Universality and herd immunity threshold: Revisiting the SIR model for COVID-19

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COVID-19 pandemic has been raging all around the world for almost a year now, as of November 1, 2020. In this paper, we try to analyze the variation of the COVID-19 pandemic in different countries in the light of some modifications to the SIR model. The SIR model was modified by taking time-dependent rate parameters. From this modified SIR model, the basic reproduction number, effective reproduction number, herd immunity, and herd immunity threshold is redefined. The re-outbreak of the COVID-19 is a real threat to various countries. We have used the above-mentioned quantities to find the reasons behind the re-outbreak of this disease. Also, the effectiveness of herd immunity to prevent an epidemic has been analyzed with respect to this model. We have also tried to show that there are certain universal aspects in the spread and containment of the disease in various countries for a short period of time. Finally, we have also analyzed the current pandemic situation in India and have attempted to discuss the possibilities in order to predict its future behavior using our model.

Keywords: SIR model; reproduction number; herd immunity; herd immunity threshold; universality; re-infection; intervention.

1. Introduction
Nowadays, the COVID-19 pandemic is spreading throughout various countries. Due to this pandemic, a total of 213 countries have been affected, 47 million people are already infected and 1.2 million people have died worldwide, as of November 1, 2020.1 Also in India, a total of 8.2 million people have been infected and 0.12 million people died, during this period.1 The worrying thing is that these numbers are still increasing on a daily basis. Also, some countries like Italy, Russia, Germany have faced a re-outbreak of this disease. COVID-19 pandemic is not only affecting public health but also affecting social health, world economy, and countries’ economy. Therefore, it is very important to understand the behavior of this pandemic to prevent such widespread damage.

In this article, we mainly take the basic susceptible-infected-recovered (SIR) model.2 SIR model is a well-known and widely used model. The SIR model and its successors like SEIR, SIRS, SEIRD, SEIAR have been used before in various epidemics like influenza, dengue, Ebola.3–9 These models are also being used to predict and understand the behavior of the COVID-19 pandemic.10–18 There are already various papers that are present on this topic,10–22 still we have tried to understand this pandemic from a different point of view.

Here, we modify the basic SIR model by taking the time-dependent rate parameters, (i) Infection rate ($\beta$), (ii) Removed rate ($\gamma$). From this modified SIR model we re-define the four important
quantities, which are, (i) Basic reproduction number ($R_0$), (ii) Effective reproduction number ($R_i$), (iii) Herd immunity of the population ($HI$), (iv) Herd immunity threshold of the population ($HIT$).

The herd immunity of a population ($HI$) is the fraction of immune people, against a disease, present in there. Herd immunity of a population is a key to decrease an epidemic. Herd immunity can increase in two different ways, (i) naturally, by increasing the number of infected people, and (ii) artificially, by vaccines.

Nowadays when an epidemic starts in a country, the administration of that country usually intervenes and imposes various restrictions in the form of partial or full lockdowns as in the COVID-19 case. As a result of this, the herd immunity of the population is forced to remain low. Despite the low herd immunity, it is also seen that, as in the case of COVID-19, the number of infected cases reached some peak value and then started to fall off in many countries. This requires a different explanation from the ones that have been previously proposed. We have tried to explain this aspect with the modified SIR model and have used the data of COVID-19 from various countries to verify them. The data used for this analysis is taken from “The Humanitarian Data Exchange”.

However, such low herd immunity of a population can bring a resurgence to the epidemic. This phenomenon is often termed in literature as reinfection or re-outbreak. Various authors have addressed this issue earlier. Here, we have tried to discuss this fact with the help of Effective reproduction number ($R_i$), Herd immunity of the population ($HI$), and Herd immunity threshold of the population ($HIT$).

As we have mentioned earlier, governments resort to several methods to mitigate a pandemic-like situation, as seen from the present COVID-19 situation. Thus the behavior and the dynamics of the COVID-19 pandemic could have common features in different countries. We have tried to address this aspect by searching for universal features in the parameters of our model.

The paper is organized as follows: Section 2 deals with a discussion of the basic and modified SIR models along with the reproduction numbers, herd immunity, and herd immunity threshold. Section 3 consists of various simulations of the modified SIR model by considering imaginary parameter values and conditions. In section 4 we try to find the time variation of the model parameters in light of the COVID-19 data for several countries. In section 5 we present a brief study of the COVID-19 behavior in India and the last section, we present our concluding remarks.

2. Model description

Here we discuss a simple epidemic model which is known as SIR model. If we assume that the population is homogeneously mixed then the model equations can be written as,

$$\frac{dS}{dt} = -\beta \frac{S}{N} I, \quad S(0) = S_0$$

$$\frac{dI}{dt} = \beta \frac{S}{N} I - \gamma I, \quad I(0) = I_0$$

$$\frac{dR}{dt} = \gamma I, \quad R(0) = 0$$

$S(t)$ = Number of susceptible people at time $t$.
$I(t)$ = Number of active cases or the number of infectious people at time $t$.
$R(t)$ = Number of removed cases or the number of infectious people at time $t$. Removed persons are those who were previously infected but now recovered or dead.
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\[N = \text{Total population in a community or a region or a country.}\]
\[\beta = \text{Infection rate.}\]
\[\gamma = \text{Removed rate of the infected people.}\]

Hence, \(S(t) + I(t) + R(t) = N\) = Total number of people in a population.

\(I_{\text{tot}}(t)\) denotes the total number or the cumulative number of infected cases at time \(t\). So, \(I_{\text{tot}}(t) = I(t) + R(t)\). Hence the rate of increase of \(I_{\text{tot}}(t)\) can be written as,

\[
\frac{dI_{\text{tot}}}{dt} = \frac{dI}{dt} + \frac{dR}{dt} = \beta \frac{S N I}{N} \tag{4}
\]

Also, we know that \(S(t) = N - I(t) - R(t) = N - I_{\text{tot}}(t)\). Hence,

\[
\frac{dI_{\text{tot}}}{dt} = \beta I \left(1 - \frac{I_{\text{tot}}}{N}\right) \tag{5}
\]

This equation looks like the logistic equation of population growth. However, the main difference is that the increment rate of the total infected cases depends on the number of active cases rather than on itself.

An epidemic will start to spread if the number of infected people in a population starts to increase with time, which means,

\[
\frac{dI}{dt} > 0. \tag{6}
\]

Hence, from equation 2 we can write,

\[
\frac{dI}{dt} = \beta \frac{S}{N} I - \gamma I > 0. \tag{7}
\]

Similarly, an epidemic will start to decrease when,

\[
\frac{dI}{dt} = \beta \frac{S}{N} I - \gamma I < 0. \tag{8}
\]

Also, at the peak of an epidemic,

\[
\frac{dI}{dt} = \beta \frac{S}{N} I - \gamma I = 0. \tag{9}
\]

2.1. Reproduction number

The reproduction number tells us about the average number of susceptible people who can be infected by an infectious individual.

