BITS Pilani, Goa

Mathematical Modelling

Project Report

Modelling the outbreak of COVID-19

Kaushik Iyer 2017A3PS0162G

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1 Literature Review

1.1 SIR Model

The SIR model, which is the acronym of Susceptible-Infected-Recovered, is the most widely used mathematical model in epidemiology. It is a compartmental model which was first proposed by Ronald Ross in [1], where he used this model for predictions in a Malaria outbreak. His work on malaria can also be found in [2] and [3]. The most simplistic model is the Kermack-McKendrick model [4] who formulated a model to predict the number of cases and the possible distribution as the disease spreads across a population through time [5]. [6] also gives a detailed study of mathematical modelling for epidemics. [7],[8] delve further into the study of epidemics by extending the idea to endemics. In [9], the basic Reproduction number (R_0) has been introduced and studied.
The Simplest SIR model began with assumptions that now seem unrealistic to be applicable to model outbreaks. Moreover, the model is completely deterministic; however, a stochastic approach has also been formulated and studied in [10],[11] and [12].

1.1.1 Assumptions

This model is based on the following assumptions [13]:
(1) **The population is fixed**. This can be thought in a way that the average number natural births and deaths are the same. (Models incorporating varying population sizes are analyzed in [14] and [15])
(2) **There is no inherited immunity in the community** i.e. the entire population is equally likely to catch the disease.
(3) All people mix homogeneously i.e. they have the same degree of interactions with each other. (The effects of heterogeneity are considered in [16])
(4) **The outbreak eventually dies out. The only way a person can leave the susceptible group is to become infected. The only way a person can leave the infected group is to recover from the disease. Once a person has recovered, the person received immunity**. (The effect of recurrent sus-

ceptibility to the disease in heterogeneous mixing of population is studied in [17])
(5) **Age, sex, social status,race and other social factors do not affect the probability of being infected.**

1.1.2 Mathematical Model

The SIR model is a system of coupled Ordinary Differential equations which which are as under:

$$\begin{aligned} \frac{dS}{dt} &= -\beta I \frac{S}{N} \\ \frac{dI}{dt} &= \beta I \frac{S}{N} - \gamma I \\ \frac{dR}{dt} &= \gamma I \end{aligned} \tag{1.1}$$

Here, time is in days, S(t) is the number of people susceptible to the disease on day t, I(t) is the number of people infected on day t and R(t) is the number of people recovered on day t. β and γ are the transmission and recovery rates per day and $N = S(t) + I(t) + R(t)$ is the total population strength which is a constant. The model parameters will be explained in the later sections of the report.

1.1.3 Limitations of the SIR model

The following limitations push for modifications to this simple model described in eq.(1.1):
(1) It assumes that all people affected will recover and there will be no deaths from the outbreak.
(2) Incubation period is assumed to be zero, which is normally not the case in any disease, because people take time to show symptoms.
(3) There is no facility to incorporate preventive measures like lock-downs, quarantines or herd immunity, which could cause the transmission rate to drop. (This is normally a time varying function of the Reproduction number R_0)
(4) There is no provision to incorporate relapses or recurrences of the diseases, which is again one of the main parameters to be modelled.
(5) Lastly, the model does not take care of the fact that a disease does not affect

all people equally and thus there is no bifurcation on the basis of age, gender or demography.

2 SEIR Model

The SEIR model (Susceptible-Exposed-Infected-Recovered) is a modification of the SIR model that overcomes some of the limitations of the SIR model. [18] models the E-bola outbreak with an SEIR model which also includes natural birth and death rates and also incorporates demographic effects. The model used in this report, however does not incorporate them but it still provides a decent prediction model and compares well with the data for the Indian subcontinent.

2.1 Assumptions and Formulation

Most of the assumptions are similar to that of the SIR model. The only changes are that this model accounts for the deaths caused by the outbreak and there is an additional 'compartment' added called Exposed, which simply means that there is a non zero incubation period associated with the outbreak.
The compartmental model is shown in the following figure:

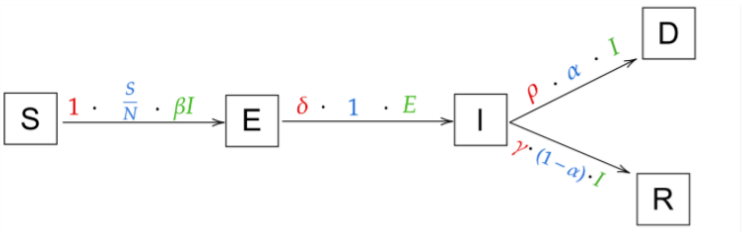


Figure 1: SEIR Compartment model [19]

The Alphabets in the blocks represent **S**usceptible, **E**xposed, **I**nfected, **D**ead and **R**ecovered on a given day t. The variables above every arrow show can be divided as follows:

Figure 2: Figure showing transitions from one compartment to another [19]

2.1.1 Explanation of the compartment model

This section gives a detailed explanation of the transitions that occur from one compartment to another. These transitions are in accordance with Figure 2. The physical relevance of the constants used are explained in section 2.2.

Transition from S to E: Here, it is assumed that the entire population is susceptible to the disease and anyone susceptible is immediately exposed to the disease hence the rate is 1. The probability of a person getting exposed is the proportion of people susceptible and lastly, the population that will get exposed depends on the number of infected people and the number of new infections (β). This somewhat helps explain the way the disease transmits.

Transition from E to I: Anyone Exposed will start showing symptoms of the infection only after the incubation period, which explains why the rate of getting infected is not 1. The probability of getting infected once exposed is 1 because we assume no inherent immunity in the population. Lastly, the target population is those that were exposed.

Transition from I to D: The number of deaths caused by the disease is modelled in this transition. An infected person does not die immediately, which is why the rate at which a person dies (ρ) is not equal 1. The probability of a person dying from the disease is α and the target population is the number of infected people.

Transition from I to R: An infected person can also get cured of the disease completely. Here we assume no relapse/recurrence of the infection. The rate again depends on the number of days a person takes to recover from the disease, and so the recovery rate (γ) is usually not 1. As for the probability, it can be argued that the number of people recovering + number of dying = number of infected people (since there are only two possibilities). Therefore, the probability is $1 - \alpha$. The target population is again the number of infected people.

