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Mathematical modeling of the spread of the coronavirus under strict social restrictions

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We formulate a simple susceptible-infectious-recovery (SIR) model to describe the spread of the coronavirus under strict social restrictions. The transmission rate in this model is exponentially decreasing with time. We find a formula for basic reproduction function and estimate the maximum number of daily infected individuals. We fit the model to induced death data in Italy, United States, Germany, France, India, Spain, and China over the period from the first reported death to August 7, 2020. We notice that the model has excellent fit to the disease death data in these countries. We estimate the model's parameters in each of these countries with 95% confidence intervals. We order the strength of social restrictions in these countries using the exponential rate. We estimate the time needed to reduce the basic reproduction function to one unit and use it to order the quality of social restrictions in these countries. The social restriction in China was the strictest and the most effective and in India was the weakest and the least effective. Policy-makers may apply the Chinese successful social restriction experiment and avoid the Indian unsuccessful one.

KEYWORDS
coronavirus, COVID-19, mathematical model, parameter estimations, social distancing, variable transmission rate

MSC CLASSIFICATION
37Nxx; 37N25; 92Bxx; 92B05

1 | INTRODUCTION

Coronavirus disease has affected most countries and has been declared as pandemic. The disease was first discovered in Wuhan, China. It is caused by a novel coronavirus known as severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) and named as COVID-19. The infection is primarily transmitted through droplets that come from coughs, wheezes, or breaths out of infected individual. As of September 25, 2020, COVID-19 confirmed cases surpassed 35 million in the globe, and roughly one million individuals have lost their lives due to this infection.[1] Currently, because of the high rate of disease transmission and the number of death records, COVID-19 is of great concern to researchers, governments, and health care organizations. As a result, many countries have started to introduce social controls and have further proposed structural changes to tackle the pandemic and economic implications. Many scientific communities have started

to look for a better way of tracking the transmission of the disease. Mathematical models are among the most tools for understanding the level of the disease as it erupts in the population and for investigating under what conditions it can be eliminated or continued.

A variety of mathematical models have been proposed to analyze the spread of the disease and to assess its transmission through simulations.[2–8] The authors[6–8] aimed on calculating the basic reproduction[6–8] number and failed to consider the effect of public health recommendations, isolate, and confinement on the transmission of COVID- 19. On the other hand, the dynamical modeling for the spread of COVID-19 has been performed by the scholars.[3–5] A dynamical model with seven compartments was also presented in Jiwei et al[2] to describe the transmission of COVID-19 in Wuhan, China. In that paper, the proposed model was fitted to 30 days of local data to estimate the model's parameter values.

COVID-19 causes infections that shift from showing no symptoms cases to death causing cases. Strict control measures have been imposed in China, such as quarantine, contact tracing, social distancing, and group surveillance, to restrict COVID-19 by February 2020.[9] It is found out in that study that imposing such controls to a sample of 100 individuals may result in a maximum of nine infected by the disease. The authors in a previous study[10] also found that nearly 50% of infected individuals are confirmed from suspected cases. It is, therefore, not a good idea to investigate the effect of the COVID-19 outbreak in a community without taking into account the effect of the implementation of control measures. The authors in a previous study[9] concluded that models that do not incorporate quarantine or contact tracing for effective policies are not good enough.

Several authors have considered the application of control measures in their model in order to predict the impact of COVID-19. For example, in Tang et al,[11] the parameters have been calculated and the impact of the virus on mainland China has been analyzed. They proposed that the quarantine and separation methodology have to be improved to minimize the disease-induced death rate. In Wu et al,[12] they developed a mathematical transmission model by taking the full consideration of the seriousness scheme implemented in Ontario: physical distancing, contact tracing, and diagnosis. By fitting the proposed model to real data, the authors parameterized this transmission model for the detailed incidence information. Using these values of parameters, they assessed the transmission risk and evaluated the effectiveness of interventions. In Hu et al,[13] an epidemic model was developed to explore the impacts of the input population and quarantine strategies on the disease variations in different scenarios of Guangdong province. The results suggest that the increased numbers of the input population can mainly shorten the disease extinction days and the increased percentages of the exposed individuals of the input population increase the number of cumulative confirmed cases at a small percentage. Increasing the input population and decreasing the quarantine strategy together around the time point of the peak value of the confirmed cases may lead to the second outbreak. The study[14] focused on changes in contact patterns shaping the dynamics of the outbreak of COVID-19 in China. The findings indicate that social distances are adequate to regulate COVID-19, whereas school closures cannot disrupt transmission on their own and only can reduce the incidence by 40%–60% and delay the epidemic.

