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Mathematical modelling of COVID-19 pandemic in Pakistan with optimal control

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ABSTRACT

We propose an innovative mathematical modeling to examine the previous coronavirus disease of 2019 pandemic or (COVID-19). This analysis has been performed qualitatively through differential equation stability theory, as well as the basic reproductive value, which indicates a pandemic index, then calculated from the maximum eigenvalue of the subsequent matrix. We establish the global asymptotic stability criteria for such disease-free state. The actual COVID-19 occurrence documents and data from 01 July, 2021 to 14 August, 2022 in Pakistan are analyzed for estimation methods, leading in fitted values for biological parameters. Sensitivity analyzation is used to identify the much more relevant attributes in the developed framework. This scientific research revealed a deterministic computational formula that assesses the impact of various mitigation measures on the propagation of COVID-19 in a worldwide population. The analysis will concentrate on Pakistan, and relevant data gathered out of that region. If the method were modified for the total number of COVID-19 reported patients as well as the total number of active patients in the Pakistan region, infection rates would be approximated fairly. This research will in some way give government authorities including local hospitals additional knowledge about how to enhance precautionary efforts to minimize infection propagation.

Contribution/Originality: We have in this regard proposed a novel mathematical model to better comprehend the transmission patterns of the frightening contemporary epidemic identified as COVID-19. The global stability of the free illness equilibrium, the fundamental reproduction number, the equilibrium state, and the invariant region are only a few of the critical innovative model elements that have been studied in the current study endeavor. The study's conclusions will serve as a roadmap for the government's decision-makers as they take safety precautions to lower the danger of infection.

1. INTRODUCTION

COVID-19 is a condition caused by a Severe Acute Respiratory Syndrome. COVID-19 was discovered as a consequence of a respiratory infection epidemic in Wuhan City, Hubei, China [1]. The report had first been submitted to the "World Health Organization" (WHO) on December 31, 2019. On January 30, 2020, the (WHO) declared the COVID-19 outbreak a worldwide health concern. COVID-19 is spread from one individual to another by direct exposure to contaminated surfaces as well as breathing respiratory drops by people with the disease [2]. Typically, individuals diagnosed with the COVID-19 virus might experience minor to serious breathing sickness and therefore survive without any additional therapy [3]. Serious sickness is more common in the elderly and individuals with preexisting medical disorders including such heart disease, diabetes, respiratory disease, and cancer [4]. COVID-19 may survive on a surface for weeks or months depending on conditions including sunshine, heat, as well as surface type. COVID-19 can be contracted by contacting a virus-infected surface and afterwards contacting one's own face [5]. Unfortunately, this is not considered to be the only way the disease mutates. Outside the house, socially isolation serves to reduce the possibilities of coming into contact with contaminated objects but also infectious persons [6]. Meanwhile, there are numerous ongoing new treatments investigating alternative therapies [7]. In order to significantly reduce COVID-19 spread, government agencies introduced numerous countermeasures such as strict and mandatory shutdowns, as well as social distancing, the prevention of populated gatherings, and the adoption of surgical masks [8]. Despite the reality that the federal government has implemented a variety of monitoring efforts [9]. Contact tracking of identified people with the disease has been increased throughout numerous countries to assist in the control of COVID-19 [10] while reported incidents are swiftly isolated for medical treatment [11]. The virus was initially identified in Pakistan on February 26th, 2020, while two cases had been reported: a teenager who had recently come from Iran and another individual in the Islamabad [12]. Cases of COVID-19 were reported in all Pakistan's four provinces on March 18, 2020, and therefore by June 17, 2020, every region in Pakistan had at least single verified patient of COVID-19. Pakistan had recorded 324,077 patients of COVID-19 as of 10 October, 2020, including 6673 casualties, 9384 active patients, as well as 308,020 cured patients. In this technique, it's really feasible to predict the conclusion of an epidemic, which is very advantageous for public healthcare provision. According to Ngonghala, et al. [13] the complex dynamics of epidemic phenomena may be investigated adopting compartmental modeling as a fundamental mathematical approach. Conceptual assumptions serve as the foundation for understanding how these two segments relate [14] so that the frameworks are developed. Ordinary differential equations (ODE's) having generally been examined to build these models. Additional populations, represented by R, that represents a description of the immune/ removed/ recovered segment, are however taken into consideration to make such models more efficient [15].

It's also commonly acknowledged that mathematical models may be used to forecast the development of contagious diseases. A significant aspect is that, proper parameters for the particular diagnosis under examination must be gathered but also applied to analyze the impact of potential preventive actions, including treatment or immunization. The issue then becomes how to integrate such measurements in an optimized way. Several significant efforts have recently been taken to adopt latest research using various sorts of integer compartmental systems [16]. Numerous mathematical and non-mathematical observations on COVID-19 have also been demonstrated by the most related research. This research paper recommends a deterministic mathematical model which evaluates the influence of various strategies on the transmission of COVID-19 in a global population; the research will concentrate on the conditions in Pakistan, relevant figures from that state will be collected. The approach would offer a reasonable approximation infection rates if adjusted with the overall number of reported patients in COVID-19 as well as the number of active patients throughout Pakistan region. We anticipate that somehow this research would provide authorities and community healthcare more information regarding how to strengthen non - pharmaceutical preventative activities to reduce illness transmission.

2. MODEL FORMULATION

The model under discussion splits the human population at time step (t) into five sections. This includes recovered R(t). infected I(t), quarantine Q(t), susceptible S(t) and exposed E(t). We expected that infants might be contaminated with the infection which induces COVID-19 after labor or after being exposed to sick caretakers. As a result, the susceptible category is recruited at a rate of θ either childbirth or immigration. The rate of progression of people exposed to sick group is ω. Persons within each of the groups have a chance of dying naturally at the rate μ.

We therefore considered overall recovery against COVID-19 doesn't really give long - lasting immunity, thus recovered people might be categorized as vulnerable at a rate σ. The number of sick and quarantined people is decreased as an outcome of COVID-19-related issues at the rate of δ, τ and ϕ reflect the treatment rates of infected as well as quarantined people, accordingly. The force of infection is depicted in Equation 1.

$$\lambda = \frac{\alpha_c(1-\Psi)(1-\nu)(E+I)S}{N(t)} \tag{1}$$

In Equation 1 Ψ is the fraction of people who establish social distance to avoid the transmission of COVID-19, and this is represented by the inequality $0 \le \psi \le 1$. Furthermore, reflects a proportion of the overall population who utilizes a surgical mask or sanitizers. We considered that wearing a surgical mask while using sanitizer seem to be incredibly efficient while being in public places, such that $0 \le \nu \le 1$. Taking the preceding statements but also hypotheses collectively yields the COVID-19 framework, which is described by the system of ordinary differential equations here below:

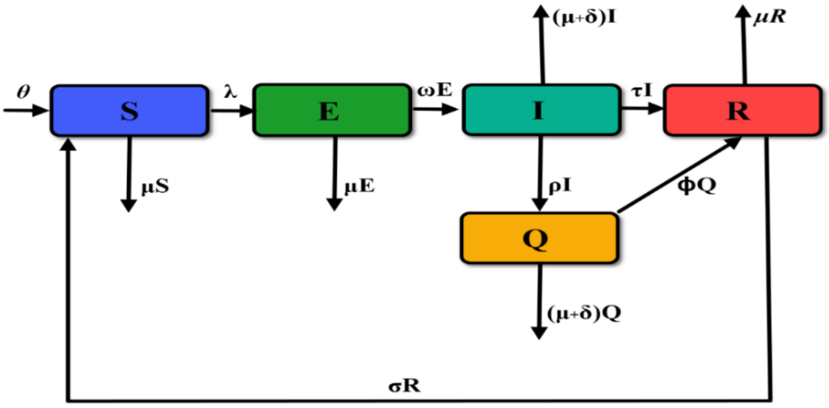


Figure 1. The suggested COVID-19 model's schematic illustration.

Table 1. Comprehensive explanation of the suggested COVID-19 model's state variables including related parameters.

