

Epidemiology : Compartmental Models

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DECLARATION

This work has not previously been accepted in substance for any degree and is not being concurrently submitted in candidature for any degree.

STATEMENT 1

This dissertation is the result of my own independent work/investigation, except where otherwise stated. Other sources are acknowledged by giving explicit references. A bibliography is appended.

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A handwritten signature in black ink, appearing to be 'ALS' followed by a stylized flourish and a horizontal line.

Signature

Abhishek Swami

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Chapter 1: Summary

The work presented in the document is in reference to the area of epidemiology compartmental model. Epidemiology is composed of analysis of several diseases. In this work the prime focus is kept on COVID-19 disease. An attempt has been made to emulate the disease behavior of COVID-19. This study of disease dynamics of COVID-19 has been done by designing a mathematical compartmental model. A variant of SIR model has been designed by amalgamating several other compartments. The revised model is SEQIHRDV. Further the design principles followed for the model development has been listed. The parameter and compartment description of the model has been mentioned as well. Literature review of other researchers work in this arena was conducted and same have be overview. Further a real world data has been applied to model by programming technique. The respective outcome has visualized for data interpretation which is part of programming implementation Forecasting of 200 days have demonstrated. The effect of precautionary measures like vaccination and testing on infection count has been analyzed generally.

Chapter 2: Introduction

Epidemiology is a wing of medical science and is study of cause and spread of diseases [1]. The disease characteristics are analyzed in a specific population [1]. Knowledge of epidemiology is also utilized for avoidance and management of the respective disease [1].

Epidemiology helps the scientists or researchers whom we can refer as epidemiologists to gain insights about the disease in the picture [2]. Epidemiologists can draw conclusions like the particular segment of population that is prone to be severely affected by the disease [2]. This can be based on age groups and several other factors [2]. Thus epidemiology contributes in prevention and to pacify effects of disorders [2].

COVID-19 is transmissible disease which is caused due to severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) virus[28] . In China 2019 the very first case of COVID-19 was detected[28] . Later virus spread almost every corner of the globe thus COVID-19 disease was declared as pandemic[28] . Some of the common symptoms of COVID-19 can be tiredness, loss of smell, fever, loss of taste, headache[28] . Senior citizens are more prone to get affected by the disease with serious health condition[28] .Certain individuals could have various other symptoms for longer duration as well[28] .COVID-19 disease can lead to serious degradation of human organs[28] .COVID-19 disease's transmission medium is through air[28] . The disease can spread through droplet particles[28] . The people in contact with each other within short distance apart can get infected to COVID-19[28] .Even if people are indoors at a greater distance as well can be infected[28] . The entry point of the virus in human body can be mouth , eyes and nose[28] . The COVID-19 virus can also spread through contact of fluids[28] . The vaccine for the COVID-19 has already been approved across the world[28] . Several vaccination campaigns have been carried out across the globe in different countries[28] . Precautionary measures apart from vaccines are also practiced in the population[28] . Some of them are regular handwashing, precaution by usage of masks, social distancing, quarantine, face cover while coughing in public[28] .

Mathematical models can be described as a set equations which are formulated to emulate a natural world crisis [3]. An effort will be made to reflect the crisis as close as possible in mathematical form [3]. Further resolving this equations will give us the interesting features about behavior of the problem [3]. We can identify the different variables that influence the behavior of the system and also the inter-relations of variables [3].

Compartmental models can be thought of as one of the prototypes of mathematical models. Consider there is certain structure or a organization [4]. Compartmental model revolves around the concept that this particular structure is segmented in various “compartments” [4]. Further compartmental models aid in gaining insights how different entities traverse these defined compartments [4]. Compartmental models are represented mathematically in the form of ordinary differential equations [4].

The epidemiology compartmental model are the mathematical models which can utilized to analyze behavior of an epidemic disease. Basically these models aid in providing an estimate of behavior of an epidemic disease. Further these differential equations are solved using numerical methods. Ultimately we shall visualize the solution of the differential equation

In my project assignment I have strived to estimate behavior of COVID-19 disease by modelling and implementing the respective compartmental model. I have analyzed the related work of different authors who have demonstrated they work in my project topic. I have applied my understanding of the domain knowledge and constructed this project assignment with foundation from the respective related work. Those referenced works are [5], [12], [17]

The data set we utilized in the project assignment is of cumulative COVID-19 deaths reported for country India. The data set has been downloaded from below mentioned website. Cumulative COVID-19 deaths were filtered out for country India for period of 22 January 2020 to 2 November 2022 amongst other countries and was used in the project assignment.

<https://data.humdata.org/dataset/novel-coronavirus-2019-ncov-cases>

As we familiarized ourselves with the data set which has been deployed in the project assignment, I have attempted to calibrate the model so as to emulate the respective outcome of the model as close as possible to the real world data.

The project assignment can be viewed as modelling → Analysis of model outcome to real world data → Visualization of the respective statistics to interpret the same. Hence in the project assignment the respective data analysis and visualization is achieved via software programming tool Python.

During the establishment of the project assignment various software libraries of respective programming language were used.

In my project assignment I have deployed the variant of SIR model SEIHRDV. The programming tool which I have utilized to implement the model is Python. The corresponding counts of the population of people in respective compartments have been extracted by solving the respective differential equations and visualized the same through Python programming language. There different statistical outcomes extracted from the implementation of respective model. Further conclusions are drawn based on the statistical data analysis of the outputs from the model.

Chapter 3: Mathematical Prerequisites

3.1 Differential Calculus

Differential equation is an arena of mathematics that deals with rate of change in respective entities [6]. The prime focus of differential calculus is derivative (change) of a function [6]. If a point is specified in a function then the derivative at the specified point offer the rate of change at the respective point [6]. As illustrated in figure 3 , the derivative at the mentioned point of the function can be thought of slope of the chosen point of the function [6]. All this comes into picture if and only if the differentiation exists at the specified point [6].

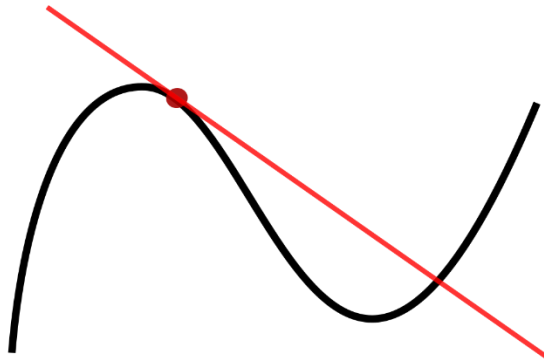


Figure 3 [6].

The equation of the slope can be given as

$$\text{Slope} = \frac{\text{Change in } Y}{\text{Change in } X} \quad (1.1) \quad [6]$$

3.2 Maxima and Minima

If a particular function is given, then maxima can be thought of as the highest value of the function and minima can be thought of as the lowest value of the function [7]. Both maxima and minima are called extrema [7]. If a certain segment or range of a function is considered then the maxima within that range is called local maxima and minima is called local minima [7]. If the

entire function is considered then the maxima is called global maxima and minima is called global minima respectively[7].

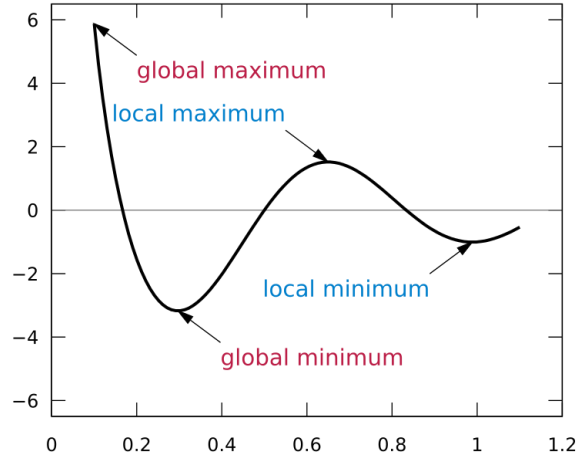


Figure 4 [7]

3.3 Gradient Descent

Gradient descent is an optimization algorithm to determine the local minima of a given function [8]. This optimization process occurs in step by step manner which can be basically thought of as an iterative process [8]. A random initial value is chosen earlier and at a specified step which can be called as learning rate, iterative movement is done towards the local minima of the function [8]. The direction of the iterative movement is done in the opposite of gradient which will eventually lead to local minima[8]. Now the question arises why we are striving to find local minima specifically. This depends on where we want to MAXIMIZE or MINIMIZE the objective function. Objective function can be thought of as function which is utilized to resolve an optimization issue [9]. In simple language if we are interested in the gain of the function then we have to maximize and if we want to minimize the loss then in that scenario we have to discover the local minima.

$$X = X - lr * \frac{d}{dx} f(X) \quad (1.2) [10]$$

Where,

X = input

$f(X)$ = output based on X

lr = learning rate

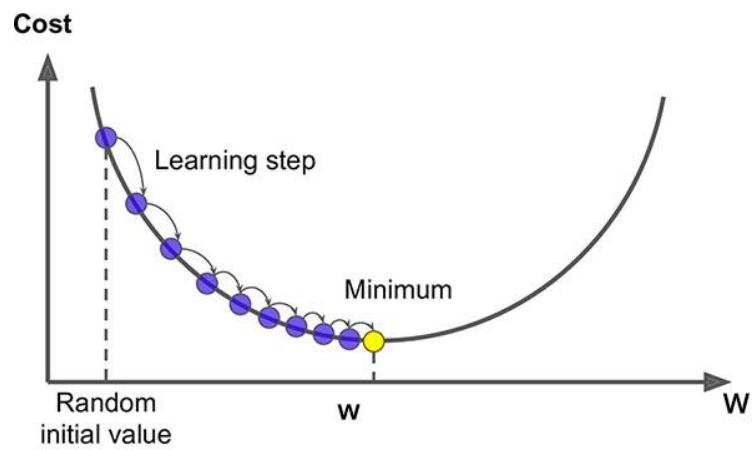


Figure 5 [11]

Chapter 4: Understanding vital parameters

4.1 Transmission rate (β)

Consider a scenario where we are dealing with an infectious disease like COVID-19. Consider a person A is infected with virus. Let's say on an average 9 individuals meet person A per day. Assume that the probability of spreading the disease to an uninfected individual from person A is 90 percent. Let's calculate $90\% \times 9$ which is 8.1 [12]. Hence we can say total count of infections created by an infected person A is 8 [12]. Hence transmission rate (β) is total infection count created by an infected individual per day [12].

4.2 Reproduction number (R_0)

Reproduction number can be thought of as the total infection count created by an infected individual [12]. Let the total duration of the infection the infected person holding the disease within him and capable of spreading the disease is 9 [12]. Transmission rate is 8 as calculated above. Hence $R_0 = \beta \times 9$ which is 8×9 which is 72 [12]. Reproduction number can be seen as the decision factor. If reproduction number is less than one then the disease may die out [13]. If reproduction number is greater than one the disease dynamic may turn into an epidemic [13]. Hence our prime focus should be on lowering the reproduction number to contain the epidemic [13].

4.3 Recovery rate (γ)

Recovery rate is inversely proportional to the number of days D the infected person holding the disease. $\gamma = 1/D$ [12]. Hence we can rewrite reproduction number $R_0 = \beta / \gamma$ [12]. Recovery rate can also be thought of as the fraction of infected individual count that will be recovering per day [12].

