

Impact of intervention on the spread of COVID-19 in India: A model based study

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Abstract

The outbreak of corona virus disease 2019 (COVID-19), caused by the virus severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has already created emergency situations in almost every country of the world. The disease spreads all over the world within a very short period of time after its first identification in Wuhan, China in December, 2019. In India, the outbreaks starts on 2nd March, 2020 and after that the cases are increasing exponentially. Very high population density, the unavailability of specific medicines or vaccines, insufficient evidences regarding the transmission mechanism of the disease also make it difficult to fight against the disease properly in India. Mathematical models have been used to predict the disease dynamics and also to assess the efficiency of the intervention strategies in reducing the disease burden. In this work, we propose a mathematical model to describe the disease transmission mechanism between the individuals. We consider the initial phase of the outbreak situation in India and our proposed model is fitted to the daily cumulative new reported cases during the period 2nd March, 2020 to 24th March, 2020. We estimate the basic reproduction number (\mathcal{R}_0), effective reproduction number ($R(t)$) and epidemic doubling time from the incidence data for the above-mentioned period. We further assess the effect of preventive measures such as spread of awareness, lock-down, proper hand sanitization, etc. in reducing the new cases. Two intervention scenarios are considered depending on the variability of the intervention strength over the period of implementation. Our study suggests that higher intervention effort

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is required to control the disease outbreak within a shorter period of time in India. Moreover, our analysis reveals that the strength of the intervention should be strengthened over the time to eradicate the disease effectively.

Key words: COVID-19, Mathematical modelling, Basic reproduction number, Intervention, Outbreak, India

1. Introduction

Coronaviruses, related to the family *Coronaviridae* are single-stranded, positive-sense RNA viruses [1]. In the year 1960, the human coronaviruses were first classified and scientists used the term ‘corona’ due to its crown-like visibility on the surface area [2]. Three major outbreaks occurred because of coronaviruses in the years 2003, 2012 and 2015. The outbreak occurred in China in the year 2003 was named as ‘Severe Acute Respiratory Syndrome’ (SARS) outbreak. Saudi Arabia in 2012 [3] and South Korea in 2015 [4] were affected by ‘Middle East Respiratory Syndrome’ (MERS) outbreak.

Recently, in December, 2019, a newly invaded coronavirus, first identified in Wuhan, the capital city of the Hubei province of China caused an outbreak [5]. This is considered as the fourth coronavirus outbreak. It has been reported that due to viral pneumonia, 27 people were infected which includes 7 critically ill cases [6], and this outbreak has grabbed substantial attentions all over the globe. The Chinese officials declared on 7th January, 2020 that this infectious disease is transmitted through a biological pathogen, named novel coronavirus and on 10th January, 2020, the World Health Organization (WHO) referred the novel coronavirus as ‘2019-nCoV’. Finally, on 11th February, 2020, WHO declared the official name of the disease and the causing virus as coronavirus disease 2019 (COVID-19) and severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) respectively [7]. WHO also published preliminary guidelines for all the countries to deal with this outbreak. The guidelines are mainly based on how to provide health care support to the infected patient and build awareness among the ordinary people about this new disease [8].

Plenty of research works indicates that COVID-19 possibly spread from animal to human (zoonotic) [9, 10]. Moreover, a rapid number of new occurrences of COVID-19 reveals the key fact that the secondary transmission can occur through human to human [11] via direct communication or through droplets spread by coughing or sneezing from an infected person [12]. This

human to human transmission is considerably growing almost everywhere in the world by means of the international movement [13] and as soon as an area of a specific country is affected then COVID-19 rapidly grows through local transmission. Person infected with SARS-CoV-2 virus shows symptoms like fever, cough, and shortness of breath, muscle ache, confusion, headache, sore throat, rhinorrhea, chest pain, haemoptysis, diarrhoea, dyspnoea and nausea and vomiting [14, 12, 10]. WHO situation report [15] reveals that the COVID-19 pandemic spread on the Western Pacific, European, South-east Asia, Eastern Mediterranean, America and African Region with their respective territories, causing a huge number of infected cases. The new cases are quickly growing in various countries like USA, Spain, Germany, France, Italy, UK, Iran, Switzerland, India, Netherlands, Austria, etc. [15].

In India, the first confirmed case of COVID-19 was reported on 30th January, 2020 [16]. Government of India declared a countrywide lock-down for 21 days as a preventive measure for the COVID-19 outbreak on 24th March, 2020 [17]. Besides the lock-down, the Ministry of Health and Family Welfare (MOHFW) of India, suggested various individual hygiene measures e.g. frequent hand washing, social distancing, use of mask, avoiding touching eyes, nose, or mouth, etc. [18, 19]. The government also continuously using various media and social networking web sites to aware the citizen. However, the factors like very high population density, the unavailability of specific medicines or vaccines, insufficient evidences regarding the transmission mechanism of the disease also make it difficult to fight against the disease properly in India.

Mathematical models have been used to predict the disease dynamics and also to assess the efficiency of the intervention strategies in reducing the disease burden. In this context, several studies have been done using real incidence data of the affected countries and examined different characteristics of the outbreak as well as evaluated the effect of intervention strategies implemented to curb the outbreak in the respective countries [6, 20, 21, 22, 23, 24].

In this work, we propose a deterministic compartmental model to describe the disease transmission mechanism between the individuals. We consider the situation of India during the initial outbreak period and fitted our model to the daily cumulative new cases reported between 2nd March, 2020 to 24th March, 2020. We estimate the basic reproduction number, effective reproduction number and epidemic doubling time from the incidence data for the above-mentioned period. The efficiency of preventive measures in reducing the disease burden is also studied for different level of intervention strength. Further, the impact of intervention in the situation where the strength of the

intervention is varied over the implementation period.