Variables	Description
S(t)	Susceptible category
E(t)	Exposed category
I(t)	Infected category
Q(t)	Quarantine category
R(t)	Recovered category
θ	Susceptible category recruited rate
μ	Natural rate of death
δ	COVID-19 proportion of deaths
ω	Progression rate from infected category exposed
σ	Immunity decline rate
τ	Treatment rate of infected people
ϕ	Quarantine patients' treatment rate
ψ	Proportion of people establish social isolation
ν	A fraction of the population wears a surgical mask with sanitizers.
ρ	Recovery time after illness
α_c	Rate of transmission efficiency

$$\frac{dS}{dt} = \theta - \mu S + \sigma R - \frac{S\alpha_c(1-\nu)(E+I)(1-\Psi)}{N(t)}$$

$$\frac{dE}{dt} = -\mu E - \omega E + \frac{S\alpha_c(1-\nu)(E+I)(1-\Psi)}{N(t)}$$

$$\frac{dI}{dt} = \omega E - I(\delta + \mu + \tau + \rho) \qquad (2)$$

$$\frac{dQ}{dt} = \rho I - (\phi + \mu + \delta)$$

$$\frac{dR}{dt} = \phi Q + \tau I - (\sigma + \mu)R$$

Equation 2 depicts the rate of infection clearly. The suggested COVID-19 model's schematic illustration and Comprehensive explanation of state variables including related parameters are effectively illustrated in Figure 1 and Table 1.

3. MODELING ASSESSMENT

3.1. The Zone of Invariance

The invariant zone determines the region wherein modeling responses are very much biologically and mathematically significant. The model's parameters and variables have all been expected to be non-negative. To a certain purpose, we determined that M(t) is the total human population.

Where, M(t) = R(t) + Q(t) + I(t) + E(t) + S(t).

We get the following simply differentiating with respect to t on both sides:

$$\frac{dM}{dt} = \frac{dR}{dt} + \frac{dQ}{dt} + \frac{dI}{dt} + \frac{dE}{dt} + \frac{dS}{dt}$$

We obtain, after simplifying:

$$\frac{dM}{dt} = \theta - \delta I - \delta Q - \mu S - \mu E - \mu I - \mu Q - \mu R$$

Hence,

$$\frac{dM}{dt} = \theta - \delta I - \delta Q - \mu M$$

In a case of absence of COVID-19 proportion of death is equal to zero, then the subsequent expression is:

$$\frac{dM}{dt} = \theta - \mu M \qquad (3)$$

Equation 3 depicts the rate of human population. Integrating on both sides of Equation 3 leads to the following result:

$$\int \frac{dM}{\theta - \mu M} \leq \int dt$$

$$\frac{-1}{\mu}\ln(\theta - \mu M) \leq t + c \qquad (4)$$

$$\theta - \mu M \geq Be^{-\mu t} \qquad (5)$$

$$M_h \leq \frac{\theta}{\mu} + \frac{\mu M_h e^{-\mu t} - \theta e^{-\mu t}}{\mu} \qquad (6)$$

Equation 4 is the integrated form and the initial condition M = M(0) and B being a constant with the initial condition as shown in Equation 5.

So t→ ∞ as shown in Equation 6, we get: $M_h \leq \frac{\theta}{\mu}$

As a result, the reasonable option in Equation 7 establishes P for the entire population in Equation 2.

$$P = \left\{(R, Q, I, E, S) \in \mathbb{R}_+^5 : M_h \leq \frac{\theta}{\mu}\right\} \qquad (7)$$

As a result, the suggested COVID-19 model is well stated and holds both epidemiological and mathematical significance. This makes it essential to investigate the dynamics of the fundamental model in domain P.

3.2. The Basic Reproductive Proportion ($\mathcal{R}$)

The basic reproducing proportion would be a baseline measurement in epidemiology which reflects the overall number of associated illnesses produced by a single infection patient in a completely vulnerable community throughout an infectious phase. F and V represent the matrices generated for the new disease and also the condition of sickness transformation.

$$\mathcal{F}(x) = \begin{pmatrix} S\alpha_c(1-\nu)(E+I)(1-\Psi) \\ \omega E \\ \rho I \end{pmatrix}$$

$$\boldsymbol{\mathcal{V}(x)} = \begin{pmatrix} \mu E + \omega E \\ I(\delta + \mu + \tau + \rho) \\ Q(\delta + \mu + \phi) \end{pmatrix}$$

At the COVID-19 free stability, the Jacobian matrix for $\mathcal{F}$ and $\mathcal{V}$ is given as F and V so as

$$F = \begin{pmatrix} S\alpha_c(1-\nu)(1-\Psi) & \alpha_c(1-\nu)(1-\Psi) & 0 \\ \omega & 0 & 0 \\ 0 & \rho & 0 \end{pmatrix}$$

$$V = \begin{pmatrix} \mu + \omega & 0 & 0 \\ 0 & \delta + \mu + \tau + \rho & 0 \\ 0 & 0 & \delta + \mu + \phi \end{pmatrix}$$

$$V^{-1} = \begin{pmatrix} \dfrac{1}{\mu + \omega} & 0 & 0 \\ 0 & \dfrac{1}{\delta + \mu + \tau + \rho} & 0 \\ 0 & 0 & \dfrac{1}{\delta + \mu + \phi} \end{pmatrix}$$

The fundamental reproduction number is determined by the spectral radius of the matrix FV^{-1}.

Table 2. Genuine incidents for 45 days throughout Pakistan during 2020. The first row of each cell represents actual incidents, the second row comprises anticipated data from the suggested system's simulated for such infecting group, while the last row displays absolute percentile errors between observed information and forecast data.

(1)	**(2)**	**(3)**	**(4)**	**(5)**	**(6)**	**(7)**	**(8)**	**(9)**
2289	2450	2708	2880	3287	3864	4970	4317	4598
2289	2746	2985	3195	3412	3642	3888	4150	4429
0	10.8	9.3	9.9	3.7	6.2	4.7	4.1	3.9
(10)	(11)	(12)	(13)	(14)	(15)	(16)	(17)	(18)
4784	5038	5374	5716	5985	6528	7016	7479	7993
4728	5046	5385	5746	6132	6543	6982	7450	7947
1.30	0.15	0.20	0.52	2.40	0.23	0.50	0.40	0.60
(19)	(20)	(21)	(22)	(23)	(24)	(25)	(26)	(27)
8420	9216	9771	10513	11155	11940	12723	13328	14079
8477	9043	9643	10282	10963	11686	12451	13266	14130
0.70	2.0	1.40	2.30	1.80	2.21	2.21	0.48	0.36
(28)	(29)	(30)	(31)	(32)	(33)	(34)	(35)	(36)
14885	15827	16817	18114	19103	20186	21501	22550	24073
15043	16011	17035	18116	19254	20454	21714	23036	24419
1.10	1.20	1.28	0.004	0.79	1.31	0.98	2.20	1.50
(37)	(38)	(39)	(40)	(41)	(42)	(43)	(44)	(45)
25837	27474	29465	30941	32081	34336	35788	37218	38799
25862	27364	28925	30534	32190	33895	35626	37378	39147
0.092	0.41	1.90	1.34	0.40	1.31	0.51	0.43	0.91

Table 3. The model's optimal-fit variables.

Variables	Description	Value	Source
θ	Susceptible category recruited rate	0.15	Fit
μ	Natural rate of death	0.054	Fit
δ	COVID-19 proportion of deaths	0.69	Fit
ω	Progression rate from infected category exposed	0.025	Fit
σ	Immunity decline rate	0.22	Fit
τ	Treatment rate of infected people	0.83	Fit
ϕ	Quarantine patients' treatment rate	0.005	Fit
ψ	Proportion of people establish social isolation	0.30	Fit
ν	A fraction of the population wears a surgical mask with sanitizers.	0.31	Fit
ρ	Recovery time after illness	0.18	Fit
α_c	Rate of transmission efficiency	0.29	Fit

$$\Re_0 = \frac{\alpha_c(1-\nu)(1-\Psi)(\delta+\mu+\tau+\rho+\omega)}{\mu(\mu+\omega)(\delta+\mu+\tau+\rho)} \qquad (8)$$

3.3. The Worldwide Sustainability of a Disease-Free Equilibrium Condition

Free of disease equilibrium refers to the steady state in the absence of COVID-19. This would be derived by equating Equation 2 right side to zero. Thus, the COVID-19 free equilibrium condition is discovered to be $E_0 = (S, E, I, Q, R) = (\frac{\theta}{\mu}, 0, 0, 0, 0)$.