Chapter 5: Methodology

We will be designing the variant of SIR model which is SEQIHRDV (Figure 3) and will be our core mathematical model. Post designing we will be deploying our model by utilizing programming techniques. Our implementation will also be having a visualization component which will aid in interpreting the data. Hence our methodology has two parts. One part gives detailed information model design and model parameters. Other part gives information about the two important implementation code component Odient function and LM fit function. Also few features incorporated in implementation are mentioned in this section

Hence to get a big picture of our project assignment the process followed is:

Designing the core mathematical → Implementing the mathematical model → Visualization of compartment curves for initial guessed parameters → Extracting the optimal mathematical parameters by optimization of real world data and model output → Visualization of compartment curves by applying optimized parameters to model and forecasting

The core concept on which the project assignment built on is epidemiology compartmental model. Below mentioned figure 1 depicts a basic version of compartmental model and the corresponding differential equations. The total population N of respective individuals of a particular country or region is divided into three compartments which are susceptible, infectious and recovered. People from the specified population transit through these compartments [4]. Initially population will be in susceptible compartment [4]. Later the people will move to infectious compartment and eventually they will enter in recovered compartment [4]. The point to be noted here is that one person can be in any “one” compartment at a given point of time and not in multiple compartments [4]. The differential equations indicate the change in population of people in respective compartments with respect to time [4]. The counts are extracted by solving the differential equations [4]. The figure 2 illustrates the visualization of count of the individuals of the respective compartments with respect to time.

The people traverse through these compartments at certain rates [4]. Hence we can draw conclusions like at which time point the peak of the curve or maximum number of people of respective compartment can be identified [4]. We shall be overviewing the various parameters involved in the functioning of differential equations in the description section of the model which we have implemented.

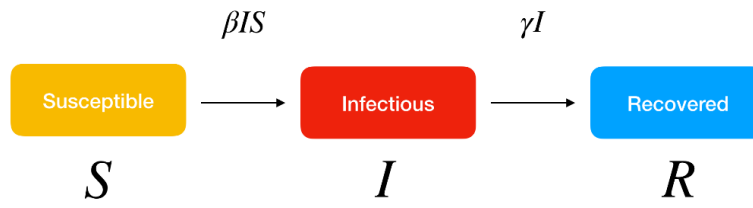


Figure 1 [14]

$$\begin{aligned}
 \frac{dS}{dt} &= -\frac{\beta SI}{N} \\
 \frac{dI}{dt} &= \frac{\beta SI}{N} - \gamma I \\
 \frac{dR}{dt} &= \gamma I
 \end{aligned}
 \tag{1.3} [15]$$

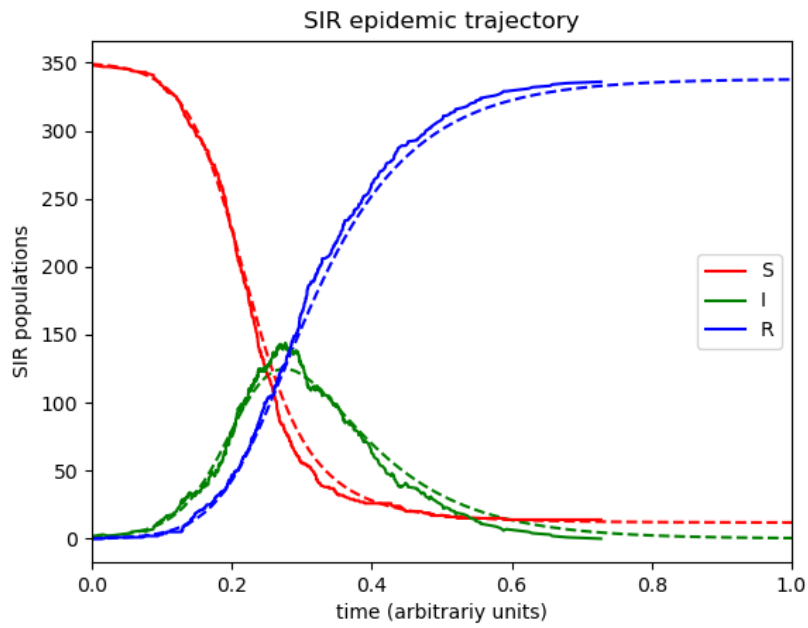


Figure 2[16]

5.1 Compartments Description of SEQIHRDV

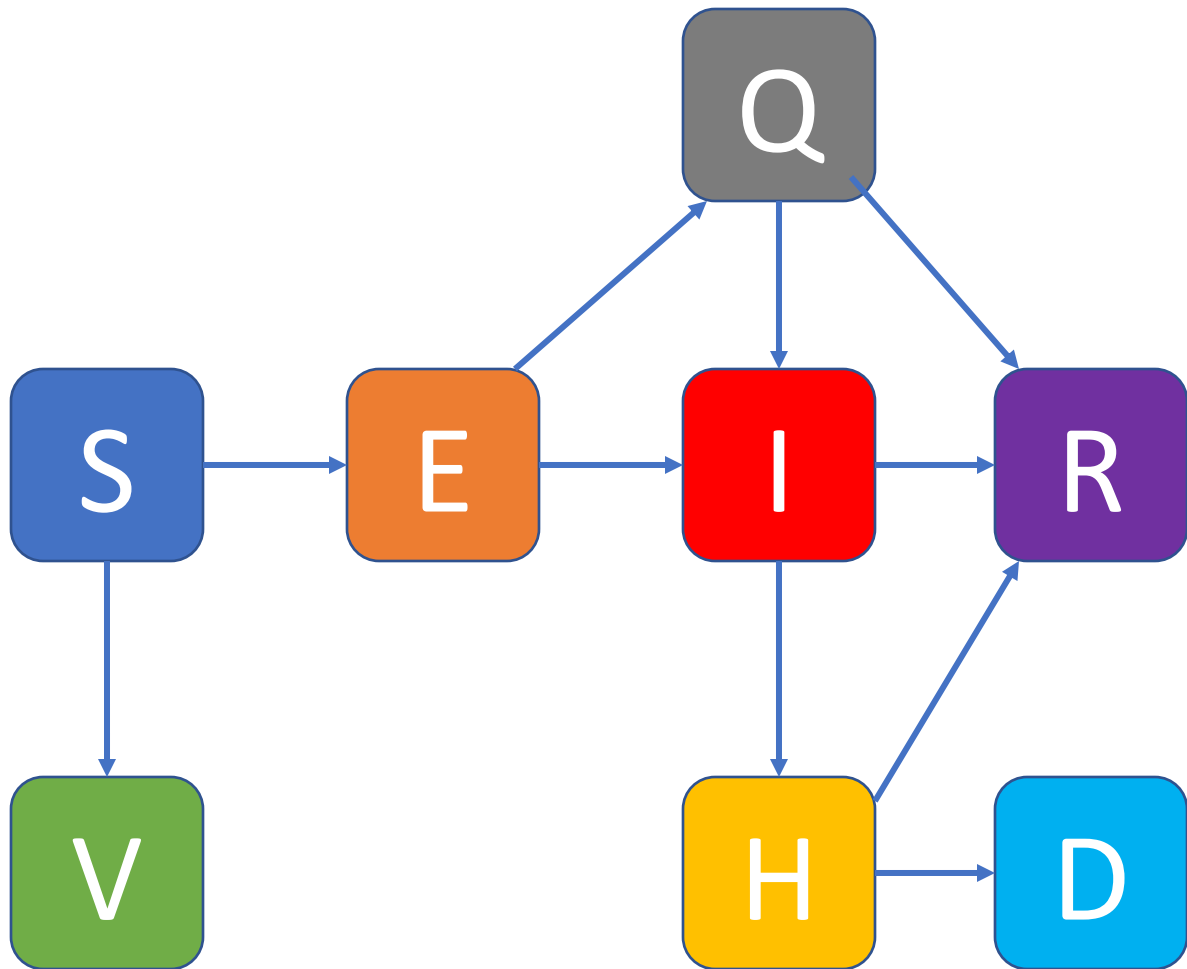


Figure 3

5.1.1 Susceptible

Susceptible compartment consist of the population that is prone to be infected. Hence we can say a very large portion of total population N will fall in susceptible compartment. The respective quantity of population will traverse from Susceptible compartment to Exposed compartment.

5.1.2 Exposed

Exposed compartment composed of the individuals who have come in contact of infected individuals or “exposed” to the virus. The individuals in exposed compartment do not exhibit any kind of symptoms of the disease. The individuals stay in exposed compartment till the defined incubation period. Individuals from Exposed compartment move to either Infected compartment or Quarantine compartment.

5.1.3 Quarantine

The quarantine compartment consists of the individual count at the given time who have identified to have come in contact with an infected individual. Hence we say people in quarantine compartment are asymptomatic and tested positive. The People from Quarantine compart transit to either Infected compartment after developing symptoms or Recovered as individuals develop more severe infections or relieved.

5.1.4 Infected

People in Infected compartment are the ones who clearly show the symptoms and are capable of spreading the disease to any susceptible person. People from infected compartment shift to Hospitalization compartment or to Recovered compartment.

5.1.5 Hospitalization

Individuals who have been severely affected and require the respective treatment to pacify the disease will reside in Hospitalization compartment. People from Hospitalization compartment are either recovered or succumbed to the disease.

5.1.6 Recovered

Individuals who have been relived from the disease are populated to recovered compartment. People from Quarantine, Infected and Hospitalization compartment enter Recovered compartment.

5.1.7 Dead

Individuals who are failed to resist the disease move to dead compartment. In our designed model individuals from Hospitalization compartment enter Dead compartment.

5.1.8 Vaccinated

People who receive the prescribed immunization against the disease enter Vaccinated compartment. Hence logically people from Susceptible compartment are eligible and traverse to vaccinated compartment.

5.2 Model Assumptions

1. We will be considering constant total population N . Hence natural births and natural deaths will be ignored. Only deaths caused due to the disease will be considered.
2. We are thoroughly not considering the result of the population who need clinical treatment however they are not receiving the treatment.
3. The Quarantine compartment is composed of ONLY the group of individuals who have been identified to be positive. Hence we can consider the respective parameters to evaluate the testing strategy.
4. Susceptible compartment is the only gateway towards Vaccination compartment. Any other compartments of model are not linked to vaccination compartment.
5. All the individuals have in susceptible compartment have equal probability of catching the infection.
6. People after entering recovered compartment are not likely to catch disease again[17].
7. Reproduction number values vary with time. We have utilized logistic function for this purpose. Hence once the R_0 number values drops down it will not rise again[17].
8. People who legitimate or rightful for the need of clinical treatment for survival are moved to Hospitalization compartment [17].

5.3 Designing the mathematical model

In this section we shall go through the analytical techniques we have utilized to design our compartmental model. We have designed our model with the approach on the basis of the transitions [5]. More precisely the transition from one compartment to other. Below mentioned figure 6 gives us more idea about this design principle.

$$\text{rate} \cdot \text{probability} \cdot \text{population} \rightarrow$$

Figure 4 [5]

Rate

Rate deals with the time related factor of the respective transition[5]. Rate can be defined as the time frame required for the completion of the transition [5].

Probability

Probability can be seen as the chance of the transition happening for a person in the respective compartment[5].

Population

The population factor corresponds to the community or the group of individual who are eligible to the respective transition[5].

Lets consider the transition from Susceptible to Exposed compartment

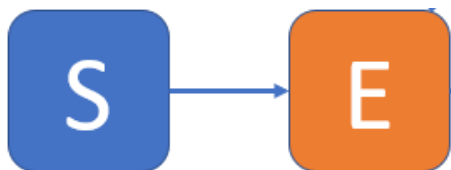


Figure 5

The equation we have formulated and implemented in code is given below

$$\frac{dS}{dt} = -I * \beta * I * (S/N)$$

In the above mentioned equation term β is the transmission rate . The entity $\beta * I$ gives the population parameter for the respective transition. Lets decode this . The transmission rate β is the total infection count from an infected individual per day and is I is number infections at given point of time. Hence $\beta * I$ gives group of individual eligible for the transition from S to E. The entity (S/N) provides us the probability parameter of the transition. The rate which is the time duration for completion of the transition is considered $\frac{1}{\tau}$ [5] which is highlighted by marker. Basically we have assumed that the susceptible person becomes infected immediately after coming in contact with an infected individual .Also the -ve sign indicates that the respective quantity is deducted from the Susceptible compartment.

