SEIR Model: A Modeling Based Approach for Analyzing COVID-19 Pandemic

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1 Introduction

In the environment of closely packed crowds, contagious diseases tend to spread due to the inter-action between individuals. The infected individuals come in close contact with other people in the crowd, making them susceptible to the disease as well. Although with proper treatment and medicines, individuals recover from the disease. With the help of advanced mathematical models, we can model such scenarios of epidemic outbreak. Such models will eventually help the front-line workers to empirically judge the extent of outbreak and prepare accordingly. We use one such mathematical model to model the spread of diseases, namely **SEIR Model**. In its core, SEIR model divides the entire population into four categories: Susceptibles, Exposed, Infectives and Recovered. Details of each type of population is described in sections later. Assuming this division of population, we then try to model the rate of change of each category of population depending upon factors like reproduction number, birth rate, death rate etc. Such mathematical models can also be used to model other identical scenarios like warfare, territorial disputes, bacterial and viral growth etc. In this report, our focus will be primarily on modeling epidemic outbursts of diseases.

In this report, we present a theoretical understanding of SIR model and SEIR model (along with different assumptions and terminologies). We have also implemented SEIR model with some arbitrary parameters, to model the outbreak of COVID-19 virus in India from the period of March - April 2021. With the help of our implemented model, we also explore and model different scenarios (by varying different parameters) like enforcement of a nation-wide lockdown from the month of March itself and the effect of vaccination drive on the overall spread of the virus. Each section is detailed with appropriate graphs and pseudo-code wherever applicable. A concise conclusion of our overall findings in presented in the end.

1.1 Terminologies

- **Compartmental Models:** It is a category of modeling methodologies, and one in which most epidemic models fall (including the SIR and SEIR models.) In these methods, the population is divided into compartments, and assumptions are made regarding the dynamics between the transfer of population from one class to another.

- **Basic Reproduction Number** (R_0)**:** For each primary infection, R_0 defines the average number of secondary infections that it is likely to generate during its entire period of infectiousness, in a completely susceptible population.

  It directly determines the growth rate of the pandemic, and is a predominant factor in the determination of the final number of infections. Hence, it is important to consider this value for optimal policy making.

1.2 SIR Model

SIR is a simple mathematical epidemic or spread of disease model. Intuitively, it works as follows: We consider the entirety of population which we have to study, and divide it into three categories,

- **Susceptibles** $S(t)$: This contains of all the people that are capable of becoming sick of infection at some point during the epidemic. Again, intuitively we know as we start, the set S is going to consists of the entire population (suppose N_0) Hence,

$$S(0) = N$$

- **Infected** $I(t)$: This contains the population that have been infected with the disease. As an individual becomes infected, it leaves the susceptible category. For most diseases, the immune response of the human body prevents them from getting infected by the same disease more than once (or at least within a reasonable time interval.) Hence, we have people previously belonging to the *susceptible set*, moving to the *infected set*. However, there is no arrow going backwards (no individual moves from the *infected set* to the *susceptible set*.)

- **Recovered** $R(t)$: Considering the rosier scenario, where people definitely do recover from the disease, everyone who has once had a disease will eventually end up in this set.

Hence, as long as the death rate is small in the population, the disjoint union of the three sets (SIR) based division can be assumed to include the entirety of the population. Here are the assumptions made by this model:

$$S(t) + I(t) + R(t) = N S(0) = S_0 I(0) = I_0 R(0) = R_0 \tag{1}$$

- S_0 is a very large number ($\approx N$)

- I_0 will be a very small number (sometimes idealized to 1)

- $R_0 = 0$

Now, we shall try to come-up with a system of differential equations which governs the dynamics of the population in each of these sets.

- $\frac{dS}{dt}$: We know that people get infected if they come in 'sufficient' contact with a disease carrier (an individual from the infected group.) The number of such interactions can be quantitatively denoted as $S \times I$. Using this, we can write our equations as:

$$\frac{dS}{dt} = -aSI$$

  where,

  - The negative sign denotes that with increasing number of infections, the size of the *susceptible set* reduces.

  - $S \times I$ gives us a quantification for the number of interactions between the *susceptible set* and the *infected set*.

  - a is just a proportionality constant.

- $\frac{dI}{dt}$: Now, in the earlier equation we saw how the susceptible population reduces, when it transitions into the infected population. Hence, we shall have the same term for the equation here, except for the negative sign (as now the same equation governs an increase in the *infected set* size.) Also, there are people that will recover from the disease (considering very few die) and hence, we need to take that into account as well. Hence, our final equation would look

$$\frac{dI}{dt} = aSI - bI$$

  where,

  - The first term follows directly from $\frac{dS}{dt}$

  - Since people recover, the second term of recovery is proportional to the number of people infected at a time. The negative sign is because the people who recover move out of the *infected set*.

  - a, b: are proportionality constants.

- $\frac{dR}{dt}$: Now, an increase in this set can only occur from the population transitioning from the *infected set*, and hence, by what we discussed in for the last scenario, we have

$$\frac{dR}{dt} = bI$$

The above system of differential equations fall in the category of non-linear differential equations. Hence, coming up with an exact solution for the same is a rather challenging task. However, due to the numerous assumptions we have made, and several invisible factors that we have possibly missed, the exact solutions of these systems are often not very useful either. Hence, we shall switch to methods of qualitative analysis to obtain qualitative information about the system, instead.

Plotting S, I and R: One of the most intuitive and straight-forward methods would be to simulate the system, and obtain the plots for the values of S, I and R, with respect to time. This would give us a qualitative insight as to how these values behave:

- with respect to time

- with respect to each-other

- with respect to proportionality constants

A few example simulations for a very rudimentary SIR model has been provided below. For the simulation, we considered the population (N) to be 100, and we used the *Runge-Kutta 4* method to solve the system of differential equations. Everything has been coded from scratch without the use of external libraries, etc. (except for of course the libraries for array operations, obtaining plots, etc.) We also assume that at $t = 0$, only one individual in the population has been infected (i.e., $S(0) = N - 1, I(0) = 1, R(0) = 0$.)
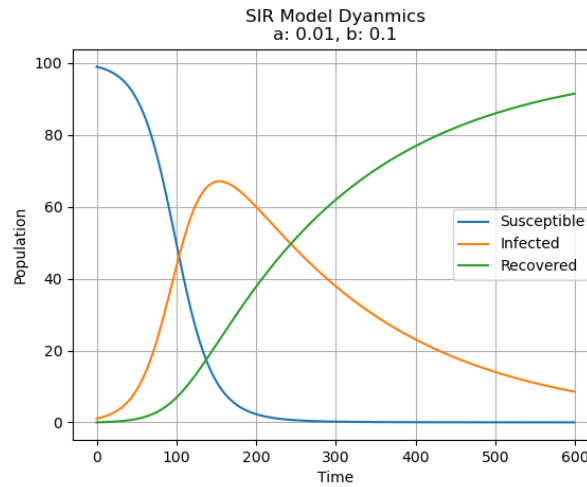

Figure 1: Typical SIR Model Dynamics

Figure 1 shows the typical dynamics of an SIR system. Let us attempt to understand this in depth

- **Susceptible**: As we know that $S(0) = N - 1$, the susceptible plot starts very near to N. Now, the equation governing S is

$$\frac{dS}{dt} = -aSI$$

S is large, and I is 1, hence $S \times I$ is also decently large. Hence, the value of S reduces. Now, we know that the maximum value of $S \times I$, since $S + I = N$(constant, at least in the initial

phase when R is small), is when $S = I = N/2$. Hence, as S reduces (and consequently I increases - which we shall discuss shortly), $\frac{dS}{dt}$ also increases in magnitude, and hence, the graph falls down faster. Once S has reduced past a limit, and R has also started increasing, resulting in a reduction in I, $S \times I$ falls, and hence, so does the slope of $\frac{dS}{dt}$. By the end of it, this slope flattens out completely.