Theorem 3.1. If $\Re_0 \leq 0$, so the COVID-19 free equilibrium $E_0 = (\frac{\theta}{\mu}, 0, 0, 0, 0)$ is stable asymptotically worldwide as in absence of pandemic. It is otherwise unstable.

Proof. The Lyapunov function has been frequently used to demonstrate the Worldwide Stability of Disease-Free Equilibrium. Consider the type of Lyapunov function that has been constructed.

$$\mathcal{L} = a_1 E + a_2 I$$

Whereas $a_1 = (\rho + \tau + \mu + \delta)$ and $a_2 = (\mu + \omega)$.

This is simple to determine that a_1 and a_2 both positive. Then let differentiate $\mathcal{L}$ in terms of time.

$$\dot{\mathcal{L}} = \dot{E}a_1 + \dot{I}a_2$$

$$\mathcal{L} = (\delta+\mu+\tau+\rho+\omega)[\alpha_c S(I+E)(1-\nu)(1-\Psi) - E(\omega+\mu)] + (\omega+\mu)[E\omega - I(\delta+\mu+\tau+\rho)] \qquad (9)$$

Computing Equation 9. We get:

$$\dot{\mathcal{L}} = [\alpha_c S(\delta+\mu+\tau+\rho+\omega)(1-\nu)(1-\Psi) - (\omega+\mu)(\delta+\mu+\tau+\rho)](I+E) \qquad (10)$$

Combine Equation 9 and Equation 10. We get:

$$\dot{\mathcal{L}} = (\delta+\mu+\tau+\rho)(\omega+\mu)(I+E)(\Re_0 - 1) \qquad (11)$$

Thus it may conclude from Equation 11 as:

$$\dot{\mathcal{L}} = 0, when\ I = E = 0$$

Thus indicates that the greatest invariance established in $(R, Q, I, E, S) \in \mathbb{R}^5_+$ seems to be the singleton Decision Feedback Equalizer (DFE) (E_0), therefore (DFE) (E_0) has been worldwide asymptotically stable in $\mathbb{R}^5_+$, according to LaSalle's Invariance Principle.

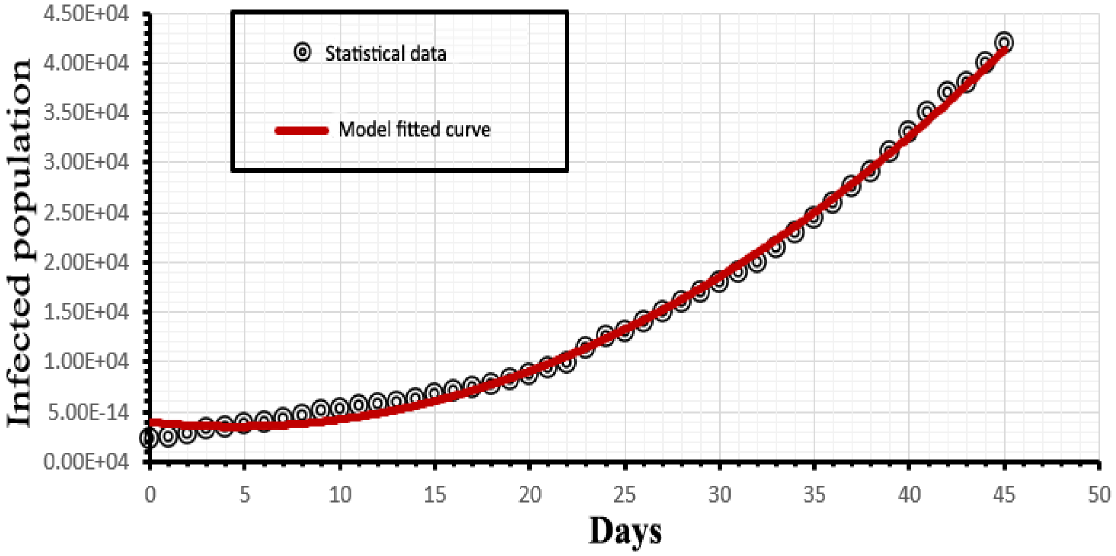


Figure 2. Ideal fit of the suggested COVID-19 prototype using actual data in Pakistan.

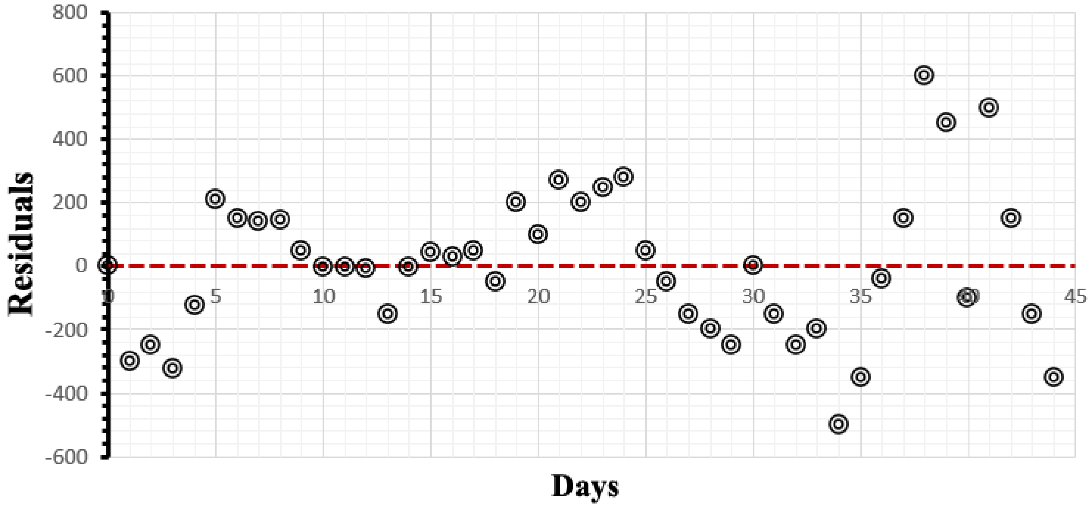


Figure 3. Corresponding residual points.

Table 4. Estimated indexes of elasticity when $\Re_0 = 4.9$ to the model variables.

Variables	Reference values	Index of elasticity
θ	0.15	Positive 1.0
μ	0.054	Negative 1.7
δ	0.69	Negative 0.006
ω	0.025	Negative 0.3
τ	0.83	Negative 0.007
ψ	0.30	Negative 0.5
ν	0.29	Negative 0.4
ρ	0.18	Negative 0.005
α_c	0.29	Positive 1.0