2.2 Mathematical model and Explanation of parameters

The SEIR model can be modelled as follows:

$$\begin{aligned} \frac{dS}{dt} &= -\beta I \frac{S}{N} \\ \frac{dE}{dt} &= \beta I \frac{S}{N} - \delta E \\ \frac{dI}{dt} &= \delta E - \rho\alpha I - \gamma(1-\alpha)I \\ \frac{dD}{dt} &= \rho\alpha I \\ \frac{dR}{dt} &= \gamma(1-\alpha)I \end{aligned} \tag{2.1}$$

2.2.1 Incubation period

It is defined as the period between exposure to an infection and the appearance of the first symptoms. This is usually non zero for any disease and is definitely the case for COVID-19. Let T_{inc} be the incubation period in days. Then

$$\delta = \frac{1}{T_{inc}} \tag{2.2}$$

which shows how fast a person exposed to the disease will start showing the symptoms on a per day basis.

2.2.2 Case fatality ratio (CFR)

The case fatality ratio is a measure of the severity of a disease and is defined as the proportion of cases of a specified disease or condition which are fatal within a specified time.

$$CFR = \frac{\text{Number of deaths till time t}}{\text{Total number of cases till time t}} \times 100 \tag{2.3}$$

Since this is a probability, the constant α can be used to model this parameter. Let T_d represent the time in days taken for an infected person to die from the disease. Then the rate at which people die per day which is modelled by ρ is

defined as:

$$\rho = \frac{1}{T_d} \tag{2.4}$$

2.2.3 Recovery rate

Let T_r denote the number of days taken for an infected patient to totally recover from the disease. Then, the recovery rate γ defined per day is:

$$\gamma = \frac{1}{T_r} \tag{2.5}$$

2.2.4 Reproduction number

The Reproduction number R_0 is the total number of people an infected person infects. This is a dimensionless number and is defined in [20] as:

$$\begin{aligned} R_0 = (\frac{\text{infection}}{\text{contact}}) \cdot (\frac{\text{contact}}{\text{time}}) \cdot (\frac{\text{time}}{\text{infection}}) \\ R_0 = \beta \cdot 1 \cdot T_r \\ R_0 = \frac{\beta}{\gamma} \end{aligned} \tag{2.6}$$

Because here it is assumed that anyone susceptible is sure to get exposed and the duration of infection is equivalent to the time taken to recover from the infection. This parameter helps also in modelling the effect of preventive measures like lockdowns, quarantines or herd immunity. If $R_0 > 1$, then the outbreak is an epidemic because then the rate of infected people is greater than 0.

3 Simulation

The simulation has been carried out in fragments of time and for the entire duration [21]. This is because the parameters are constantly varying and do not follow a specific trend. The model parameters are assumed to be a constant in the interval so specified and this constant is mostly taken as the mean value in that interval. The data is collected on a daily basis from [22] and the interpolated values for the continuous graph have been rounded off to the nearest integer.

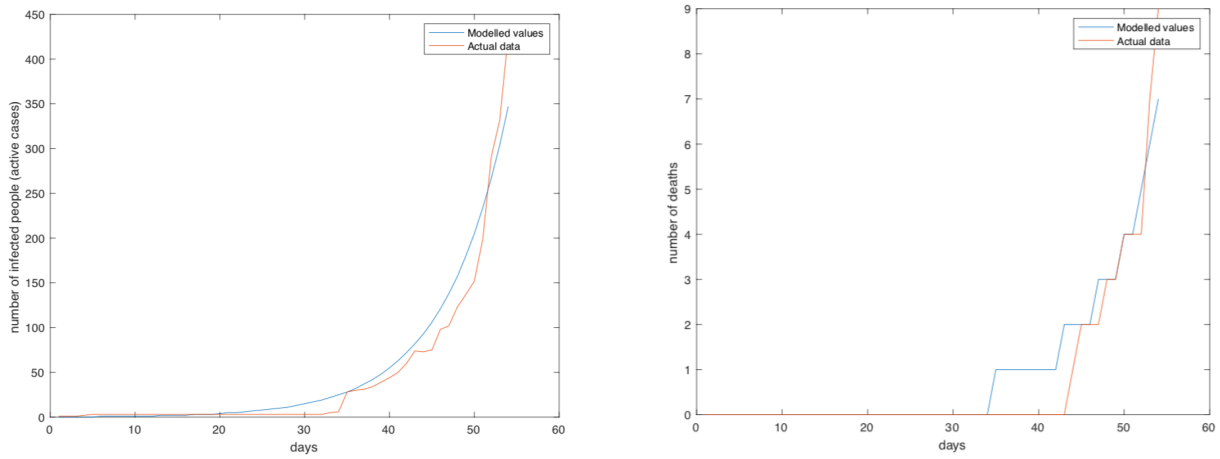
The parameter values here have been taken from the official websites of WHO. However, they are slightly different from these values and the corresponding justifications are given wherever applicable.
The model has been divided into 5 phases which are described in detail in the following subsections.
The generic code used for the simulation purposes has been given in the Appendix.

3.1 Phase I

This phase is the time from January 30 (date when the first case was reported in India) to March 22 (date of the first national lock-down).
1) The reproduction number R0 has been taken around 4.6, although the range of values has been stated to be from 2-4 in several countries. The reason for taking a higher value is because R_0 depends on the density and India has a very high density.
2) The value of α has been found by taking the average of the ratio of daily deaths to daily active cases.
3) Other parameters have been taken in accordance with the data obtained from the official websites of the Health ministry of India and other news sources.
The graph comparing the model with the actual data is shown in figure 3.

3.2 Phase II

This phase is the time from March 23 to April 14 (duration of the second national lock-down).
1) The reproduction number R_0 has been taken around 3.7, although the value was predicted around 2.2. The reason for taking a higher value is because R_0 should not be taken as an average with respect to all states but should be a weighted average depending on where the cases are maximum. Most cases during this phase was seen in Maharashtra and Delhi, which have one of the highest densities and the reported values of R_0 in these areas are near the value taken for the simulation.
2) The value of α has been found by taking the average of the ratio of daily deaths to daily active cases.



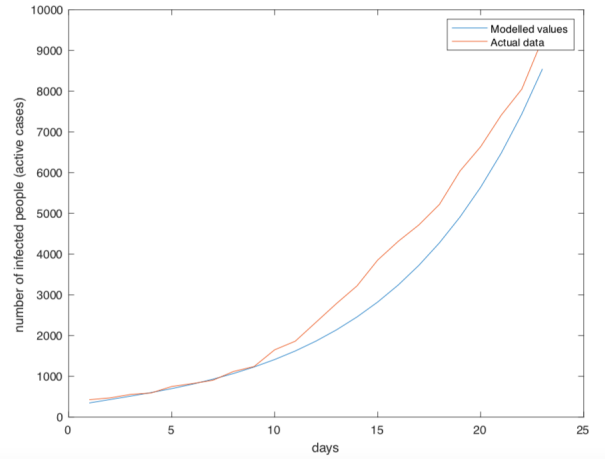
(a) infected (b) deaths

Figure 3: (a) shows the trend of the number of infected people and (b) shows the trend of the number of deaths. Simulation values for the duration are $\alpha = 0.034$, $\gamma = 1/12$, $\delta = 1/6$, $\rho = 1/15$, $R_0 = 4.6$.