The rest of the paper is organized as follows. In section 2, we briefly describe our proposed model. Section 3 is devoted in describing the procedure of model fitting. The estimation of basic reproduction number, effective reproduction number and epidemic doubling time from actual incidence data is described in section 4. In section 5, the efficiency of the intervention is studied. Finally we discuss the findings obtained from our study in section 6.

2. Description of the model

We adopt deterministic compartmental modelling approach to describe the disease transmission mechanism. Depending on the health status, the total human population is categorized into seven compartments: susceptible (S), exposed (E), symptomatic (I), asymptomatic (I_a), quarantined (I_q), hospitalized (H) and recovered (R). Susceptible population becomes exposed with the disease after experiencing close contacts with the symptomatic as well as asymptomatic individuals. We assume that the rate of disease transmission from asymptomatic individuals to susceptible individuals is less than that of from symptomatic individuals. The rate of new infection is given by $\frac{\beta S(I+\eta I_a)}{N}$, where β denotes the transmission rate of the disease and $\eta (< 1)$ is the modification parameter that accounts the reduction in the transmission rate from the asymptomatic individuals. At any instant of time, the total population is given by $N = S + E + I + I_a + I_q + H + R$. Since we consider the outbreak situation which usually persists for a shorter period of time, we do not incorporate any demographic factors (i.e birth, death, etc.) into the model. We assume that after the incubation period (σ^{-1}), ρ_1 fraction of the exposed individuals move to symptomatic compartment, ρ_2 fraction move to the asymptomatic compartment and the remaining fraction, ($\rho_3 = 1 - \rho_1 - \rho_2$) move to the quarantined compartment. The individuals in the symptomatic compartment (I) show severe symptoms of the disease and after α^{-1} period of time they are hospitalized. On the other hand, the asymptomatic individuals who do not show any symptom of the disease get natural recovery at a rate γ_a and move to the recovered class (R). The individuals in the quarantined compartment (I_q) are those individuals who exhibit mild symptoms and are advised to be quarantined. From quarantined class (I_q), individuals move to the hospitalized class (H) at a rate α_q . They can also get natural recovery and move to the recovered class (R) at a rate γ_q . Individuals admitted in the hospitals move to recovered class at a rate γ . We also consider that the

hospitalized individuals die due to the disease at a rate δ . The recovered population increases due to the recovery of asymptomatic, quarantined and hospitalized individuals at the rates γ_a , γ_q and γ respectively. The following set of ordinary differential equations represents the transmission dynamics of the disease:

$$\begin{aligned}
\frac{dS}{dt} &= -\frac{\beta S(I + \eta I_a)}{N}, \\
\frac{dE}{dt} &= \frac{\beta S(I + \eta I_a)}{N} - \sigma E, \\
\frac{dI}{dt} &= \rho_1 \sigma E - \alpha I, \\
\frac{dI_a}{dt} &= \rho_2 \sigma E - \gamma_a I_a, \\
\frac{dI_q}{dt} &= \rho_3 \sigma E - (\alpha_q + \gamma_q) I_q, \\
\frac{dH}{dt} &= \alpha I + \alpha_q I_q - (\gamma + \delta) H, \\
\frac{dR}{dt} &= \gamma_a I_a + \gamma_q I_q + \gamma H.
\end{aligned} \tag{2.1}$$

The schematic diagram and the description of the parameters used in the model (2.1) is presented in Fig. 1 and Table 1 respectively.

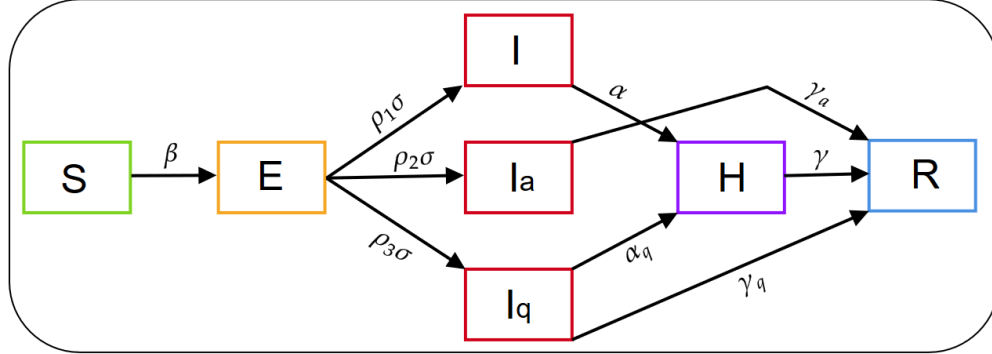


Figure 1: Schematic diagram of the model (2.1).

Parameters	Description	Value	Reference
β	Rate of disease transmission	1.1164	Estimated
η	Modification parameter	0.2	Estimated
σ	Rate of transition from exposed to infected class	0.1923 day^{-1}	[11]
ρ_1, ρ_2, ρ_3	Fractions of population move from the compartment E to the compartments I , I_a and I_q respectively	0.5210, 0.2740, 0.2050	Estimated
α	Rate of transition from symptomatic to hospitalized class	0.2174 day^{-1}	[11]
α_q	Rate of transition from quarantined to hospitalized class	0.1429 day^{-1}	Assumed
γ	Recovery rate of the individuals in hospitalized compartment	0.0701 day^{-1}	[25]
γ_a	Recovery rate of asymptomatic population	0.13978 day^{-1}	[6]
γ_q	Recovery rate of quarantined population	0.11624 day^{-1}	[6]
δ	Rate of disease induced death	0.0175 day^{-1}	[25]

Table 1: Description of parameters used in the model (2.1).

3. Model fitting

Though the first confirmed case of COVID-19 was reported on 30th January, 2020 [16], from 2nd March, 2020 onwards, the new cases are being reported continuously. Therefore, we consider 2nd March, 2020 as the starting date of the outbreak in India. It is also to be noted that, Government

of India declared a countrywide lock-down from 25th March, 2020 for 21 days [17]. Therefore, we assume that during the period 2nd March, 2020 to 24th March, 2020 no such preventive measures was taken by the Government of India. Since we do not incorporate any intervention in our model (2.1), we fit our model to the daily cumulative new reported COVID-19 cases of India during the period 2nd March, 2020 to 24th March, 2020. The daily cumulative cases data are obtained from [26].