Now lets consider transition from S susceptible to V vaccinated compartment



Figure 6

$$\frac{dS}{dt} = -\beta * I * (S/N) - \omega * (S - (\beta * I)) * (1 - (S/N))$$

The negative sign indicates that the quantity is getting deducted from the susceptible compartment. ω represents the rate component of transition. The population this transition applies to $(S - (\beta * I))$. The quantity $(\beta * I)$ from Susceptible compartment traverses to E exposed compartment. Hence population left over from susceptible compartment $S - (\beta * I)$ moves to vaccinated compartment V. $(1 - (S/N))$ is the chance of this S to V transition taking place for the person in S susceptible compartment

Lets have a look at one more transition from Exposed compartment to infected compartment to get more clarity on the design foundation

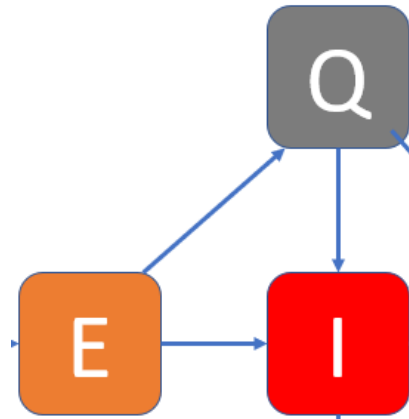


Figure 7

The equation we have formulated and implemented in code is given below

$$\frac{dE}{dt} = \text{beta} * I * (S/N) - \text{delta} * \text{giga} * E - \text{tera} * (1 - \text{giga}) * E$$

The entity $\text{beta} * I * (S/N)$ corresponds to the quantity that was deducted from Susceptible compartment is added into Exposed compartment. In reference to transition from E to I in entity $\text{delta} * \text{giga} * E$, delta is the incubation rate which defines the rate parameter. Giga is probability or portion of individuals going for transition E to I. Hence $(1 - \text{giga})$ is the probability or portion of individuals for transition E to Q. E is population eligible for the transition.

Further rest of transitions of model are computed by applying these design principles.

5.4 Designed differential equations for all the compartments

$$\frac{dS}{dt} = - \text{beta} * I * (S/N) - \text{omega} * (S - (\text{beta} * I)) * (1 - (S/N))$$

$$\frac{dE}{dt} = \textit{beta} * I * (S/N) - \textit{delta} * \textit{giga} * E - \textit{tera} * (1 - \textit{giga}) * E$$

$$\frac{dQ}{dt} = \textit{tera} * (1 - \textit{giga}) * E - \textit{nano} * \textit{mega} * Q - \textit{kilo} * (1 - \textit{mega}) * Q$$

$$\frac{dI}{dt} = \textit{delta} * \textit{giga} * E - \textit{gamma} * (1 - \textit{pi}) * I - \textit{theta} * \textit{pi} * I + \textit{nano} * \textit{mega} * Q$$

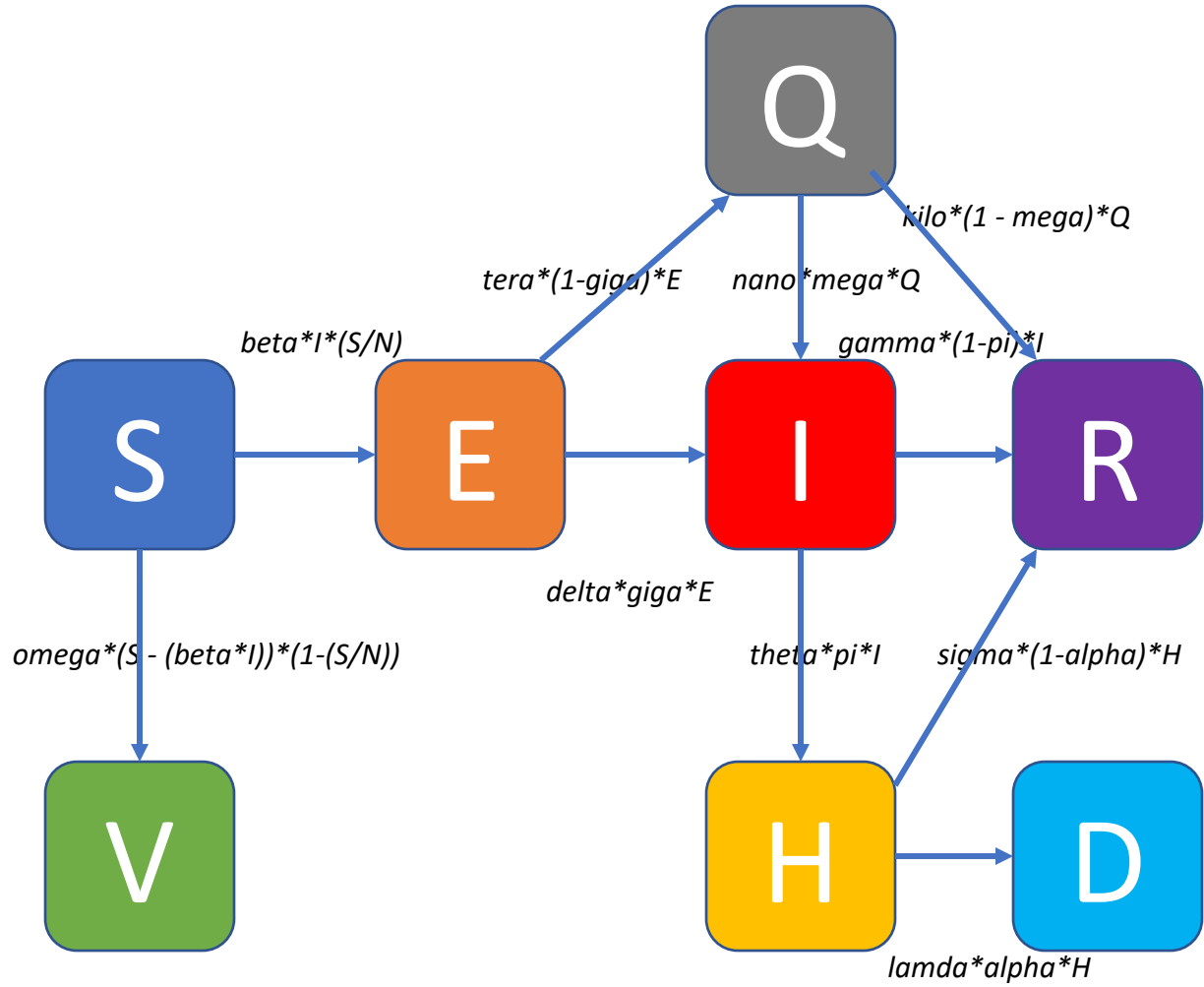
$$\frac{dH}{dt} = \textit{theta} * \textit{pi} * I - \textit{sigma} * (1 - \textit{alpha}) * H - \textit{lamda} * \textit{alpha} * H$$

$$\frac{dR}{dt} = \textit{gamma} * (1 - \textit{pi}) * I + \textit{sigma} * (1 - \textit{alpha}) * H + \textit{kilo} * (1 - \textit{mega}) * Q$$

$$\frac{dD}{dt} = \textit{lamda} * \textit{alpha} * H$$

$$\frac{dV}{dt} = \textit{omega} * (S - (\textit{beta}(t) * I)) * (1 - (S/N))$$

5.5 Parameter Definitions



Beta - Infection transmission rate

Omega – Rate of transfer of individuals from Susceptible (S) to Vaccinated (V) compartment

Delta – Incubation rate

Giga – Fraction of individuals moving from Exposed (E) to Infected (I) compartment

Tera – Rate of transfer of Individuals from Exposed(E) to Quarantine (Q) compartment

Nano – Rate of transfer of Individuals from Quarantine(Q) to Infected (I) compartment

Mega – Fraction of individuals moving from Quarantine(Q) to Infected (I) compartment

Kilo – Rate of transfer of Individuals from Quarantine(Q) to Recovered (R) compartment

Gamma – Recovery rate

Pi - Fraction of individuals moving from Infected (I) to Hospitalization (H) compartment

Theta - Rate of transfer of Individuals from Infected (I) to Hospitalization (H) compartment

Sigma - Rate of transfer of Individuals from Hospitalization (H) to Recovered (R) compartment

Alpha - Fraction of individuals moving from Hospitalization (H) to Dead (D) compartment

Lamda - Rate of transfer of Individuals from Hospitalization (H) to Dead (D) compartment

N – Total Population

S - Number of Susceptible population in S compartment at given point of time

E – Number of Exposed population in E compartment at given point of time

Q – Number of Quarantine population in Q compartment at given point of time

I – Number of Infected population in I compartment at given point of time

H – Number of Hospitalized population in H compartment at given point of time

R – Number of Recovered population in R compartment at given point of time

D – Number of Dead population in D compartment at given point of time

V - Number of Vaccinated population in V compartment at given point of time

5.6 Odeint Function

Our project assignment's core computational component is ordinary differential equations. Hence we need to utilize certain algorithm to solve the respective differential equations. In my work I have implemented odeint function. Odeint is a built in function of scipy module in python language. We need to pass three parameters into the odeint function. First one is the model which has the actual differential equations [18]. Model is basically the function that encapsulates the differential equations. Second one is the initial conditions or we can say the start values of the variables [18]. The variables are the ones of which we are estimating the derivative like S, E, Q etc. The third parameter is the entire time frame till when we are striving to estimate derivative [18]. The time is passed in the form of an array [18]. Fourth entity *args* can also be passed [18]. However this entity is non-mandatory [18]. Basically *args* includes the scaling the parameters of the respective differential equations [18]. Odeint function utilizes LSODA numerical algorithm to solve the respective differential equation [19]. Basically the output of odeint function is an array of continuous numerical values

We can see below mentioned block of code from our implementation which has built in odeint function.

```
outc = odeint(core, [Start_S, Start_E, Start_Q, Start_I, Start_H, Start_R,
Start_D, Start_V, Start_N], t, args=(giga, tera, mega, kilo, nano, gamma,
theta, delta, pi, alpha, sigma, lamda, omega, start_R, end_R, Stch, x0))
```

1. Parameter *core* is the respective user defined function which encapsulates the model differential equations.

2. Parameter *[Start_S, Start_E, Start_Q, Start_I, Start_H, Start_R, Start_D, Start_V, Start_N]* represents the initial conditions of the variables that needs to be differentiated

3. Parameter *t* is the respective time frame for the derivative needs to be computed.

4. *args=(giga, tera, mega, kilo, nano, gamma, theta, delta, pi, alpha, sigma, lamda, omega, start_R, end_R, Stch, x0))* represents the scaling the parameters of the differential equations.

5.7 LM fit

In my implementation a section of code exists which is LM fit that performs curve fitting. Basically LM fit is deployed to carry out the task of curve fitting in my project assignment. As we have fed real world data to our system, LM fit is implemented to optimize the real data and our model output and estimate a best fit curve which as close as possible to real data. Further the extracted parameters after this optimization are our area of interest. LM fit method utilizes Levenberg-Marquardt algorithm. The Levenberg-Marquardt algorithm is primarily used to fix least squares issues [20]. Least squares can be thought of as a technique that cut downs the difference between actual information fed to system and model computed results so as to resolve

a set of equations[21].These are the system of equations which holds less unknown variable than total number of equations [21].In our project assignment we have deployed Levenberg-Marquardt algorithm to tackle non-linear least square minimization. Levenberg-Marquardt algorithm operates on gradient descent approach to compute the minimum [20].The minimum can be thought of as the scenario where the parameters that we have used in our differential equations have settled down for optimal value such that the real data and computed best fit for the real data result is very low. This process is carried out in iterative manner [20].The respective equation has been mentioned below.

$$\sum (\text{distinction})^2 = \sum [(\text{real data point}) - (\text{Model computed data point})]^2$$

(1.4)[20]

5.8 Other features incorporated in implementation

Two key characteristics which we have incorporated in our model is the Total count plot visualization and Reproduction number varying with time. Total count gives the count of individuals in all the compartments at given point of time. As we have considered the total population to be constant the total T can be given as

$$T = S(t) + E(t) + I(t) + Q(t) + R(t) + H(t) + D(t) + V(t) \quad (1.5)$$

This also gives us the surety that the designed model is valid. This idea has been considered from the article work [5].