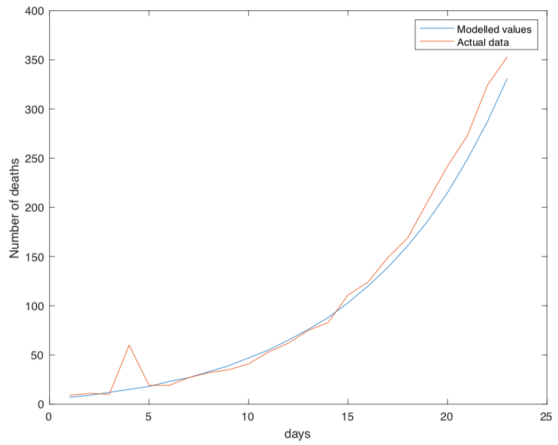
3) The initial values for this phase were set as the values of the last date of the previous phase for continuity.
4) Other parameters have been taken in accordance with the data obtained from the official websites of the Health ministry of India and other news sources.
The graph comparing the model with the actual data is shown in figure 4.

3.3 Phase III

This phase is the time from April 15 to May 3 (duration of the second phase of the national lock-down).
1) The reproduction number R_0 has been taken around 2, although the value was predicted around 1.5. Here, the higher value is taken to account for the Tablighi Jammat event that occurred in Delhi, causing unexpectedly high transmission rates.
2) The value of γ is being reduced to incorporate the rising recovery rate in the country.
Other parameters are similar to the previous phase. The graph comparing the model with the actual data is shown in figure 5.

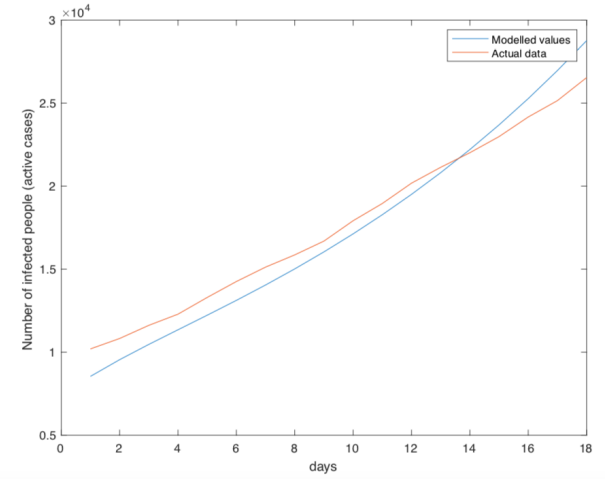


(a) infected

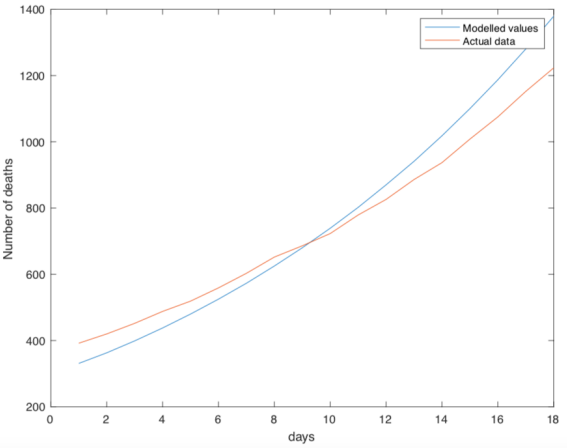


(b) deaths

Figure 4: (a) shows the trend of the number of infected people and (b) shows the trend of the number of deaths. Simulation values for the duration are $\alpha = 0.037$, $\gamma = 1/12$, $\delta = 1/4$, $\rho = 1/7$, $R_0 = 3.7$.



(a) infected



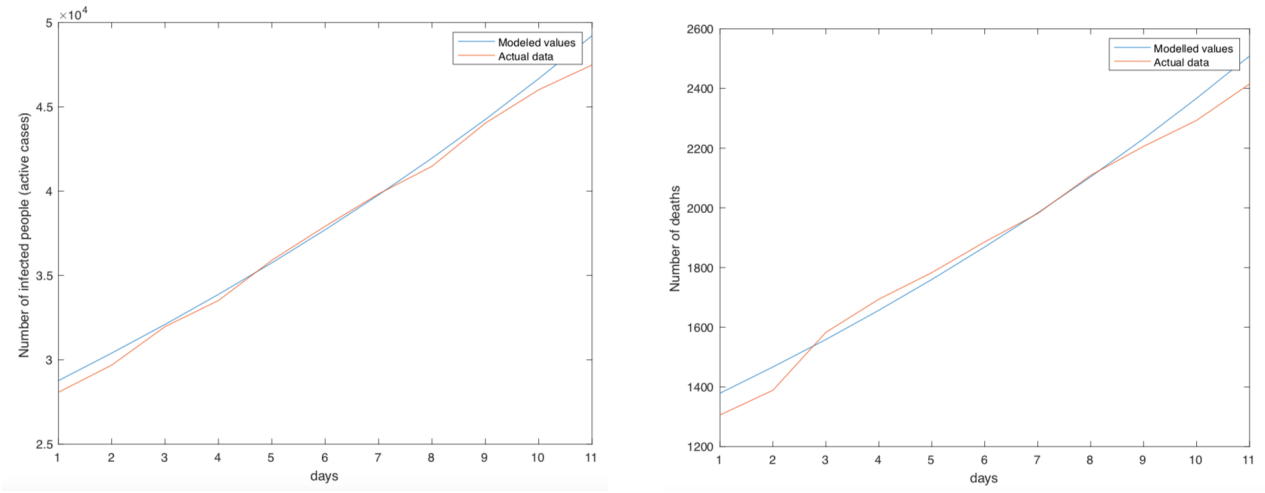
(b) deaths

Figure 5: (a) shows the trend of the number of infected people and (b) shows the trend of the number of deaths. Simulation values for the duration are $\alpha = 0.037$, $\gamma = 1/10$, $\delta = 1/4$, $\rho = 1/11$, $R_0 = 2$.

3.4 Phase IV

This phase is the time from May 4 to May 14 (duration of the third phase of the national lock-down).

. The graph comparing the model with the actual data is shown in figure 6.



