

# Mathematical Modeling And Forecasting The Spread Of Covid-19 Using Python

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**Abstract:** Numerous Mathematical models are being produced to predict the trend of spreading of corona virus disease (COVID19) epidemics in INDIA and worldwide, which has become a pandemic. On 23rd Feb 2020, first case of covid-19 was reported, when we were writing this paper cases crossing 70000 in India. We present here data driven models for COVID-19 in India where we used minimal number of parameters to provide insights into the spread of the disease. Here in this paper we are presenting the Susceptible-Infected (SI), Susceptible-Infected-Recovered (SIR), SEIR and SEIR-D models, implemented on Python language with their transition diagrams. All four models presented here are related quantitatively and based on Indian data. In this paper our aim is to deliver an overview of these models and the outcome of simulation by using the dataset of Covid-19. Numbers of plots are presented here for analysis which makes the prediction easy.

**Index Terms:** Susceptible-Infected-Recovered (SIR), SI, SEIR, SEIR-D, Covid-19, Mathematical Models, Python.

## 1 INTRODUCTION

As the whole world is facing a very difficult situation now a days due to COVID19 and our country is also facing the same situation but as the news are coming from the other countries like USA, UK, Italy, Spain, Iran this virus is showing different behavior in different environment. The outbreak of the novel coronavirus disease (Covid-19) brought considerable turmoil all around the world. Statistics show that the mortality of COVID-19 is 20 times higher than seasonal flu so now it should be the priority for every Indian states and central agencies to take efficient measure to limit the transmission of COVID-19. Worldwide, Mathematical Models are playing important role in the making of key policy discussions on these kinds of epidemics like EBOLA, corona, measles and COVID-19. [2] presented the analyses in epidemiology for plant diseases. [1] discussed a very simple model for Africa regarding EBOLA virus. Similarly [3] presented SIR Model to forecast the Outbreak of Ebola Virus Diseases using Euler and 4<sup>th</sup> Order RK method. Lashari et al. (2019) discussed the spread of two successive SIR epidemics through modeling.[5] explained the SIR-type network epidemics based on non-Markovian concept. [6] gave the idea about the epidemics transition in Varroa-infested honeybee colonies. [7] presented the concept regarding SIR Model for different applications. Here We have discussed some mathematical model like SIR, SEIR, SEIR-D describing the structure of how the infectious disease spreading. This work attempts to use python as a language to implement the classic infectious disease model. Because infectious disease model research belongs to the research direction of infectious disease dynamics, I only use the differential equations in the model to implement in Python2 Procedure for Paper Submission

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## 2 MATHEMATICAL MODELS

Mathematical Models are useful tools which are very much capable to make us aware about the trend of disease, may be its spread rate, and effects of policies to be implemented. These mathematical Models are also very useful in scenarios where perfect data are not available with us or collection of such type of data is also not possible, same problems are arising now with data of COVID-19 as this virus is changing day by day and region by region.

### 2.1 Notations

In this paper we have used following symbols to depict the states and transition rate as mentioned in the table-1

**TABLE 1**  
SYMBOLS USED FOR STATES AND TRANSITION RATES

S	Susceptible
I	Infectious
R	NUMBER OF CONTACTS PER UNIT TIME
E	Exposed human being
N	Total population
$\beta$	PROBABILITY OF DISEASE TRANSMISSION PER CONTACT (THE CONTAGION RATE OF THE PATHOGEN)
$\gamma$	RECOVERY RATE
$\mu$	DEATH RATE
$\Omega$	DEATH RATE AFTER INFECTION (IN SEIR-D MODEL)
$\Phi$	RECOVERY RATE AFTER INFECTION (IN SEIR-D MODE)
A	RATE OF PROGRESSION TO INFECTIOUS STATE
$R_0$	REPRODUCTIVE NUMBER