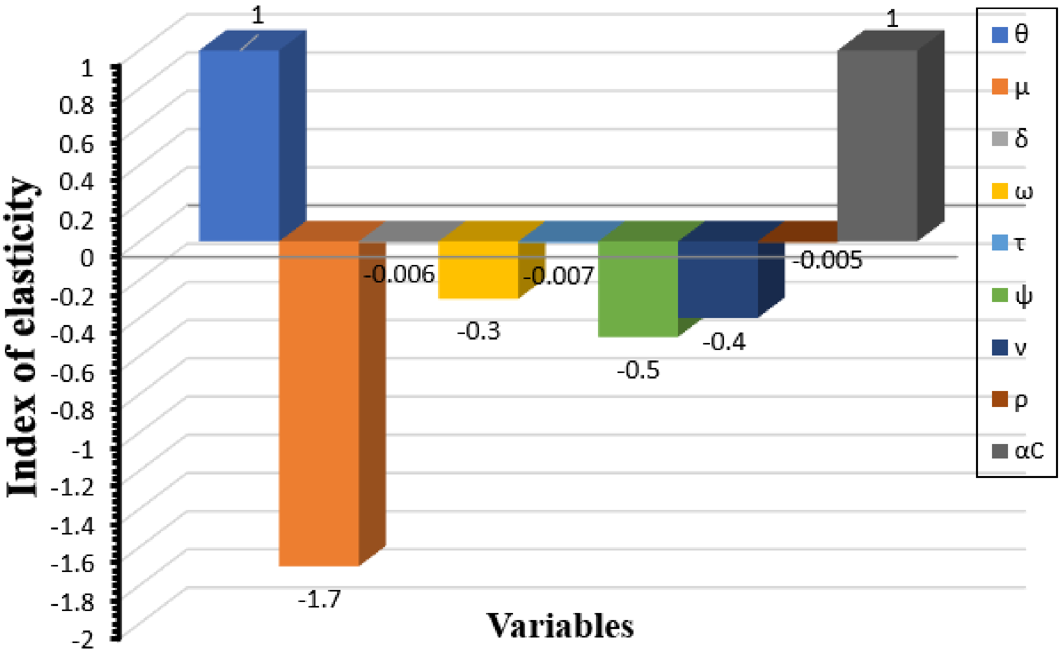


Figure 4. $\Re_0$ local sensitivity indexes normalized for each variables.

4. FIXING VARIABLES

The idea of modeling a data collection is common in practically all applicable fields of research. Checking that the information is repeated is an important step since it will make assumptions about objects connected to our dataset easier. In such a curve fitting strategy, researchers take existing dataset and try to fit it into a line or a curve. When examine the statistics for deaths cases, or hospitalizations related to the Covid-19, it has been observed that the first row of Table 2, the curve shows an increase tendency from July 1st, 2020 to August 14, 2020 throughout the Pakistani territory. There are several ways to modify the parameters of differential systems so the data can be fit easily. Typically, so it might be start with a model of the system, which could resemble an ordinary differential equation, and thereafter the data will be gathered at a specific period, such as that shown from the first rows in Table 2. This table compares actual statistics to modeling assumptions as well as absolute percentile errors. It is clear from the table that while most mistakes are quite minor, the second section suggests has the largest error, reaching in at approximately 10%. The unknown parameters of the suggested modeling, which are presented in Table 3, were obtained in the current section using a nonlinear curve fitting method. The aim was to achieve the lowest squared sum of the residuals, which is expressed as:

$$SSE = \sum_{j=1}^{n} (x_j - k(t_j))^2 \tag{12}$$

Here, respectively, x_j and $k(t_j)$ represent the observed values as well as anticipated data points derived from simulated infected component with in modeling. Hence, this aggregated data points shows the number of incidents that regularly happened in Pakistan between July 1 and August 14, 2020. While the essential regenerative rate as indicated in Equation 8 is computed as $\Re_0 = 4.90$ while applying fitted parameters given in Table 3, so it has been achieved average absolute relative error of being equivalent to around 0.023 while reaching the goal of attaining the least amount of error feasible. Furthermore, one best suitable fitted curve in contrast to actual observed data points of coronavirus instances is depicted in Figure 2, where residuals are also visually depicted in Figure 3. The graphic shows how effective the nonlinear least-squares curve fitting technique seems to be in our modeling conditions, which finally enabled us get missing key metrics for validation of the suggested coronavirus modeling, as demonstrated by Equation 2.

5. PARAMETRIC SENSITIVITIES

The idea of sensitivity method is used in this portion to assess the persistent relevance of the specified requirements identified in the unique specified reproduction number. Additionally, the numerical and analytical estimates of the different parameters in $\mathfrak{R}_0$ are calculated from reasonable hypotheses using model parameters. Unless the dynamics satisfy the model, then analytical formulas generated might be utilized to provide some information regarding how to monitor the appearance of coronavirus at various sites. $\mathfrak{R}_0$ would be a figure that is regarded to represent the essential to reducing and preventing the propagation of victimization through reducing the amount to fewer than unity. The modeling most responsive specifications are determined using the sensitivity index strategy; others with non - negative signs have been thought for being remarkably as well as substantially sensitive to elevating the value of $\mathfrak{R}_0$, whereas those having the signs of negative would be less vulnerable to reducing $\mathfrak{R}_0$, and indeed the final stage would be neutrally responsive. It is well known that the basic reproductive value $\mathfrak{R}_0$ is strongly linked to the mechanism of raping transmission. it has been calculated the following sensitivity indices for the state variables:

$$\Upsilon_{P_i}^{X_i} = \frac{\partial X_i}{\partial P_i} \times \frac{P_i}{X_i} \tag{13}$$

Here P_i are indeed the corresponding parameters in X_i, while Xi refers for the points during which the sickness occurs as shown in Equation 13. The basic reproduction number's elasticity indices to the corresponding parameters are similarly characterized as:

$$\Upsilon_{P_i}^{\mathfrak{R}_0} = \frac{\partial \mathfrak{R}_0}{\partial P_i} \times \frac{P_i}{\mathfrak{R}_0} \tag{14}$$

Here $\mathfrak{R}_0$ would be the basic reproduction factor as shown in Equation 14. As a result of several calculations, it has been observed that:

$$\begin{gathered}
\Upsilon_{\alpha_c} = Unity \\
\Upsilon_{\theta} = Unity \\
\Upsilon_{\psi} = -(1-\psi)^{-1}\psi \\
\Upsilon_{\nu} = -(1-\nu)^{-1}\nu
\end{gathered}$$

$$\begin{aligned}
\Upsilon_{\delta} &= \mu\delta(\delta+\mu+\tau+\rho)(\omega+\mu)\left(\frac{\theta\alpha_c(1-\nu)(1-\psi)}{\mu(\delta+\mu+\tau+\rho)(\omega+\mu)} - \frac{\theta\alpha_c(1-\nu)(1-\psi)(\delta+\mu+\tau+\rho+\omega)}{\mu(\delta+\mu+\tau+\rho)^2(\omega+\mu)}\right)\left(\frac{1}{\theta\alpha_c(1-\nu)(1-\psi)(\delta+\mu+\tau+\rho+\omega)}\right) \\
\Upsilon_{\rho} &= \mu\rho(\delta+\mu+\tau+\rho)(\omega+\mu)\left(\frac{\theta\alpha_c(1-\nu)(1-\psi)}{\mu(\delta+\mu+\tau+\rho)(\omega+\mu)} - \frac{\theta\alpha_c(1-\nu)(1-\psi)(\delta+\mu+\tau+\rho+\omega)}{\mu(\delta+\mu+\tau+\rho)^2(\omega+\mu)}\right)\left(\frac{1}{\theta\alpha_c(1-\nu)(1-\psi)(\delta+\mu+\tau+\rho+\omega)}\right) \\
\Upsilon_{\tau} &= \mu\tau(\delta+\mu+\tau+\rho)(\omega+\mu)\left(\frac{\theta\alpha_c(1-\nu)(1-\psi)}{\mu(\delta+\mu+\tau+\rho)(\omega+\mu)} - \frac{\theta\alpha_c(1-\nu)(1-\psi)(\delta+\mu+\tau+\rho+\omega)}{\mu(\delta+\mu+\tau+\rho)^2(\omega+\mu)}\right)\left(\frac{1}{\theta\alpha_c(1-\nu)(1-\psi)(\delta+\mu+\tau+\rho+\omega)}\right) \\
\Upsilon_{\omega} &= \mu\omega(\delta+\mu+\tau+\rho)(\omega+\mu)\left(\frac{\theta\alpha_c(1-\nu)(1-\psi)}{\mu(\delta+\mu+\tau+\rho)(\omega+\mu)} - \frac{\theta\alpha_c(1-\nu)(1-\psi)(\delta+\mu+\tau+\rho+\omega)}{\mu(\delta+\mu+\tau+\rho)^2(\omega+\mu)}\right)\left(\frac{1}{\theta\alpha_c(1-\nu)(1-\psi)(\delta+\mu+\tau+\rho+\omega)}\right)
\end{aligned} \tag{15}$$

Table 4 exhibits the numerical figures indicating the relative relevance of the $\Re_0$ factors. According to the results in Table 4, it can be demonstrated that α_c and θ have an obvious influence on the disease stability and a very comparable connection. As a result, simply raising α_c then by 1%, $\Re_0$ effect might grow by 1%. Table 4 illustrates that there are factors with such a positive association and others that have a negative association. This negative association implies as raising the levels of those parameters would contribute in reducing the COVID-19 severity. Whereas a positive association suggests that increasing the levels of such factors would have a significant impact on the frequency of the COVID-19 as a whole. Figure 4 depicts the numerical indications mentioned in Table 4. The significant factors depicted in Figure 4 permit the coronavirus to propagate rapidly.