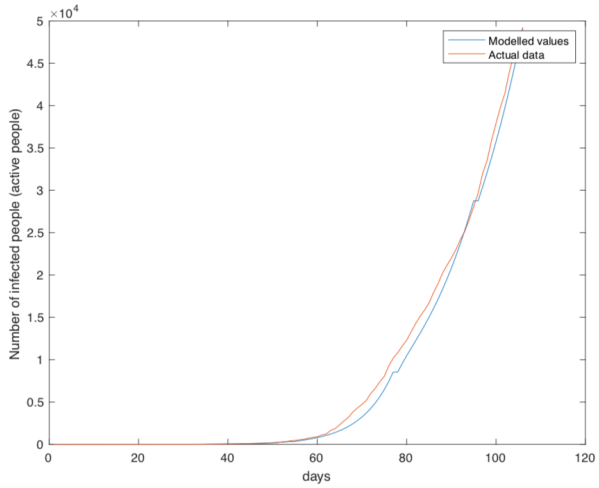
(a) infected (b) deaths

Figure 6: (a) shows the trend of the number of infected people and (b) shows the trend of the number of deaths. Simulation values for the duration are $\alpha = 0.035$, $\gamma = 1/9$, $\delta = 1/4$, $\rho = 1/13$, $R_0 = 1.7$.

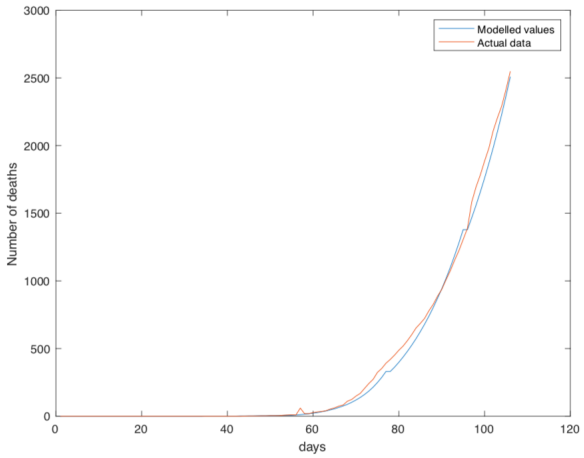
It must be noted here that the time axis starts from 1 because the graphs for each phase start and end at the dates specified above. The cumulative graph along with the errors in the deaths and infected cases are plotted in figures 7 and 8.
One more thing worth mentioning is that the actual data does not match with the modelled data in terms of the number of recoveries. The main reason for this is that the model assumes that the probability of recovering once infected is $1 - \alpha$. This is not the case usually because the direct consequence of this is that we assume infected people to either recover or die every day, but in reality, they can remain infected the next day too. Also, most people in the **'Exposed'** compartment are assumed to recover, which is why predicted number of recoveries will be very high.

4 Prediction Model

The prediction of COVID-19 in India is presented for two cases here. The main parameter that is varied is the Reproduction number (R_0). Following the trend till

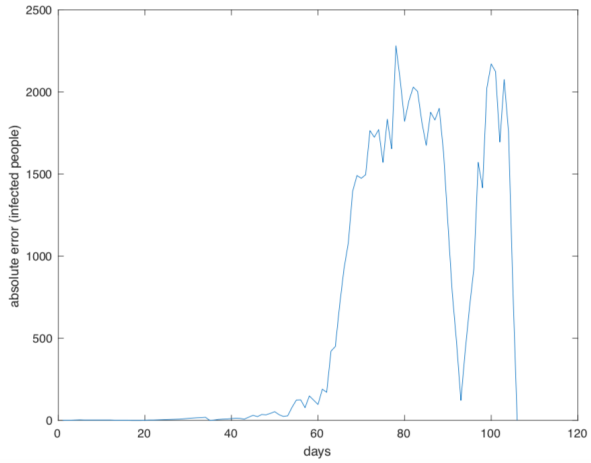


(a) infected

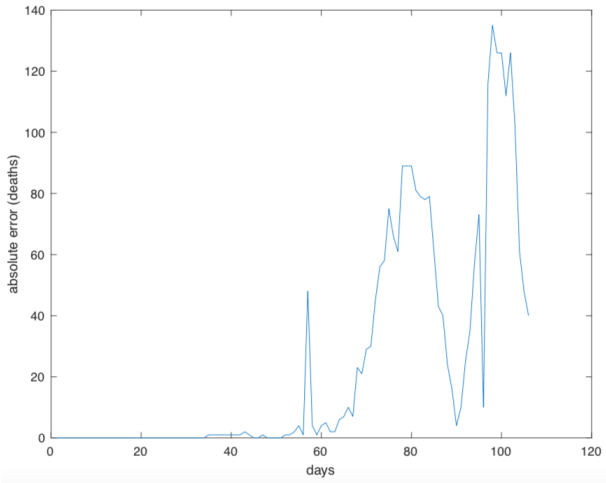


(b) deaths

Figure 7: (a) shows the trend of the number of infected people and (b) shows the trend of the number of deaths for the entire duration of 106 days from January 30 to May 15



(a) infected

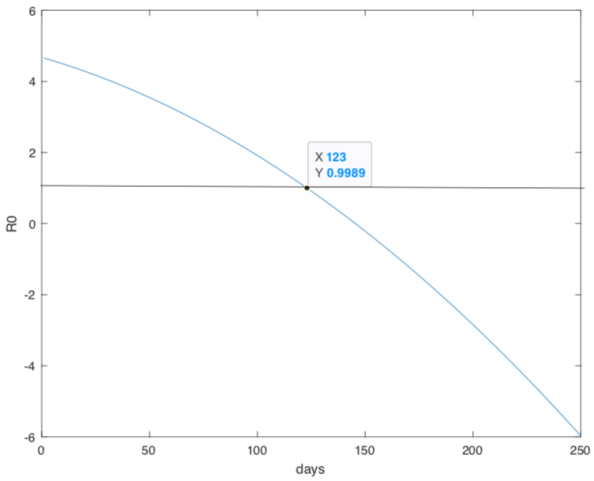


(b) deaths

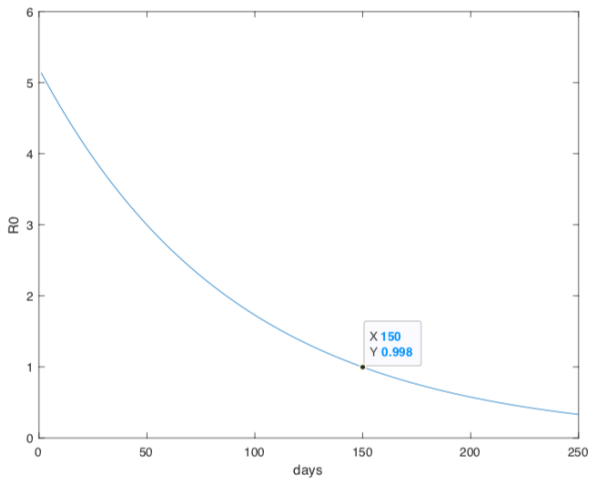
Figure 8: (a) shows the absolute error of the number of infected people and (b) shows the absolute error of the number of deaths.