We estimate four unknown model parameters: (i.) the transmission rate (β), (ii.) modification parameter (η), (iii.) fraction of population move to symptomatic class from exposed class (ρ_1) and (iv.) fraction of population move to asymptomatic class from exposed class (ρ_2) by fitting the model to the cumulative reported cases data.

The cumulative new reported cases from the model is given by

$$C(t, \Theta) = C(0) + \int_0^t (\alpha I(\tau) + \alpha_q I_q(\tau)) d\tau, \quad (3.1)$$

where $\Theta = \{\beta, \eta, \rho_1, \rho_2\}$ and $C(0)$ denotes the initial cumulative cases.

We perform our model fitting by using in-built function *lsqnonlin* in MATLAB (Mathworks, R2014a) to minimize the sum of square function. In our case, the sum of square function $SS(\Theta)$ is given by,

$$SS(\Theta) = \sum_{i=1}^n (C^d(t_i) - C(t_i, \Theta))^2,$$

where, $C^d(t_i)$ is the actual data at t_i^{th} day and n is the number of data points.

The model fitting to the cumulative new reported cases is displayed in Fig. 2. The values of the estimated parameters are given in Table 1.

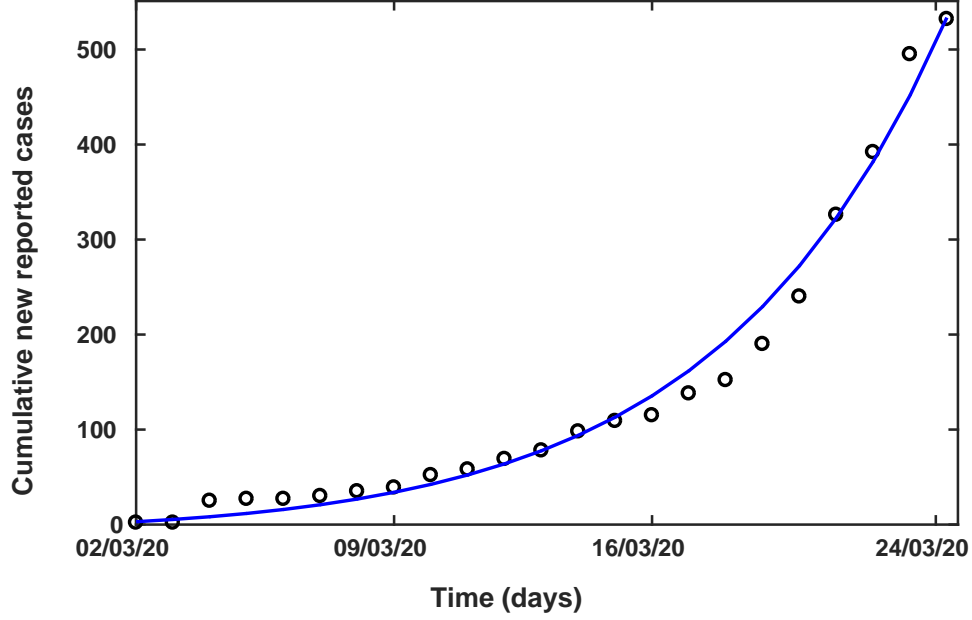


Figure 2: Model fitting to cumulative new COVID-19 reported cases for the time period 2nd March, 2020 to 24th March, 2020. The blue solid line represents the model solution and black circles are the discrete data points.

4. Basic reproduction number

Basic reproduction number is a key quantity in epidemiology which quantifies the average number of secondary cases generated from a single primary cases during the his infectious period. This quantity can be calculated from a mathematical model by following next generation matrix approach. Following [27], the new infection matrix F and the transmission matrix V are given by,

$$F = \begin{pmatrix} 0 & \beta & \eta\beta & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}, V = \begin{pmatrix} \sigma & 0 & 0 & 0 \\ -\rho_1\sigma & \alpha & 0 & 0 \\ -\rho_2\sigma & 0 & \gamma_a & 0 \\ -\rho_3\sigma & 0 & 0 & \alpha_q + \gamma_q \end{pmatrix}.$$

The basic reproduction number, \mathcal{R}_0 is defined as the spectral radius of the matrix FV^{-1} ,

$$\mathcal{R}_0 = \frac{\rho_1 \beta}{\alpha} + \frac{\eta \rho_2 \beta}{\gamma_a}. \quad (4.1)$$

It is to be noted that, the first term is the number of new infection caused by symptomatic individual (I) whereas the second term is the number new infection due to the infection by asymptomatic individual (I_a).

4.1. Estimation of basic reproduction number from actual epidemics

The basic reproduction number (\mathcal{R}_0) for communicable diseases can be estimated through the actual epidemic data by using various statistical as well as mathematical methods [28]. In this study, we estimate \mathcal{R}_0 from the initial growth phase of the epidemics [29, 30, 31]. At the early stage of the epidemic, there is a non-linear relationship between the cumulative number of cases $C(t)$ and the force of infection Λ which can be mathematically written as $C(t) \propto \exp(\Lambda t)$. So the number of exposed, symptomatic and asymptomatic population progress in the following form,

$$\begin{aligned} E &\propto E_0 \exp(\Lambda t), \\ I &\propto I_0 \exp(\Lambda t), \\ I_a &\propto I_{a0} \exp(\Lambda t). \end{aligned} \quad (4.2)$$

where E_0 , I_0 and I_{a0} are constants. Further, the number of non-susceptible population can be assumed negligible i.e. $S(t) = N$. Substituting the equation (4.2) into the model (2.1), we have

$$\begin{aligned} E_0(\Lambda + \sigma) &= \beta(I_0 + \eta I_{a0}), \\ I_0(\Lambda + \alpha) &= \rho_1 \sigma E_0, \\ I_{a0}(\Lambda + \gamma_a) &= \rho_2 \sigma E_0. \end{aligned} \quad (4.3)$$