- **Infected**: Now, I is governed by

$$I = aSI - bI$$

We just discussed that $S \times I$ increases in the beginning, and hence, I gets a positive slope. Since I it self starts at 1, bI in itself is small, and hence, I has an increase overall. Once I becomes large enough, and S becomes small enough, bI dominates aSI and the curve gets a negative slope, and the value of I reduces.

- **Recovered:** This is rather straight-forward in comparison to the first two. We have

$$R = bI$$

As I is first small, and then gradually increases, we have a similar behavior of the slope $\frac{dR}{dt}$. So the slope starts small, then increases, till I peaks. After I begins reducing, the slope for R also begins reducing and hence, we obtain the green plot.

Analyzing Equation Values: Another effective way of understanding the qualitative behavior of the epidemics is to analyze the equations for certain values. Suppose we look at the equation of I

$$\frac{dI}{dt} = aSI - bI$$

Now, what happen if $bI > aSI$ as $t = 0$? In this scenario, we do have infections, or new individuals contracting the disease, however at all times, we have that the recovery is going to be faster than the new number of infections. In such a scenario, we shall never reach the phase of an epidemic at all, as the number of infections will be highly constricted. This scenario can be represented as follows:

$$bI_0 > aS_0I_0$$
$$b > aS_0$$
$$aS_0/b < 1$$

This term $a\frac{S_0}{b}$ is also denoted as R_0 or the **Basic Reproduction Number.** Let us try and understand this using the plotting method:

This case is depicted in *Figure 2.* Since the rate of recovery is faster, the infections plot remains flat through-out the interval, and hence, we do not have an epidemic at all.
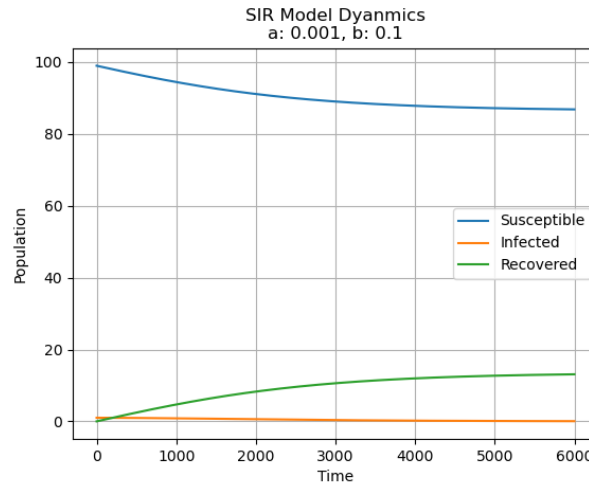
Figure 2: SIR Model Dynamics: No Epidemic ($R_0 < 1$)

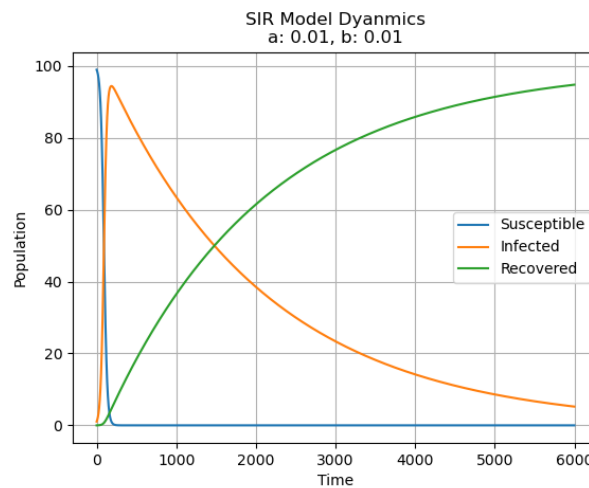Now let us look at the degenerate case at the other end of the spectrum, i.e., $aSI >> bI$

Figure 3: SIR Model Dynamics: $R_0 >> 1$

Figure 3 depicts this scenario. Since the rate of infections is very fast, almost the entire population gets infected as soon as the epidemic begins. This is shown by a massive drop in the *susceptible* population, a massive increase in the *infected population*, while the *recovered* population remains close to 0. In real life, this scenario corresponds to the when the health-case systems usually get overwhelmed because there are a lot of infected or diseased individuals appearing in a very short time. In real life scenarios, this also leads to a high number of deaths.

How can we use the information to help us during a pandemic? In a very simple scenario, we can consider our goal to bring $R_0 < 1$. Now, R_0 depends upon three terms, it is directly proportional to a and S_0, where as inversely proportional to b. Hence, we can try to achieve the following three goals:

- **Decrease a**: This refers to the case where the rate of transmission is reduced. This can be done by various methods like social distancing, masking, etc. In case of SARS Covid-19, this can be achieved by steps like frequent sensitization, social distancing, wearing masks, washing hands, not touching your face, etc.

- **Decrease S**: This refers to reducing the susceptible population. The primary method of reducing the susceptible population is to vaccinate the population so they cannot contract the disease even if they come in contact to it. Such a population can be put directly from the *susceptible set*, to the *recovered set* (assuming that the immunity from vaccination lasts forever, or practically for a really long duration.)

- **Increase b**: This refers to increase in the recovery rate. This is a little tricky, as it primarily depends on the individual's immune system. However, one way to affect this (albeit to a small extent) would be to spread awareness regarding activities which bolster's the immune system, coming up with effective drugs to counter the disease, etc. In reference to SARS Covid-19, some activities which *might* fall under this would be to encourage steam inhalation, make drugs like *remdesivir* available, etc., however, there is no prominent scientific backing behind most of these methods.

Solving the Equations: The next, and probably the most obvious method is to solve for the equation to come up with a function of different sets in terms of time. Clearly, the most intriguing set for this analysis is the *infected set.* Let us see how we solve for the same:

$$\frac{dI}{dt} = aSI - bI$$
$$I(t) = e^{(aS_0 - b)t}$$

Here, in the third step we considered the assumption that at $t = 0, I(t) = I_0 = 1$, i.e., we start with one infected individual. Clearly, we can see that the following is an exponential curve, which would look like

Having seen this over a number of times this past year, this is how a typical infection curve looks for a pandemic.

1.3 SEIR Model

As discussed earlier, SEIR model is another *compartmental model* for modeling an epidemic. It is similar to the SIR model, however, it introduces vital additional complexity.

Figure 5 shows how a typical SEIR Model appears. It has four compartments:

- **Susceptible** (S) : Same as the susceptible set for the SIR model.