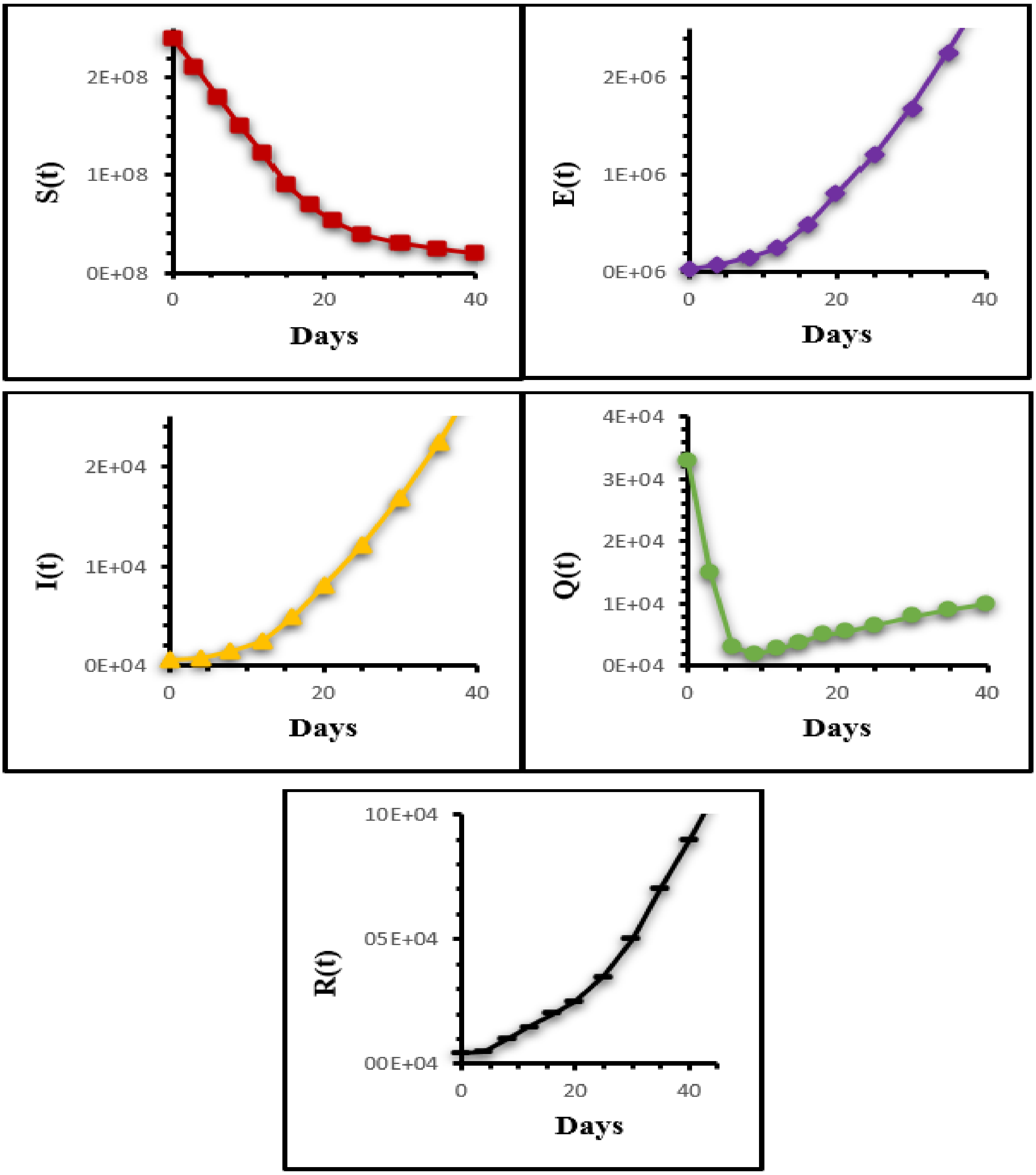


Figure 5. Each stage parameters proficiency throughout the suggested COVID-19 modeling (1) during the timeframe 0 to 45.