Second characteristic is the Reproduction number changing with time. We have made use of logistic function to shape the change of reproduction number with time.

$$R_0(t) = \frac{R_{0START} - R_{0END}}{1 + e^{-k(-x+x_0)}} + R_{0END}$$

[5]

R_{0START} – Initial value of R_0 for the chosen for the corresponding start day

R_{0END} - End value of R_0 chosen for the corresponding last day

X_0 - Defines the day of immediate drop in R_0 value

K – defines the stretch of the function

This approach gives a real world approach for variation in reproduction number over time. The decline in value of reproduction number can be seen as the imposition of lock down like measures in the respective country. This idea has been considered from the article work [5]. Further transmission rate β is calculated by formula (1.6) in code implementation by defining a function.

$$\beta = R_0 * \gamma \quad (1.6)$$

```
def beta(t):
    return Chang_R(t, start_R, Stch, x0, end_R) * gamma
def Chang_R(t, start_R, Stch, x0, end_R):
    return (start_R - end_R) / (1 + np.exp(-Stch*(-t+x0))) + end_R
```

Chapter 6: Literature Survey

The author [22] has clearly mentioned the objective of the work. The author has strived to model the COVID-19 pandemic as close as possible to the real world scenario. Also compare and evaluate the precautionary steps which one to them would mitigate the pandemic to appropriate level.

Author has developed a variant of SIR model by including different compartments to make it as realistic as possible. The regular compartments are susceptible, exposed, recovered and dead. The author has added new compartments to model like Vaccination, Asymptomatic, symptomatic and Quarantine, Asymptomatic and quarantine. Considerations and Assumptions are clearly mentioned by the author.

Covid-19 data of Santa Clara county of around 300 days has been applied to the designed model. The author has utilized two different varying infection rates. One infection rate due to Asymptomatic group and other for symptomatic groups. Both the infection rates are divided by certain scaling factors. Hence the scaling factor for asymptomatic infection rate aids in examining individual precautionary measures like social distancing and mask usage amongst individuals [22]. Scaling factor for Symptomatic infection rate helps to evaluate degree of quarantine as symptomatic people will be quarantined according to model [22]. The proportion of people moving to Symptomatic and Quarantine compartment is measured in terms of testing rate [22]. Infection rates, testing rate and death rate are estimated which are varying with time. As per author as the actual symptomatic count is unknown and same he has ignored in estimating total infection, author assumed scaling factor for asymptomatic infection rate to be one and he calculated Scaling factor for Symptomatic infection rate via experimentation. Further statistical

comparison of from known actual data and predicted infection and death cases is done. Author has not mentioned any usage of programming tool to evaluate the prediction in the paper however the is mention of only of utilization of Runge Kutta numerical method. From statistical comparison of from known actual data and predicted infection it is known that many asymptomatic cases are not captured in the data [22].

Further in evaluation of results section, author has strived to capture the effects of parameters which are in relation to precautionary measures on the outbreak. Author has followed a principle that effects on total number of infection and total number of deaths are captured by varying and calibrating parameters individually has been captured. Hence this gives better insights which precautionary measure parameters is better in curbing the outbreak.

Increasing both the scaling factor for asymptomatic infection rate and symptomatic infection rate reduces number of deaths and number of infections significantly. Hence having a critical impact on the pandemic.

The testing rate is also scaled with a parameter. The difference here testing rate is multiplied with the scaling parameter not divided. Increasing or decreasing this parameter do have a useful impact on the infection and death curves. The relationship is linear.

Vaccination rate has also been defined in the paper by the author. Its the proportion of individual moving from susceptible to vaccination compartment. Increasing vaccination rate to certain level has a reasonable impact on the infection and death count curves as gradual decrease is observed.

Also as varying infection rates are considered with time. The infection rates are divided in 5 stages. In the stage 1 there was steep decrease in infection rate. If this infection rate was maintained with the respective social interaction amongst the population then the outbreak would have diminished in comparatively short span of time.

The Author [23] in this work has presented a variant of SEIRD model. The author has strived to enhance the effect of three characteristics which are incorporated in the model. Those key entities are quarantine compartment, Asymptomatic population compartment and changing mortality rate. The outcomes of the model which have been considered to evaluate the model are confirmed infection count and death count.

One of the good observation made the author which has been stated in the introduction is the variations in susceptible compartment. The author has said that non linear variations occur in susceptible compartment due to factors like lockdown , social behavior etc. This has repercussions on the transmission rate[23].

Further author has briefed about his review on other works. Author has made a mention about research work where variable transmission rate that adapts and changes with restrictive rules like lock down. Another work author has reviewed where the SEIRD model has been modified with addition of hospitalization compartment. This was done to analyze the influence of quarantine on

hospitalizations[23]. In this work symptomatic and asymptomatic population has been kept separate. Followed by this work author has surveyed a work which studies age entity of the people who has receiving clinical treatment.

Further author has explained about definition of reproduction number and its importance. One of the important point made author is that reproduction number varying according to region[23]. Reproduction number also depends on the social etiquettes and practices of the respective land[23]. Hence reproduction number estimated for a particular country cannot be implemented for analysis of disease dynamics of other region[23]. Reproduction number can also seen as the deciding factor like if the pandemic will stay longer or diminish[23].

Author has proposed a SEQAIRD model in which the quarantine compartment is linked to the susceptible compartment. Hence this gives a realistic approach where suppose if a lockdown is imposed people from S compartment will traverse to Q compartment at a defined rate. People can move from Q compartment to S compartment at defined rate. People from exposed E compartment can move to either Asymptomatic compartment or Symptomatic compartment. Two different infection transmission rate are defined for symptomatic and asymptomatic compartment. A variable death rate has been defined with a thought that deaths can be controlled with the knowledge exchange between different regions. Another real world effect which author included in the model is by defining a rate of transfer from recovered compartment to susceptible compartment. This allows to model mutation in the virus.

The observed infection count and death count data of USA for march 2020 to December 2020. was segmented in 3 months segment[23]. Later this data was fitted with model output data. The segmentation was done with the thought of achieving higher accuracy[23]. Variable death rate was estimated by the designed model. Further author estimated the parameters that have critical effect on epidemic graph. Initial quarantine count and transmission rate can change the disease dynamics to major extent even both the parameters are varied minutely. However it was evaluated that initial asymptomatic count, incubation rate and fraction of population moving from E to I have more critical impact in lengthy phase of epidemic as compared to Initial quarantine count and transmission. Reproduction number was computed using eigen formula by using all the parameters extracted from real data fit. Further prediction was done for period after dec 2020 to July 2021. Parameters used for prediction were the ones that were extracted from third segment of real data curve fits. Further summary of all model estimation versus the observed real data used was presented by author with the all relevant conclusions.

The author in the work [24] has started with brief introduction to mathematical modelling and emergence of COVID-19. The author has proposed a mathematical model to analyze the COVID-19 disease dynamics of Nigeria by utilizing COVID-19 data for Nigeria. The author [24] has implemented two mathematical approaches in the study. One is through designing by ordinary differential equation. Other mathematical approach used is of fractional differential equation.

The second mathematical approach is out of scope for our project assignment, hence we will be diverting our focus more on the detailing of first approach.

The proposed epidemiological model by the author is composed of total six compartments. The compartments are Susceptible, Quarantine, Exposed, Symptomatic, Asymptomatic and Recovered. The population applied for the model is not considered constant and author has considered natural births and natural deaths to model. This can be considered as addition to naturalistic approach factor compared to the other papers we have reviewed. People from susceptible compartment can move to Quarantine and Exposed compartment. Population from Exposed compartment can traverse to Symptomatic, Asymptomatic compartment and Quarantine Compartment. Individuals from Quarantine Compartment can transit to Symptomatic and Asymptomatic compartment only. Further community transition from Symptomatic and Asymptomatic compartment is enabled to recovered compartment. People from Symptomatic compartment can die due to the disease along with natural death as well however author has not added any separate Dead compartment in the model. Individuals from all the compartments can die out due to natural death.

The author has stated that the reproduction number is calculated with through a numerical method next generation matrix[24]. The infection count of Nigeria has been applied to model output for fitting and extracting respective parameters. Further sensitivity analysis of the parameters were performed to estimate their influence on reproduction number. Natural birth rate and transmission rate were found positively related to reproduction number which means, changes in these values may result critical change in reproduction number. Death rate, Exposed to symptomatic compartment rate, Exposed to Asymptomatic compartment rate, Susceptible to Quarantine rate, recovery rates were negatively related which means rise in weights in these value would decline reproduction number [24]. From the fitting model to the infection count of Nigeria, it was discovered that the Symptomatic and Asymptomatic compartment counts decline with time[24]. Hence it was explored that government policies in limiting the social interaction within the community aided in decreasing the infection count.

The author has focused on estimating the reproduction number through numerical algorithms more, missing the analysis of other parameters. Adding analysis of about quarantine and analysis of mortalities by including dead compartment would have enhanced the model design to a level above. Analysis of parameters with respect to the changes in infection count apart from only reproduction number would also have helped to gain more insights.

The research analysis of these [5], [12], [17] works have also been carried out however these have been referenced in other part of the document.

Chapter 7: Results and Discussion

The real world data I have utilized is of country India. I have fed total number of COVID-19 deaths occurred in India for period of 22 January 2020 to 2 November 2022. I have strived to design a realistic model so that the outputs of the model fits as accurately possible to the respective total number of deaths of real world model. The implementation is divided in three sections. The total population of India has been referenced from webpage

<https://www.worldometers.info/world-population/india-population/>

7.1 Section 1

In this section is importing the real world death count for the mentioned period of time. Following this the respective imported data is visualized so that we can get a rough and clear picture of the counts over the time.

7.2 Section 2

In this section certain initial counts are specified and initial parameter guesses are specified as well. In this part of implementation we can analyze the normal behavior of the designed model. We shall observe simulation of system for 180 days. The X-axis represents the number of days data and the Y-axis represents count of the individuals. We can investigate and estimate how the respective number of counts of respective compartments vary with respect to time when we slide over and change the parameter values. Also we can view the changing values of reproduction number as we have implemented reproduction number that varies according to time.

7.3 Section 3

In section 3 , the model output of death compartment is fitted to the real world death count for entire mentioned period of time through LM fit algorithm. Further this best fit is visualized to get the sense of accuracy of the curve fitting. From the best fit the optimized parameters are extracted. The fit statistics are also displayed which gives information like revised fitted parameter values. The correlation between all the parameters are displayed as well. Further the compartments counts are simulated with the newly computed optimized parameter values.