### 2.2 SI Model

To get the information about the trend of infection, we have used various mathematical models. Here in this section first we discuss the simplest model named SI Susceptible-Infectious Model which is mainly applicable to HIV like disease but this model is not applicable for Covid19 type disease

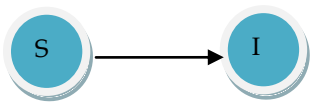


Fig. 1 Transition diagram for SI model

Differential Equation for SI model:

$$dS/dt = -(SI\beta r)/N \tag{1}$$

$$dI/dt - (SI\beta r)/N = 0 \tag{2}$$

**2.3 SIR Model**

SIR (Susceptible, Infected, Recovered) is a simple model that considers a population that belongs to one of the following states and it is Applicable to rubella, COVID-19 and measles

The SIR model is described by the below mentioned system of nonlinear ODE



Fig. 2 Transition diagram for SIR model

$$dS/dt = -(SI\beta r)/N \tag{3}$$

$$dI/dt - (SI\beta r)/N + \gamma I = 0 \tag{4}$$

$$dR/dt - \gamma I = 0 \tag{5}$$

$$N = S + I + R = (\text{Recovered human beings}) \tag{6}$$

$$R_0 = r\beta/\gamma \tag{7}$$

: recovered

human beings, where  $N = S + I + R$

R:

Where  $R_0$  is known as reproductive number which is a dimensionless quantity but it is not a rate, it is defined as a number of secondary infections that one person (infected by others) affect the other persons.

For most of the models  $R_0$  plays a very important role as it works as the threshold parameter.

when  $R_0 < 1$ : the disease dies out

when  $R_0 > 1$ : disease becomes an epidemic.

Python code for ODE equations (3-7)

```
def derivative(y, t, N, r, beta, gamma):
    S, I, R = y
    dSt = -beta * S * I * r / N
    dIt = beta * S * I * r / N - gamma * I
    dRt = gamma * I
    return dSt, dIt, dRt
```

**2.4 SEIR Model**

Many infectious diseases have an incubation period, before being infectious during which the host is still unable to transmit the disease. We will call such individuals, and the entire

compartment, Exposed. This SEIR model is very much applicable for measles, rubella, Corona and Covid-19 also. This model is perfectly suitable for COVID-19 case as it involves exposed state which is missing in the SIR model. The only new transition is the one from E to I, and the rate gets a new variable,  $\alpha$  (alpha). We have the transition diagram as depicted by Fig. 3

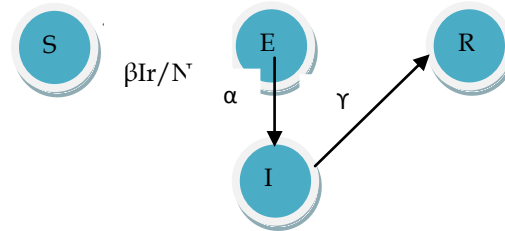


Fig. 3 Transition diagram for SEIR model

$$dS/dt = -(SI\beta r)/N \tag{8}$$

$$dE/dt - (SI\beta r)/N + \alpha E = 0 \tag{9}$$

$$dI/dt - \alpha E + \gamma I = 0 \tag{10}$$

$$dR/dt - \gamma I = 0 \tag{11}$$

If  $R_0 < 1$ , the disease not exists, otherwise ( for  $R_0 > 1$ ) epidemic spreads in the populations.

Python code for derivatives functions ( ODE ,equations 8-11)

```
def derivative(y, t, N, beta, r, gamma, alpha):
    S, E, I, R = y
    dSt = -beta * S * I * r / N
    dEt = beta * S * I * r / N - alpha * E
    dIt = alpha * E - gamma * I
```

**2.5 SEIR-D MODEL**

When can a person die from the disease? Only while infected!, this means that we need to add a transition from I to D .Of course, people don't die immediately.so we have to add one more compartment in the transition diagram.SIR/SEIR/SEIR-D models are key mathematical models, best suited to covid-19 that separates the persons into different sets like S,E,I,R,D also called compartments and then applies a set of mathematical formulas which will give the strategy about the movement of people in between the compartments