- **Exposed** (E) : This is an additional compartment as compared to the SIR model. This denotes the individuals who have come in contact with infected individuals, and have contracted the
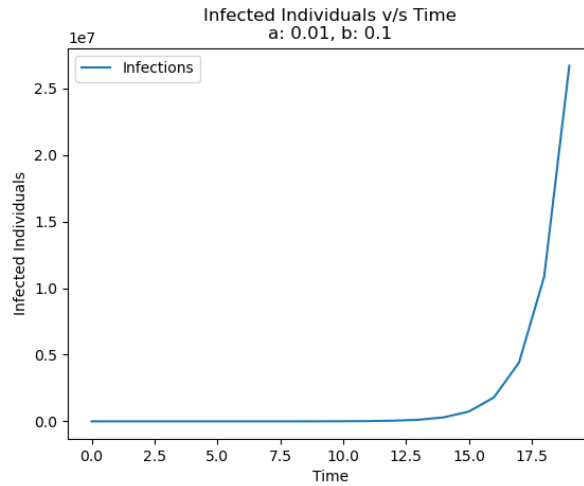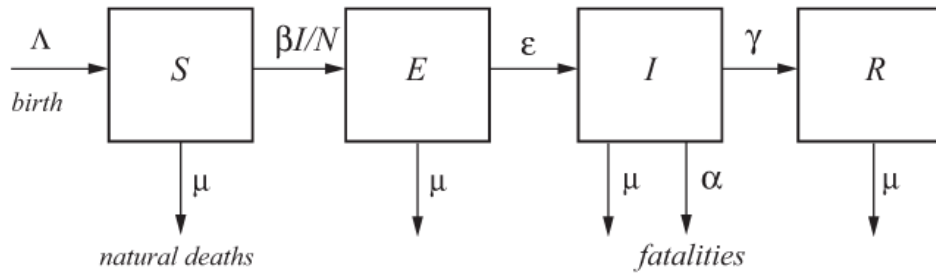
Figure 4: Infections v/s Time

Figure 5: SEIR Model Basics

disease, but the disease is in a latent stage. With respect to SARS Covid-19, this duration can range from 4-14 days (well-known for this disease.) These individuals are infected, but not infectious yet. The dynamics goes from compartment S to compartment E, and from compartment E to compartment I.

- **Infected** (I) : Same as the susceptible set for the SIR model.

- **Recovered** (R) : Same as the susceptible set for the SIR model.

As we can see, there are also a bunch of other parameters as against to the two proportionality constants in the SIR model. Let us look at what they denote:

- $\wedge$: Natural births (independent of the disease.)

- μ: Natural deaths (independent of the disease). The inverse of this quantity is interpreted as normal life expectancy.

- α: Fatality rate[1] due to the disease.

- β: Probability of disease transmission per contact times the number of contacts per unit time.

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[1]Fatality rate refers to the proportion of deaths from a certain disease compared to the total number of people diagnosed with the disease

- η: Rate of progression from exposed to infectious (the reciprocal of this quantity is the incubation period[2] of the disease.)

- γ: Recovery rate of infectious individuals

- N_0: Total population.

- t: time variable.

$$N = S + E + I + R \leq N_0$$

For this model, if we have the following:

$$\wedge = 0$$

$$\mu = 0$$

$$\eta = \inf$$

This would give us the classical SIR model. However, as we know that most diseases (including SARS Covid-19) have an incubation period. Hence, having this compartment provides more validity to the methodology.

Since we assume life-long immunity in case of most diseases (or at least for the entire duration of simulation), we do not have the dynamics going from *recovered set* to the *susceptible set*. However, recent research supports that this might not be true for SARS Covid-19.

For this scenario, the **reproduction ratio** is given as follows:

$$R_0 = \frac{\beta \eta}{(\eta + \mu)(\gamma + \alpha + \mu)}$$

The interpretation is the same as before, i.e., average secondary infections per infected individual. We also define *IFR (Infection Fatality Rate)* and *CFR (Case Fatality Rate)*. Where the prior represents the number of deceased individuals to the number of total infected individuals. This can be represented by the equation:

$$IFR = \frac{D_{\text{inf}}}{D_{\text{inf}} + R_{\text{inf}}}$$

The subscript inf denotes that we are considering the numbers all the way to the end of the pandemic to evaluate this. Similarly, CFR refers to the number of deceased individuals to the number of identified individuals. In this case, the denominator is always smaller than the prior, and hence, $CFR > IFR$ always holds.

1.3.1 SEIR Assumptions

The following assumptions are usually associated with epidemic modeling using SEIR methodology:

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[2]Incubation period is the time elapsed between exposure to virus till the time when symptoms and signs are first apprent

- The natural death rate is balanced by the natural birth rate. That is, the only change in population can be brought about by deaths due to the disease being modeled. To mathematically model the prior assumption we use:

$$\wedge = \mu * N$$

Hence, at all times, the number of deaths (due to all other causes except for the disease being modeled) is exactly equal to the number of births.

- No immigration or emigration of population takes place in the duration of simulation. Hence, our total population is constant, and $N_0 = N + D$ (initial population = remaining living population + number of individuals deceased because of the pandemic.)

- Individuals directly get recruited to the *susceptible compartment* at birth.

- The dynamics from the *susceptible compartment* to the *exposed compartment* is controlled by a complex bi-linear term denoted by:

$$\frac{\beta S I}{N}$$

This denotes a simple (*simplest* to be precise) model for *mass-action* transmission in a homogeneously-mixed host population. The scaling factor (N) allows the reproduction ratio to be independent of the actual population size, and instead just represent proportionality to the local density.

- The recovered individuals are assumed to be immune for life.

- The population is considered homogeneous in all aspects.

1.4 Experimentation

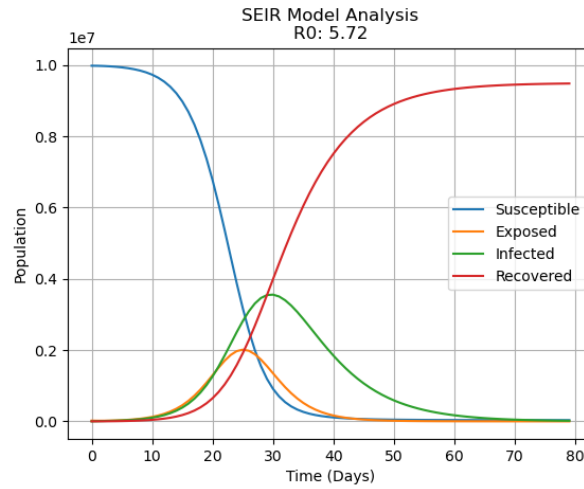Let us run some experiments using our present SEIR model.

Figure 6: Typical SEIR Model Dynamics

Figure 6 shows us how the population size in the four different compartments vary with time. Here, a more precise and informative time-axis has been used (in comparison to earlier plots) and it denotes time in *days.* The data used has been done considering prior research on SARS Covid-19. Some of these parameter-values include:

```
Parameters:
    N0      = 10000000 (10 million)
    alpha   = 0.006/day
    beta    = 0.75/day
    gamma   = 0.125/day
    eta     = 0.33/day
    wedge   = mu * N (to balance the birth and natural deaths)
    E0      = 20000
    I0      = 1
    R0      = 0
    S0      = N0 - (S0 + I0 + R0)
```

Figure 7: SEIR Model Parameter Values

We can also analyze the deaths separately to gain a better insight regarding the same. There are two fundamental ways to analyze the number of deaths in the scenario:

- **Deaths per day**: This denotes the number of people that are expected to die on each day. This is directly related to when the health-care facilities of a region will be under maximum stress.