The parameters that have pre defined biological values are not included in the curve fitting algorithm. The respective parameters are listed below. The values of the parameters are referenced from article *gamma* and *delta* have been referenced from article[25]

The values of parameters *theta* , *sigma* and *lamda* are referenced from article[17]

Gamma – Recovery rate

Delta – Incubation rate

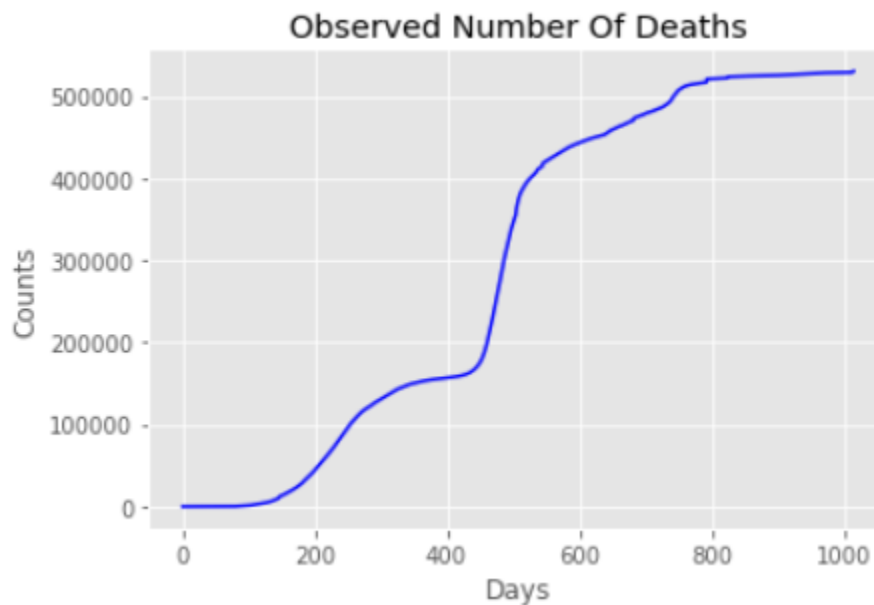
Theta - Rate of transfer of Individuals from Infected (I) to Hospitalization (H) compartment

Sigma - Rate of transfer of Individuals from Hospitalization (H) to Recovered (R) compartment

Lamda - Rate of transfer of Individuals from Hospitalization (H) to Dead (D) compartment

7.4 Section 1 Discussion

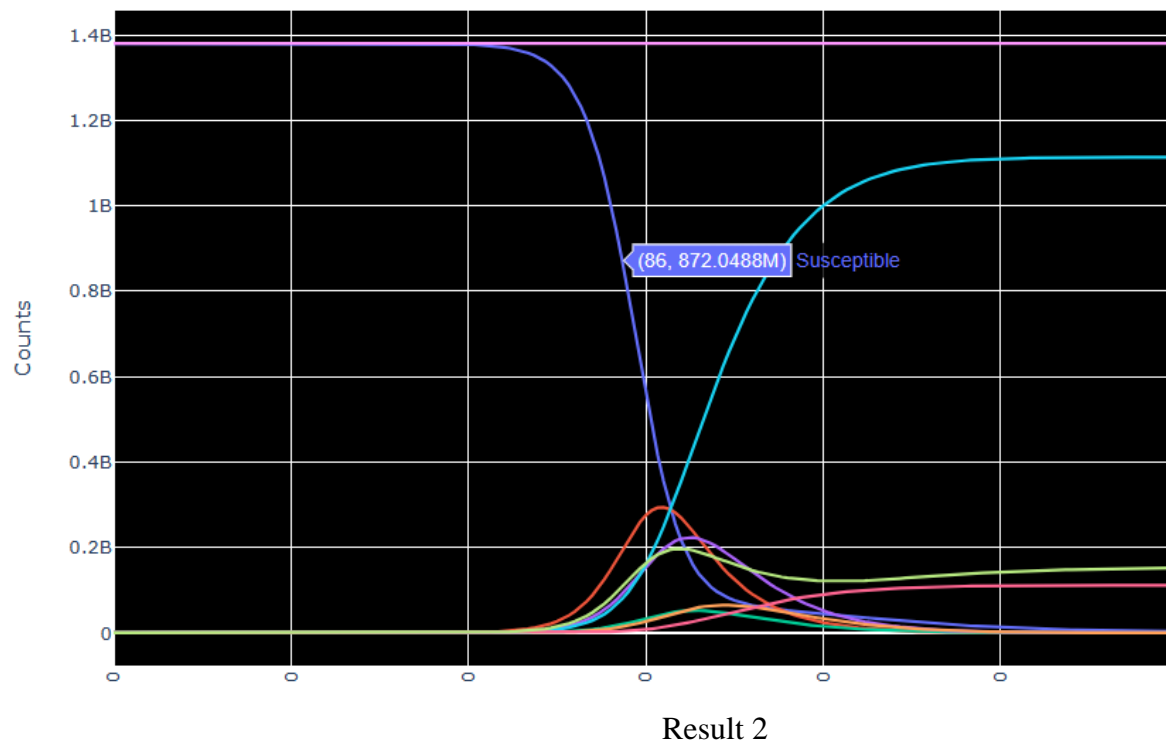
The total deaths occurred are visualized. Please find the below plot Result 1 of the same from the implementation. This plot represent cumulative deaths count of India



Result 1

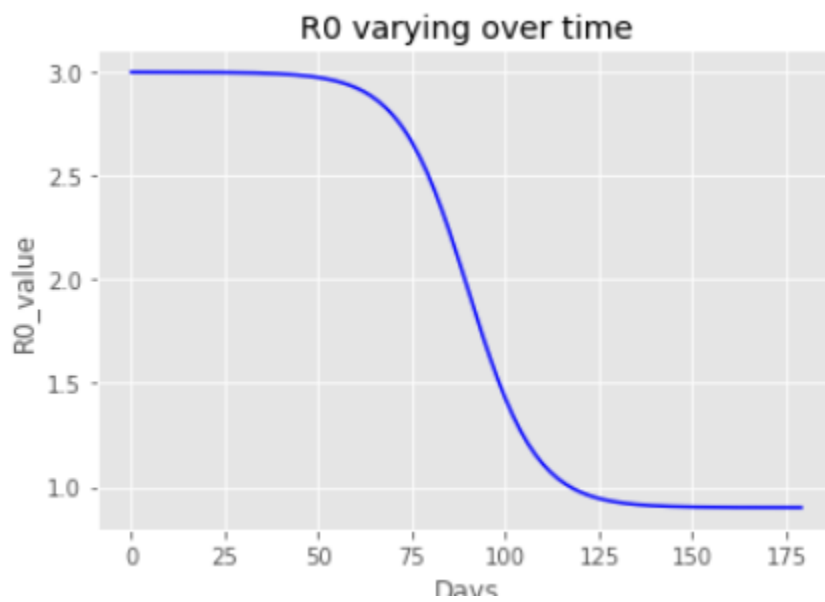
7.5 Section 2 Discussion

A slider layout is provided in visualization component of the implementation. This interactivity provision enables us to vary the corresponding parameter values. The slider definitions for respective values of R0 logistic function are Start_Val, End_val, Stretch, D-Day . D-Day corresponds to the X0 value. Rest of the slider values corresponds to the parameter values utilized in the model. Tooltip enables to view the number of counts of any compartment by point on the respective curve of the that compartment as seen in Result 2. Also zoom feature is also added as part of interactivity and deeper data exploration.



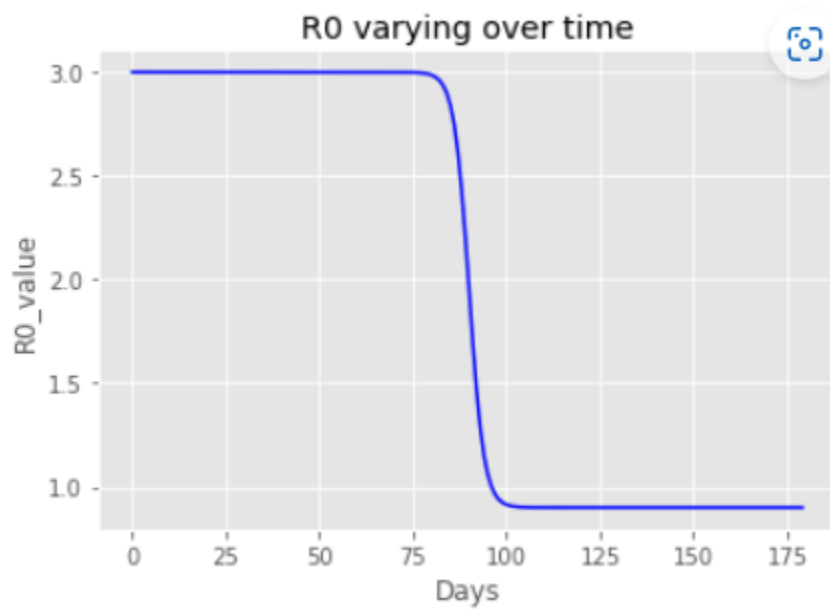
Below mentioned outputs from the section 2 implementation illustrates how the curve of R0 varies with change in the value of stretch k.