Basic reproduction number \(R_0\) is a very important quantity that tells us whether an epidemic will start or not. \(R_0\) can be defined as the number of secondary infections due to a single primary infected individual at the initial time of an epidemic.

If at any time \(t\), \(S(t)\) and \(I(t)\) are the numbers of susceptible and infected people respectively then the number of people who will be infected newly is \(\beta \frac{S}{N} I\) per unit time. Now initially the number of infected people in a population is very less, so we can assume \(S(0) \approx N\). Hence initially an infected person can infect \(\beta\) number of susceptible people per unit time. The removed rate is \(\gamma\), hence on average, an infected person will remain infected for \(\frac{1}{\gamma}\) unit of time. So, in this period, an infected person can spread the disease to \(\frac{\beta}{\gamma}\) number of people. Hence this is the number of secondary infections due to a single infected individual. Thus \(R_0 = \frac{\beta}{\gamma}\).

So, from equation 7 we can say that initially, an epidemic will start to grow if,

\[
\frac{\gamma}{\beta} < \frac{S(0)}{N} \quad (I \neq 0) \tag{10}
\]
or,
\[ \frac{\beta}{\gamma} > \frac{N}{S(0)} \overset{\approx}{=} 1 \] (11)

or,
\[ R_0 = \frac{\beta}{\gamma} > 1 \] (12)

So, if \( R_0 > 1 \) then a disease will start to spread, and if \( R_0 < 1 \) then the spread of the disease will die down.

\( R_0 \) describes only the initial behavior but not the late-time behavior of an epidemic. So, we introduce another important quantity which is known as the instantaneous reproduction number or effective reproduction number and denoted as, \( R_i(t) \). At any time \( t \), the number of susceptible people can be infected by a single infected individual is \( \frac{\beta S}{N} \) per unit time. Hence on average, a single infected individual can infect a total of \( \frac{\beta S}{\gamma} \) number of people until that individual is removed. Thus,
\[ R_i(t) = \frac{\beta S(t)}{\gamma} \] (13)

Now if we assume that the infection rate \( \beta \) and recovery rate \( \gamma \) are constants then, \( R_0 = \frac{\beta}{\gamma} \) and \( R_i(t) = R_0 \frac{S(t)}{N} \).

As, \( S(t) \leq N \), so, \( R_i(t) \leq R_0 \). So as time goes by, \( R_i(t) \) decreases from \( R_0 \).

Like the previous way, we can find that an epidemic will increase if \( R_i(t) > 1 \) and will decrease if \( R_i(t) < 1 \).

At the peak of an epidemic, the effective reproduction number, \( R_i(t) = 1 \) (from equation 9).

### 2.2. Herd immunity

Immune people in a population are those who are currently infected \( (I) \) and who were infected, which means the removed people \( (R) \). So, at any time \( t \) total number of immune people in a population is \( I(t) + R(t) = I_{\text{tot}}(t) \).

Herd immunity in a population is defined as the fraction of the population which is immune to a disease\(^{27,28}\). So, to stop the spread of the disease there have to be a minimum fraction of immune people in a population and which is called the "Herd immunity threshold (HIT)".

From equation 8, we can say that an epidemic will start to decrease when,
\[ \frac{\gamma}{\beta} < \frac{S}{N} \] (14)

Now fraction of immune people at time \( t \) is
\[ \frac{I(t) + R(t)}{N} = \frac{N - S(t)}{N} = HI_i(t) \] (15)

\( HI_i(t) \) is the instantaneous herd immunity of a population at any time \( t \). So from equation 14, we can write,
\[ 1 - \frac{\gamma}{\beta} < 1 - \frac{S}{N} = HI_i(t) \] (16)

Hence an epidemic will stop if,
\[ HI_i(t) > 1 - \frac{\gamma}{\beta} = HIT \] (17)
Hence herd immunity threshold defined as,

$$HIT = 1 - \frac{\gamma}{\beta}$$

If $\beta$ and $\gamma$ are constant of time then we can write,

$$HIT = 1 - \frac{\gamma}{\beta} = 1 - \frac{1}{R_0}$$

So, if $HI_i(t) < HIT$ then the epidemic will increase and will decrease if, $HI_i(t) > HIT$.

So, at the peak of an epidemic, $HI_i(t) = HIT$ (from equation 9).

### 2.3. Modifications to the SIR model

In this section, we present certain modifications to the SIR model. The spread of an epidemic depends on the infectivity of a disease which is an universal property of the virus. However, it also depends on the social behavior and social interaction of a region, which can vary with time. Also, when an epidemic starts, governments in those regions try to contain the spread of the disease by locking that region down or part of it, making rules to prevent infections (like maintaining social distancing, wearing masks, and spreading awareness among the people). Hence the rate of infection $\beta$ will not be constant always. Here we assume that the rate of infection $\beta$ is a time-dependent quantity.

Also removed rate $\gamma$ can be time-dependent. It is mentioned earlier that increment of the removed rate depends not only on the recovery of infected people, also on the death rate or fatality rate of the disease. So, in general, the removed rate can be changed if the recovered rate or death rate is changed. Initially, knowledge among the doctors and scientists is limited for a new disease. But as time goes by the knowledge about that disease will increase and this may help to improve the recovered rate. On the other hand, there are factors such as medical infrastructure, infectivity of the disease etc. which directly affect the recovered rate and the death rate. Thus it is difficult to disentangle these two effects in the current purview of our model and it would be only possible to predict the total increment of the removed rate as a function of both. We would be interested to extend this model and study these two effects separately in future to better predict the behaviors of the deceased rate and the recovered rate.

Due to these modifications, the relation of basic reproduction number becomes $R_0 = \frac{\beta(t)}{\gamma(t)}$ because the basic reproduction number is a quantity that is measured initially. Also, the instantaneous reproduction number or effective reproduction number is given by, $R_i(t) = \frac{\beta(t)}{\gamma(t)} \frac{S(t)}{N}$.

As we discussed in subsection 2.1, an epidemic will increase if $R_i(t) > 1$ and will decrease if $R_i(t) < 1$. At the peak of the epidemic $R_i(t) = 1$.

The instantaneous herd immunity of a population, $HI_i(t)$ is given by, $HI_i(t) = 1 - \frac{N(t)}{N}$. Now, for the basic SIR model, herd immunity threshold ($HIT$) is a constant in time since $\beta$ and $\gamma$ are constant quantities. But here herd immunity threshold is a time-dependent quantity and is given by, $HIT(t) = 1 - \frac{\gamma(t)}{\beta(t)}$. Hence the maximum possible value of herd immunity threshold is $HIT_{max} = 1 - \left(\frac{\gamma(t)}{\beta(t)}\right)_{\text{max}}$.

As we discussed in subsection 2.2, an epidemic will increase if $HI_i(t) < HIT(t)$ and will decrease if $HI_i(t) > HIT(t)$. At the peak of the epidemic $HI_i(t) = HIT(t)$.