- **Total number of deaths**: This denotes the total number of individuals that are expected to die during the entire duration of the pandemic. This allows us to interpret the total cost on human-life of the pandemic.
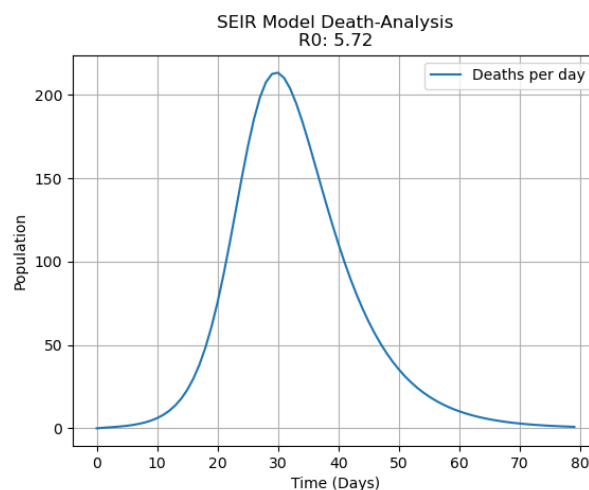

Figure 8: SEIR Model: Deaths per day

Figure 8 shows the expected number of deaths per day. This predicts that the health-care systems will be under maximum stress around $30^{th} - 40^{th}$ day.

Figure 9 shows us the total number of deaths, which here is 7000. Considering we began with a
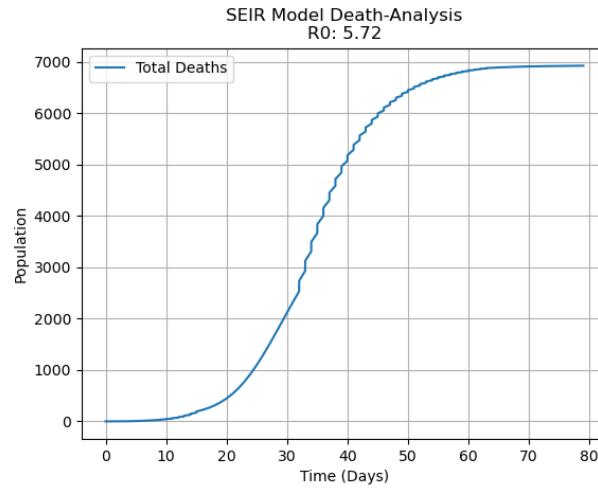
Figure 9: SEIR Model: Total number of deaths

population size of 10,000,000, this predicts a mortality rate of $\approx 0.07\%$, which as we know is quite far off from the observed rate at most places. Hence, we shall need to fine-tune the parameters for this particular model before applying it to real-life instances. This is also a methodology to verify the authenticity and reliability of the model.

Now, we shall attempt to draw comparisons for different values of R_0. We shall vary R_0 by varying β essentially.
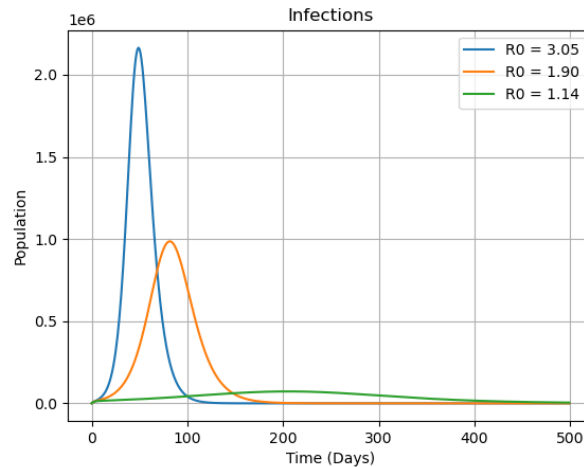
Figure 10: SEIR Model: Infections

Figure 9, 10, 11, 12 show how the infections, total infections, deaths and total deaths vary, as the value of reproduction ration varies. As we can see, a higher reproduction rate not only corresponds to a higher peak, but to a faster one as well (which usually does not give the time for the population and the health-care system to adapt.) Moreover, it also leads to both, a higher number of infections and a higher number of deaths in total.

The number if brought down significantly as the reproduction rate comes down. It can be brought
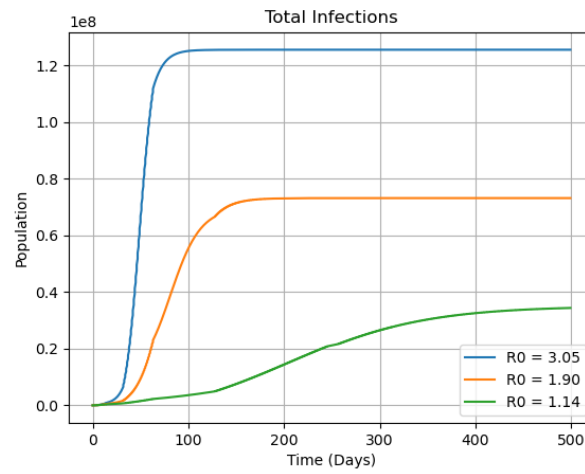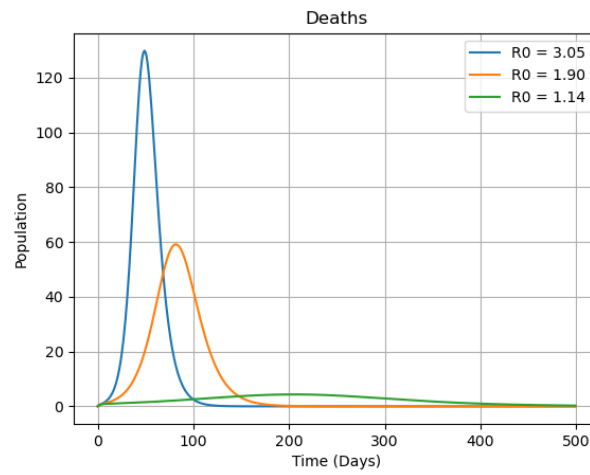
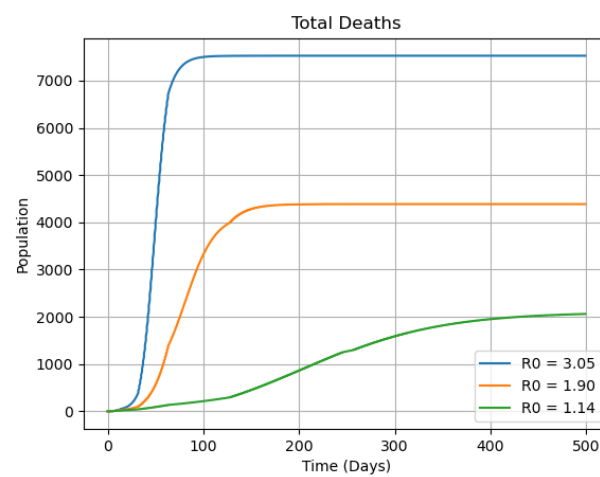Figure 11: SEIR Model: Total Infections