For $k = 0.11$



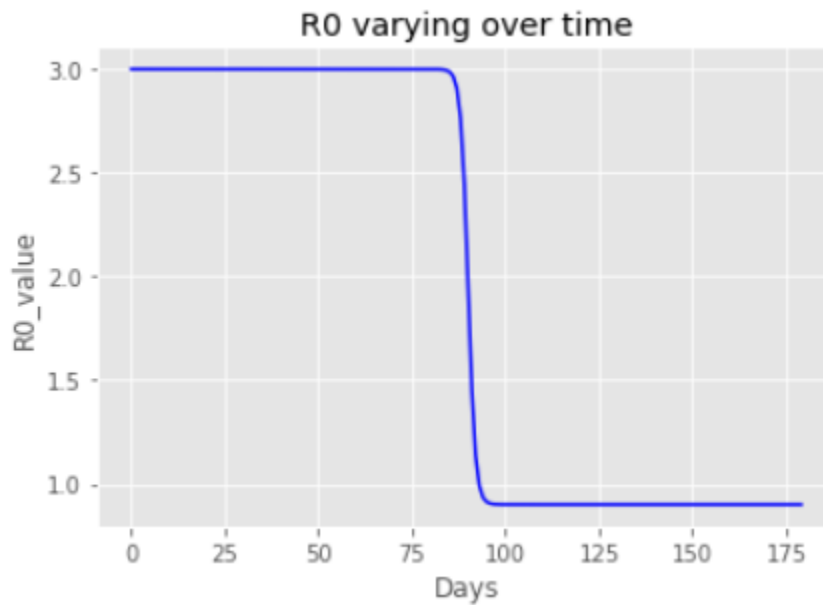
Result 3

For $k = 0.5$



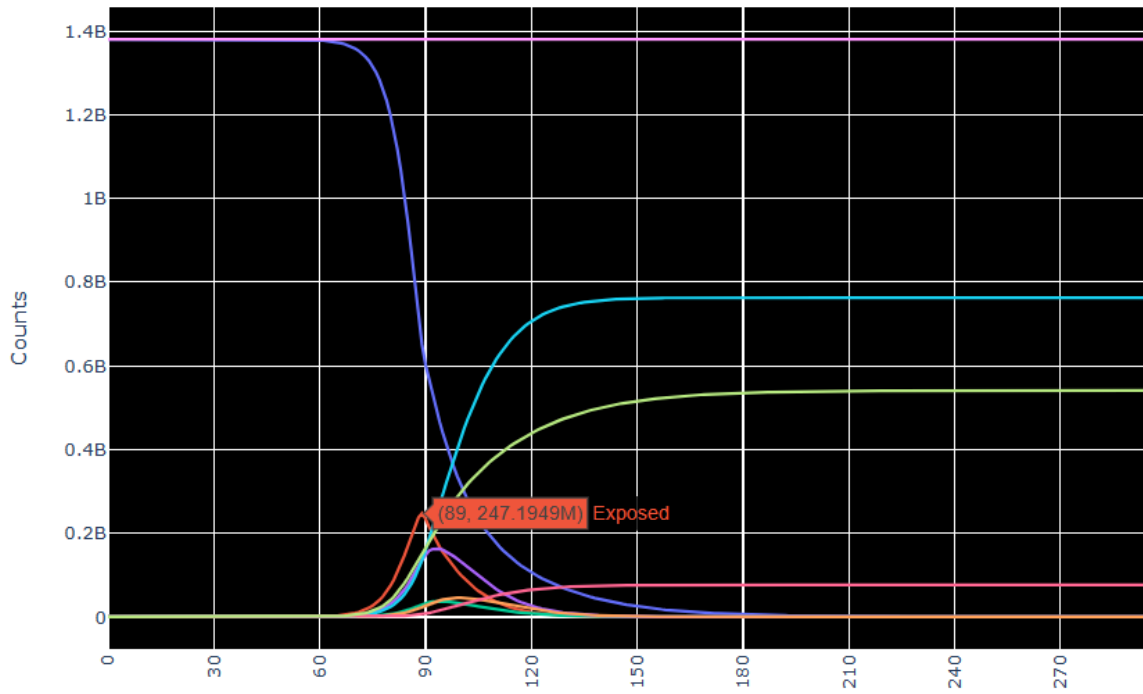
Result 4

For $k=1$



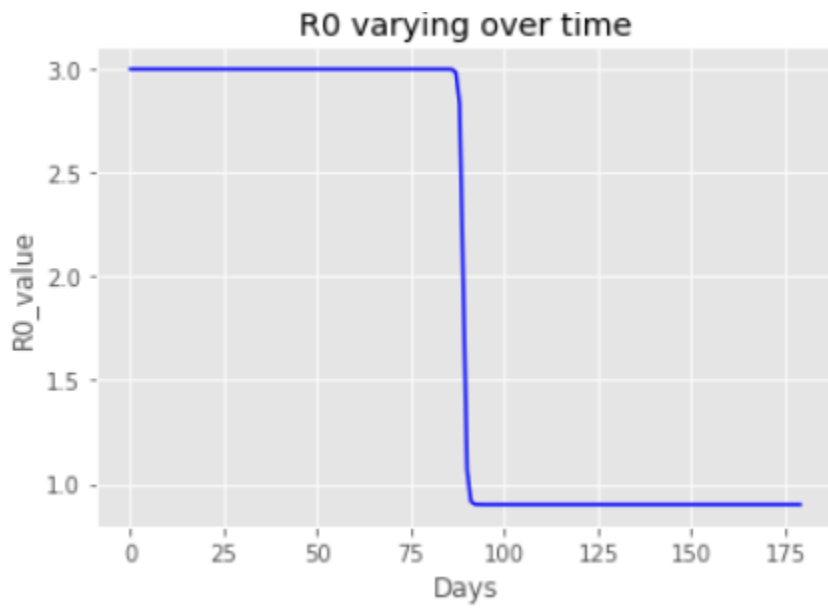
Result 5

Lets analyze the changes in the simulation with respect to stretch k . The X_0 has been set to 89 and stretch $k = 2.45$. Hence the value of R_0 at day 89 will drop immediately. Due to the drop of value in R_0 the red curve which represents exposed compartment can be seen declining instantly.



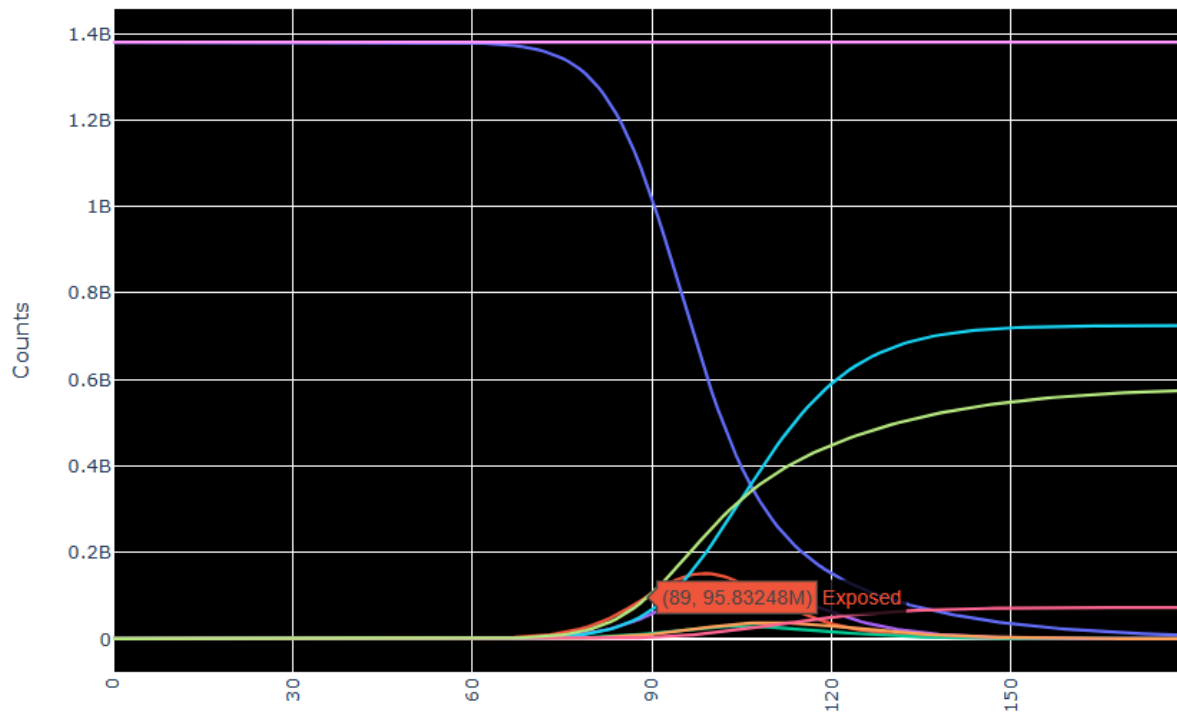
Result 6

$k = 2.45$



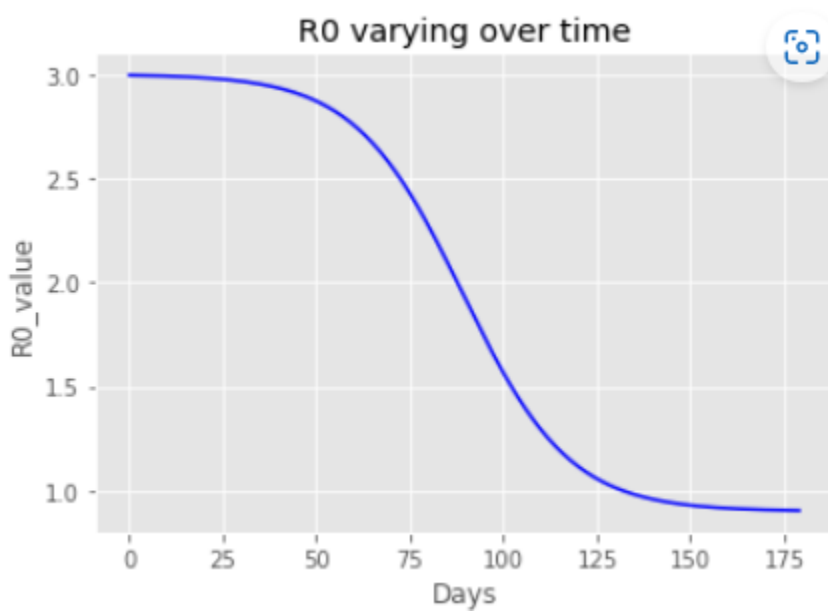
Result 7

Now if we stretch the value of $k = 0.07$ the decline in the count of exposed compartment is not immediate but needs longer duration for the decline compared to $k=2.45$ as function R_0 stretched. This can be seen in Result 8



Result 8

$k=0.07$



Result 9

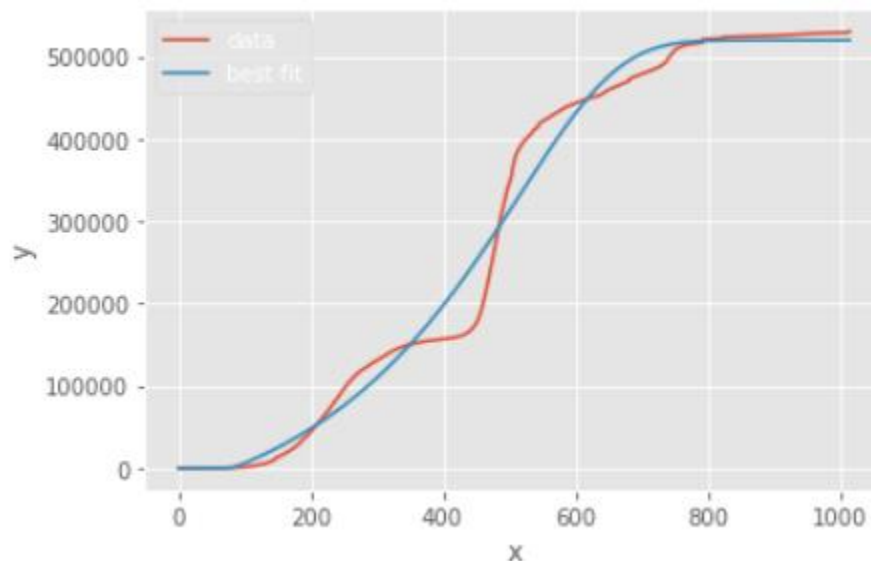
Hence the designed model is responding appropriately with the variations in value of reproduction number R_0 .

7.6 Section 3 Discussion

In section 3 of implementation curve fitting with the real death count of India for mentioned entire period of time has been performed. The model output 6 defines the death array computed by the model. This output is optimized with the real death count and respective optimized parameters are extracted. The curve fit is also visualized. Please find the below mentioned output. The reproduction number start value estimated is nearly 2.988 and the corresponding end value estimated is 0.91. The initial guess for x_0 was chosen 80. This was done with the thought that the data of death count of India starts from 22 January 2020 and lockdown was imposed India on 24 March 2020[26]. Hence a near by day was chosen.

```
{'giga': 0.39516796959207756,  
'tera': 0.09446150292086693,  
'mega': 0.14679650125326807,  
'kilo': 0.09804183519578794,  
'nano': 0.10964426949440642,  
'pi': 0.5842870885765072,  
'alpha': 0.38714007448561283,  
'R_0_start': 2.988313396095232,  
'R_0_end': 0.918072790218488,  
'k': 2.500714012589111,  
'x0': 79.97186846703079,  
'omega': 0.010109528588129519}
```

Below mentioned output is the curve fit with red curve illustrating the real death count data and blue curve represents the best fit computed



The report statistics provides more details about the parameters and the curve fit. The report statistics outcome has been documented below

```
[[Fit Statistics]]
# fitting method      = least_squares
# function evals      = 39
# data points         = 1016
# variables           = 12
chi-square            = 6.3053e+11
reduced chi-square    = 6.2801e+08
Akaike info crit      = 20594.1314
Bayesian info crit    = 20653.2149

[[Variables]]
giga:      0.39516797 +/- 0.03503879 (8.87%) (init = 0.4)
tera:      0.09446150 +/- 7.37947959 (7812.16%) (init = 0.11)
mega:      0.14679650 +/- 103.501099 (70506.52%) (init = 0.2)
kilo:      0.09804184 +/- 7.34636702 (7493.09%) (init = 0.12)
nano:      0.10964427 +/- 130.052123 (118612.79%) (init = 0.11)
pi:        0.58428709 +/- 93.5547723 (16011.78%) (init = 0.6)
alpha:     0.38714007 +/- 107.492685 (27765.84%) (init = 0.4)
R_0_start: 2.98831340 +/- 131.314254 (4394.26%) (init = 3)
R_0_end:   0.91807279 +/- 104.652798 (11399.18%) (init = 0.9)
k:         2.50071401 +/- 10549.1148 (421844.11%) (init = 2.5)
x0:        79.9718685 +/- 819.149912 (1024.30%) (init = 80)
omega:     0.01010953 +/- 0.02153347 (213.00%) (init = 0.05)

[[Correlations]] (unreported correlations are < 0.100)
C(tera, kilo) = -1.000
C(R_0_start, R_0_end) = 0.996
C(pi, alpha) = -0.972
C(alpha, R_0_end) = 0.969
C(k, x0) = 0.957
C(alpha, k) = -0.951
C(pi, k) = 0.949
C(pi, x0) = 0.947
C(alpha, R_0_start) = 0.945
C(R_0_end, k) = -0.896
C(alpha, x0) = -0.894
C(pi, R_0_end) = -0.885
C(R_0_start, k) = -0.877
C(mega, R_0_start) = 0.857
C(mega, R_0_end) = 0.849
C(pi, R_0_start) = -0.843
C(mega, nano) = -0.830
C(R_0_start, omega) = -0.822
C(R_0_end, omega) = -0.811
C(R_0_end, x0) = -0.784
C(mega, alpha) = 0.764
C(R_0_start, x0) = -0.749
C(mega, omega) = -0.735
C(alpha, omega) = -0.695
C(nano, omega) = 0.689
C(mega, k) = -0.651
```