From the basic SIR model, we can describe only one way to prevent an epidemic in terms of herd immunity and herd immunity threshold. This is,

- An epidemic can be prevented by increasing herd immunity ($HI_i(t)$) of the population than the herd immunity threshold value ($HIT$).
However, in the modified SIR model, the herd immunity threshold is a time-dependent quantity. So, we can describe two different ways to prevent an epidemic. The first way is the same as the previous one. The second way is,

- An epidemic can be prevented by decreasing the herd immunity threshold ($HIT(t)$) to the current herd immunity of the population ($HI(t)$).

Herd immunity threshold ($HIT$) can be reduced by decreasing the infection rate ($\beta(t)$) or increasing the removed rate ($\gamma(t)$).

### 2.4. Estimating $\beta(t)$ and $\gamma(t)$ from the SIR model

From equation 2 and equation 3 we can write,

$$\beta(t) = \frac{N}{I(N - I - R)} \left( \frac{dI}{dt} + \frac{dR}{dt} \right)$$

(20)

where,

$I$ = Number of infected or active cases at time $t$.  
$R$ = Number of removed cases at time $t$.

From equation 3 we can write,

$$\gamma(t) = \frac{1}{I} \frac{dR}{dt}$$

(21)

Hence, from equations 20 and 21, we can estimate $\beta(t)$ and $\gamma(t)$. From these time dependent rate parameters, we can easily estimate the variation of $HIT(t)$ and $R_i(t)$.

### 3. A thought experiment

Let a region initially contain a total of $N = 10000$ people where a disease starts to spread with infection rate $\beta = 0.7 \text{ day}^{-1}$. Also, let the removed rate for this disease be $\gamma = 0.15 \text{ day}^{-1}$. Hence, the basic reproduction number $R_0$ has a value, $R_0 \approx 4.6667 > 1$, implying an epidemic will start to grow in this region.

Let there initially be only one infected person in the region, which means $I(0) = 1$. Thus, the initial number of susceptible people is $S(0) = N - I(0) = 9999$ and removed people is $R(0) = 0$. If we simulate the SIR system with the above-mentioned values of the parameters and the initial conditions, we get the results which are shown in Figure 1.

In this system, the herd immunity threshold has value $HIT = 0.7857$. Thus, when 78.57% of people of this population are immune from the disease, the epidemic will start to decrease. From figure 1, we further see that the effective reproduction number $R_i(t)$ is reduced from $R_0$ to unity, and then it is reduced further. Similarly, we can see that herd immunity $HI_i(t)$ is increased from zero to $HIT$, and then it is increased further and has a value greater than $HIT$. Recalling that an epidemic will start to decrease after $I(t)$ attains the peak (as previously discussed). Let, at $t = t_p$, $I(t)$ attains its peak. So, from figure 1 we can see that at $t_p$, $R_i(t_p) = 1.0$ and $HI_i(t_p) = HIT = 0.7857$. Here, $t_p = 19.47$ days. Hence, approximately 20 days are needed to start to decrease the spread of the disease. At the end of the epidemic, which means, at $t \rightarrow \infty$, the number of susceptible persons left in the population is $S(\infty) \approx 97$. This is very small compared to the whole population. Also at, $t \rightarrow \infty$, $R_i(\infty) = 0.0457$ and $HI_i(\infty) = 0.9902$. Hence, at the end of the epidemic, the herd immunity of the population is increased than the $HIT$ which has the value 0.7857 and the effective reproduction number reduced from one. Thus, there is no chance of a re-outbreak in this population.
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Fig. 1: Simulation of the SIR model. The left picture of row one shows how $S(t)$, $I(t)$, and $R(t)$ is varying with time. The right picture of row one shows how effective reproduction number $R_i(t)$ varies with time. The picture of row two shows us the variation of herd immunity $HI_i(t)$ with time.

So, we can see that almost all of the people are infected once during this epidemic. If the fatality rate of this disease is very low then technically fewer people will die. But the problem is that the large number of infected cases will create pressure on the medical facilities, which can make the situation worse. Thus many people can die because of not getting proper treatment. But if the fatality rate is large then the situation will be very grave. In this situation, the government and local authorities will intervene and will put some restrictions and safety rules to prevent the epidemic. Due to these restrictions and rules, the infection rate will decrease and thus fewer people will be infected during this epidemic.

Let, at time $t = t_I = 10$ government starts to intervene. Here we consider two cases of the government interventions,

1. Intervention-1: At $t = 10$, $\beta$ decreases from $0.7 \text{ day}^{-1}$ to $0.25 \text{ day}^{-1}$. Means, $\beta(t) = 0.7 \text{ day}^{-1}$ when $t < t_I$ and $\beta(t) = 0.25 \text{ day}^{-1}$ when $t \geq t_I$.

2. Intervention-2: At $t = 10$, $\beta$ decreases from $0.7 \text{ day}^{-1}$ to $0.35 \text{ day}^{-1}$. Means, $\beta(t) = 0.7 \text{ day}^{-1}$ when $t < t_I$ and $\beta(t) = 0.35 \text{ day}^{-1}$ when $t \geq t_I$.

From the $I(t)$ vs. $t$ plot of figure 2 we can see that due to the government’s intervention, the peaks are flattened than the no intervention case. Also, it is seen in figure 2 that due to government’s intervention at $t = t_I = 10$, the curve of $R_i(t)$ decreases fast as compared to no intervention.
Fig. 2: Plots for the number of active cases $I(t)$ and the effective reproduction number $R_i(t)$ for different interventions. The left plot is $I(t)$ vs. $t$ plot for three different interventions. The right plot is $R_i(t)$ vs. $t$ plot for three different models for interventions.

We found that at the end of the epidemic, the number of susceptible people left in the population is approximately 3111 and 1290 for intervention-1 and intervention-2 respectively. So, interventions help to decrease the total number of infections. Also from figure 2, we can see that if the intervention is more strict then the epidemic will take more time to reach the peak.

Fig. 3: The plot of the variation of herd immunity $H_i(t)$ with time for intervention-1 (left) and intervention-2 (right).

Figure 3 shows the variation of herd immunity $H_i(t)$ for the two interventions. But we can see that there are some basic differences between these herd immunity plots. For both cases, the maximum value of herd immunity threshold is $HIT_{\text{max}} = 0.7857$. Due to the intervention, the herd immunity threshold value is reduced from the maximum value to 0.4 and 0.5714 for intervention-1 and intervention-2 respectively. Here, the reduced value of the herd immunity threshold due to the intervention is represented by $HIT_{\text{in}}$. As, the difference between the $HIT_{\text{max}}$ and $HIT_{\text{in2}}$ for intervention-2 is small, thus the herd immunity at the end of the epidemic ($H_I(\infty)$) not just goes beyond the $HIT_{\text{in2}}$ also it crosses $HIT_{\text{max}}$. But for intervention-1, the herd immunity of the population crosses $HIT_{\text{in1}}$ but could not able to cross the $HIT_{\text{max}}$. 
Fig. 4: Two possible examples of re-outbreak of the epidemic due to negligence of safety rules by the population or easing restriction by the government. The first column is an example where negligence starts at $t_N = 55$ and the second column is an example where negligence starts at $t_N = 90$. The top row shows how $I(t)$ is varying with time. The middle row shows how effective reproduction number $R_i(t)$ vary with time. The bottom row shows us the variation of herd immunity $HI_i(t)$ with time.