Recent studies show that social distancing was implemented in China to control the COVID-19 outbreak. So in this work, we are fitting the death data for various countries in the standard susceptible-infectious-recovery (SIR) mathematical model with parameters depending on social restrictions. The data relevant for this study are taken from the World Health Organization (WHO). Previous studies show that there exist many relations between the spreading of SARS and COVID-19. Therefore, in this study, we are using the approach applied to SARS.[15] First, we present the SIR mathematical model to describe the dynamics of COVID-19 under social restrictions. Next, we fit the model to death data for various nations to assess the model's parameter values. Further, we utilize the estimated parameter values and the basic reproduction number to examine the effectiveness of the current social restrictions for all considered nations to control the COVID-19.

The rest of the paper is organized as follows. In Section 2 we introduce the mathematical model with social restrictions, and also we describe the parameters. We present the basic reproduction number to analyze the impact of the virus in Section 3. Further, we have discussed the methodology for estimating the parameters and results in Section 4. Finally, we conclude with a summary in Section 5.

2 | FORMULATION OF THE MODEL

We divide the population into three classes, depending on the individual disease status, that are susceptibles class S, infected class I, and recovered class R. Susceptible individual can acquire infection due to contact with infected individual. The force of infection $\lambda(t)$ is given in (2). Infected recover at the natural rate r and the disease-induced death rate μ_d. The

TABLE 1 Definition of the model's parameters

Parameter	Definition	Unit
β_0	The background disease transmission rate	day^{-1}
k	Exponential decreasing rate for the transmission rate	day^{-1}
r	The disease recovery rate	day^{-1}
μ_d	The disease death rate	day^{-1}

ordinary differential equations (ODEs) that represent the dynamics in this model are given in the following:

$$\frac{dS}{dt} = -\lambda(t)S$$
$$\frac{dI}{dt} = \lambda S - (r + \mu_d)I \tag{1}$$
$$\frac{dR}{dt} = rI$$

$$\lambda(t) = \frac{\beta(t)I}{N} \tag{2}$$

The transmission rate $\beta(t)$ decreases exponentially in time and given by

$$\beta(t) = \beta_0 e^{-kt}$$

where β_0 is the transmission rate in the absence of strict social restrictions which includes but not limited to social distancing, lockdown, cleaning, and quarantine. k is the exponential decreasing rate and measures the strength of social restrictions. Similar exponential decreasing rate can be found in Wu et al,[16] in which $\beta(t) = \delta C(t)$, where δ is the probability of transmission and $C(t) = C_0 e^{-kt}$ exponentially decreasing contact rate.

The model's parameters are described in Table 1.

Note that $\frac{S}{N} \approx 1$ in the early stages of the disease. Therefore, the differential equation for the infected class is reduced to

$$\frac{dI}{dt} \approx \beta(t)I - (r + \mu_d)I \tag{3}$$

which has the solution

$$I(t) \approx I_0 \exp\left(\frac{\beta_0}{k}(1 - exp(-kt)) - (r + \mu_d)t\right) \tag{4}$$

Introducing the cumulative number of infected I_c given by

$$I_c(t) = \int_{t_0}^{t} I(s)ds \tag{5}$$

The number of cumulative death from the disease D_c is defined as follows

$$D_c(t) = \frac{\mu_d}{r + \mu_d} I_c(t) \tag{6}$$

3 | BASIC REPRODUCTION FUNCTION

Note that the differential Equation (3) can be written as follows:

$$\frac{dI}{dt} = (r + \mu_d)(R(t) - 1)I$$

with $R(t) = \frac{\beta_0 e^{-kt}}{r+\mu_d}$ which represents the disease threshold quantity and measures the average number of secondary infections generated by a single infected individual at time t when placed in a population of susceptibles. Note that $R(t)$ is decreasing function in time with the maximum value $R(0) = \frac{\beta_0}{r+\mu_d}$. Also, $R(t) = 1$ if and only if $t = t_c \equiv \frac{1}{k} \ln\left(\frac{\beta_0}{r+\mu_d}\right) > 0$. Moreover, $I(t)$ is increasing in the interval $(0, t_c)$ and decreasing in the interval (t_c, ∞). Therefore, $I(t_c)$ is an absolute maximum value. From (4), we have