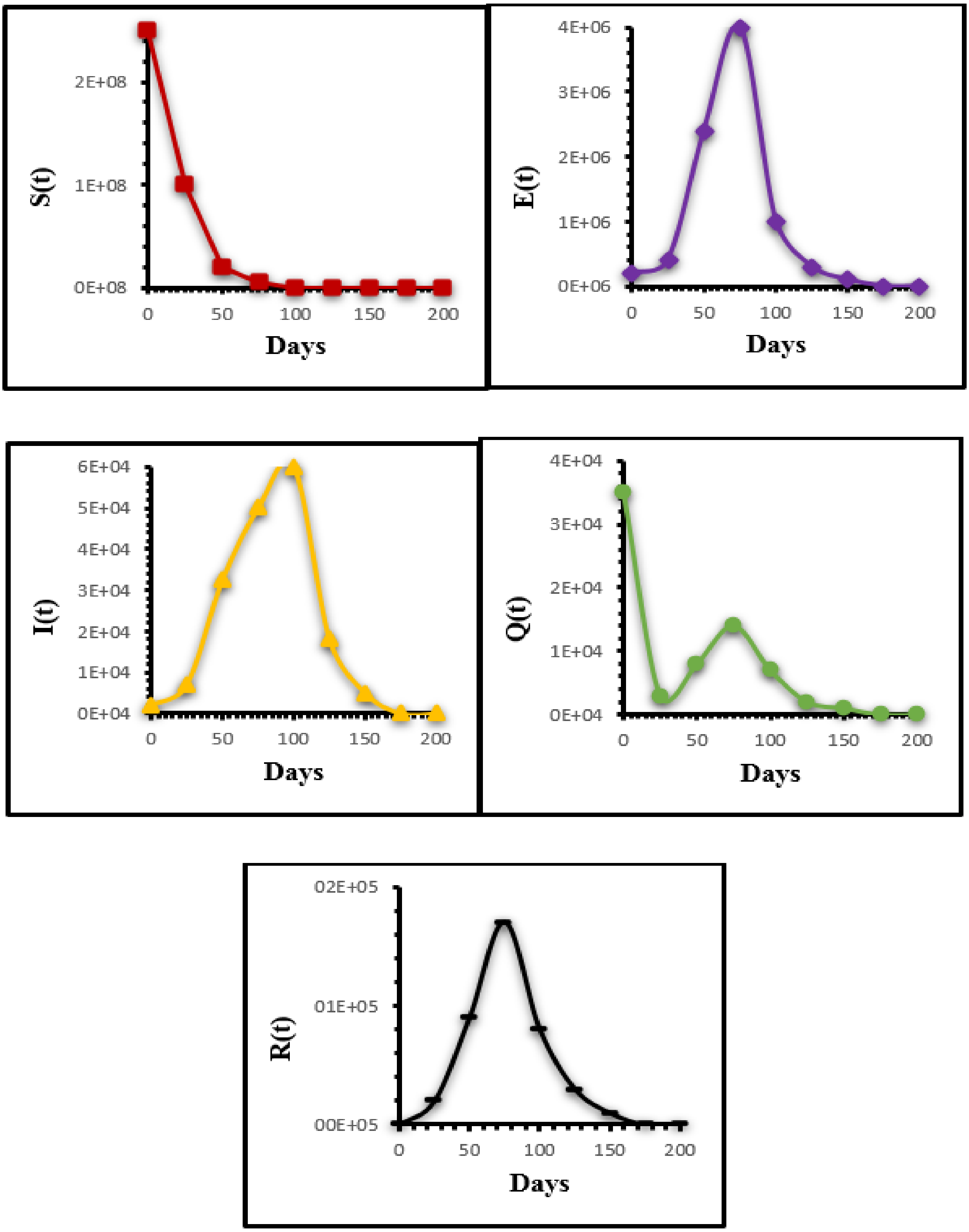
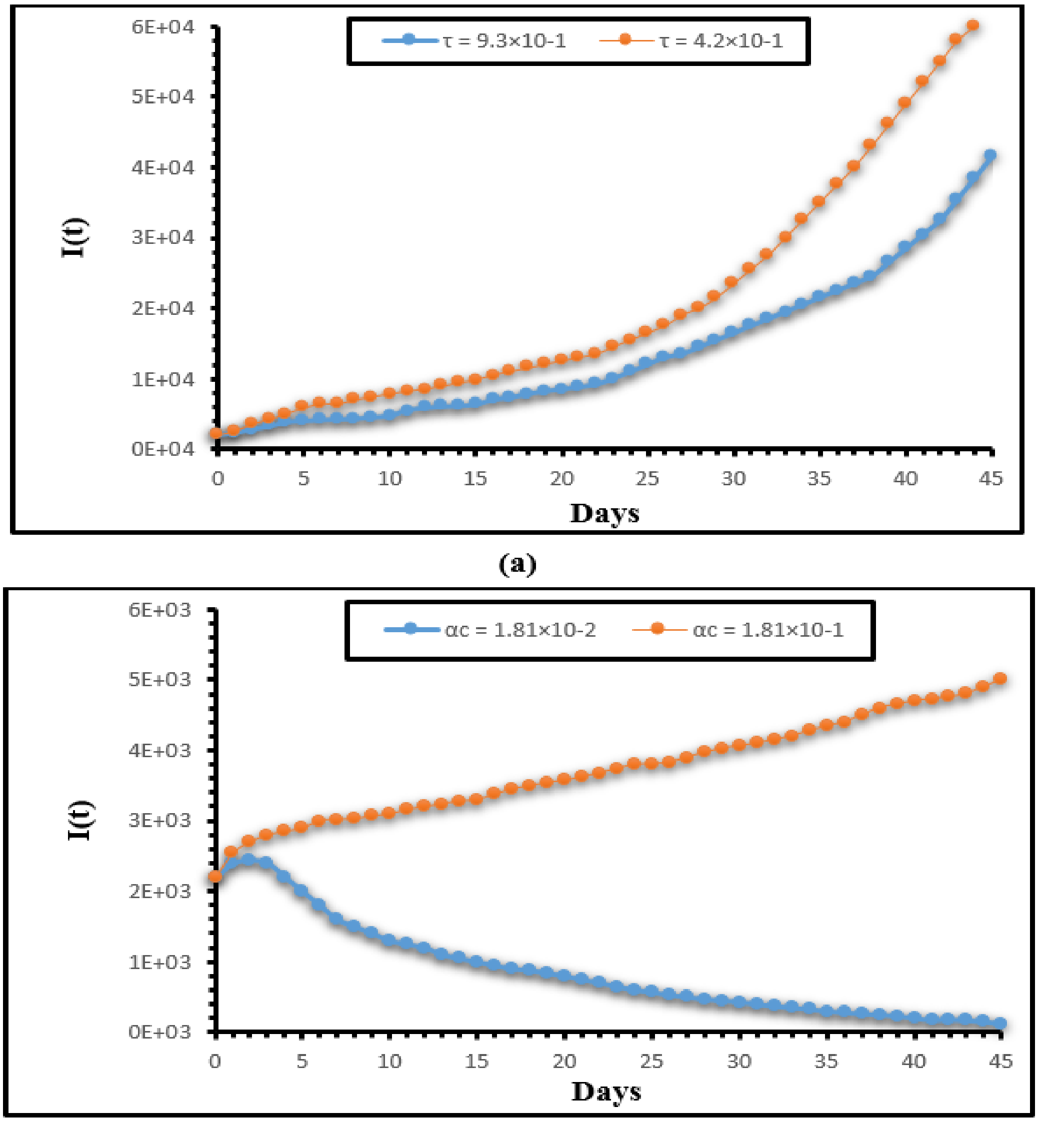


Figure 6. Each stage parameters proficiency throughout the suggested COVID-19 modeling (1) during the timeframe 0 to 45.

6. DYNAMICAL NUMERICAL ANALYSIS

In this perspective, we achieve comprehensive understanding of the model's sophisticated dynamics. The suggested modeling of state variables may be computationally simulated in a variety of ways to fully comprehend how a contagious virus spreads. In order to comprehend the complicated response of asymptomatically infected patients and thus the number of reproductive control $\Re_0$, it has been run a lot of simulations in this section. By adjusting the model parameters under the factors generated through fitting technique of nonlinear minimumsquares in Section 5, several types of time series graphs have been displayed. Additionally, the dynamics of $\mathfrak{R}_0$ are obtained for the majority of the model's major factors. Several parameters with various values are tested in the recovered R(t), quarantined Q(t), infected I(t), exposed E(t) and susceptible S(t) populations. As illustrated in Figure 5 and 6, the S(t) is dropping across the interval 0 to 44, E(t) is rising, I(t) is rising, Q(t) is dropping and R(t) is rigorously rising. Thus performance of the state variables significantly changes when the interval is modified from 0 to 200.