Figure 12: SEIR Model: Deaths

Figure 13: SEIR Model: Total Deaths

down through measures like social isolation, wearing masks, etc., and hence, these practices can lead to a significant reduction in the total number of causalities. One can argue that for lower reproduction number, the pandemic does appear to temporally last-longer (because of the wider curves in this scenario), however, the significantly lower number of causalities more than makes up for it. Next, we shall look at how the quantity of initially exposed individuals influences the over-all dynamics of the simulation. *Figure 14, 15* show the influence of initially exposed individuals (i.e.,
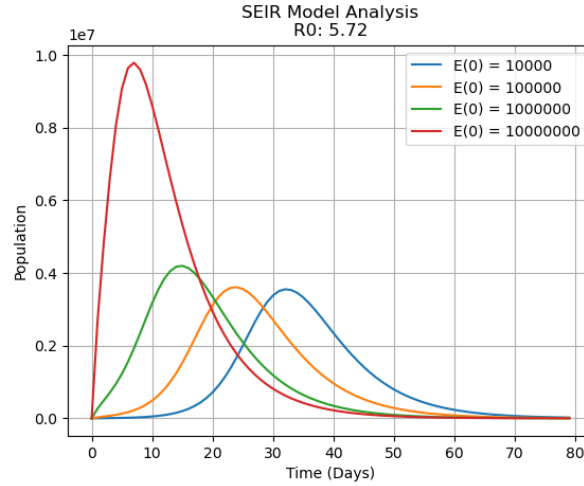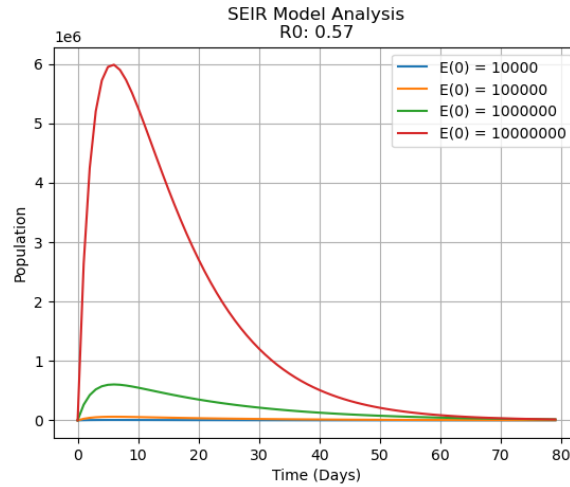

Figure 14: SEIR Model: Infections

Figure 15: SEIR Model: Infections

$E0$) on the model dynamics. We analyze it for two sets of reproduction rates 5.72 and 0.57. The first figure represents that $E0$ has a very prominent effect on both the intensity of the peak, and the spread. The intensity of the peak is directly related to the magnitude of the initially exposed population. This shows that if there are a very high number of individuals exposed, the high rise in infection shortly after can wreck havoc on the health-care system which is under stress, and may result in a lot higher number of deaths than predicted by the model.

For $R_0 < 1$ however, we have do have a similar scenario when considering the intensity of the peak, but the position of the peak remains the same irrespective of the value of E_0. Also, this high rising peak delays the suppression of the epidemic, as now it gets prolonged significantly more than when E_0 is small.

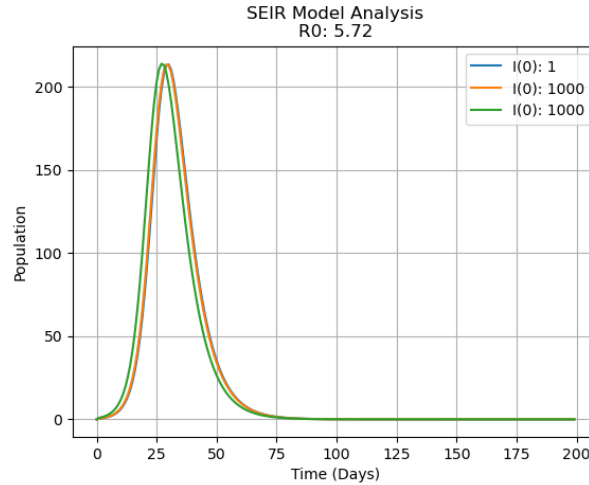Now we shall extend this to analyzing other parameters as well.
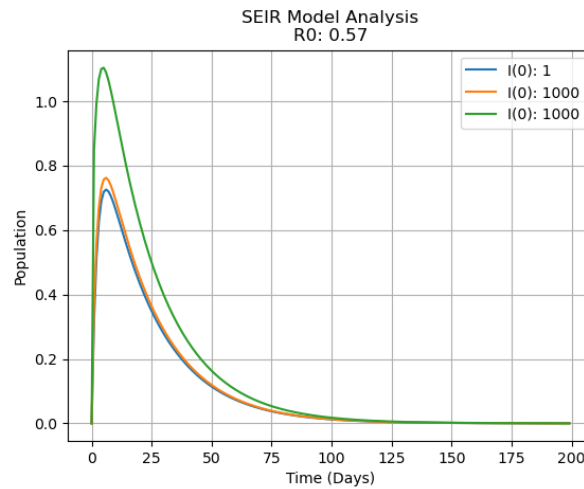

Figure 16: SEIR Model: Infections

Figure 17: SEIR Model: Infections

Figure 16, 17 represent the scenario where we start with different $I(0)$ values, or where a different quantity of population is initially infected with the disease. The peak intensity is shown to be unaffected by the magnitude of $I(0)$ for $R_0 > 0$, and there is some, but not a significant effect for $R_0 < 0$. It is however, to note that historical evidence lines up against this observation and $I(0)$ indeed has a prominent effect on the dynamics in reality.

Figure 18, 19 show the effect of different values of η on the dynamics of the epidemic. As discussed
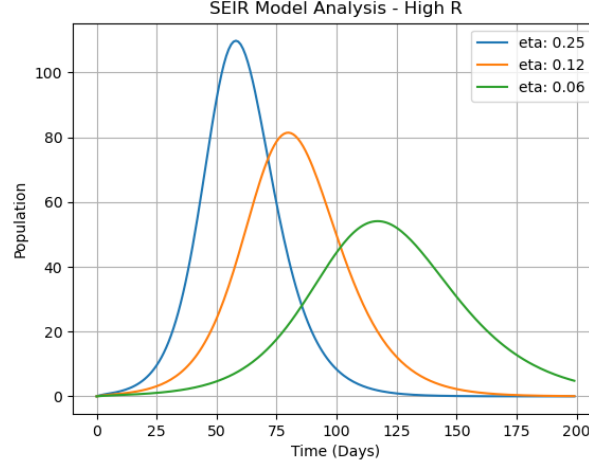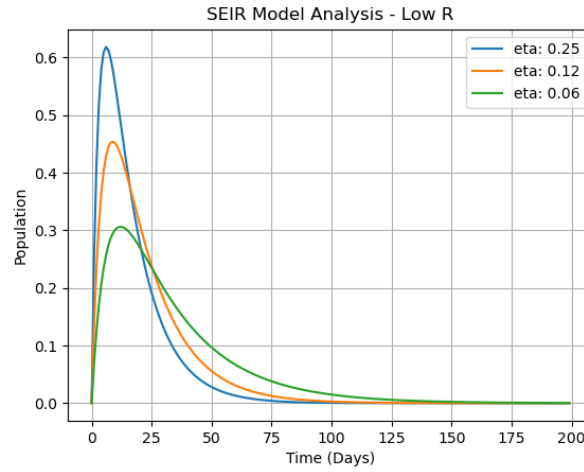
Figure 18: SEIR Model: Infections

Figure 19: SEIR Model: Infections

earlier $1/\eta$ corresponds to the incubation period of the disease, hence, for larger values of η, an individual is more likely to become infected soon after being exposed, and for a smaller value we have the opposite. It is also important to note that in this scenario we are not considering a constant reproduction rate, as it is a function of η and hence, changes for different values of η.