Using the expression of \mathcal{R}_0 from equation (4.1) and applying the above equations (4.3) we have determined relation between the \mathcal{R}_0 and the force of infection Λ as follows:

$$\mathcal{R}_0 = \left(\frac{\rho_1}{\alpha} + \frac{\rho_2 \eta}{\gamma_a} \right) \left[\frac{\Lambda + \sigma}{\frac{\rho_1 \sigma}{\Lambda + \alpha} + \frac{\eta \rho_2 \sigma}{\Lambda + \gamma_a}} \right]. \quad (4.4)$$

Here we first estimate the force of infection Λ and then estimate \mathcal{R}_0 by using equation (4.4). Following [32, 31], the relation between the number

of new cases per day and the cumulative number of cases per day $C(t)$ as: number of new cases $\sim \Lambda C(t)$.

The force of infection (Λ) can be calculated from the COVID-19 incidence data in the following ways [30]:

- Step 1. We plot the number of new COVID-19 cases (per day) in x -axis versus the cumulative number of COVID-19 cases (per day) in y -axis.
- Step 2. In the scatter plot, we point out the threshold of cumulative cases up to which new cases show the exponential growth.
- Step 3. Then we fit a linear regression model using the least square technique to this exponential growth data.
- Step 4. The slope of the fitted line is considered as the force of infection (Λ).

We obtain $\Lambda = 0.2073 \pm 0.0151 \text{ day}^{-1}$ based on the slope shown in Fig. 3. Using the equation (4.4) along with the parameter values from Table 1, we obtain the estimate of $\mathcal{R}_0 = 4.1849$ with upper and lower bounds 4.5014 and 3.8799 respectively. This estimate of \mathcal{R}_0 indicates that the initial transmissibility of COVID-19 is pretty much higher than 1, which in turns implies that it is essential to control the disease at the initial phase.

4.1.1. Epidemic doubling time

The doubling time of an epidemic is a measure of the rate of spread of a disease. It is the required time to double the number of cases in the epidemic. There is an inverse relationship between epidemic strength and the doubling time i.e. if an epidemic declines, the doubling time increases and vice versa. Following [22], we obtain the epidemic doubling time for our study is $T_2 = \frac{\ln(2)}{\Lambda} \approx 3.34$ days. Therefore, it is necessary to apply some preventive measures else the epidemic appears in a large scale within a short time.

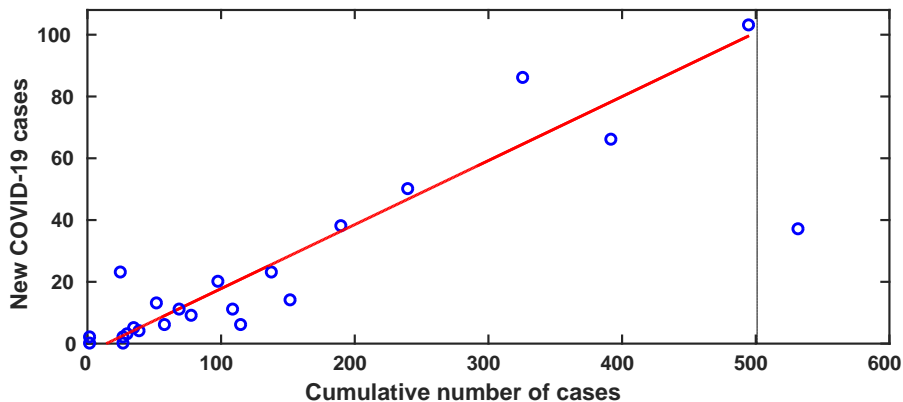


Figure 3: The daily number of new COVID-19 cases against the cumulative number of COVID-19 cases in India, from 2nd March, 2020 to 24th March, 2020. The box indicates the growing linear parts of the plots corresponding to the initial growth of the epidemics. The least squares linear fit of the linear phase corresponding to data in dot box gives $\Lambda = 0.2073 \pm 0.0151$ with correlation coefficient $R \approx 0.9507$.

4.2. Effective reproduction number $R(t)$

Study regarding the time span of an epidemic is very crucial and can be achieved to a certain extent through the estimation of $R(t)$, the effective reproduction number. It is defined as the actual average number of secondary cases from a typical primary case at time t [33]. The value of $R(t)$ provides information about the severity of the disease over different time points and alert epidemiologists to suggest about the control measures [30]. We estimate $R(t)$ from the daily new infection curve of the infected COVID-19 cases data by using the following equation derived from the renewal equation of a birth process:

$$R(t) = \frac{b(t)}{\int_{a=0}^{\infty} b(t-a)g(a)da}, \quad (4.5)$$

where, the term $b(t)$ corresponds to the number of new cases in the day t and the term $g()$ is the generation interval distribution for a disease [31].

We derive the expression of the generation interval distribution $g(t)$ from the model (2.1) by applying the method discussed in [31, 34]. The rates of leaving the exposed and infectious compartments are indicated by b_1, b_2

and b_3 . These quantities are constant and extracted from the model (2.1) as $b_1 = \sigma$, $b_2 = \alpha$ and $b_3 = \gamma_a$. Moreover, the generation interval distribution is the convolution of three exponential distributions with a mean $T_c = 1/b_1 + 1/b_2 + 1/b_3$. Following [31, 35], we have the following explicit expression for the convolution:

$$g(t) = \sum_{i=1}^3 \frac{b_1 b_2 b_3 \exp(-b_i t)}{\prod_{j=1, j \neq i}^3 (b_j - b_i)}, \quad (4.6)$$

with $t \geq 0$. The validity of the above relation (4.6) holds for a minimum threshold value of the force of infection Λ , defined as $\Lambda > \min(-b_1, -b_2, -b_3)$ [34].