$$
\begin{aligned}
I(t_c) &= I_0 \exp\left(\frac{\beta_0}{k}\left(1 - \frac{1}{R(0)}\right) - \frac{r+\mu_d}{k}\ln(R(0))\right) \\
&= I_0 \frac{1}{R(0)^{\frac{r+\mu_d}{k}}} \exp\left(\frac{\beta_0}{k}\left(1 - \frac{1}{R(0)}\right)\right) \\
&= I_0 \left(\frac{r+\mu_d}{\beta_0}\right)^{\frac{r+\mu_d}{k}} \exp\left(\frac{\beta_0}{k}\left(1 - \frac{r+\mu_d}{\beta_0}\right)\right) \\
&= I_0 \left(\frac{r+\mu_d}{\beta_0}\right)^{\frac{r+\mu_d}{k}} \exp\left(\frac{\beta_0 - (r+\mu_d)}{k}\right)
\end{aligned}
$$

which represents the maximum number of daily infected.

We have found a formula for the critical time needed to reduce the basic reproduction number to less than one unit and the maximum possible number for daily infected cases.

4 | PARAMETER ESTIMATIONS AND ANALYSIS

The cumulative number of deaths from January 21 to August 7, 2020 for Italy, United States, Germany, France, India, Spain, and China are obtained from the WHO (http://www.who.int). We estimate the values of the parameters for Model (1) by fitting the cumulative death function D_c (6) to these data from the first reported death case till August 7, 2020. The least squares method is applied here and implemented in MATLAB using the built-in function *lsqcurvefit* with the initial values for the parameters $[\beta_0, k, r, \mu_d] = [0.7, 0.06, 0.03, 0.03]$, the lower bounds $lb = [0.0001, 0, 0.001, 0.001]$, and the upper bounds $ub = [2, 0.5, 1, 0.04]$. Also, the 95% confidence intervals for the parameters are estimated using the MATLAB built-in function *nlparci*.

4.1 | Italy

In Table 2 we have estimated the values for the parameters of the model and their 95% confidence intervals for Italy.

Cumulative death graphs for Italy are added to support our results. Figure 1A shows excellent fit between cumulative number of deaths from the model and the reported data for the period Februar 21 to August 7, 2020. Here February 21 is the date of the first reported death case in Italy and August 7 is the final date for the study that is the last date for the data that is available when this work started. In Figure 1B we have the basic reproduction function of time $R(t)$ over the same period. It is clear that $R(t)$ is decreasing with time and reaches one unit after 40 days. As we assumed that strict social restriction were applied in Italy in this period, the 40 days can be translated as the critical time spent under social restrictions to reach the disease controlling threshold.

4.2 | United States

In Table 3 we have estimated the values for the parameters of the model and their 95% confidence intervals for the United States. The confidence interval for the positive parameter μ_d should be ignored here as it has negative lower bound.

TABLE 2 Estimated values and confidence intervals for the parameters of the model in Italy

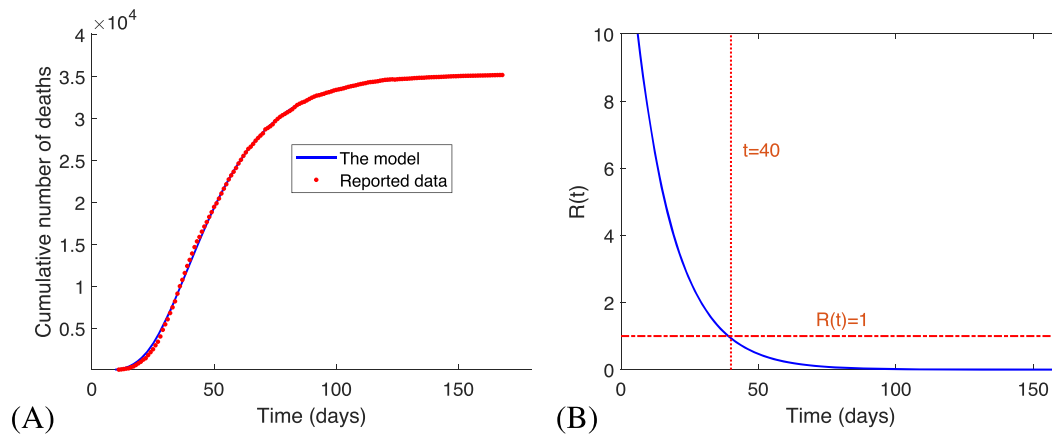| Parameter	Value (day^{-1})	95% confidence interval
β_0	0.7227	(0.6457, 0.7996)
k	0.0702	(0.0662, 0.0741)
r	0.0332	(0.0254, 0.0410)
μ_d	0.0135	(0.0047, 0.0223)

