crossover function	Intermediate
Migration direction	Forward
Migration fraction	0.3
Migration interval	30
Stopping criteria	40000

the number of individuals when $q_1(t) = 0.9$ and $q(t) = 0.9 + \frac{0.1}{1+exp(-t)}$. As it is evident from this figure, when the value of fractional derivative varies by time, the results are different, and it can dramatically affect the behavior of the model.

6.1 Optimal decision rules

Herein, we propose a genetic optimization approach to find optimal decision rules. Genetic optimization is an appropriate technique to handle such problems, since there is a trade-off between all possible values. Table 3 lists the parameters and configuration of the applied multi-objective genetic algorithm. The fractional-order derivative is considered to vary over time as $q(t) = 0.9 + \frac{0.1}{t+1}$.

We consider δ_I as the decision variable. The following is the cost functions that have been chosen:

$$J = \sum E(t) + I(t) + A(t). \tag{15}$$

We have chosen this cost function to reduce the accumulated infected people. In what follows the results of the optimization are provided.

Figure 5 shows the value of the cost function from the genetic algorithm optimization. As it is shown in this figure, we could choose the optimal controllers, which

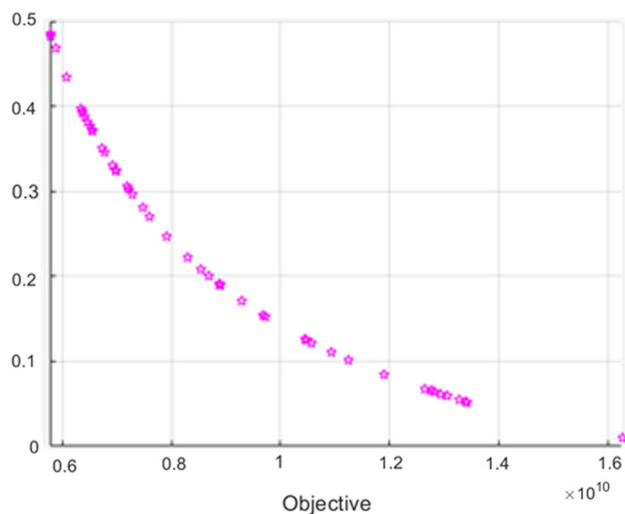


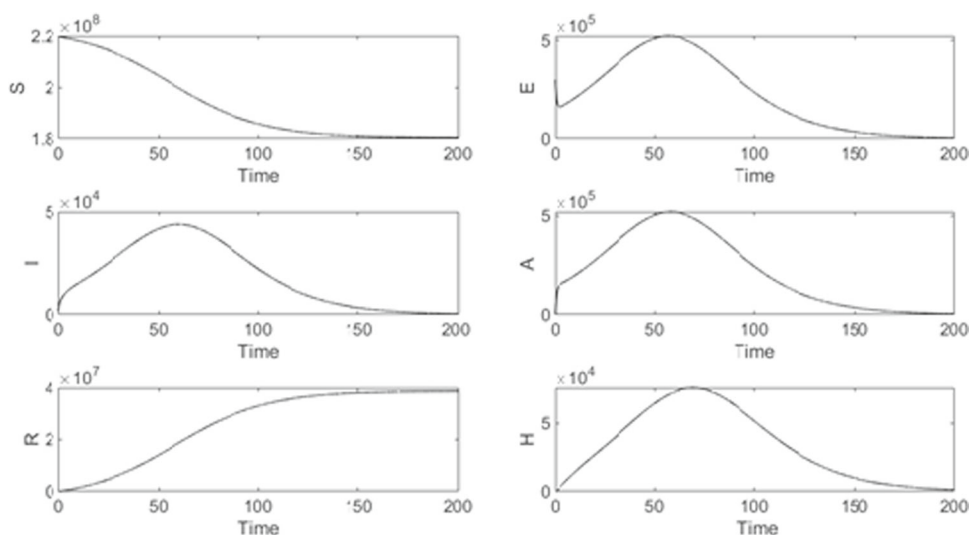
Fig. 5 Objective function

effectively reduce both cost functions. Herein, we chose $\delta_I = 0.18$ as the optimal value for the control purpose. The time histories of individuals are illustrated in Fig. 6. As can be seen, the maximum number of infected people has decreased when compared to the case where no optimal control effort was made. Also, the decreasing rate of infectious people is noticeably quicker.

7 Conclusion

Here, in the present investigation, an attempt has been made to study a new mathematical model for the dynamics of novel coronavirus. We first formulated a new mathematical model for the better understanding of the virus by considering the hospitalized class. After formulation the model, we presented in details the model analysis for the integer-order case and obtained the stability results in detailed. We found the local and global asymptotical stability of the model when $\mathcal{R}_0 < 1$.

Fig. 6 The number of individuals with optimal control



Furthermore, we estimated the parameters using the real cases of coronavirus from Pakistan and obtained the results for the data fitting. The realistic parameters for the considered data gave the basic reproduction number $\mathcal{R}_0 = 1.2036$. Using further parameter values, some graphical results are obtained that indicate the infection can be minimized by following the reduction in contact rate, asymptomatic contact, rapid testing of individuals to isolate the individuals with no clinical symptoms. The numerical results for the integer cases can be useful for the minimization of infection by following the suggestions given in figures in numerical results section. Finally, a variable-order fractional model of SARS-CoV-2 in Pakistan was introduced. Then, through an evolutionary algorithm, the control of the variable-order fraction model was studied. Through numerical simulations, it was shown that using the proposed optimal strategy, the number of infected people has decreased significantly, and the third wave is controlled more efficiently.

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Data availability statement This manuscript has associated data in a data repository. [Authors' comment: The data is available from the corresponding author on a reasonable request.]

Declarations

Conflicts of interest No conflicts of interest exist regarding the publishing of this work.

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