Now, if we have a small value of η, the incubation period is large, and hence, the rate of infection slows down. This is shown in the *Figure 18*, when the peak corresponding to smaller values is less intense, and also shifted towards the left (as the infection 'kicks-in' at a latter stage.)

For a lower values of $R(< 1)$, there is no shift of peak (as expected since new infections are rather small in number), but there still is a prominent effect of η on the intensity of the peak.

Finally, in *Figure 20, 21* we look at the effect of different values of γ on the epidemic dynamics. As for η, reproduction number is also a function of γ and hence, we do not consider a constant value for it as it changes with our choice of γ. However, like in the previous scenario we adjust the other
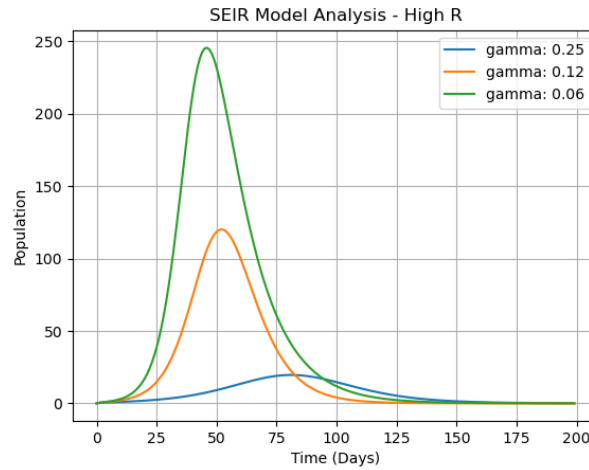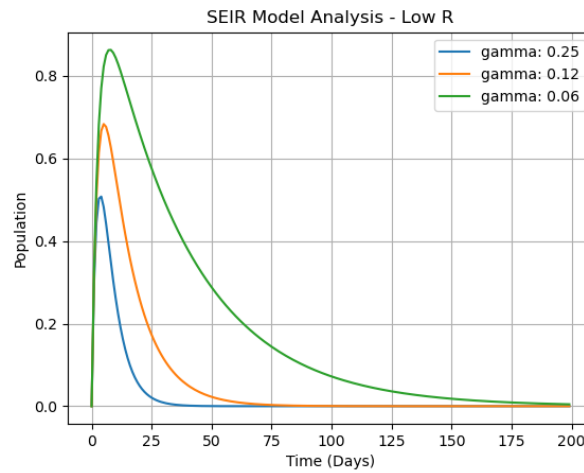
Figure 20: SEIR Model: Infections

Figure 21: SEIR Model: Infections

parameters in a manner such that we can analyze the case with both $R_0 > 1$ and $R_0 < 1$.

As discussed earlier, gamma refers to the recovery rate of individuals, hence, the larger its value the faster is recover, and more mathematically, the faster is the transition from the compartment of *infected* to the compartment of *recovered*. Hence, as we would expect. a lower γ corresponds to a high peak, since a lot of individuals are infected during the same time, and they further cause more infections, and so on. Whereas, a smaller γ results in a significantly flatter peak. The position of the peak is however, almost the same for both the scenarios. This carries over to the case where $R_0 < 1$, where though the different in peak is not that signification (because the rate of infections is anyway low), but it is still higher for lower values of γ.

Hence, with this we have developed a good understand of both the **SIR** model and the **SEIR** model, its parameters, its physical and mathematical interpretations, etc. Now, we are ready to model an epidemic using an SEIR model.

2 Model

2.1 Introduction

For the purpose of our model, we attempt to model the global pandemic of SARS Covid-19, for the entirety of Indian population in the duration of March 1st, 2021 to April 21st, 2021. Consequently, right before this duration we had a period where the pandemic seemed to have reduced in intensity. As a result, most of the country was fully functioning at this point, with public places like malls, gymnasiums, sports facilities, etc., open for the masses to use. There was no real lockdown or enforced social distancing during this period, and a social complacency had set in. This perhaps was the reason which lead to a second-wave of infections, which turned out to be much worse than the first.

As unfortunate as it is, it does provides us with a relatively easy scenario to model, as a traditional SEIR model (which does not account for measures such as lock-down, enforcement of social-distancing, etc.) can be applied to obtain a satisfactory fit with the data. Also, it allows us modify the SEIR model to introduce these notions of policy-making, and estimate how the trajectory of the pandemic could have been altered if certain policies were employed.

2.2 Methodology

All the data has been obtained using REST-API from

`https://api.rootnet.in/covid19-in/stats/history`. All the code used for this project (from the basic modeling, to the numerical methods involved) have been coded from scratch in Python (as this is a course project, and the goal of this course was to understand modeling, simulation and numerical methods, instead of merely using it.) We used a traditional SEIR model, where the parameters were estimated through the means of parameter space exploration, and least-squared error optimization with the predicted number of infections to the actual number of infections. The code for these were also written from scratch in Python. The numerical methods involved were *euler method* for integration, and the *Runge-Kutta 4* method for secondary analysis.

2.3 Parameters

The following parameter values were used for the simulation:

Parameter	Value
N_0	1380000000
E_0	1000
I_0	16835.8
R_0	10786457
D_0	157157
S_0	1369038550.2

These were the parameter values which we use for the simulation. The $\wedge$ and μ parameters are kept to be 0, which basically indicate that our overall population is static, if not for the dynamics induced by pandemic. This is an appropriately sound assumption over a short duration of time (i.e., for our case of a 52 days long simulation.)

Moreover, we have the parameters η, γ β and α, values for which we shall search using repeated parameter-space exploration.

2.3.1 Parameter Space Exploration

Parameter space exploration is a relatively standard methodology for model optimization, when the number of parameters are usually few and have an associated physical significance. It is often used to identify various parameters in brain-network simulations, etc. The idea is simple, we constraint a parameter between a lower-bound and an upper-bound, and then divide this interval uniformly. Then, we proceed with a simulation using each of these values, and obtain the error term with respect to each (in our case it is the squared-error obtained by comparing the number of infections per-day to the actual number of infections per-day in the same duration.)

To whichever set of parameters we obtain the least possible error, we pick those for our simulation, or we can refine it further by searching in a smaller interval around this obtained value. The time-complexity of the method increases as $O(n^p)$, where p is the number of parameters whose space we are attempting to search. Also, the space searched, and its granularity has a direct adverse impact on the time complexity as well. Here, we present the pseudo-code algorithm for parameter space exploration over the parameters α, β, γ and η.