FIGURE 1 (A) Model fitting results and reported cumulative number of deaths in Italy. Here, the blue curve is the best fitting curve, while the red doted curve is the reported cumulative number of deaths. (B) The basic reproduction function $R(t)$ in Italy. In the later, horizontal and vertical dashed lines are added to find the critical time needed to reach $R(t) = 1$

Parameter	Value (day^{-1})	95% confidence interval
β_0	0.9198	(0.2319, 1.6076)
k	0.0799	(0.0581, 0.1017)
r	0.0167	(0.0123, 0.0211)
μ_d	0.0010	(−0.0048, 0.0068)

TABLE 3 Estimated values and confidence intervals for the parameters of the model in the United States
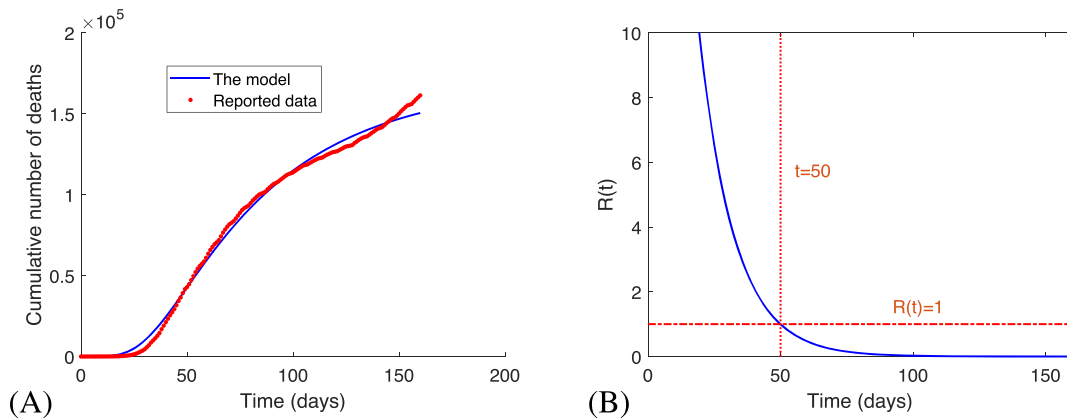

FIGURE 2 (A) Model fitting results and reported cumulative number of deaths in the United States. Here, the blue curve is the best fitting curve while the red doted curve is the reported cumulative number of deaths. (B) Basic reproduction function $R(t)$ in the United States. In the later, horizontal and vertical dashed lines are added to find the critical time needed to reach $R(t) = 1$

Parameter	Value (day^{-1})	95% confidence interval
β_0	0.8356	(0.7029, 0.9683)
k	0.0783	(0.0716, 0.0851)
r	0.0558	(0.0543, 0.0574)
μ_d	0.0022	(−0.0000, 0.0045)

TABLE 4 Estimated values and confidence intervals for the parameters of the model in Germany

Figure 2A shows excellent fit between cumulative number of deaths from the model and the reported data for the period February 21 to August 7, 2020. Figure 2B shows how the basic reproduction function changes with time when applying social distancing. The figure shows that $R(t)$ is decreasing with time and reaches one unit after 50 days.

4.3 | Germany

In Table 4 we have estimated the values for the parameters of the model and their 95% confidence intervals for Germany. The confidence interval for the positive parameter μ_d has negative part and should be ignored. Note that the percentage of death for Germany is $\frac{\mu_d}{\mu_d+r} = 3.8\%$.

Figure 3A shows excellent fit between cumulative number of deaths from the model and the reported data for the period March 9 to August 7, 2020. Figure 3B shows that the basic reproduction function decreases with time after applying social distancing. The figure shows that $R(t)$ in Germany reaches one unit after 34 days.