Using the daily COVID-19 incidence data and applying the expression of $g(t)$ in equation (4.6), we estimate $R(t)$ from equation (4.5). Fig. 4 shows the time evolution of the effective reproductive number $R(t)$ to the COVID-19 outbreak in India, from 2nd March, 2020 to 24th March, 2020. The result is shown here for $t \geq 3$, since, the method used here to derive the expression of $R(t)$ is not applicable for lower values of t . Here the value of $R(t)$ lies between 2 to 6 most of the times. The low value of $R(t) = 0$ appears on the second point (see Fig. 4) due to non occurrence of new cases at 6th March 2020 also the high value of $R(t) \approx 7.54, 8.86$ occurs on 6th, 17th day of the outbreak due to the high number of new cases found on these days. It implies that the disease continues to infect the more and more people during that period. It is worthy to remember that, at this point Govt. of India announced a lock-down to break the chain of infection spread else it will be almost impossible to control the spread after a certain period of time.

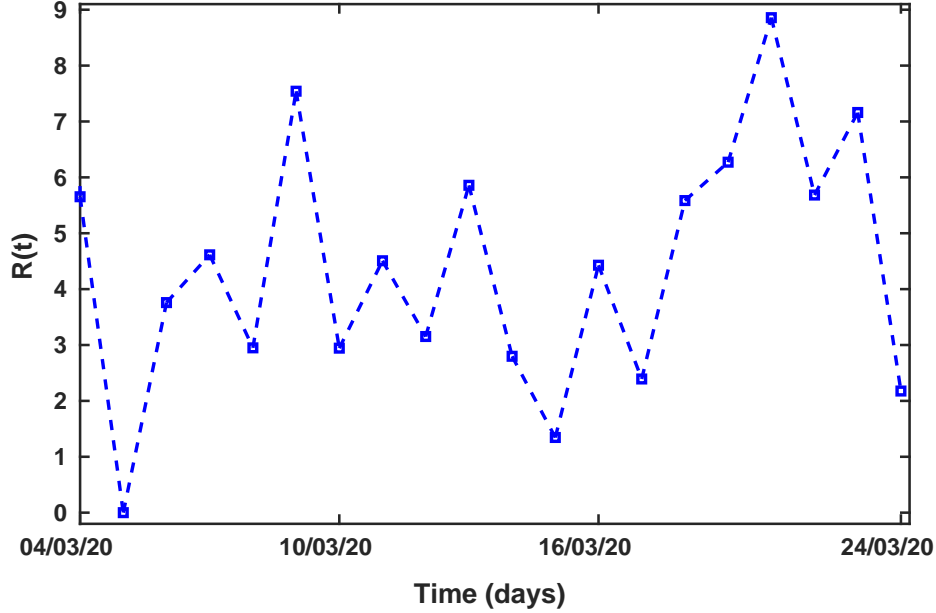


Figure 4: The effective reproductive number $R(t)$ versus time t (days) of the COVID-19 outbreak in India during 2nd March, 2020 to 24th March, 2020. The parameter values are taken from Table 1.

5. Effect of intervention

In this section, we study the effect of intervention strategies in reducing the new COVID-19 cases through our model. Intervention strategies includes the control measures such as lock-down, spreading awareness program through media, proper hand sanitization, etc. which results in slowing down the disease transmission process. In terms of model parameter, the implementation of intervention implies that there would be a reduction in the disease transmission rate β . This reduction in the transmission rate is considered as the strength of the intervention, k . In the presence of intervention, the parameter β is modified as $(1 - k)\beta$ throughout the period of implementation.

Starting from the initial date of outbreak, we consider a period of 210 days (i.e 7 months) and study the impact of intervention during that period.

Speaking in terms of actual date, we consider the time period 2nd, March, 2020 to 27th September, 2020.

We consider two types of intervention scenarios: (i.) the strength of the intervention (k) is fixed throughout the implementation period, (ii.) the strength of intervention is varied over the implementation period.

5.1. Scenario 1

In this intervention scenario, the strength of the intervention k is taken to be fixed over the implementation period. We first consider the situation without any intervention (i.e $k = 0$). Our model (2.1) is simulated for 210 days to observe the dynamics of the disease in the absence of any intervention, using the in-built function `ode45` in MATLAB (Mathworks, R2014a). From Fig. 5, we see that the number new cases grows exponentially and attains the maximum at the end of the June. It is also observed that maximum of 26.3593 million new cases can occur in the absence of any intervention during the period (see Table 2). However, in the subsequent time, decreasing trend in the new cases is noted.

Now we study the efficiency of the intervention by varying the strength of the intervention (k). Regarding the initiation of the control, we follow the same date when Govt. of India implemented nation-wide lock down i.e 25th March, 2020. Throughout the study we consider this date as the initial date of implementing the intervention.

For the low value of the intervention strength (i.e for $k = 0.20$), it is observed that the time for the occurrence of peak of the outbreak is slightly delayed than that of without intervention scenario (see Fig. 5). The peak of the outbreak is shifted to the end of the month July. In this case, maximum 19.7233 million new cases can occur (see Table 2). If the strength of the intervention is increased further (for $k = 0.40$), the peak of the outbreak decreases and the occurrence of the peak shifted to the end of September (see Fig. 5). In this case, the maximum number new cases in a single day reduces to 11.2784 million (see Table 2).

Now we consider the higher values of intervention strength. For $k = 0.75$, the new cases tend to decrease within a week (see Fig. 5) from the date of implementation and in such a case maximum of 102 new cases can occur (see Table 2). If the strength is increased further (i.e for $k = 0.85$ and 0.95) we see that the disease can be effectively eradicated within 1 to 2 months from the initial date of implementing intervention (see Fig. 5).