date, a quadratic approximation and exponential approximation has been derived which are shown in figure 9

The reason for considering only variations in R_0 is because it helps model a trend



(a) $R_0 = -0.0001t^2 - 0.0176t + 4.6766$



(b) $R_0 = 5.1968e^{-0.011t}$

Figure 9: (a) shows quadratic approximation of R_0 and (b) shows exponential approximation of R_0.

significantly, but the other parameters show oscillations or very slow decay, which are not significantly reflected in the model. The predicted models for both the cases have been considered for different lengths of time because the quadratic approximation decays very quickly whereas the effect of the exponential approximation is seen only after certain days. These have been plotted in figures 10 and 11.

Important inferences can be drawn from these plots.

Quadratic Approximation

The pandemic seems to peak at **day 126** from January 30 to a value of **70435** and then starts falling down. The final of R_0 is 0.0221 (beyond this, R_0 becomes negative, which is not permissible). This is quite unrealistic, considering that the cases are still sharply rising in the country

The number of deaths saturate at a value of **8927**. This is quite a valid prediction, because the death rate has started to fall in several regions of the country.

Exponential Approximation

The pandemic seems to peak at **day 153** from January 30 to a value of **113698** and then starts falling down. The final value of R_0 is 0.5822. This seems somewhat close to the time when the Indian sources state the pandemic would start receding.

Moreover, the number of cases can mount to this value considering present data. The number of deaths seem to saturate around **887914**. This value is highly unlikely.

Thus the quadratic approximation seems to predict the data and especially the number of deaths correctly, but the pandemic seems to end very soon in that scenario. Whereas, the exponential approximation predicts the duration and the number of infected people correctly but the number of deaths is quite off the charts.

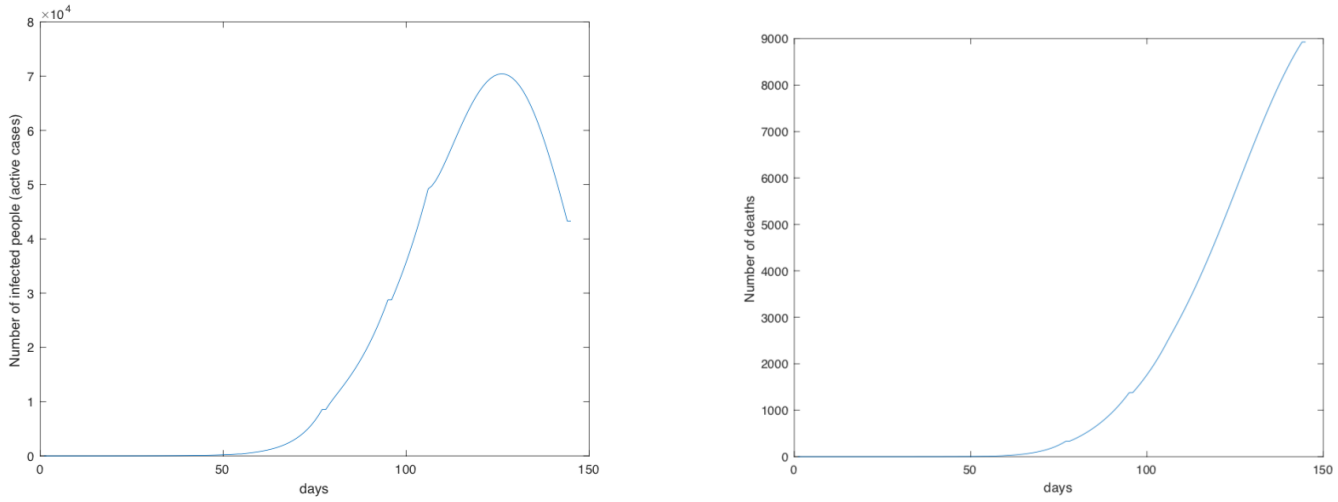


Figure 10: Figure on the left shows prediction of infected people and on the right shows prediction of deaths for quadratic approximation of R_0.

The variation of the probability of deaths from the disease, α, can also be approximated using a 3^{rd} order polynomial as shown in figure 12. The reason for varying α is because:
1) It models the probability of deaths directly.
2) The reducing value of α shows indirectly that the medical facilities in the countries are improving, which are preventing deaths.
The recovery rate was not varied because it is modelled for a daily basis and being defined as the inverse of the number of days taken to recover, its variation will be close to 0 or will cause sudden jumps (because the number of days to recover is

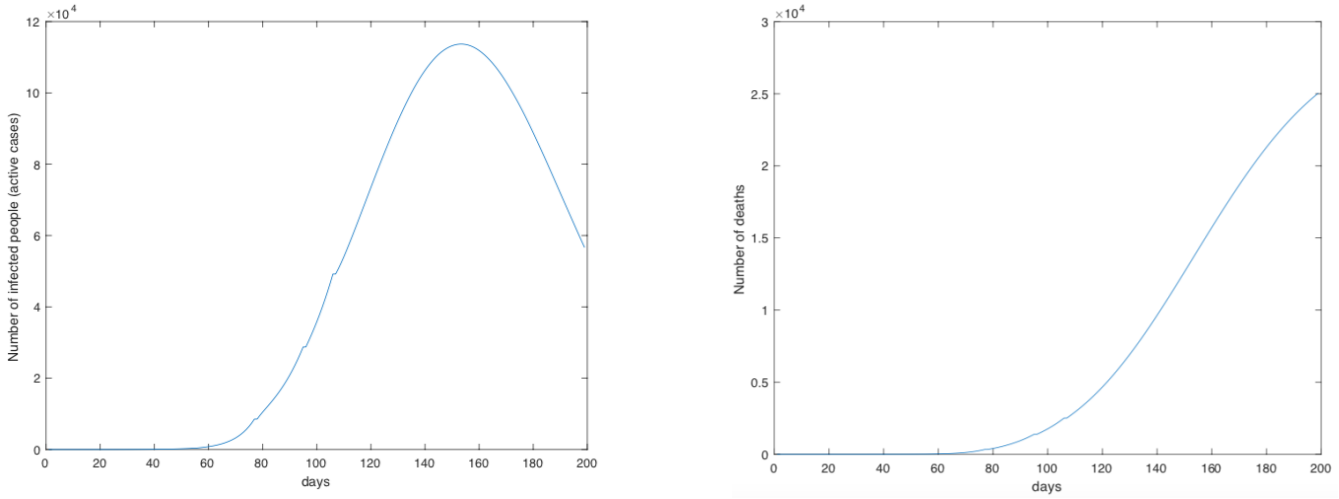


Figure 11: Figure on the left shows prediction of infected people and on the right shows prediction of deaths for exponential approximation of R_0.

an integer and cannot be a fraction). Although, it is not how the actual would be carried out, this is a good approximation, serving the required prediction purposes.