4.4 | France

In Table 5 we have estimated the values for the parameters of the model and their 95% confidence intervals for France. The confidence interval for $\mu_d > 0$ should be ignored as it has negative lower bound. Note that percentage death for France is $\frac{\mu_d}{\mu_d+r} = 1.2\%$.

Figure 4A shows excellent fit between cumulative number of deaths from the model and the reported data for the period February 15 to August 7, 2020. Figure 4B shows that the reproduction function decreases with time after applying social distancing. In France, it took 58 days, after the first death, to reduce $R(t)$ to one unit.

4.5 | India

In Table 6 we have estimated the values for the parameters of the model and their 95% confidence intervals for India. r and μ_d confidence intervals, with negative lower bounds, should be ignored.

Figure 5A shows excellent fit between cumulative number of deaths from the model and the reported data for the period March 11 to August 7, 2020. Figure 5B shows that the social distancing in India in this period was not enough to reduce $R(t)$ to one unit.
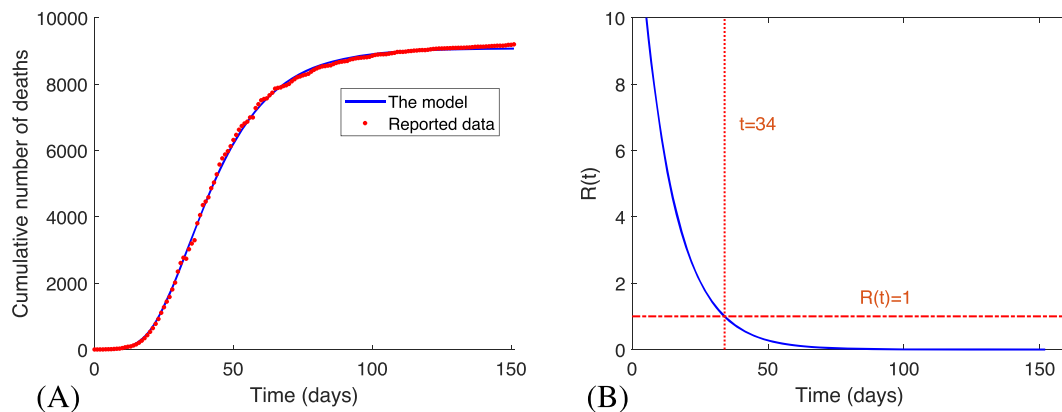

FIGURE 3 (A) Model fitting results and reported cumulative number of deaths in Germany. Here, the blue curve is the best fitting curve while the red doted curve is the reported cumulative number of deaths. (B) Basic reproduction function $R(t)$ in Germany. In the later, horizontal and vertical dashed lines are added to find the critical time needed to reach $R(t) = 1$

TABLE 5 Estimated values and confidence intervals for the parameters of the model in France

Parameter	Value (day^{-1})	95% confidence interval
β_0	0.6619	(0.5185, 0.8052)
k	0.0239	(0.0110, 0.0368)
r	0.1683	(0.0909, 0.2456)
μ_d	0.0024	$(-0.0065, 0.0112)$

TABLE 6 Estimated values and confidence intervals for the parameters of the model in India

Parameter	Value (day^{-1})	95% confidence interval
β_0	0.1425	(0.1035, 0.1815)
k	0.0176	(0.0087, 0.0265)
r	0.0010	(0, 0.0027)
μ_d	0.0027	$(-0.0106, 0.0160)$

4.6 | Spain

In Table 7 we have estimated the values for the parameters of the model and their 95% confidence intervals for Spain. The confidence interval for μ_d should be ignored here as it contains negative lower bound.

Figure 6A shows excellent fit between cumulative number of deaths from the model and the reported data for the period March 3 to August 7, 2020. Figure 6B shows that the reproduction function decreases with time after applying social distancing. After the first death in Spain, the social distancing took 30 days to reduce $R(t)$ to one unit.