C(mega, pi)	= -0.639
C(kilo, x0)	= 0.637
C(tera, x0)	= -0.637
C(tera, k)	= -0.599
C(kilo, k)	= 0.598
C(nano, R_0_start)	= -0.574
C(tera, R_0_start)	= 0.567
C(kilo, R_0_start)	= -0.565
C(pi, omega)	= 0.548
C(k, omega)	= 0.539
C(tera, R_0_end)	= 0.538
C(kilo, R_0_end)	= -0.536
C(nano, R_0_end)	= -0.529
C(tera, alpha)	= 0.519
C(kilo, alpha)	= -0.517
C(tera, pi)	= -0.468
C(kilo, pi)	= 0.467
C(mega, x0)	= -0.440
C(giga, tera)	= 0.407
C(giga, kilo)	= -0.406
C(x0, omega)	= 0.378
C(nano, alpha)	= -0.336
C(tera, omega)	= -0.287
C(kilo, omega)	= 0.281
C(giga, R_0_start)	= 0.276
C(giga, k)	= -0.269
C(giga, x0)	= -0.265
C(giga, R_0_end)	= 0.261
C(giga, alpha)	= 0.239
C(giga, pi)	= -0.206
C(nano, k)	= 0.192
C(giga, omega)	= -0.186
C(tera, mega)	= 0.139
C(mega, kilo)	= -0.138
C(nano, pi)	= 0.133
C(giga, mega)	= 0.118

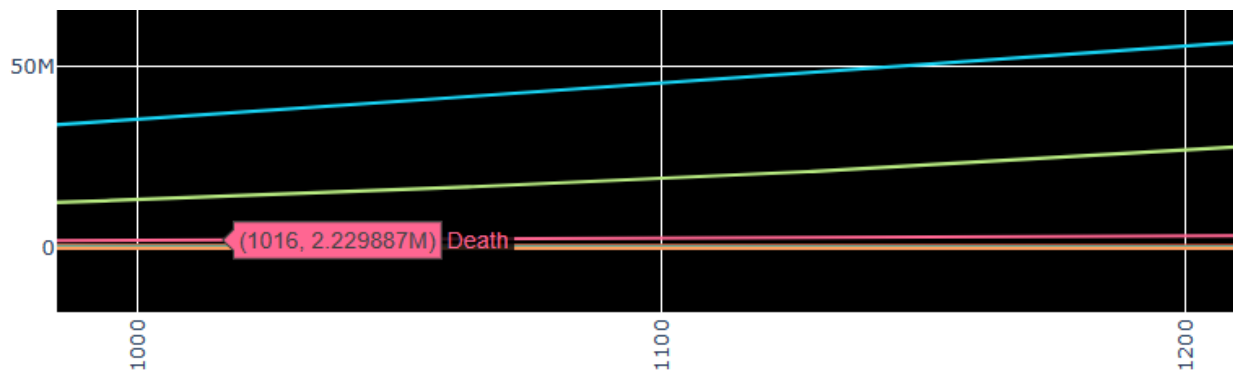
The chi-square can be associated to below mentioned equation. Hence the chi-square function should minimized to get the accurate and closest possible fit to the real world data.

$$\sum (\text{distinction})^2 = \sum [(\text{real data point}) - (\text{Model computed data point})]^2 \quad [20]$$

The correlation coefficient values are displayed as well. Basically correlation can be seen as the association or dependence of two variables with respect to each other[27]. The relationship is seen as linear relation with respect to each other[27]. If two variables are strongly positively correlated the correlation coefficient is near by to +1 and if conversely if the parameters are strongly negatively correlated then value is near by to -1. The highlighted parameters are strongly positively and negatively correlated to each other.

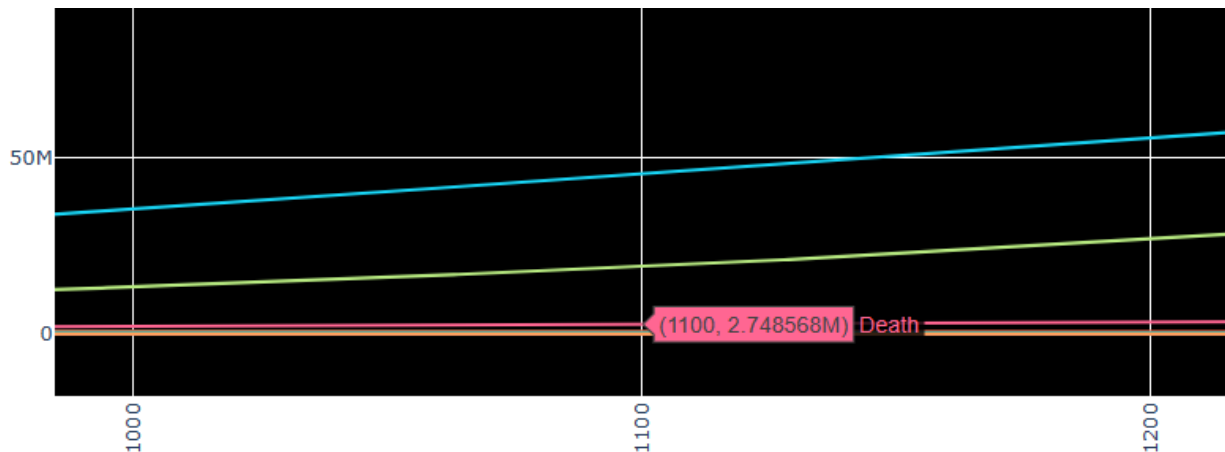
7.7 Forecasting Death count for 200 days

We have fed the optimized parameters to our model. The Death Count on the day till the last day in real data is 1016th day. The model predicted death count is around 2229887 twenty two lakhs twenty nine thousands . The actual death count on the 1016th day is 530461 five lakhs thirty thousands. M entity in the quantity 10^6



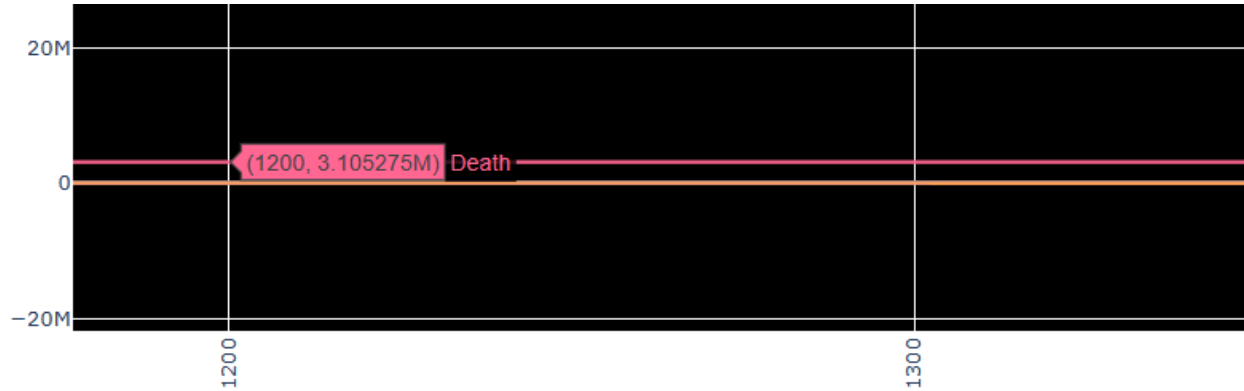
Result 10

Below output shows the prediction for 1100th day. The total estimated death count by the model is around 2748568 which is around 27 lakhs forty eight thousand.



Result 11

Below output shows the prediction for 1200th day. The total estimated death count by the model is around 3105275 which is around 31 lakhs



Result 12

Hence we can conclude that the disease will persist after 200 days after 2 November 2022 as the deaths are still active

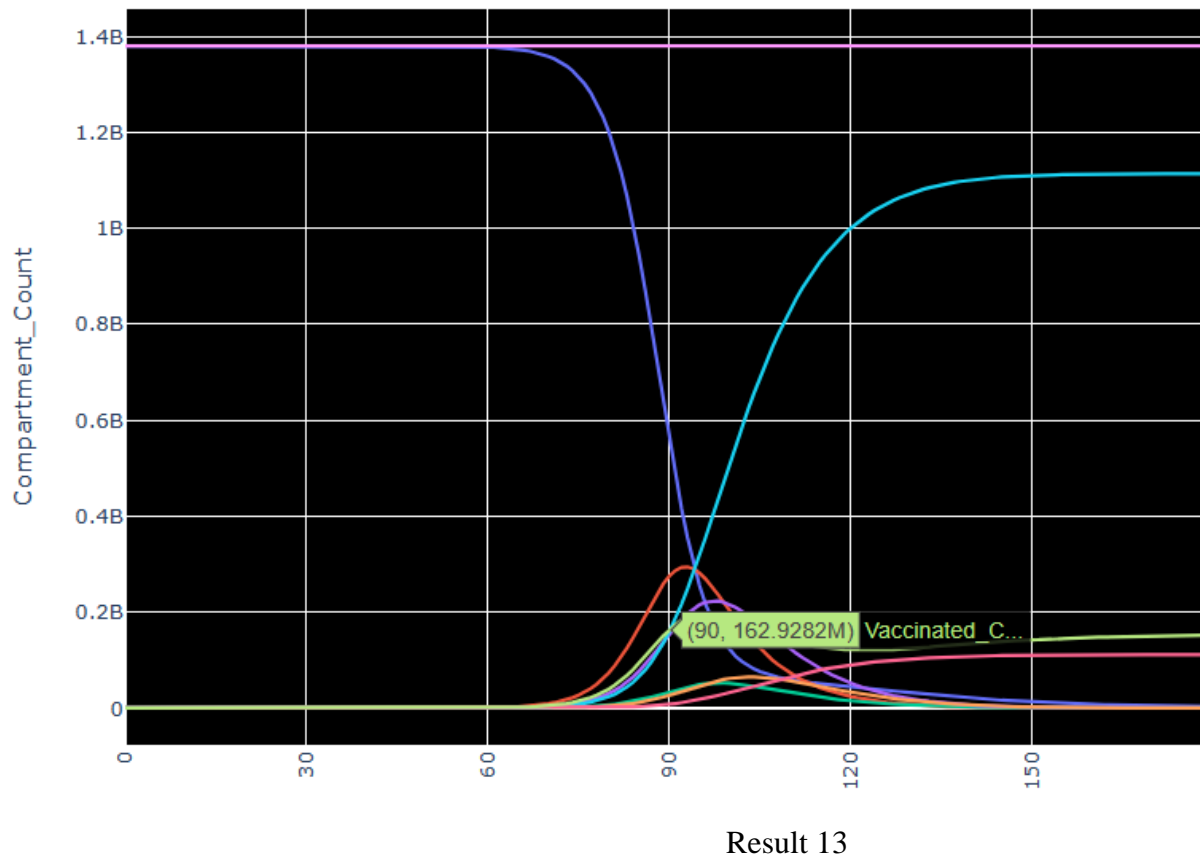
7.8 Analyzing precautionary Measure Parameters