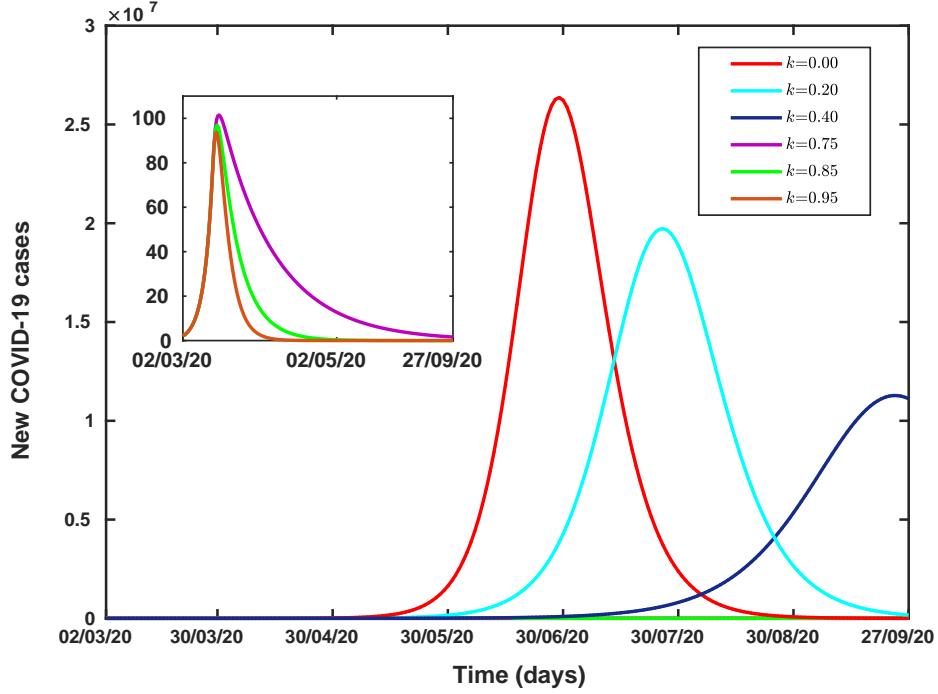


Figure 5: Trajectories of the new COVID-19 cases for different values of the strength of the intervention (k). The zoomed in figures for $k = 0.75, 0.85$ and 0.95 are displayed in the insets. All the parameters are taken from Table 1.

Next we quantify the cumulative number of new cases at the end of the time duration under consideration (i.e at the end of 27th September, 2020) for different values of strength of intervention (k). From Fig. 6, we see that, the final number of cumulative new cases gradually decreases if the strength of the intervention is increased. However, for higher values of k (i.e for $k \in [0.7, 0.95]$), the final cumulative cases are reduced significantly. The actual number of final cumulative cases for different values of k are presented in Table 2.

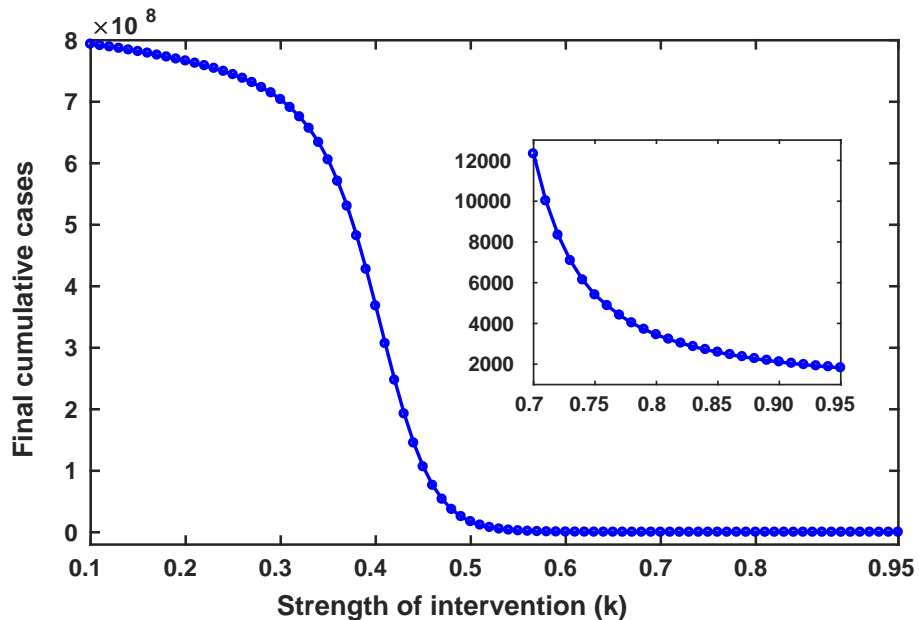


Figure 6: Final cumulative new cases for different values of strength of intervention (k). The zoomed in figure is displayed in the inset.

Strength of the intervention (k)	Final cumulative cases	Maximum number of new cases
0.0	810.5521 million	26.3593 million
0.2	766.2467 million	19.7233 million
0.4	367.8458 million	11.2784 million
0.6	0.3141 million	0.0072 million
0.7	12359	107
0.75	5424	102
0.85	2587	97
0.95	1814	94

Table 2: Actual number of final cumulative cases and maximum number of new cases for different values of k .

Next we evaluate the maximum number of new cases during the time period 2nd March, 2020 to 27th September, 2020 for different values of k (see Fig. 7). The actual number of maximum new cases for different values of k are tabulated in Table 2.