3.1. Re-outbreak possibilities for interventions

For intervention-1

For intervention-1, the herd immunity of the population $HI_i(\infty)$ does not cross the $HIT_{max}$, so there can be a re-outbreak of the epidemic because of the increment of $\beta$. $\beta$ can be increased due
to the negligence of the safety rules by the population or maybe easing the restrictions by the
government. We assume that negligence starts at $t_N$. So, there can be two possibilities: (a) $\beta$
increases to such an amount that $HIT(t_N) > HI_i(\infty)$, (b) $\beta$ increases to such an amount that
$HIT(t_N) < HI_i(\infty)$.

Figure 4 shows the two possible scenarios of the first case. As, in this case $HIT(t_N) > HI_i(\infty)$,
thus there will always be a chance of re-outbreak of the epidemic. Here we consider two examples
and it has been assumed that the negligence starts at $t_N = 55$ and $t_N = 90$ respectively. Also, let $\beta$
increased from 0.25 to 0.6 in both examples.

From figure 4 we can see that the second peak occurs at $t_{p2} = 64.12$ and $t_{p2} = 123$ for the
two consecutive examples. After the second outbreak, we can see that the herd immunity of the
population goes beyond the $HIT_{max}$ for both examples.

![Graphs](image.png)

Fig. 5: Re-outbreak for the intervention-1. The left picture of row one shows how $I(t)$ is varying with time.
The right picture of row one shows how effective reproduction number $R_0(t)$ vary with time. The picture
of row two shows us variation of herd immunity $HI_i(t)$ and herd immunity threshold $HIT(t)$.

Here, we have to remember that the accurate value of $HIT_{max}$ of an epidemic is impossible to
find. Because $HIT_{max}$ not only depends on the virus characteristics, it also depends on the social
behavior of a region. Also, $HIT_{max}$ can change from country to country and between various
mutation states of a virus. Hence, after these outbreaks, there will be no chance of re-outbreak
again. For this example, herd immunity reaches $HIT_{max}$ after the second outbreak. But there can
be a system where herd immunity reaches $HIT_{max}$ after several outbreaks. Also, it is hard to say
when a re-outbreak will start because re-outbreak starts whenever the population will start to neglect the rules or the government will lift the restrictions.

Here, a re-outbreak can also occur when the epidemic is almost at the end ($I(t) \approx 0$). Of course, this re-outbreak cannot occur due to the internal infected people. However, if somehow a small number of susceptible people become infected (maybe for migration, from the tourists, or by some external carrier) then a re-outbreak can again start. Figure 5 shows an example of this kind. Here we assume that the negligence starts at $t_N = 150$ and the $\beta$ value increased to 0.65. But at the time $t_N$, $I(t_N) \approx 0$ thus no outbreak can possible. Let, at time $t_f = 175$, ten susceptible people are somehow infected. Hence $I(t_f) = 10$. Because of this small disturbance, we can see that a second outbreak occurs and the peak of it is at $t_{p2} = 248.2$. So, we can say, until a population crosses the $HIT_{\text{max}}$ there will always be a chance of re-outbreak.

Figure 6 shows an example of the second case. Now, for this second case we assume that $t_N$ is a little bit far from the peak time. At this time herd immunity of the population $HI_i(t_N) \approx HI_i(\infty)$. As, for the second case, $HI_i(\infty) > HIT(t_N)$ hence, $HI_i(t_N) > HIT(t_N)$. So, there is no possibility of re-outbreak. But if $t_N$ is close to $t_p$ then there can be a re-outbreak if $HI_i(t_N) < HIT(t_N) < HI_i(\infty)$. Here we assume that $t_N = 75$ and from this time $t_N$, $\beta$ increased from 0.25 to 0.4.
For intervention-2

For intervention-2 the herd immunity of the population very quickly crosses $HIT_{\text{max}}$ after crossing $HIT_{\text{in}}$. So, there is no chance of re-outbreak.

![Graphs showing no re-outbreak for intervention-2]

Fig. 7: No re-outbreak for intervention-2. The left picture of row one shows how $I(t)$ is varying with time. The right picture of row one shows how effective reproduction number $R_i(t)$ vary with time. The picture of row two shows us variation of herd immunity $HI_i(t)$ and herd immunity threshold $HIT(t)$.

Here we have assumed that the negligence time is $t_N = 55$ and due to this negligence $\beta$ increases to 0.6. Figure 7 shows that there is no increment of active cases, which means no re-outbreak.

### 3.2. Summary

So, the differences between the two interventions are

1. As intervention-1 is stronger than the intervention-2, thus fewer people are infected for intervention-1 than the intervention-2 during this epidemic.
2. For intervention-2, herd immunity of the population crosses the maximum herd immunity threshold value but for intervention-1, herd immunity of the population does not cross the maximum herd immunity threshold value.

So, we can see that there can be various types of interventions, different from strictness. Let, reduced value of the infection rate is represented by $\beta_{in}$. If $\beta_{in}$ is close to the $\beta_{max}$ then we will
say that intervention is a loose one. However, if $\beta_{in}$ lies a little bit far from $\beta_{max}$, then we will say the intervention is a strict one.

Now for both no intervention case and loose intervention case, we saw that the herd immunity of the population crosses the maximum herd immunity threshold. But fewer people are infected in the loose intervention case than the no intervention case. So, we can say that if the government and local authorities decide to fight an epidemic by increasing the herd immunity of the population, then loose intervention will be a good option than the no intervention one.

Now for the strict intervention case, we saw that number of infections is small compared to the others. But problem is that there will always chances of re-outbreak in the population when strict interventions are lifted or loosen (As it is impossible to maintain strict interventions for a very long time).

So, from our model, we can say that, if the goal is to decrease the number of infections then strict intervention will be a good option. Also, if the goal is to increase the herd immunity of the population beyond the maximum herd immunity threshold value then loose intervention will be a good option. However, we have to remember that in real life situation the herd immunity and maximum herd immunity depends on many factors. So, these interventions can have different impacts on the population and might not work well.