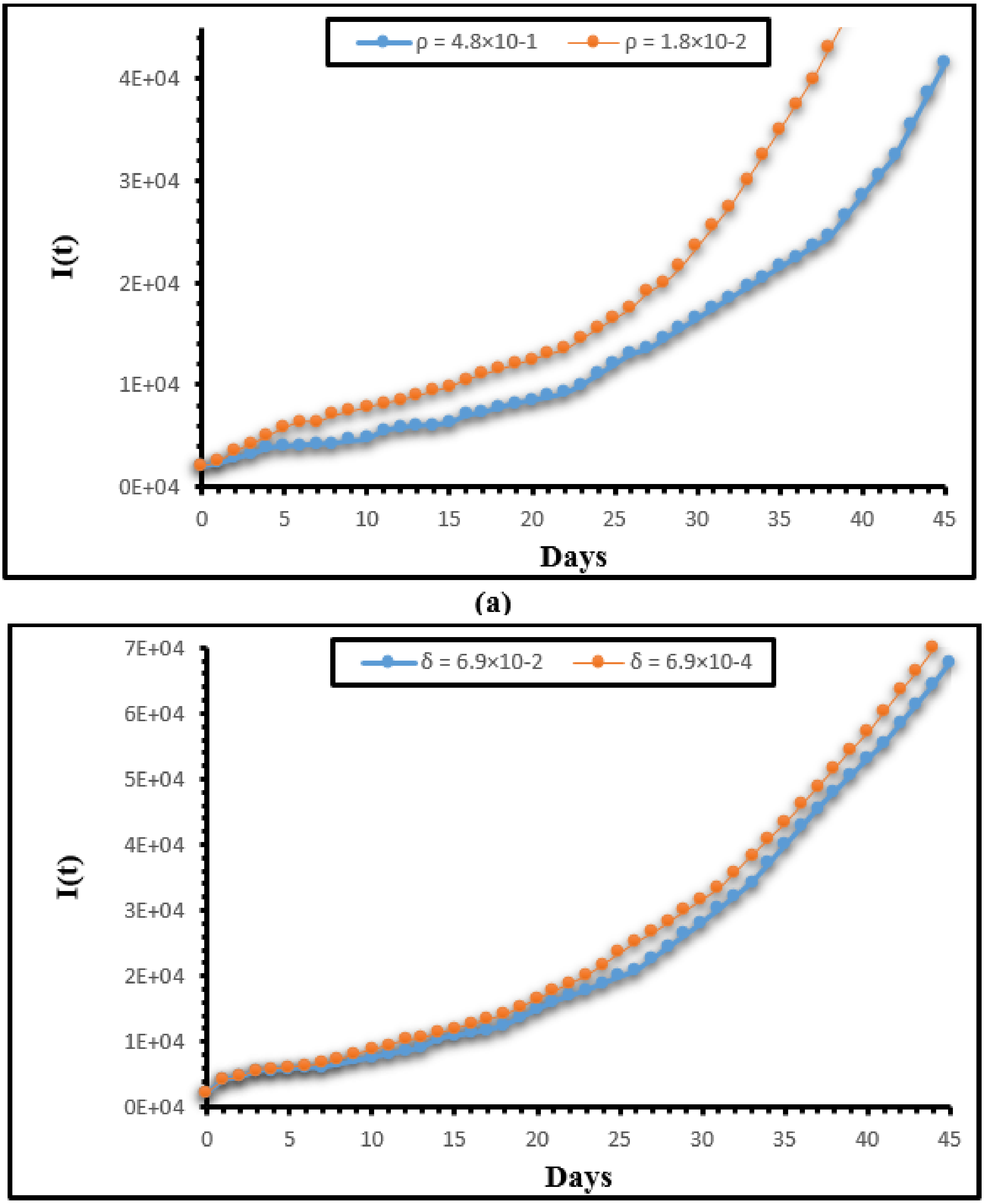
Figure 7(a) illustrates the dynamic characteristics of the I(t) having certain values of the τ (infected patient's treatment rate), whereas Figure 7(b) illustrates the I(t) individuals having certain values of α_c (rate of effective transmission). I(t) is illustrated in Figures 8(a) and (b) while adjusting ρ (rate of recovery infection rate) as well as δ (mortality rate). Furthermore, the influence of ψ (fraction of people who keep social isolation) and ν (fraction of the entire population who fully implement a surgical mask plus hand wash) upon I(t) individuals shown in Figure 9(a) and (b). Figures 10(a) and (b) demonstrate the behavior of $\mathfrak{R}_0$ vs several parameters in two dimensions. According to the illustrations, it's indeed clear that the techniques employed by the sector of public health and the government responsible to fix the condition that is causing the pandemic to spread might be extraordinary effective if the transmission rate could be controlled as shown in Figure 6.



(a)

(b)

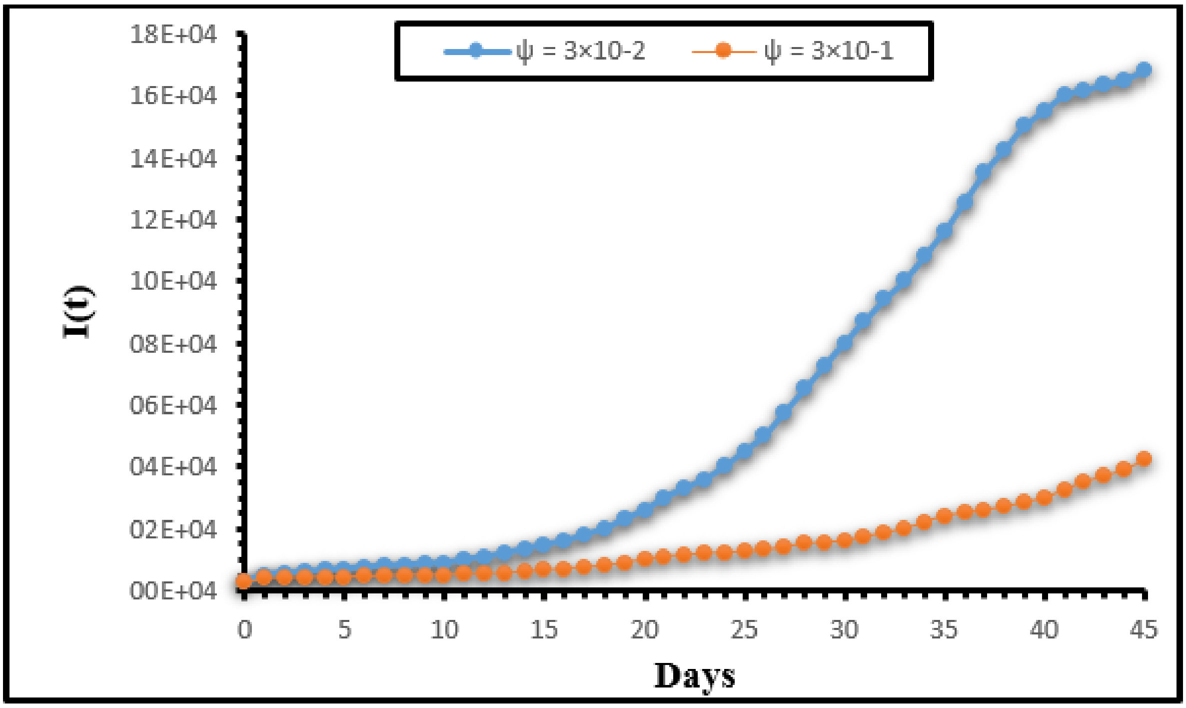
Figure 7. (a) I(t) dynamical system over τ. **(b)** I(t) dynamical system over α_c.



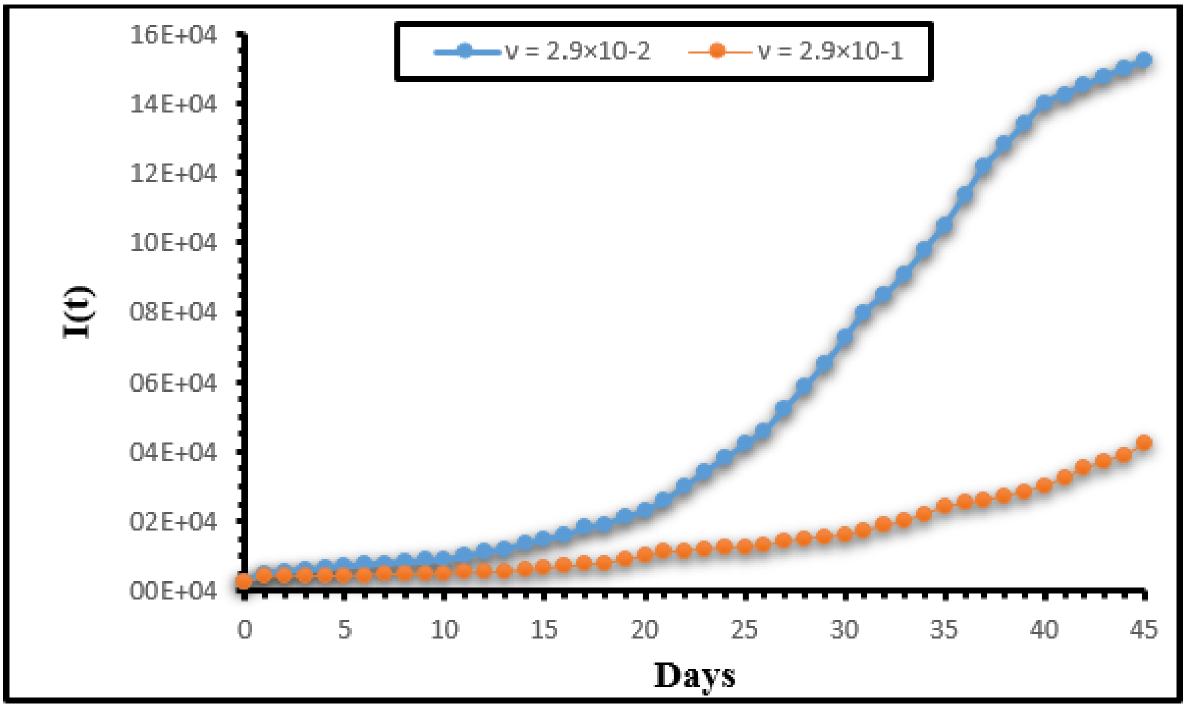
(a)

(b)

Figure 8. (a) I(t) dynamcal system over ρ. **(b)** I(t) dynamical system over δ.