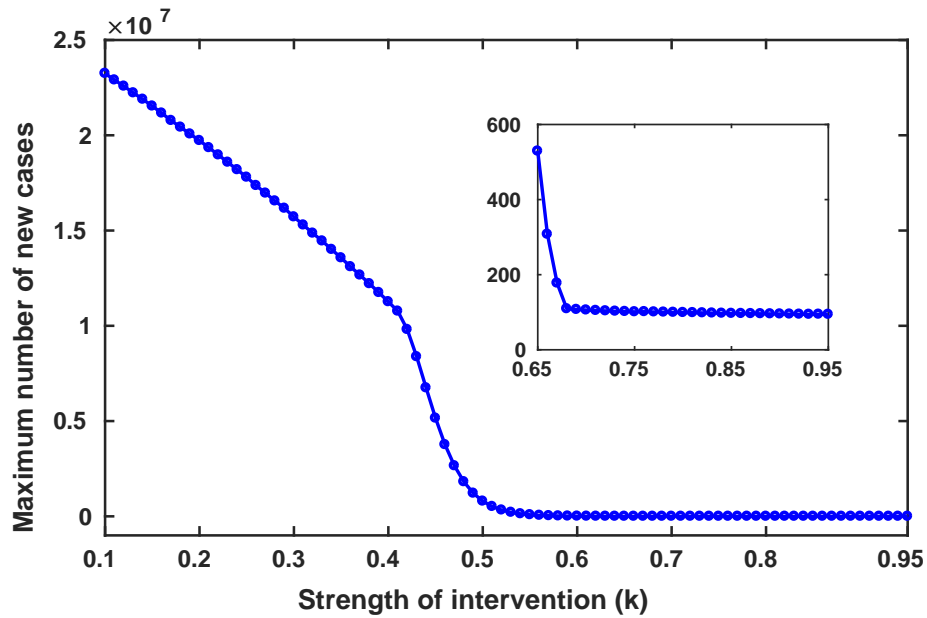


Figure 7: Maximum number of new cases for different values of strength of intervention (k) for the time period 2nd March, 2020 to 27th September, 2020. The zoomed in figure is displayed in the inset.

The percentage of relative reduction in the final cumulative new cases for different k is presented in Fig. 8. It is observed that interventions having lower strengths (i.e for $k \in [0.1, 0.4]$), can reduce up to 54.6% final cumulative cases. However, if the strength of the intervention is considered to be higher then almost 99.8% reduction in the final cumulative cases can be achieved.

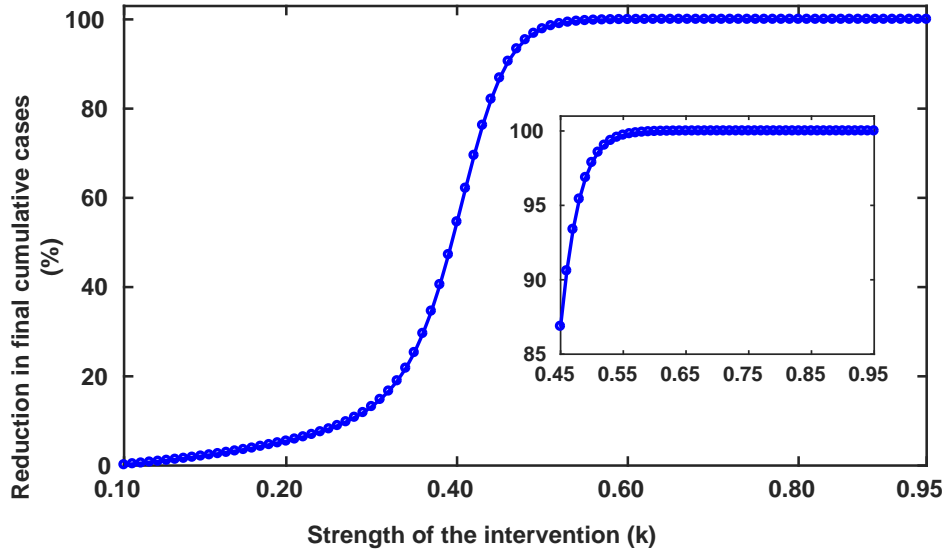


Figure 8: Percentage of relative reduction in the final cumulative new cases for different values of strength of intervention (k).

5.2. Scenario 2

In this scenario, instead of considering the fixed value of k over the whole time interval after the initiation of intervention as in scenario 1, we vary the value of k over the implementation period. The implementation period i.e 25th March, 2020 to 27th September, 2020 is divided into three time windows. The first window consists of 21 days whereas the second and third window consists of 35 days and 131 days respectively.

We first decrease the value of k from first window to third window. The values of k taken in the three windows are 0.9, 0.7 and 0.6 respectively. We observe from Fig. 9 that in this case, the new cases decreases in the first window and remains almost unchanged in the second window where the value of k is decreased slightly than first window. However, when the value of k is decreased further in the third window, the new cases tend to increase rapidly. This implies that the relaxation in the interventions strategy over the time does not end up with the disease eradication.

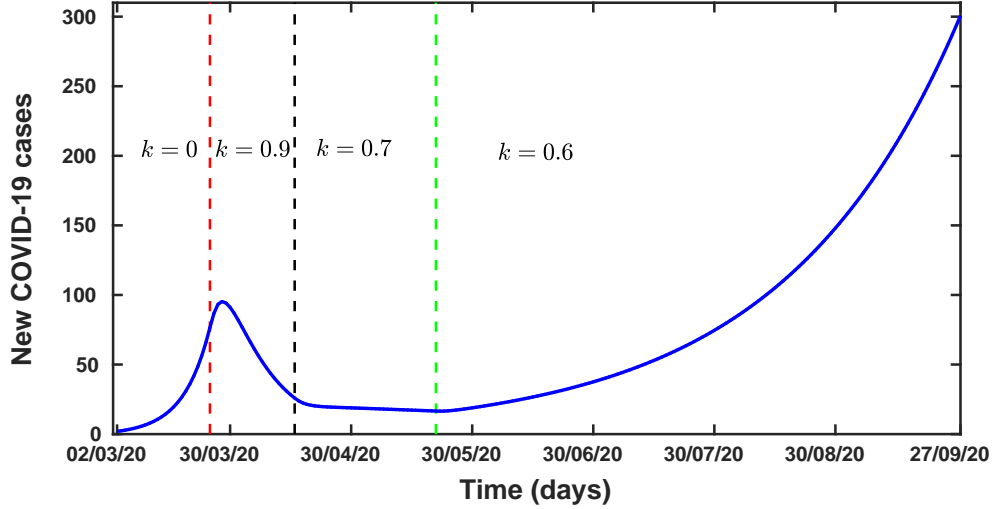


Figure 9: Time evolution of the new COVID-19 cases for the period 2nd March 2020 to 27th September, 2020. In each time window the strength of the intervention (k) is given. The strength of the intervention is decreased in the subsequent time windows after the initiation of the intervention

Next we consider the opposite case i.e we increase the value of k from first window to third window. The values of k are taken as 0.3, 0.65 and 0.8 respectively in the respective time windows. It is observed from Fig. 10 that the new cases tends to increase in the first two windows. However, in the third window where the value of k is high enough, the new tend to decrease. This essentially implies that the intervention should be strengthened over the time to eradicate the disease effectively.