4. Our model and Data from Various Countries

In this section, we take COVID-19 pandemic data\textsuperscript{23} of various countries and fit that data by a piece-wise continuous function. From these fitted functions, we calculate the infection rate ($\beta(t)$), removed rate ($\gamma(t)$), and herd immunity of the population ($HI(t)$). Also, we calculate the herd immunity threshold ($HIT(t)$) and effective reproduction number ($R_i(t)$) from fitted active cases ($I$), removed cases ($R$), and estimated infection rate ($\beta$), removed rate ($\gamma$). Here data are taken from that date when the recovered cases and deaths both start to increase steadily with time (except for Brazil). There are large discontinuities in Brazil’s data at the initial time and around the end (01/11/2020) of the data. Thus we have rejected the initial part of the data. We have retained the end part of the $I$ and $R$ data. However, the end part of the active cases data has not been used for the analysis. Table 1 shows such range of dates for various countries. For a country, the first date of the range is considered as the initial time $t=0$.

| Country   | Data were taken from | Data were taken till |
|-----------|----------------------|----------------------|
| USA       | 18/03/2020           | 1/11/2020            |
| India     | 24/03/2020           | 1/11/2020            |
| Peru      | 29/03/2020           | 1/11/2020            |
| Russia    | 29/03/2020           | 1/11/2020            |
| Colombia  | 29/03/2020           | 1/11/2020            |
| Bangladesh| 11/04/2020           | 1/11/2020            |
| Italy     | 18/03/2020           | 1/11/2020            |
| Brazil    | 15/04/2020           | 1/11/2020            |

Table 1: Range of the dates of data taken for various countries.
Fig. 8: Piece-wise continuous function fitting to the data of active cases ($I$) for different countries.
Fig. 9: Piece-wise continuous function fitting to the data of removed cases ($R$) for different countries.
Fig. 10: Time variation of infection rate ($\beta$) of various countries. Insets of the infection rate plots show the part in which we fit it exponentially.
Fig. 11: Time variation of removed rate ($\gamma$) of various countries.
Figures 8 and 9 show how the active cases and removed cases of various countries are varying with time. In figures 8 and 9, the black dashed lines indicate the 95% prediction interval of the fitted data. We don’t show this interval in some plots or some portions of the plot because the intervals are very close to the best fit line.

Figure 8 shows that the active case curves have different behaviors for different countries. Active cases curves are increasing for the countries like USA and are decreasing in countries like India, Bangladesh, Colombia. Also, we find that a re-outbreak of the disease has started in Italy, Russia, Brazil and has ended in Peru. Figures 10 and 11 show how the infection rate ($\beta$) and removed rate ($\gamma$) vary with time in different countries. In these figures, the gray dashed lines represents the discontinuities that come because of the piece-wise continuous fitting of $I$ and $R$ data and not from the model. So, the discontinuities do not have any physical significance. The variation of removed rate is different for different countries. But removed rates are varying in the order of $\sim 10^{-2}$. Besides, we can roughly say that the removed rates are linearly varying with time. Countries like Russia, Bangladesh, Italy, and Brazil have removed rate which is approximately constants with time. Also for India and Colombia, we can approximate that the removed rate is increasing linearly with time. In the USA removed rate is approximately decreasing linearly with time. In the case of Peru, we will also get a linear region in a particular period of time.

The variation of $\beta$ is also different for different countries. However, the initial variation of $\beta$ for different countries are approximately the same. We can see that initially, all the $\beta$s have an approximately exponential decrease. Here we take an exponentially decreasing function $f(t) = ae^{-b(t-t_0)} + c$. We fit this function to that portion of the $\beta$ in which it is approximately decreasing exponentially.

Table 2: This table shows the parameter values of the fitted function in different countries. This also shows the time range in which $\beta$ is decreasing exponentially.

| Country   | a       | b       | c       | $t_0$ in day | time range in days |
|-----------|---------|---------|---------|--------------|--------------------|
| USA       | 0.3639  | 0.0958  | 0.02372 | 1            | 1-71               |
| India     | 0.2032  | 0.2231  | 0.09874 | 0            | 0-69               |
| Peru      | 0.2278  | 0.05027 | 0.03617 | 9            | 9-95               |
| Russia    | 0.2024  | 0.03751 | 0.02375 | 0            | 0-137              |
| Colombia  | 0.1762  | 0.2803  | 0.06477 | 0            | 0-77               |
| Bangladesh| 0.2865  | 0.09588 | 0.03955 | 0            | 0-152              |
| Italy     | 0.3026  | 0.05244 | 0.063245| 5            | 5-94               |
| Brasil    | 0.1074  | 0.04652 | 0.07227 | 10           | 5-140              |

Table 2 shows the parameter values of the fitted function in different countries. We can see that initially, the fitted function has values of order $\sim 10^{-1}$ for all of the countries. Then the values of this function quickly decreased to an order of $\sim 10^{-2}$ (except Italy). So, we can see that there lies a universal feature among the infection rates ($\beta$) for a limited period of time.
Fig. 12: Time variation of instantaneous herd immunity ($H_{I_t}$), herd immunity threshold ($HIT$) of various countries.
Fig. 13: Time variation of effective reproduction number ($R_i$) of various countries.
Figures 12 and 13 show how herd immunity ($HI_i(t)$), herd immunity threshold ($HIT(t)$), and effective reproduction number ($R_i(t)$) vary with time in different countries. In figures 12 and 13, the gray dashed lines again represent the discontinuities that appear because of the same reason as discussed earlier. We can see that herd immunity of the population is very close to zero and this is true for all of the countries. This happens because the total number of infected cases in a country is very small compared to the country’s total population. Now, there are many reasons behind the small number of infected people compared to the country’s population. First of all, as we mentioned earlier, countries take various actions and restrictions to reduce the spread of the disease. Besides that, we only work with the reported cases. However, there can be many unreported cases due to the lack of testing or awareness, which are not taken care of in our model. Under-reporting and asymptomatic cases can affect our work and results. This is one of the major drawbacks of our model.

The variation of the herd immunity threshold is different between the countries. This happens because of the different variations of both $\beta$ and $\gamma$ between the countries. Table 3 shows the maximum values of herd immunity threshold ($HIT_{max}$) in different countries. We can see that the values of $HIT_{max}$ lie between 0.9 to 1.0, except for Peru, Colombia and Brazil.

Table 3: Maximum values of herd immunity threshold ($HIT_{max}$) in different countries.

| Country     | $HIT_{max}$ |
|-------------|-------------|
| USA         | 0.9618      |
| India       | 0.9688      |
| Peru        | 0.7055      |
| Russia      | 0.9690      |
| Colombia    | 0.8123      |
| Bangladesh  | 0.9027      |
| Italy       | 0.9595      |
| Brazil      | 0.6027-0.6951 |

Figure 13 shows that, initial value of $R_i(t)$ varies so much. $R_i(t)$ is not directly calculated from the data. It is estimated from the model. Now, in our model, initial value of $R_i(t)$ is approximately related to the $HIT_{max}$. Also, $R_i(t)$ is sensitively depends on the $HIT_{max}$. So, when $HIT_{max}$ varies from $\sim 0.7$ to $0.97$ then $R_i(t)$ varies from $\sim 3.3$ to $33.3$.

From figures 12 and 13 we can infer:

- In USA, $HI_i(t) < HIT(t)$ and $R_i(t) > 1$. So, infection is still increasing for these countries.
- Whereas in countries like Colombia, Bangladesh, and India $HI_i(t) > HIT(t)$ and $R_i(t) < 1$. So, the infection is in a downward trend.
- In Italy, Russia, and Brazil, $HIT(t)$ and $R_i(t)$ goes below $HI_i(t)$ and 1.0 respectively. So, the infection has started to decrease. But after some time $HIT(t)$ and $R_i(t)$ goes above $HI_i(t)$ and 1.0. Hence the infection starts to rise again and the re-outbreak occurs. A similar thing happens for Peru.