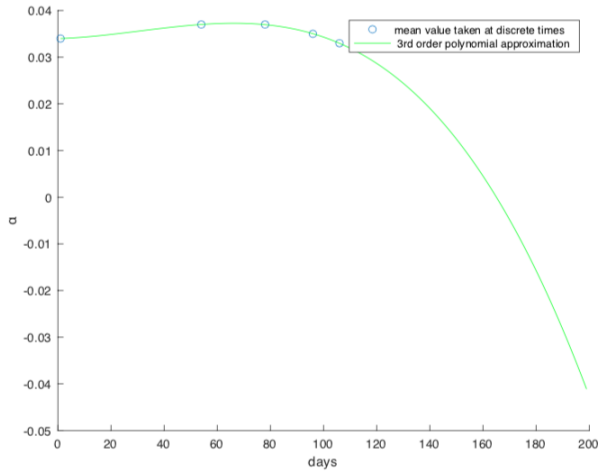


Figure 12: variation of α with time shown with the mean value taken at the start of each phase. $\alpha = -1.8594e-8t^3 + 1.7153e-6t^2 + 1.7693e-05t + 0.034$

Although, this approximation shows that the value of α eventually goes below 0, the interpretation of this is quite different. Since the probability of dying from a disease can practically tend to 0 only when a vaccine is found, and theoretically

always positive, a minimum threshold value can be decided for α. Beyond this threshold, α will take the same value for the rest of the duration for which the prediction is being made.

For the final prediction model, only the exponential case has been presented, with variation in α as described by the equation mentioned in figure 12. The threshold for α has been kept at 0.0159 (1.59%). The predictive model is shown in figure 15. Moreover, the variation in SEIR model variables (infected,recovered,dead) are shown in figure 19.

As a final step to see how the prediction has worked out, the data from May 15 to June 3 has been taken and plotted against the approximations (quadratic and exponential) in the reproductive number R_0 and α. These are shown in figures 13 and 14 along with the absolute error with respect to each approximation. Note here that the time axis goes from 1 (May 15) to 19 (June 3).
As can be readily seen and as was pointed out earlier, the quadratic approximation matches more closely with the actual data, but predicts that the pandemic will become an endemic sooner, which seems unlikely considering the present scenario.

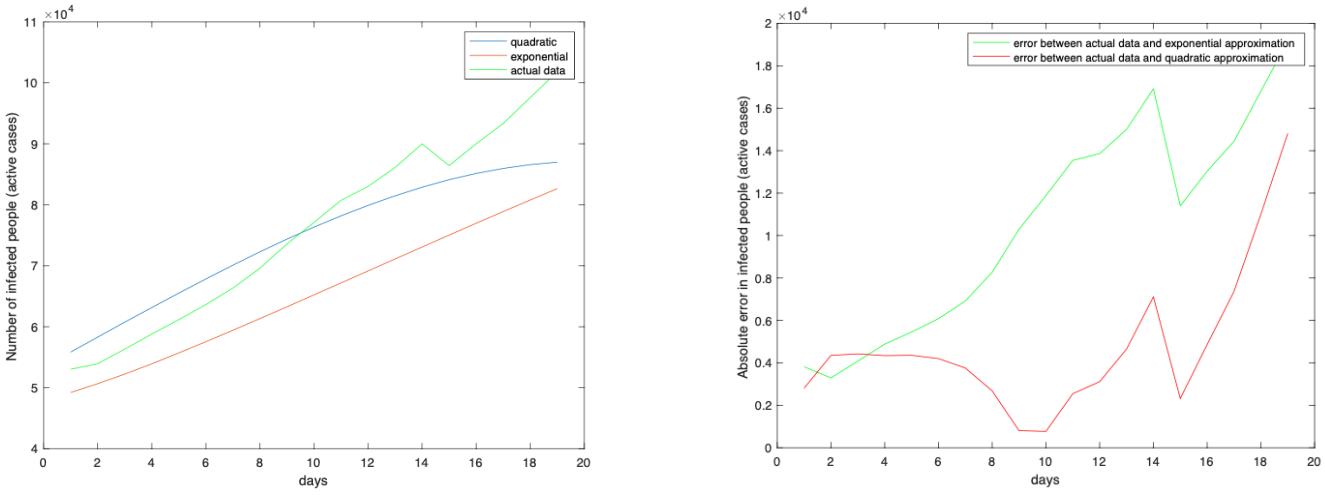


Figure 13: Figure on the left shows prediction of infected people from May 17 to June 3 and on the right shows the error in case of both the approximations

The predictive model has also been subject to the scenario after the lock-down

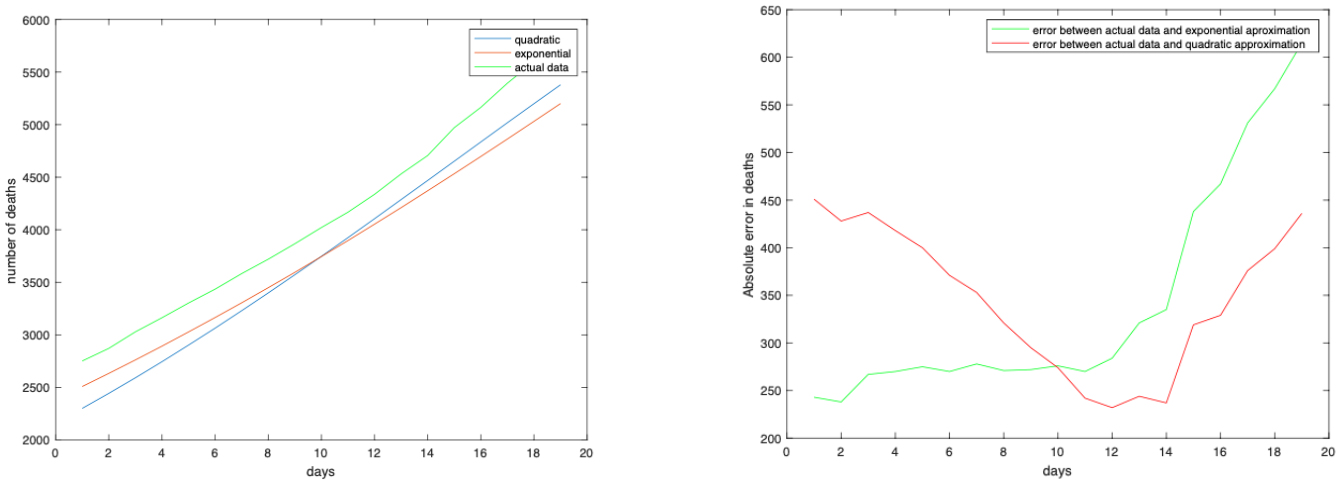


Figure 14: Figure on the left shows prediction of infected people from May 17 to June 3 and on the right shows the error in case of both the approximations