4.7 | China

In Table 8 we have estimated the values for the parameters of the model and their 95% confidence intervals for China. All confidence intervals here have negative lower bounds and should be ignored.
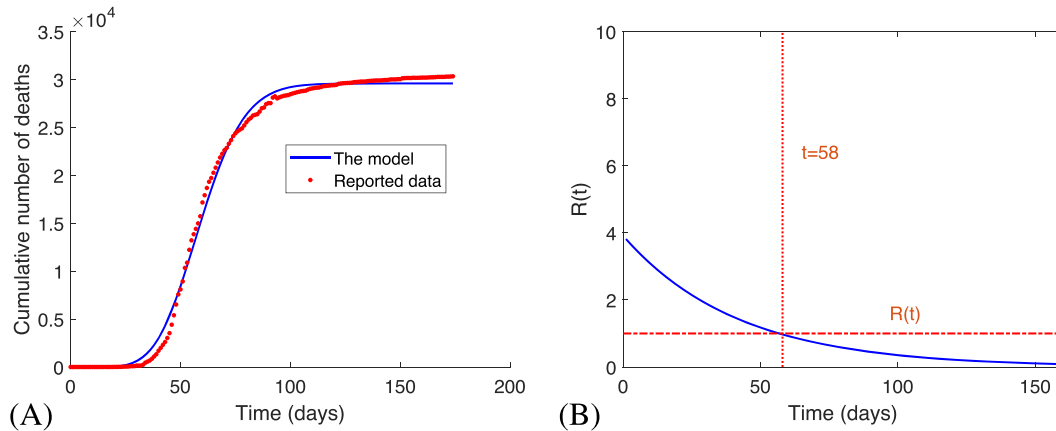
FIGURE 4 (A) Model fitting results and reported cumulative number of deaths in France. Here, the blue curve is the best fitting curve while the red doted curve is the reported cumulative number of deaths. (B) Basic reproduction function $R(t)$ in France. In the later, horizontal and vertical dashed lines are added to find the critical time needed to reach $R(t) = 1$
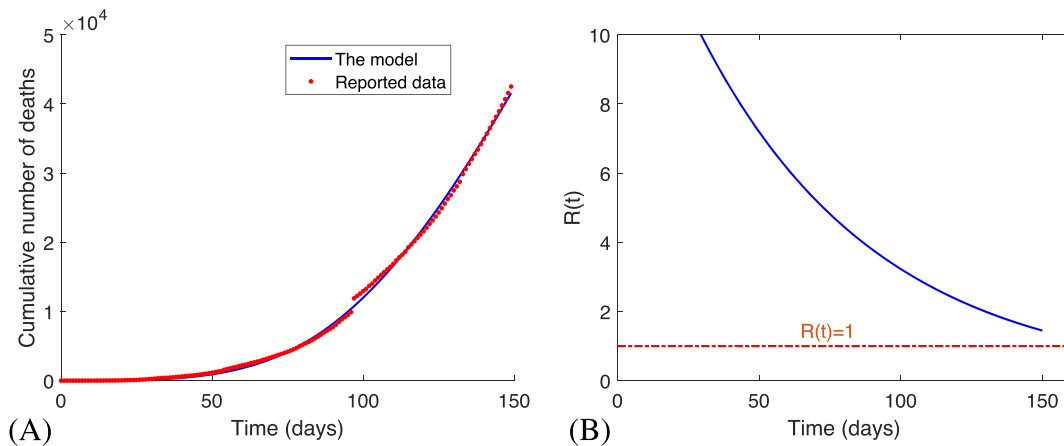
FIGURE 5 (A) Model fitting results and reported cumulative number of deaths in India. Here, the blue curve is the best fitting curve while the red doted curve is the reported cumulative number of deaths. (B) Basic reproduction function $R(t)$ in India. In the later, horizontal and vertical dashed lines are added to find the critical time needed to reach $R(t) = 1$

TABLE 7 Estimated values and confidence intervals for the parameters of the model in Spain