In some plots of herd immunity threshold, $HIT(t)$ goes into the negative region. This happens because at that time removed rate ($\gamma$) becomes larger than the infection rate ($\beta$). We can also say that a negative herd immunity threshold of a population means there is no need for any immune people to prevent the disease. The disease will automatically decrease with time.

So from these discussions, we can see that the herd immunity threshold ($HIT(t)$) is a major player than the herd immunity $HI_i(t)$ to decrease the COVID-19 infections. As, governments of
the countries, intervene in the situation and imposed restrictions on the population, so, infection rates are reduced. Thus, herd immunity threshold \((HIT(t))\) is changed and becomes the main quantity which describes the decrease of infections. Later, if this restrictions are eased or lifted then a re-outbreak of the disease can happen (like Italy, Russia, and Brazil).

5. COVID-19 pandemic in India

In this section, we will try to analyze the current COVID-19 pandemic situation in India. Also we will try to find the possibility to predict the future behavior of the COVID-19 pandemic by effective reproduction number \((R_i(t))\) and herd immunity threshold \((HIT(t))\), as has been studied by several authors.\(^{33\text{-}35}\)

Figure 13 shows that, in India, the effective reproduction number initially decreases quickly from a large value. But then it starts to decrease very slowly and becomes less than unity. Also, figure 12 shows that, in India, the herd immunity \((HI_i(t))\) of the population is very low. But herd immunity threshold \((HIT(t))\) goes below the herd immunity \((HI_i(t))\) of the population and then into the negative region. Thus the infection is decreasing.

If, in future the herd immunity threshold \((HIT(t))\) and the effective reproduction number \((R_i(t))\) remains below than the herd immunity \((HI_i(t))\) and 1.0 respectively, then the infection will decrease continuously. However, the herd immunity of the population is very low thus a re-outbreak can occur at any time in countries like Russia, Brazil, and Italy. We can’t speculate the time of the re-outbreak because we don’t know how the infection rate \((\beta)\) and removed rate \((\gamma)\) will vary with time. So, only in future we will able to get the actual variation of the COVID-19 pandemic in India and the rest of the world.

6. Conclusion

In this paper, we have modified the basic SIR model by considering the infection rate \((\beta)\) and the removed rate \((\gamma)\) both as time-dependent parameters. We have redefined the four important variables, basic reproduction number \((R_0)\), effective reproduction number \((R_i(t))\), herd immunity \((HI_i(t))\) of the population, and herd immunity threshold \((HIT)\), according to the modifications that are suggested in the SIR model. Since infection rate and removed rate are both time-dependent parameters, the herd immunity threshold \((HIT)\) is also time-dependent.

The salient points of this study are presented below:

- The herd immunity threshold \((HIT)\) is related to \(\beta\) and \(\gamma\) as, \(HIT(t) = 1 - \frac{\gamma(t)}{\beta(t)}\). Hence, \(HIT(t)\) can be varied with the variation of \(\beta\) and \(\gamma\). For example, herd immunity threshold \((HIT)\) can be reduced by decreasing infection rate, \(\beta(t)\) or by increasing removed rate, \(\gamma(t)\).
- An epidemic will start decreasing when \(HI_i(t) > HIT(t)\), which means herd immunity has greater value than the herd immunity threshold. Thus we propose two different ways of reducing the spread of a disease: (i) by increasing herd immunity of the population over the herd immunity threshold, and (ii) by decreasing the herd immunity threshold below the herd immunity of the population.
- We fit the COVID-19 data of various countries with piece-wise continuous functions. From these fitted functions, we have estimated the time variation of the infection rate \((\beta)\) and the removed rate \((\gamma)\) of the SIR model. Using these rate parameters \((\beta\) and \(\gamma)\), we have estimated the variations of the effective reproduction number \((R_i(t))\), the herd immunity of the population \((HI_i(t))\), and the herd immunity threshold \((HIT(t))\).
- For this COVID-19 pandemic, we see that the herd immunity of the various countries’ is close to zero. Also, we have found that the initial value of the herd immunity threshold is
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∼0.9. However there are many countries, where COVID-19 pandemic is decreasing. This means, the herd immunity threshold went below the herd immunity at a certain time.

• We observe that the infection is currently decreasing in the countries like Colombia, Bangladesh, India and had decreased sufficiently like Italy, Russia, and Brazil. In these countries, the herd immunity threshold went below the herd immunity of the population at a certain time. We have also found that the removed rate $\gamma(t)$ does not change much in these countries. However, infection rate $\beta(t)$ is greatly decreased from the initial value and thus herd immunity threshold ($HIT(t)$) is also reduced. We also observe that the infection rate $\beta(t)$ can be decreased by imposing restrictions, like lockdown, or increasing awareness about the disease.

• Hence, the countries are trying to prevent COVID-19 pandemic by the second method that is taking measures so that $HIT(t)$ goes below $HI_i(t)$. However, for the same reason the herd immunity of the population also remains low. Thus, a country might face a re-outbreak of the disease very easily.

• In countries like Italy, Russia and Brazil, we see that there a re-outbreak of the COVID-19 disease has occurred now. Here, the herd immunity threshold has increased again due to the increment of the infection rate ($\beta$) or decrement of the removed rate ($\gamma$). We understand that infection rate ($\beta$) will increase if people start to neglect restrictions or if the government decides to lift lockdown. Thus imposing restrictions and lockdown is a good way to prevent the spread of the disease. However, there always remains a chance of re-outbreak of the disease and this is the major drawback of this method.

• In COVID-19 pandemic we see that the epidemic is prevented mainly by the second method, where herd immunity threshold ($HIT$) goes below the herd immunity ($HI_i(t)$) of the population. This makes herd immunity of the population ($HI_i(t)$) insignificant.

In addition to these, we have also tried to find some universal features between the variations of these components in different countries.

• We have found that initially there is an exponential drop in the infection rates of various countries. Infection rates decrease from a value of the order of $\sim 10^{-1}$ to a value of order $\sim 10^{-2}$ exponentially in a very short period of time.

• Also, we have found that the maximum value of herd immunity threshold in different countries has a value between 0.9 to 1.0.

• In the end, we have tried to discuss the upcoming COVID-19 behavior in India from the point of view of effective reproduction number and herd immunity threshold. We see that the COVID-19 pandemic is currently decreasing in India. This is because the herd immunity threshold ($HIT$) has gone below the herd immunity ($HI_i(t)$) of the population. Since herd immunity ($HI_i(t)$) of the population is close to zero, we predict that with the smallest of fluctuations, there is a possibility of re-outbreak in India.

We would like to conclude that COVID-19 pandemic might be a curse on humanity, but we can defeat it together. We will hope that our future will be COVID-19 free very soon.

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Appendix A. Fitted functions

The fitted functions of the active cases and the removed cases for the various countries are given below.