2.4 Result and Observation

Figure 23 shows the plots for infections vs time, for both the real-data and data obtained through model-simulation. The curvature of both the curves are almost similar. It is to be noted that parameter values which do not exactly overlap with the actual data, but instead lead it by a small amount

```python
def parameterSpaceExploration(I_real, dt=.01, days=52, gran=5):
    all_values      = []
    gran            = gran
    alpha           = [0.030, 0.04]
    beta            = [0.36, 0.40]
    eta             = [.043, .048]
    gamma           = [.055, .075]
    alpha_explore   = np.linspace(alpha[0], alpha[1], num=gran)
    beta_explore    = np.linspace(beta[0], beta[1], num=gran)
    eta_explore     = np.linspace(eta[0], eta[1], num=gran)
    gamma_explore   = np.linspace(gamma[0], gamma[1], num=gran)
    for alphaI in alpha_explore:
        for betaI in beta_explore:
            for etaI in eta_explore:
                for gammaI in gamma_explore:
                    model = getSEIRModel(I0, R0, D0, eta=etaI, gamma=gammaI, alpha=alphaI, beta=betaI)
                    iterator = 0
                    I        = []
                    I_total  = []
                    while iterator*dt < days:
                        if iterator*dt - int(iterator*dt) < dt/2:
                            T.append(iterator*dt)
                            I.append(model.I)
                            if iterator == 0:
                                I_total.append(I0 + I[-1])
                            else:
                                I_total.append(I_total[-1] + I[-1])
                        model.simulate(dt)
                        iterator = iterator + 1
                    error = getError(I_total, I_real)
                    all_values.append(Value(alphaI, betaI, etaI, gammaI, error))
    return sorted(all_values, key=lambda elem: elem.error)
```

Figure 22: Pseudo-code Algorithm for Parameter Space Exploration
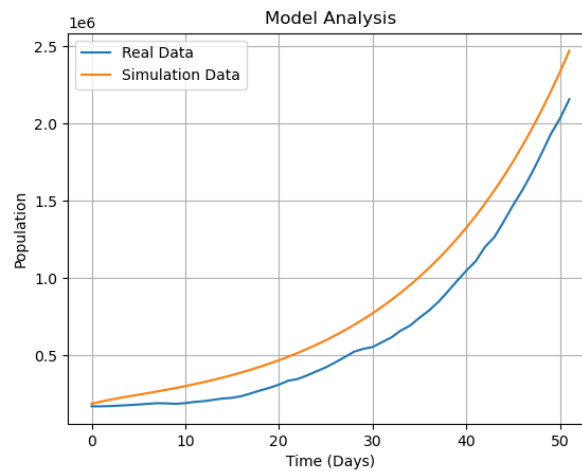

Figure 23: Model Analysis

was purposely chosen, because the real-data corresponds to reported cases of infection which are always a little lower than the actual number of infections. The values of parameter were obtained through parameter space exploration. The final values were:

Parameter	Value
α	0.06
β	0.435
γ	0.15
η	0.1

Moreover, when $\mu = 0$, we have:

$$R_0 = \frac{(\beta \eta)}{((\eta + \mu) * (\gamma + \alpha + \mu))}$$
$$R_0 = \frac{(\beta \eta)}{((\eta) * (\gamma + \alpha))}$$
$$R_0 = \frac{(0.435 \times 0.1}{(0.1 \times (0.15 + 0.06))}$$
$$R_0 = 2.071$$

Hence, the obtained reproduction number is $2.071 (> 1)$ and hence, the pandemic is not likely to end without external measures. If things stay the way they are, the pandemic is expected to get worse at this rate, and lead to a lot many infections which can cause the health-care system to collapse.

2.4.1 Effect of Lockdown

Now we shall look at what would happen if there was a lock-down imposed (enforcement of social distancing.) If in a lockdown, susceptible population does not come in contact to the infected population as often, and hence, this reduces the magnitude of population transitioning from the *susceptible compartment* to the *exposed compartment*. In mathematical terms, this would result in a reduction of the value of β. However, a very low value of β that is a complete lockdown would have a disastrous impact on the economy. Hence, for optimal policy making we need to understand the optimal amount of enforcement of social distancing that is required to ease the ongoing spread of infections, while also leading to the minimum possible economic backlash. *Figure 24* shows what would have happened if we had a draconian lockdown ($\beta = 0.215$) for 52 days beginning from the 1st of March. This would have lead to a near flattening of the curve, as would be expected with the value of R_0 falling down to 1.02.

A $\beta = 0.315$ (*figure 25*) corresponds to a much less severe lockdown as compared to the first case, however, it still would have gotten the curve a lot flatter than where it actually is. The curve however, is still exponential, but the growth is much flatter, and hence, appears to be manageable. Its economic and welfare backlash however, would be much less compared to the first scenario.

Finally we see what happens when we relax β further (in *figure 26)*, and have it as 0.385. The reproduction rate at this value is pretty significant, and as expected, the curve of infections has an exponential growth which is close to where we currently are. Hence, such loose enforcement of social-distancing would have probably not helped altering the dynamics of the pandemic by much,
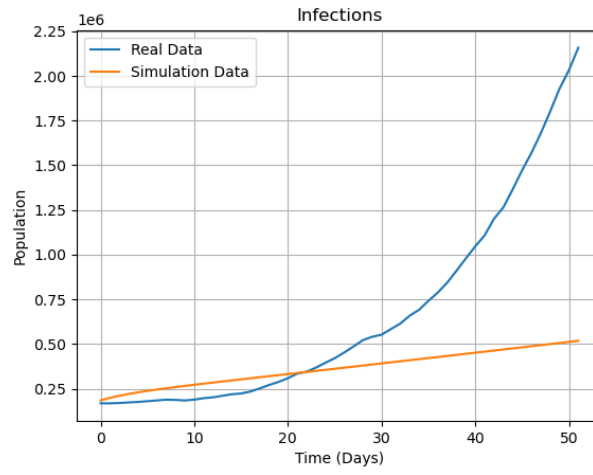
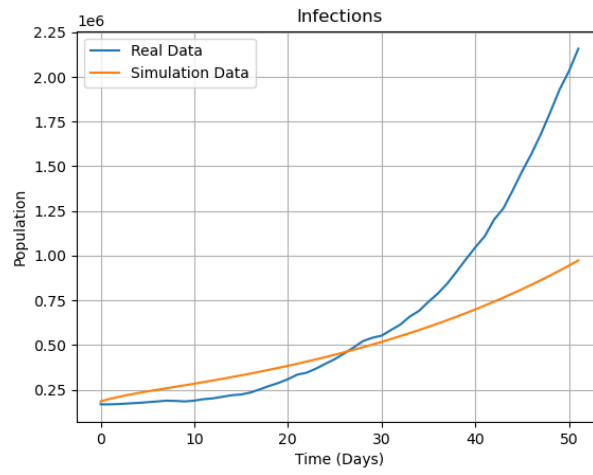Figure 24: $\beta = 0.215, R_0 = 1.02$

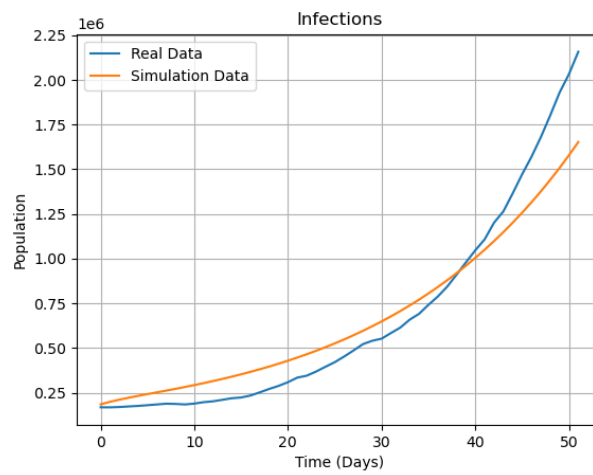

Figure 25: $\beta = 0.315, R_0 = 1.5$

Figure 26: $\beta = 0.385, R_0 = 1.83$

and would have only resulted in hurting the economy and welfare of the population.