Omega

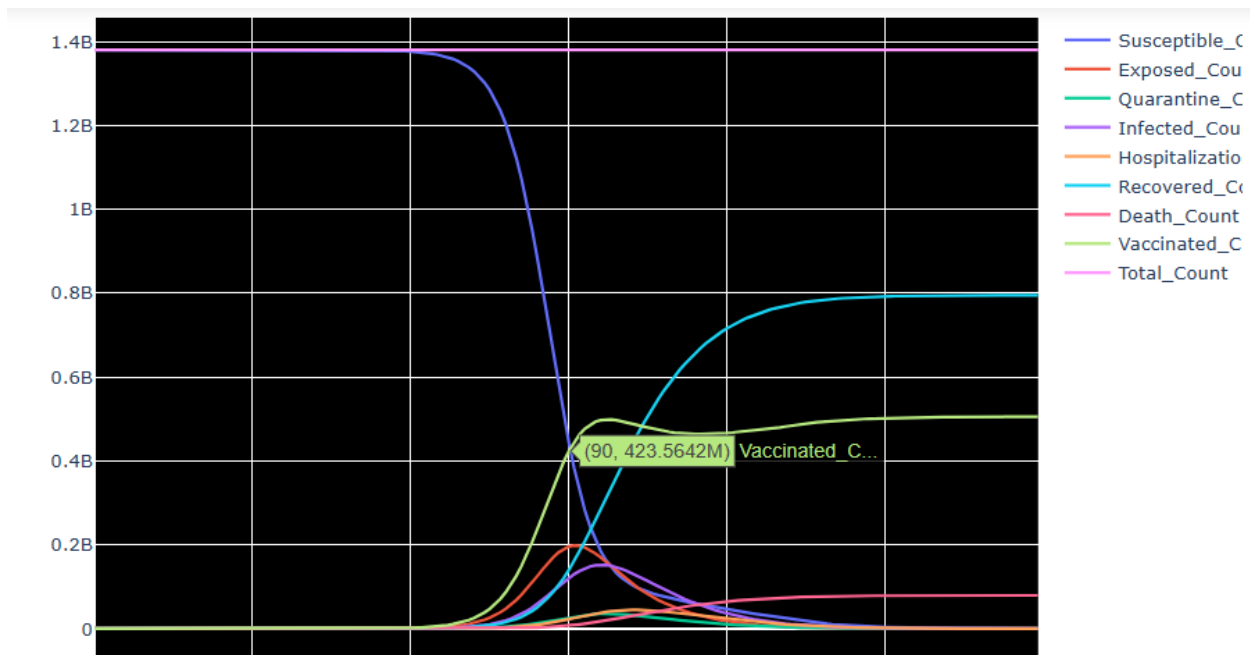
Omega is defined as time entity for transfer of individuals from Susceptible to Vaccinated compartment. To dive deeper into understanding of rate , the rate can defined in form mentioned in equation below where the T represents the actual time entity which can be days or any other measure[17].

$$\text{Rate} = \frac{1}{T}$$

Hence in case of analyzing effect of omega we need to reduce the number days of transfer of individuals from susceptible to vaccinated compartment. Hence we need to maximize the rate omega. We shall analyze the omega rate changes on vaccinated ,exposed and infected compartment on initial parameter simulation for better clarity through visualization. Below mentioned output Result 13 from initial guess model simulation displays vaccinated compartment count for omega 0.05 on 90th day.



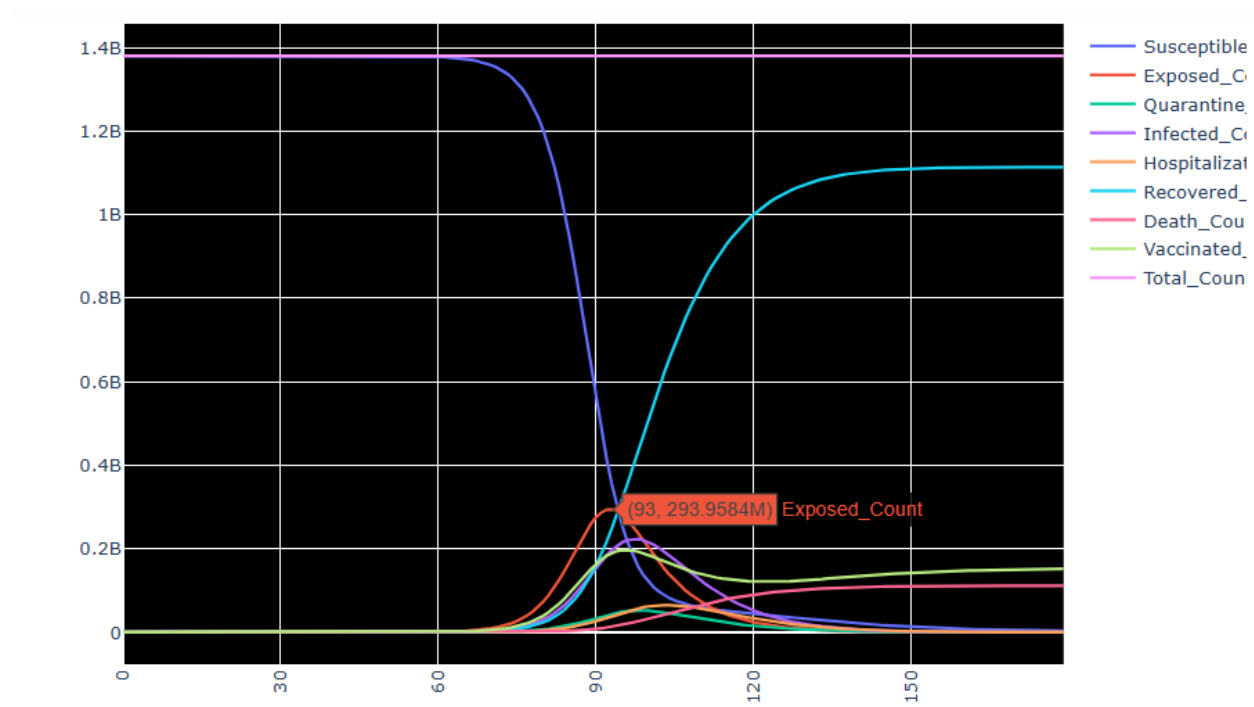
If we slide over ω to 0.11, the vaccinated compartment count is increased to 423.564M on 90th day as seen in Result 14. Hence more individuals are vaccinated in less span of time. Significant reduction in exposed and infected individuals can also be observed. Hence vaccination rate can play vital role in reduction of infection count.



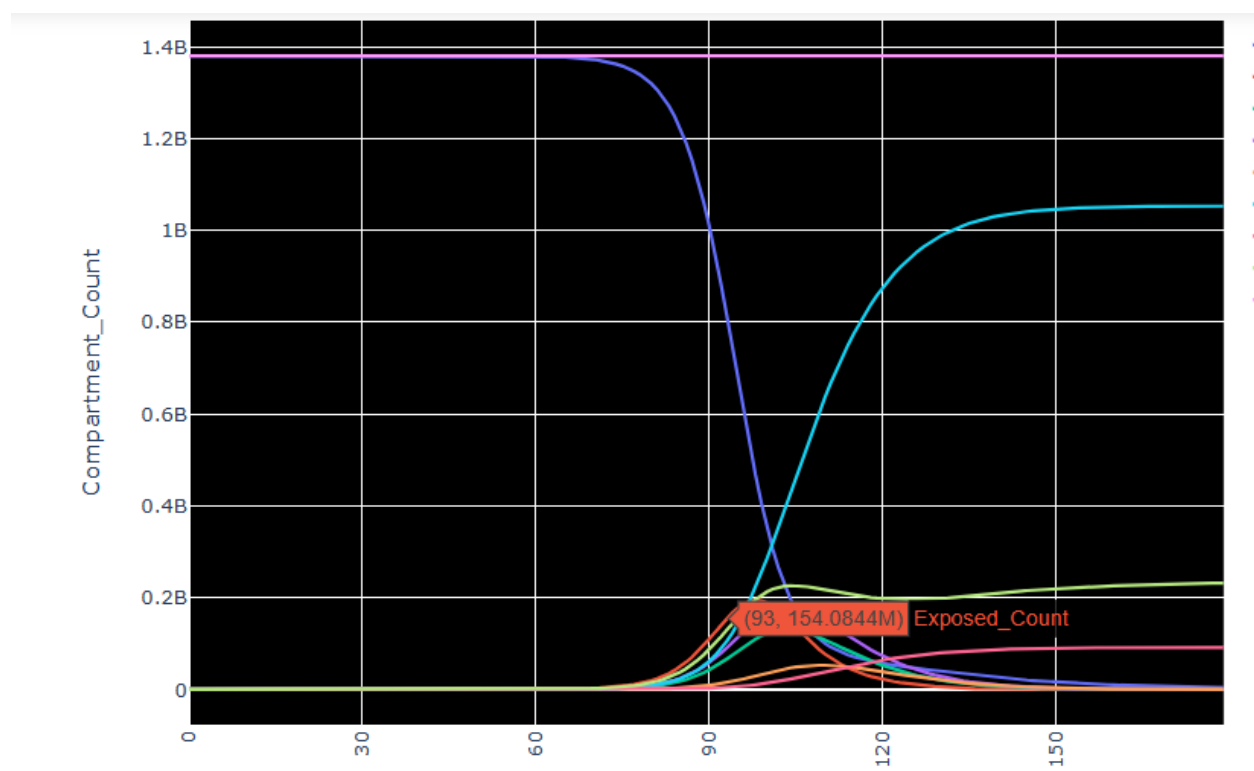
Result 14

Tera

Tera represents the rate of transfer of individuals from Exposed compartment to Quarantine compartment. We shall analyze the variations in exposed and infection curves with respect to change in parameter tera. Result 15 illustrates the exposed and infected curves for tera value 0.15. Increasing the value of tera to 0.57 decrease the value of exposed and infection count. Hence tera can be seen as the testing rate. This testing rate can be expanded to detect the asymptomatic individual. Hence by increasing the testing rate infections can be pacified.



Result 15



Result 16

Chapter 8: Conclusion

The COVID - 19 pandemic has shown its presence now and then for a quiet long time. The disease has some series effects on human race. The dynamics of the disease has to be understood with the right approach to pacify it. There are multiple ways to understand the dynamics of COVID-19. One of the way is to model the disease behavior in the perception of mathematical models. This gives critical insights of the behavior of the disease. An estimate of preventive measures that can be applied can also be drawn to restrict the consequences of the disease.

In my project a variant of SIR model SEQIHRDV was designed by modifying the base model from work[17]. The model is designed with compartments susceptible, exposed, quarantine, hospitalized, dead, recovered, vaccinated. I added visualized total count which gives the sum of all the compartments at given point. This aids in checking the hygiene of the model equation and approves the model functionality. Varying reproduction number was incorporated in the model implementation to take consideration of the lock down restrictions. Further the designed model was implemented via python programming. The death count of country India and model computed output of death compartment were optimized to extract the model parameters of optimal values. Optimized reproduction number was extracted with other optimized parameters. The detailed curve fit statistics were obtained as well.

Further these optimized parameters were fed to model. We overviewed the prediction of death count for 200 days post the last day of data fed.

In the end we analyzed the effects of susceptible to vaccinated rate. The increase in vaccination in shorter period of time aid in declining the infection count. Next we analyzed the effects of testing rate. Testing rate as well aids in pushing the infection count to a certain extent.

Chapter 9: Future Work

The future work with respect to this project assignment can be thought of many directions. Our designed model mildly lags in prediction component considering a large population is analyzed, but still mathematical models with highlight factor on accuracy could be designed so as to get a nearest estimate of the disease behavior.

One of other future perception might be the analysis and readiness in term of mutations of COVID-19 [22]. The prime reason why COVID-19 waves float after certain frequency is the virus mutation. Hence complex models explaining the COVID-19 behavior with mutations may aid quick precautionary measures.

Mathematical models with parameter values changing with time can be designed. [22]. By incorporating the maximum parameter with varying values may offer quite realistic approach to real world scenarios.

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10.1 Implementation Code References

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