**USA**

For USA the fit function for active cases is,

\[
\begin{align*}
    a + b \times t + c \times t^2 + e \times t^4 + f \times t^5 & \quad 0 \leq t \leq 50, \\
    a1 + b1 \times (t - 50) + c1 \times (t - 50)^2 + d1 \times (t - 50)^3 + e1 \times (t - 50)^4 & \quad 50 < t \leq 139 \\
    + e2 \times (t - 139)^2 + d2 \times (t - 139)^3 + c2 \times (t - 139)^4 & \quad 139 < t \leq 228 \\
\end{align*}
\]

The value of the parameters are,

\[
\begin{align*}
    a &= 9.688 \times 10^5, b = 2.373 \times 10^4, c1 = -899.5, d1 = 18.74, e1 = -0.09631, e2 = 0.0209, \\
    a1 &= 3.083 \times 10^5, b2 = 2.676 \times 10^4, c2 = -218.1, d2 = 0.4034, e2 = 0.0209. \\
\end{align*}
\]

**India**

For India the fit function for active cases is,

\[
\begin{align*}
    a + b \times t + c \times t^3 + e \times t^4 + f \times t^5 + g \times t^6 & \quad 0 \leq t \leq 129, \\
    a1 + b1 \times (t - 129) + c1 \times (t - 129)^2 + d1 \times (t - 129)^3 + e1 \times (t - 129)^4 & \quad 129 < t \leq 177 \\
    + f1 \times (t - 129)^5 & \quad (A.3) \\
    a2 + b2 \times (t - 177) + c2 \times (t - 177)^2 + d2 \times (t - 177)^3 + e2 \times (t - 177)^4 + f2 \times (t - 177)^5 & \quad 177 < t \leq 223 \\
\end{align*}
\]

The value of the parameters are,

\[
\begin{align*}
    a &= 486, b = 152.8, d = 0.4716, e = -0.001239, f = -4.67 \times 10^{-5}, g = 3.364 \times 10^{-7}, \\
    a1 &= 5.575 \times 10^5, b1 = 9798, d1 = -24.74, c1 = 1.089, f1 = -0.012, \\
    a2 &= 1.025 \times 10^5, b2 = -1.459 \times 10^4, c2 = 1265, d2 = -58.71, e2 = 0.9071, f2 = -0.004006. \\
\end{align*}
\]

**Peru**

For Peru the fit function for active cases is,

\[
\begin{align*}
    a + b \times t + c \times t^2 + e \times t^4 + f \times t^5 & \quad 0 \leq t \leq 106, \\
    a1 + b1 \times (t - 106) + c1 \times (t - 106)^2 + d1 \times (t - 106)^3 + e1 \times (t - 106)^4 & \quad 106 < t \leq 223 \\
\end{align*}
\]

The value of the parameters are,

\[
\begin{align*}
    a11 &= 50, b11 = 13, c11 = -2.287, d11 = 0.2378, f11 = 1.789 \times 10^{-5}, \\
    a21 &= 4.724 \times 10^5, b21 = 2.139 \times 10^4, c21 = 262.5, d21 = 5.476, e21 = -0.04073. \\
\end{align*}
\]
The value of the parameters are,
\[ a = 818, \quad b = 55.29, \quad d = 1.089, \quad e = -0.01283. \]
\[ a1 = 4.787 \times 10^4, \quad b1 = 1948, \quad c1 = 71.62, \quad d1 = -3.747, \quad e1 = 0.04906, \quad f1 = -0.0001964. \]
\[ a2 = 1.328 \times 10^3, \quad b2 = -0.1234, \quad c2 = -106.4, \quad d2 = 1.41. \]

The fit function for removed cases is,
\[
\begin{align*}
& a11 + b11 \times t + c11 \times t^2 + d11 \times t^3 + e11 \times t^4 + f11 \times t^5 \quad 0 \leq t \leq 54 \\
& a21 + b21 \times (t - 121) + c21 \times (t - 121)^2 + d21 \times (t - 121)^3 \quad 54 < t \leq 165 \\
& + e21 \times (t - 121)^4 + f21 \times (t - 121)^5 \\
& a31 + b31 \times (t - 165) + c31 \times (t - 165)^2 + d31 \times (t - 165)^3 \quad 165 < t \leq 217
\end{align*}
\]

The value of the parameters are,
\[ a11 = 34, \quad b11 = 132.1, \quad c11 = -5.678, \quad d11 = 1.2, \quad e11 = -0.03648, \quad f11 = 0.0003907. \]
\[ a21 = 4.938 \times 10^4, \quad b21 = 1445, \quad c21 = 117.9, \quad d21 = -2.429, \quad e21 = 0.02103, \quad f21 = -5.689 \times 10^{-5}. \]
\[ a31 = 5.687 \times 10^3, \quad b31 = 7160, \quad c31 = 3.441, \quad d31 = -0.6423. \]

**Russia**

For Russia the fit function for active cases is,
\[
\begin{align*}
& a + b \times t + d \times t^3 + e \times t^4 + f \times t^5 \quad 0 \leq t \leq 33 \\
& a1 + b1 \times (t - 33) + c1 \times (t - 33)^2 + d1 \times (t - 33)^3 \quad 33 < t \leq 165 \\
& + e1 \times (t - 33)^4 + f1 \times (t - 33)^5 \\
& a2 + b2 \times (t - 165) + d2 \times (t - 165)^3 + e2 \times (t - 165)^4 \quad 165 < t \leq 217 \\
& + f2 \times (t - 165)^5 + g2 \times (t - 165)^6
\end{align*}
\]

The value of the parameters are,
\[ a = 1462, \quad b = 347.6, \quad d = 1.824, \quad e = 0.1441, \quad f = -0.003847. \]
\[ a1 = 1.003 \times 10^3, \quad b1 = 1.025 \times 10^4, \quad c1 = -279.3, \quad d1 = 3.551, \quad e1 = -0.02304, \quad f1 = 6.014 \times 10^{-5}. \]
\[ a2 = 1.638 \times 10^3, \quad b2 = 809.1, \quad d2 = -1.995, \quad e2 = 0.3368, \quad f2 = -0.008406, \quad g2 = 5.989 \times 10^{-5}. \]

The fit function for removed cases is,
\[
\begin{align*}
& a11 + b11 \times t + d11 \times t^3 + e11 \times t^4 + f11 \times t^5 \quad 0 \leq t \leq 44 \\
& a21 + b21 \times (t - 44) + c21 \times (t - 44)^2 + e21 \times (t - 44)^4 \quad 44 < t \leq 217 \\
& + f21 \times (t - 44)^5
\end{align*}
\]

The value of the parameters are,
\[ a11 = 72, \quad b11 = 11.13, \quad d11 = 0.7236, \quad e11 = -0.0298, \quad f11 = 0.005763. \]
\[ a21 = 3.494 \times 10^4, \quad b21 = 7121, \quad c21 = 20.55, \quad e21 = -0.003328, \quad f21 = 1.51 \times 10^{-5}. \]