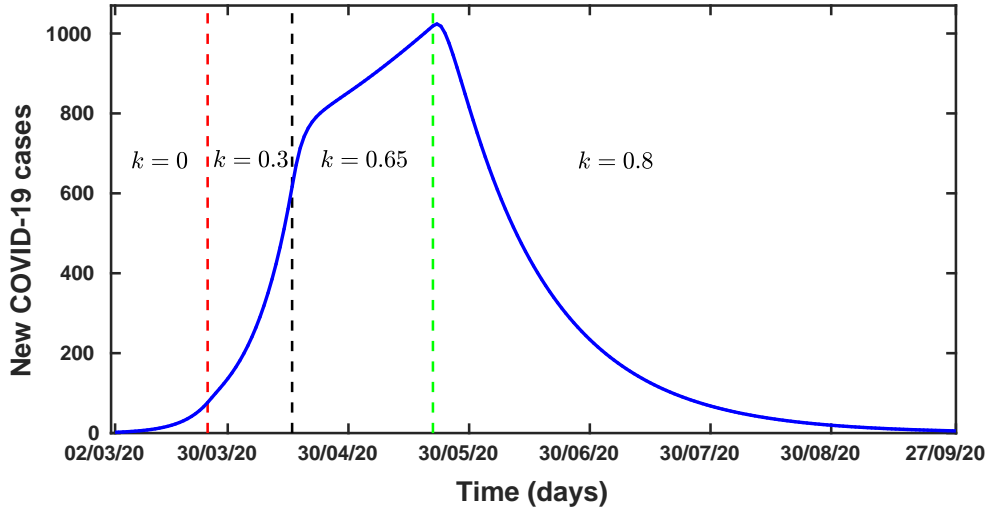


Figure 10: Time evolution of the new COVID-19 cases for the time period 2nd March 2020 to 27th September, 2020. In each time window the strength of the intervention (k) is given. The strength of the intervention is increased in the subsequent time windows after the initiation of the intervention.

6. Discussion and conclusion

The COVID-19 outbreak in India is a potential threat to the country due to its rapid spread. Mathematical models are very effective tools to predict the time span and pattern of the outbreak. Moreover, mathematical models can also provide useful insights regarding the impact of intervention in lowering the disease incidence.

In this study, we proposed a deterministic compartmental model to describe the disease transmission mechanism among the population. We considered the initial phase of outbreak of the disease COVID-19 in India and fitted our proposed model to the cumulative new reported cases during the period 2nd March, 2020 to 24th March, 2020. Some model parameters are estimated by fitting our model to the cumulative new reported cases during the above mentioned period. By looking at the estimated parameters, it is observed that the rate of disease transmission is quite high which basically implies the high infectiousness of the disease. The percentage of the symptomatic individuals coming from exposed individuals is estimated to be more than 52%,

whereas the percentage of the asymptomatic and quarantined individuals are estimated as more than 27% and 20% respectively. This indicates that the contribution of the asymptomatic population to COVID-19 cases in India is not negligible.

Based on the estimated parameters and actual COVID-19 incidence data, we estimated basic reproduction number, effective reproduction number and epidemic doubling time to get an overview of this initial phase of outbreak. We obtained the estimate of basic reproduction number \mathcal{R}_0 as 4.1849 with upper and lower bounds are 4.5014 and 3.8799 respectively. This high value of \mathcal{R}_0 basically captures the outbreak scenario in India. The effective reproduction number ($R(t)$) provides information about the severity of COVID-19 over different time points. In our study, the values of $R(t)$ lie between 2 and 6 most of the time. This is also confirms high transmissibility of the disease. The epidemic doubling time is also estimated to be approximately 3.34 days. This suggests that the rate of disease transmission need to be controlled otherwise a large proportion will be affected within a very short period of time

We studied the impact of intervention in reducing the disease burden. We basically considered the preventive measures such as lock-down, spreading of awareness program through media, proper hand sanitization, etc. which slow down the disease transmissibility. Two intervention scenarios are considered depending on the variability of the intervention strength over the period of implementation. In the first scenario, we fixed the strength of the intervention throughout the period of implementation and studied the impact of intervention for different level of intervention efforts. In this scenario, our study reveals that higher intervention effort is required to control the disease outbreak within a shorter period of time. In the second scenario, the whole implementation time are divided into three time windows and in each of the window, the intervention strength is taken to be different. In such a scenario, our analysis shows that the strength of the intervention should not be relaxed over the time rather the intervention should be strengthened to eradicate the disease effectively. Designing the efficient intervention strategy is one of the crucial factor to curb the disease spread in an outbreak situation. In this regard, our study suggests that strict intervention should be implemented by the Government in the subsequent period of this outbreak. We believe that the findings obtained from this study can provide fruitful insights in framing policies regarding the control of COVID-19 in India.

Acknowledgements

Abhishek Senapati is supported by the research fellowship from Council of Scientific & Industrial Research, India (Grant no: 09/093(0167)/2015/EMR-I), Government of India.

Conflict of interest

The authors declare that there is no conflict of interest.

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