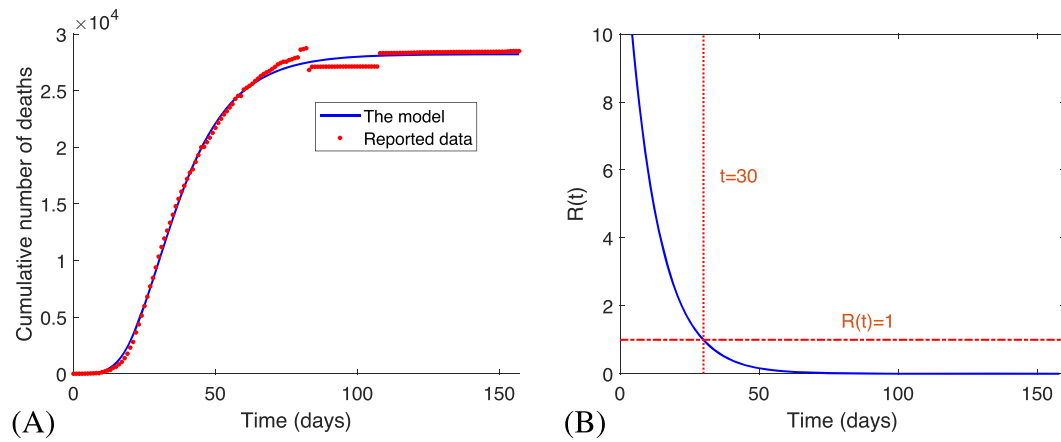| Parameter	Value (day^{-1})	95% confidence interval
β_0	0.9838	$(0.6711, 1.2966)$
k	0.0897	$(0.0746, 0.1048)$
r	0.0528	$(0.0273, 0.0782)$
μ_d	0.0143	$(-0.0153, 0.0440)$

FIGURE 6 (A) Model fitting results and reported cumulative number of deaths in Spain. Here, the blue curve is the best fitting curve while the red doted curve is the reported cumulative number of deaths. (B) Basic reproduction function $R(t)$ in Spain. In the later, horizontal and vertical dashed lines are added to find the critical time needed to reach $R(t) = 1$

TABLE 8 Estimated values and confidence intervals for the parameters of the model in China

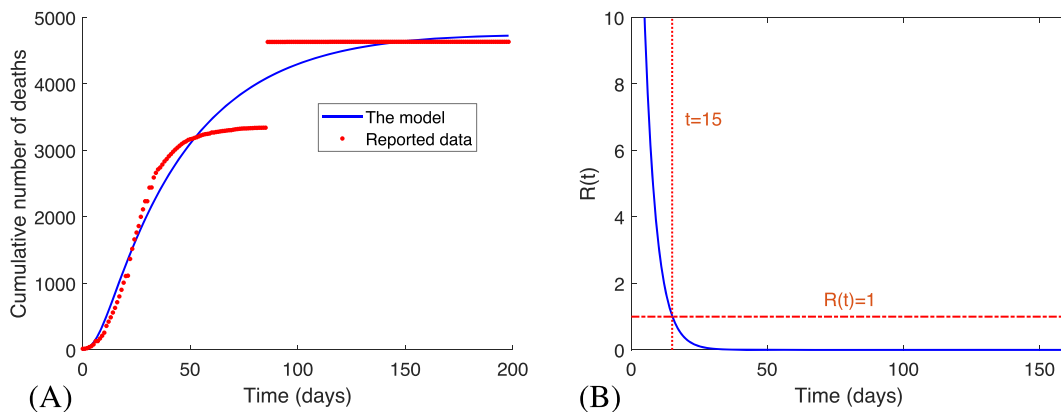| Parameter	Value (day^{-1})	95% confidence interval
β_0	0.7240	$(-1.1520, 2.6000)$
k	0.2242	$(-0.0262, 0.4747)$
r	0.0164	$(-0.0228, 0.0556)$
μ_d	0.0080	$(-0.0314, 0.0474)$

FIGURE 7 (A) Model fitting results and reported cumulative number of deaths in China. Here, the blue curve is the best fitting curve while the red doted curve is the reported cumulative number of deaths. (B) Basic reproduction function $R(t)$ in China. In the later, horizontal and vertical dashed lines are added to find the critical time needed to reach $R(t) = 1$

Figure 7A shows fair fit between cumulative death function and the reported death data for the period January 22 to August 7, 2020. Note that the death data reported for both China and Spain had unreasonable jumps. We ignored these unreasonable reported data in our work. Figure 7B shows that the reproduction function decreases with time after applying social distancing. After the first reported death in China, social distancing reduces $R(t)$ to one unit in 15 days.

We have estimated the values for the parameters of the SIR model under strict social distancing in Italy, United States, Germany, France, India, Spain, and China. We have found the 95% confidence intervals for these estimated parameters too. Moreover, we have estimated the critical time spent under social restrictions in each country to reach the disease controlling threshold $R(t) = 1$.