Figure 27 shows us how the total number of deaths would have been affected for different values
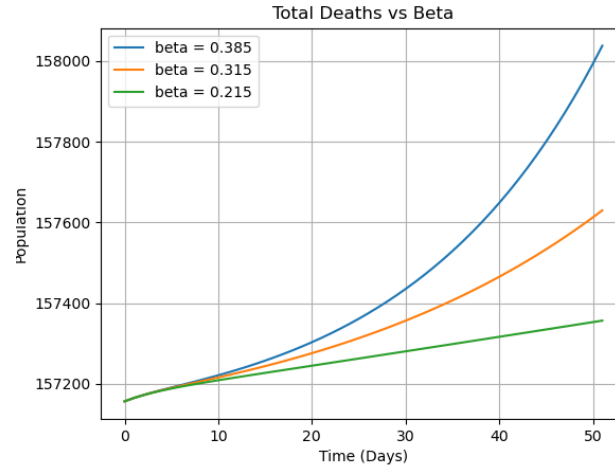

Figure 27: Total deaths for different values of β

of β. The lower the value (the draconian is the lockdown), and the lesser number of deaths we have. This is an expected result, and can also be seen from the simulation results. Here, it shows that both $\beta = 0.215, \beta = 0.315$ would have been good choices to govern an optimal policy for the lockdown.

2.4.2 Effect of Vaccination

Finally, we have attempted to do something interesting with our SEIR model. We tried to modify it for the scenario where the population is vaccinated at a rate of θ. We make the following assumptions for the same:

- We consider that the vaccinated population becomes immune to the disease with immediate effect. This might not be a completely accurate assumption, however, it is an appropriate place to begin.

- A person can get vaccinated only if it is not infected. This falls in line to the current guidelines following the vaccination where only a person who is Covid-free at the moment can get vaccinated.

- The entire population has access to vaccination. This is again a slightly inaccurate assumption for the current scenario, however, again it does provide us a place to conveniently begin our analysis.

- A vaccinated individual moves directly to the recovered population.

- Only one shot of vaccine is required to be effective.

Now, our set of equations become

$$dS = \wedge + (\theta - \mu)S - \frac{\beta SI}{N}$$

$$dE = \frac{\beta SI}{N} - (\mu + \eta + \theta)E$$

$$dI = \eta E - (\gamma + \mu + \alpha)I$$

$$dR = \gamma I + \theta(S + E) - \mu R$$

and with a bit of algebra, we get the reproduction number as:

$$R_0 = \frac{\beta \eta}{(\eta + \mu + \theta)(\gamma + \alpha + \mu)}$$

Figure 28 shows the dynamics for the SEIR model which models vaccination. As expected, there is a
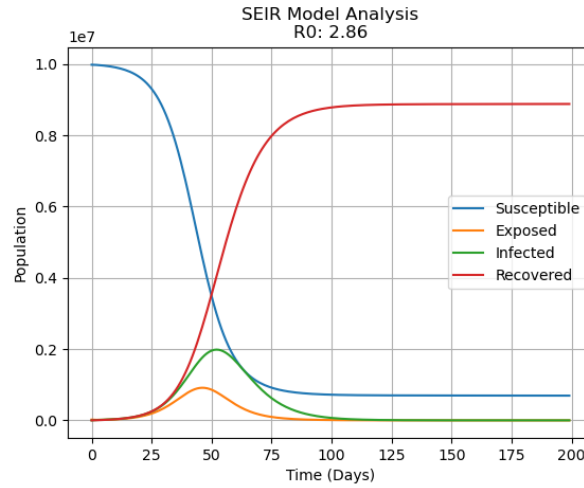

Figure 28: SEIR Dynamics with $\theta = 0.0001$

steep increase in the recovered population as now it also contains the vaccinated population. Population from $compartment S$ and $compartment E$ move directly into the $recovered compartment$. This population does not infect anyone either, not is susceptible to the infection, and hence, the number of infections are much smaller than for when we did not have vaccination. Also the duration of the pandemic has been largely reduced even for a relatively high reproduction rate of 2.86, which again bolsters the fact that vaccination is an effective methodology.

Now, we shall look at what would have happened if we had a full-fledged vaccination drive from early March in India.

For a $\theta = 0.01$ (*Figure 29*), the simulation shows that the curve would have flattened to an equal extent as having a social-distancing enforced to bring $\beta = 0.315$ from $\beta = 0.435$. Also, vaccination does not have long-term ill effects on the economy, nor on the well-fare of the population, and hence, is always preferred over a lockdown.
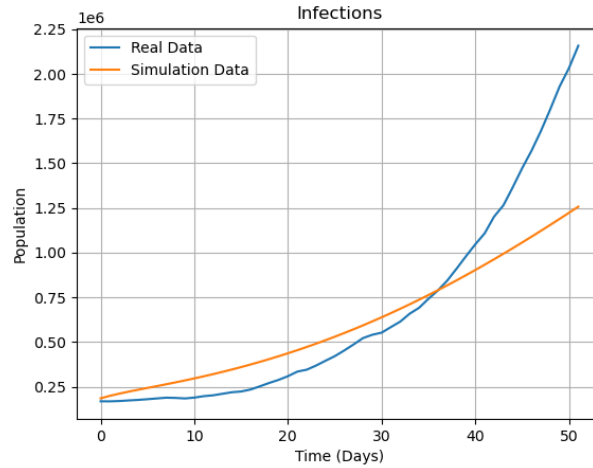
Figure 29: Total infections for $\theta = 0.01$

2.5 Conclusion

We studied the SEIR model of epidemic modeling, and used it to analyze the SARS Covid-19 pandemic in India over the period of beginning of March to 3rd week of April. We saw how the current scenario was, what mathematical inferences can be made (such as the various parameters, estimating reproduction number, etc.) and used various methodologies to fit our model approximately to the real-world data. Following this, we used the obtained fine-tuned model to analyze how things could have been different if we have different policies enforced. Namely, what would have happened if we have a lockdown enforced (of varying strictness) and what would have happened if there was a very successful (and rather too ideal) vaccine drive. We modified our model (and the system of equations) to account for the vaccination, and carried out experiments over the same as well. We found that lockdown is effective but only if its strict to more than a certain degree, otherwise it might just end up harming the socioeconomic welfare of the population while not significantly altering the current dynamics of the pandemic. Then we saw how the SEIR model would behave in case of a successful vaccination drive, and we found that it would be (albeit too ideal) the most effective way to flatten the curve of infections in the present scenario, while also propelling us towards the end of the pandemic more effectively.

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