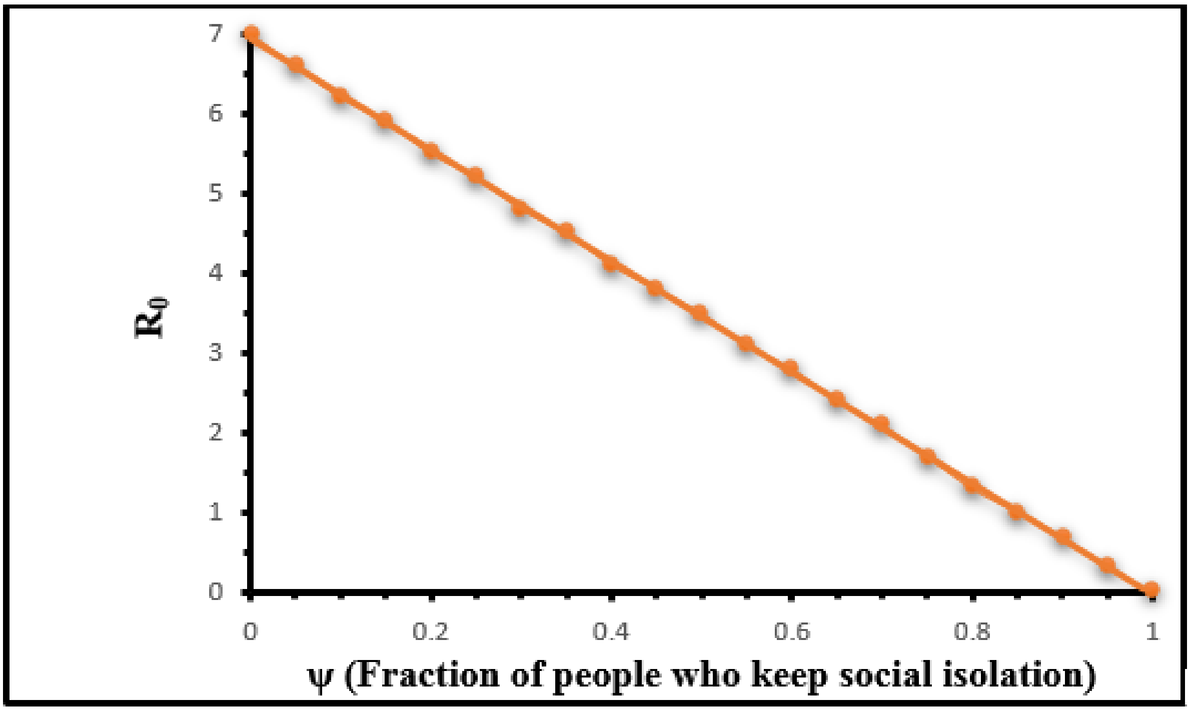


(a)

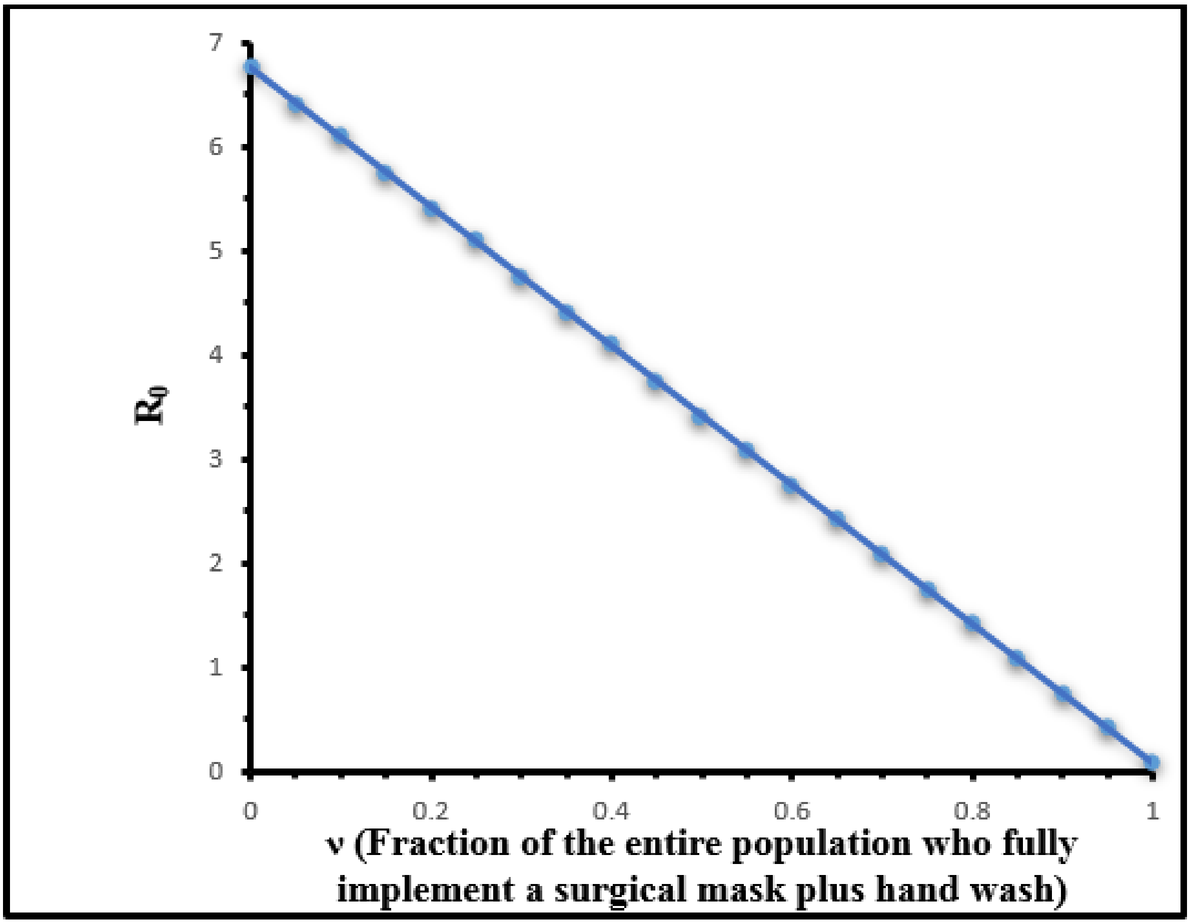


(b)

Figure 9. (a) I(t) dynamical system over ψ. **(b)** I(t) dynamical system over ν.



(a)



(b)

Figure 10. **(a)** R_0 dependency on ψ. **(b)** R_0 dependency on ν.

7. CONCLUSION

The “Severe Acute Respiratory Syndrome Coronavirus 2” (SARS-CoV-2) virus is the contagious disease classified as coronavirus (COVID-19). The majority of virus-infected individuals will have a mild to severe lung infections and thus survive without the need for special care. Being knowledgeable about the disease and the virus's propagation is the greatest strategy to stop or slow down propagation. The mathematical method is one of the useful approaches that helps to enhance awareness of the infection. To better understand the transmission patterns of the alarming modern pandemic known as COVID-19, we have in this regard suggested a novel mathematical model. The present study effort has examined a number of essential novel model features, including the global stability of the free disease equilibrium, basic reproduction number, equilibrium state and invariant region. Additionally, an actual statistical data from July 01 to August 14, 2020, from Pakistan is utilized to determine the nonlinear least squares estimating method's appropriate model for a few factors using the curve fitting “Matrix Laboratory” (MATLAB) function. The significant sensitive factors of such suggested model have been identified by a sensitivity method of the model parameters. These data have been supported by numerical simulations, and indeed the suggested model's best fitting curve has been found. According to the result of this research, the public health industry as well as the state will be able to handle the scenario that is fueling the pandemic more efficiently if the rate of transmission is controlled.

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