**Colombia**

For Colombia the fit function for active cases is,
The value of the parameters are,

\begin{align}
 a &= 664.5, b = 127.4, d = -0.2445, e = 0.01288, f = -0.000192, g = 9.507 \times 10^{-7} \\
 a &= 4.967 \times 10^4, c = 341, d1 = -19.47, e1 = 0.4733, f1 = -0.004023 \\
 a &= 1.711 \times 10^5, b2 = -2264, d2 = 0.1695
\end{align}

Bangladesh

For Bangladesh the fit function for active cases is,

\begin{align}
 a + b \times t + d \times t^3 + e \times t^4 + f \times t^5 + g \times t^6 & \quad 0 \leq t \leq 89 \\
a1 + c1 \times (t - 89)^2 + d1 \times (t - 89)^3 + e1 \times (t - 89)^4 & \quad 89 < t \leq 138 \\
 & \quad + f1 \times (t - 89)^5 \\
a2 + b2 \times (t - 138) + d2 \times (t - 138)^3 & \quad 138 < t \leq 217
\end{align}

\begin{equation}
 (A.9)
\end{equation}

The fit function for removed cases is,

\begin{align}
 a11 + b11 \times t + c11 \times t^4 + f11 \times t^5 & \quad 0 \leq t \leq 97 \\
a21 + b21 \times (t - 97) + c21 \times (t - 97)^2 + d21 \times (t - 97)^3 & \quad 97 < t \leq 217 \\
 & \quad + f21 \times (t - 97)^4 + g21 \times (t - 97)^5
\end{align}

\begin{equation}
 (A.10)
\end{equation}

The value of the parameters are,

\begin{align}
 a11 &= 20, b11 = 29.43, c11 = 0.0004539, f11 = 9.232 \times 10^{-7} \\
 a21 &= 5.106 \times 10^4, b21 = 1494, c21 = 42.39, d21 = 3.275, f21 = -0.05163, g21 = 0.0002101
\end{align}

\begin{equation}
(A.11)
\end{equation}

Italy

For Italy the fit function for active cases is,

\begin{align}
 a + b \times t + d \times t^3 + e \times t^4 & \quad 0 \leq t \leq 94 \\
a1 + b1 \times (t - 94) + c1 \times (t - 94)^2 + d1 \times (t - 94)^3 & \quad 94 < t \leq 131 \\
 & \quad + e1 \times (t - 94)^4 + f1 \times (t - 94)^5 \\
a2 + b2 \times (t - 131) + d2 \times (t - 131)^3 + e2 \times (t - 131)^4 & \quad 131 < t \leq 204
\end{align}

\begin{equation}
 (A.12)
\end{equation}

The value of the parameters are,

\begin{align}
 a &= 416, b = 155.1, d = 0.4037, e = -0.003359 \\
 a &= 8.476 \times 10^4, b1 = 721.6, c1 = 132.6, d1 = -14.52, e1 = 0.532, f1 = -0.006333 \\
 a &= 1.149 \times 10^5, b2 = -1050, d2 = 0.2373, e2 = -0.001881
\end{align}

The fit function for removed cases is,

\begin{align}
 a11 + b11 \times t + f11 \times t^5 + g11 \times t^6 & \quad 0 \leq t \leq 104 \\
a21 + b21 \times (t - 104) + c21 \times (t - 104)^2 & \quad 104 < t \leq 152 \\
 & \quad + d21 \times (t - 104)^3 + e21 \times (t - 104)^4 \\
a31 + b31 \times (t - 152) + c31 \times (t - 152)^2 & \quad 152 < t \leq 204 \\
 & \quad + d31 \times (t - 152)^3 + e31 \times (t - 152)^4
\end{align}

\begin{equation}
 (A.12)
\end{equation}

The value of the parameters are,

\begin{align}
 a11 &= 66, b11 = 31.08, f11 = 4.687 \times 10^{-5}, g11 = -3.551 \times 10^{-7} \\
 a21 &= 1.238 \times 10^5, b21 = 2559, c21 = -121, d21 = 4.979, e21 = -0.05306 \\
 a21 &= 2.376 \times 10^5, b21 = 2819, c21 = -48.14, d21 = 0.8254, e21 = -0.005229
\end{align}
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\[ a + b \times t + c \times t^2 + d \times t^3 \quad 0 \leq t \leq 40 \]
\[ a1 + b1 \times (t - 40) + c1 \times (t - 40)^2 + d1 \times (t - 40)^3 \quad 40 < t \leq 172 \]
\[ + e1 \times (t - 40)^4 \]
\[ a2 + b2 \times (t - 172) + c2 \times (t - 172)^2 + e2 \times (t - 172)^4 \quad 172 < t \leq 194 \]

The value of the parameters are,
\[ a = 1.452 \times 10^4, b = 34.86, c = 114.2. \]
\[ a1 = 2.056 \times 10^5, b1 = 1.069 \times 10^4, c1 = -69.16, d1 = -0.3049, e1 = 0.002232. \]
\[ a2 = 3.925 \times 10^3, b2 = -4398, c2 = 1277, e2 = -0.7863. \]

For Brazil the fit function for removed cases is,
\[ a1 + b1 \times (t - 24) + c1 \times (t - 24)^2 + d1 \times (t - 24)^3 + e1 \times (t - 24)^4 \]
\[ 24 < t \leq 91 \]
\[ a2 + b2 \times (t - 91) + c2 \times (t - 91)^2 + d2 \times (t - 91)^3 + e2 \times (t - 91)^4 + f2 \times (t - 91)^5 \]
\[ 91 < t \leq 196 \]
\[ a3 + b3 \times (t - 196) + c3 \times (t - 196)^3 + d3 \times (t - 196)^4 + e3 \times (t - 196)^5 \]
\[ 196 < t \leq 248 \]

The value of the parameters are,
\[ a = 862.2, b = 169.3, c = 28.79, d = 2.225. \]
\[ a1 = 4.795 \times 10^4, b1 = 3586, c1 = -23.34, d1 = -1.408, e1 = 0.01436. \]
\[ a2 = 4.792 \times 10^3, b2 = -1598, c2 = 21.16, d2 = 0.003922, e2 = -0.002203, f2 = 1.469e - 05. \]
\[ a3 = 3.527 \times 10^4, b3 = 1036, d3 = -2.201, e3 = 0.08203. \]

Brazil

For Brazil the fit function for active cases is,
\[ a + b \times t + c \times t^2 + d \times t^3 \quad 0 \leq t \leq 24 \]
\[ a1 + b1 \times (t - 24) + c1 \times (t - 24)^2 + d1 \times (t - 24)^3 + e1 \times (t - 24)^4 \]
\[ 24 < t \leq 91 \]
\[ a2 + b2 \times (t - 91) + c2 \times (t - 91)^2 + d2 \times (t - 91)^3 \]
\[ + e2 \times (t - 91)^4 + f2 \times (t - 91)^5 \]
\[ 91 < t \leq 196 \]
\[ a3 + b3 \times (t - 196) + c3 \times (t - 196)^3 + e3 \times (t - 196)^4 + f3 \times (t - 196)^5 \]
\[ 196 < t \leq 248 \]

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