Parameter	Global confidence interval
β_0	(0.1035, 1.6076)
k	(0.0087, 0.1048)
r	(0, 0.2456)

TABLE 9   Global 95% confidence interval for the estimated parameters

Country	k (day^{-1})	Lockdown levels
Italy	0.07	4
United States	0.08	3
Germany	0.08	3
France	0.02	5
India	0.02	5
Spain	0.09	2
China	0.22	1

TABLE 10   Lockdown strength in descending order

Country	Time (days) till $R(t) = 1$	Effectiveness level
Italy	40	4
United States	50	5
Germany	34	3
France	58	6
India	-	7
Spain	30	2
China	15	1

TABLE 11   Time spent under social restrictions, from the first reported death case till reaching $R(t) = 1$

5 | SUMMARY AND CONCLUSION

We have introduced a simple SIR model to describe the spread of the COVID-19 under social distancing. The disease transmission rate was considered exponentially decreasing time-dependent because of strong social restrictions considered in considered countries at the disease starting period. The model has been fitted to induced death data country wise to estimate the model's parameters' values. The 95% confidence intervals for the model parameters are estimated in Italy, United States, Germany, France, India, Spain, and China. We have shown that these estimated values make sense by comparing them with literature estimated values.

In Table 9 we have the shortest possible confidence intervals for the model's parameters that work for all the considered six countries (excluding China).

Our work can be considered as the first work estimates parameters' values for SIR model using induced death data for almost 160 days period in Italy, United States, Germany, France, India, Spain, and China. Even if the work shows excellent fitting between the curve $D_c(t)$ and the reported cumulative death data in the countries considered, we need to investigate the quality of the parameters' values produced by this fitting. The disease death rate in China, in Table 8, is exactly the same value estimated in Tang et al.[11] In Ding and Gao[17] the estimated disease death and recovery rates are 0.00027 and 0.0082, respectively, which are within the interval for disease death rate in Table 2 and the global interval for death rate in Table 9. The value of $k = 0.0632$ in Ontario, Canada,[16] is very close to that in Italy ($k = 0.0702$) in Table 2 and within the 95% confidence interval for the United States; Table 3. Finally, the estimated percentage induced death $\frac{d}{d+r}$ in Germany and France 3.8% and 1.2% are close to the worldwide percentage of death value 3.6% reported by the WHO.

It should be mentioned that the function $I_c(t)$ (5) has been fitted to cumulative infected cases. The results show excellent fitting between $I_c(t)$ and the reported cumulative infected data in both Italy and China. The results are not presented here as the estimated induced death rates from this fitting are different from that in literature. The is because reported death data could be more accurate than infected reported data in which many asymptomatic untested cases were not reported.

To compare the strength of social restrictions in the seven countries, we have added Table 10. In this table an average value for k rounded to two decimals is calculated. The lockdown strength in these countries is ordered using the numbers 1–5 depending on the value of k, in which the lower the number given, the higher the level of restriction in the country. As expected from the COVID-19 data reported, the social restrictions in China were the strictest and in India was the weakest. The strength of restriction for other countries is in the following order: Spain, United States-Germany, Italy, and France. Estimated value for k in France is almost equal to that in India and that could mean that France social restriction at that time was as low as that in India.

Time spent under social restrictions till reaching $R(t) = 1$ is used to measure social restrictions' success in controlling COVID-19 in the seven countries. In Table 11 we order the success of social restrictions in the seven countries using the time from the first induced death till the time of $R(t) = 1$. The effectiveness is ordered using the numbers 1–7, with the lower the number, the faster to control COVID-19 using social restrictions. As expected, the stronger the restriction, the faster the control of COVID-19.

In sum, we have estimated the transmission, recovery, induced death, and the exponential rates with 95% confidence interval for each of the seven countries. The confidence intervals have been unified to global range for each of these rates. We have ordered the strength of social restriction programs and their effectiveness in the considered seven countries. Health agencies should make use of Chinese successful social distancing experiment and avoid unsuccessful experiment like the Indian one.

The work has some limitations: In some countries we could not estimate the confidence interval for the disease death rate. The parameters values estimated here are average values and vary within the estimated confidence interval; readers should take extra care before using them. The parameters values are estimated for specific period when social restrictions were too strong; some parameter values may change when restrictions are eased. For future work, more countries will be considered to check the validity of the results.

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