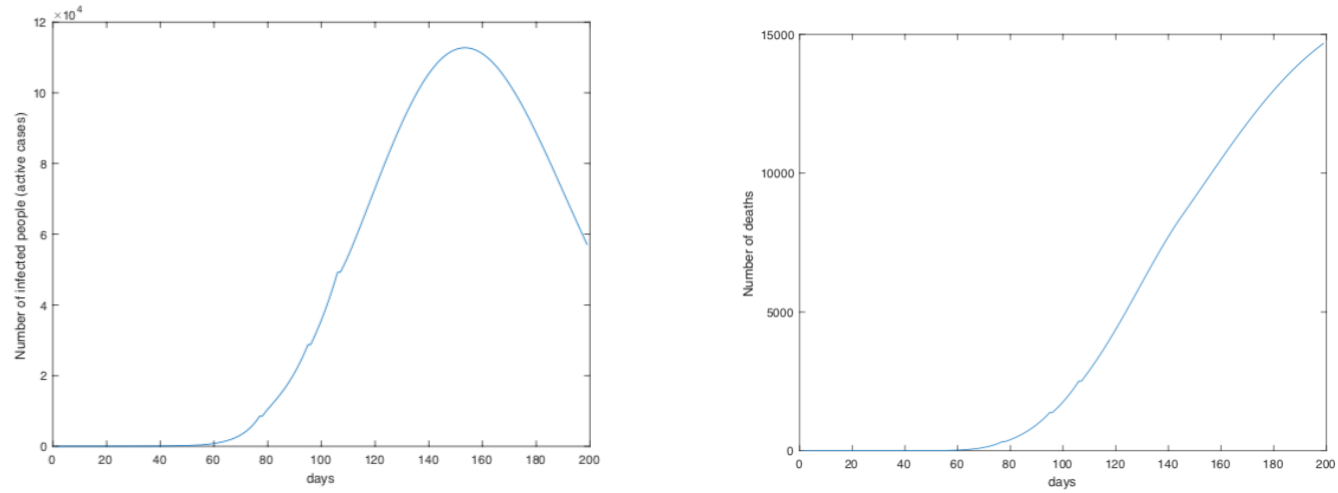


Figure 15: Figure on the left shows prediction of infected people and on the right shows prediction of deaths for exponential approximation of R_0 and variation of α.

ended on June 8 to see how effects of relaxing the restrictions are reflected in the model. Here, as shown in figures 16,17 and 18 that the model no longer predicts the outbreak correctly. This can be justified as under:

The main parameters that were extrapolated from the actual values over different periods of time (i.e α and R_0) were done so considering

that the restrictive measures would be followed in the country as they were then. However, after unlock 1.0, the number of cases and deaths in the country recorded all time high values on a daily basis, which cannot be accounted for in the functions used to extrapolate these parameter values.

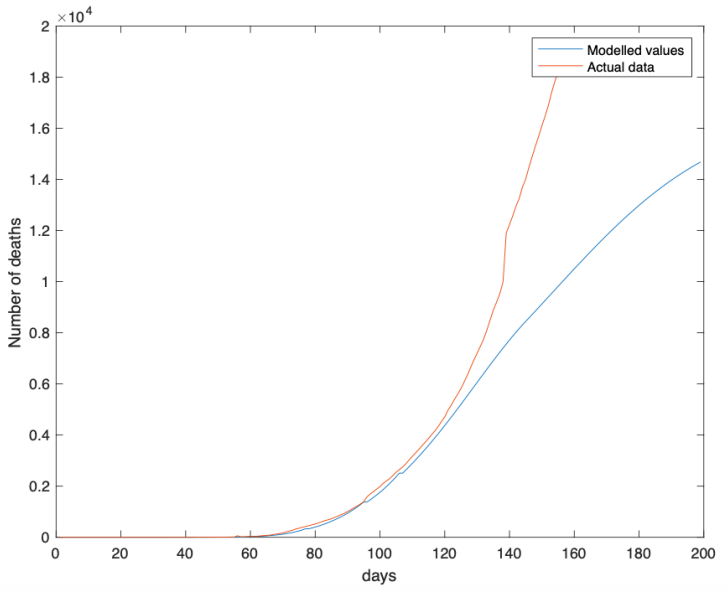


Figure 16: number of deaths predicted vs actual number of deaths till date

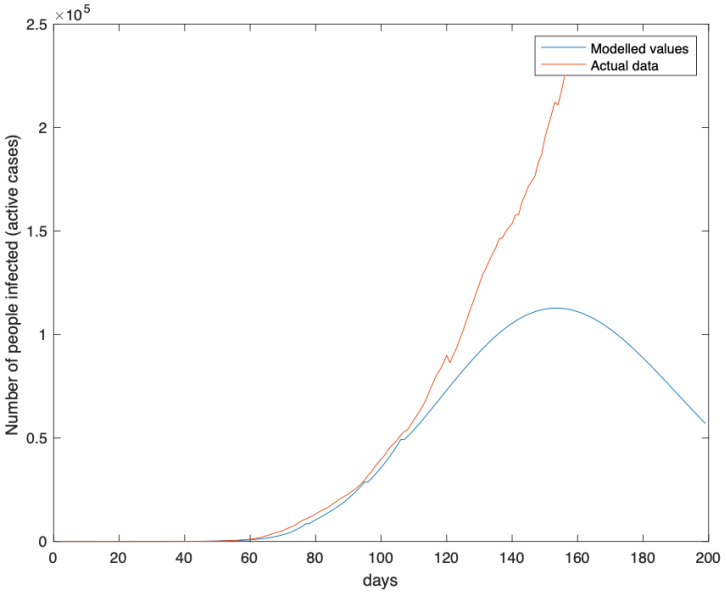


Figure 17: number of active cases predicted vs actual number of active cases till date

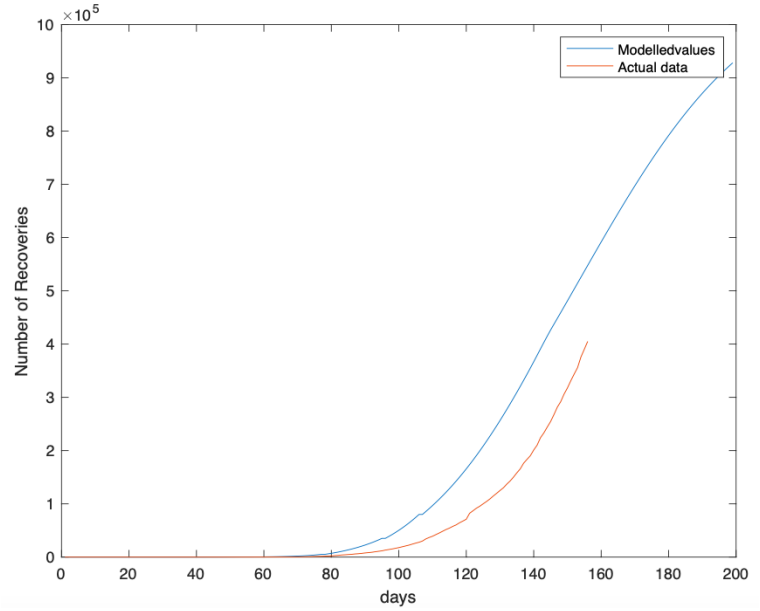


Figure 18: number of recoveries predicted vs actual number of recoveries till date

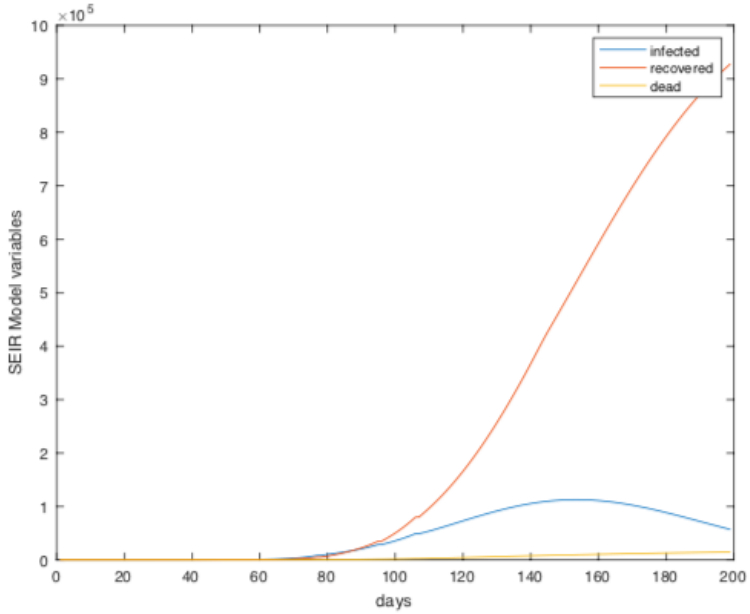


Figure 19: SEIR variables' variation with time

5 Conclusions

This project has mathematically modelled the outbreak of COVID-19 pandemic in India. The mathematical model is divided into two parts: the first where data was collected to help understand how the parameters varied; second was to predict how the outbreak would proceed, for which the parameters from the first part was used to extrapolate future values. The actual data was then plotted against the predicted model. The main parameters that were varied for the prediction model were R_0 and α, and each case has been presented along with the respective errors. The errors, although ranging from a few hundreds to early ten-thousands can be rightly justified as presented in [23] where it says:
"However, for countries that have tested a smaller fraction of their populations, the number of people with COVID-19 (most of them asymptomatic) could be higher than the number that tested positive. Thus, although it's nearly impossible to determine the exact number of people in India already affected by COVID-19, it should not be surprising if that number turns out to be 10-100-times the number of cases detected thus far – most of them asymptomatic many of whom would have recovered."

The values of the parameters have also been taken more than what was mentioned in the various news sources, because a 'weighted average' should be taken and not a regular average, owing to high number of cases in densely populated states.

Although, the model has several idealistic assumptions, the result is quite satisfactory in terms of the trend that both the predictions models have described. A final and concrete prediction model cannot be proposed because variations in several parameters and combinations of theirs could produce several prediction models, which would become very exhaustive, hence only two types of approximations have been considered here.
The theoretical analysis is not presented here because the equilibrium point is turning out be 0 owing to the fact that there is no feedback in the compartment model.

6 Appendix

The generic code used for simulation remains same for every phase of the simulation and also for the prediction model. The only change is that the time varying parameters have to specified in the form of a time-varying function directly in the **'odefun'** function wherever applicable.

```
N = 1.3e9; % total population
y0 = [N-1 1 0 0 0]; %initial conditions for the variables
t_max = input('Enter number of days from the day of infection:'); % number of days to run the simulation
t = linspace(1,t_max,t_max-1);
alpha = input('Enter the probability of death from the disease'); % death rate in India (probability in percentage)

T_r = input('Enter number of days to recover after infection');
gamma = 1/T_r; % recovery rate per day

T_inc = input('Enter incubation period'); % (average is 5-6 days but can extend to 14 days)
delta = 1/T_inc; % 1/incubation period (number of infections per day)

T_d = input('Enter number of days to die after infection');
rho = 1/T_d; % 1/number of days to die after infection (number of deaths per day)

[t,y] = ode45(@(t,y) odefun(t,y,alpha,gamma,delta,rho,N),t,y0); % solving the system of ODEs
y = round(y,0); % rounding off the values to the nearest integer
save y;
load('covidcases.mat') % loading the file containing the actual data
% the SEIR model variables as defined in the 'odefun' function
% S = y(1) Susceptibile
% E = y(2) Exposed
% I = y(3) Infected
% R = y(4) Recovered
% D = y(5) Dead

% R0 = 5.1968.*exp(-0.011.*t; using the exponential model
% beta = R0*gamma;
function dydt = odefun(t,y,alpha,gamma,delta,rho,N)

    dydt = zeros(5,1);
    dydt(1) = - (5.1968.*exp(-0.011.*t))*gamma * y(1) * y(3)/N ;
    dydt(2) = (5.1968.*exp(-0.011.*t))*gamma * y(1) * y(3)/N  - (delta * y(2));
    dydt(3) = delta * y(2) - (1-alpha) * (gamma) * y(3) - alpha * rho * y(3);
    dydt(4) = (1-alpha) * (gamma) * y(3);
    dydt(5) = alpha * rho * y(3);

end
```

Figure 20: MATLAB code

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