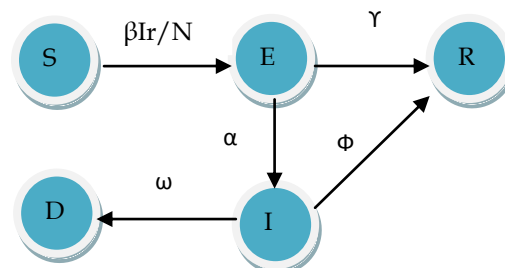


Fig. 4 Transition diagram for SEIR-D model

$$dS/dt = -(S\beta r)/N \tag{12}$$

$$dE/dt + (S\beta r)/N + \alpha E + \gamma E = 0 \tag{13}$$

$$dI/dt - \alpha E + (\phi + \omega)I = 0 \tag{14}$$

$$dR/dt - \phi I - \gamma E = 0 \tag{15}$$

$$dD/dt = \omega I \tag{16}$$

Python code for derivatives functions ( ODE ,equations 12-16)

```
def derivative(y,t,N,beta,gamma,omega, alpha,r,phi):
    S, E, I, R, D = y
    dSt = -beta * S * I * r / N
    dEt = beta * S * I * r / N - (alpha + gamma) * E
    dIt = alpha * E - (omega + phi) * I
    dRt = phi * I + gamma * E
    dDt = omega * I
    return dSt, dEt, dIt, dRt, dDt
```

We have used RK 4<sup>th</sup> order method to solve these equations of all 4 models and we have also used python as a software language to get the plots as an output which is very useful for the policy makers.

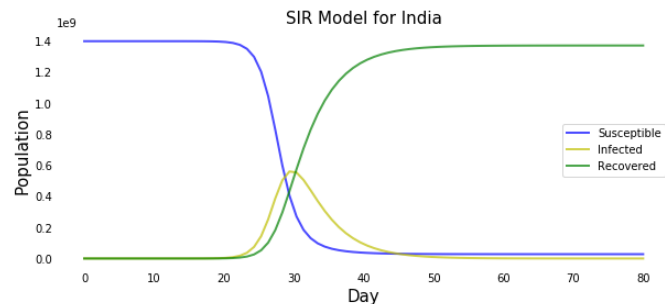


Fig. 5 Temporal evolution for SIR model

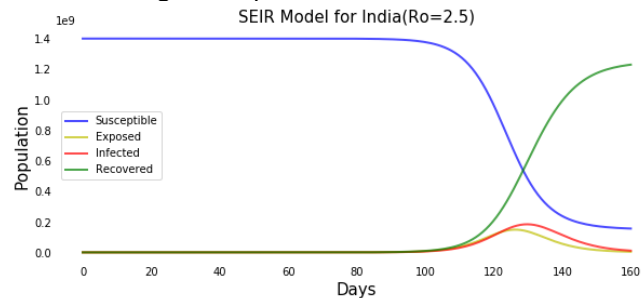


Fig. 6 Temporal evolution for SEIR(for R<sub>0</sub>=2.5) model

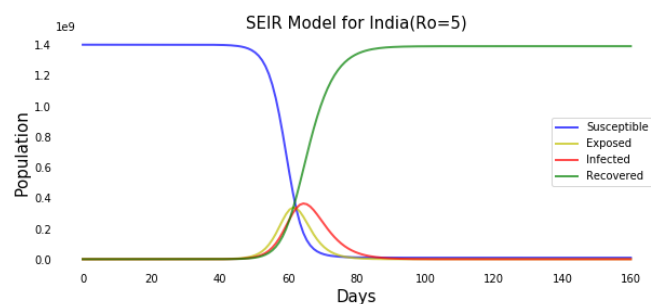


Fig. 7 Temporal evolution for SEIR(for R<sub>0</sub>=5) model

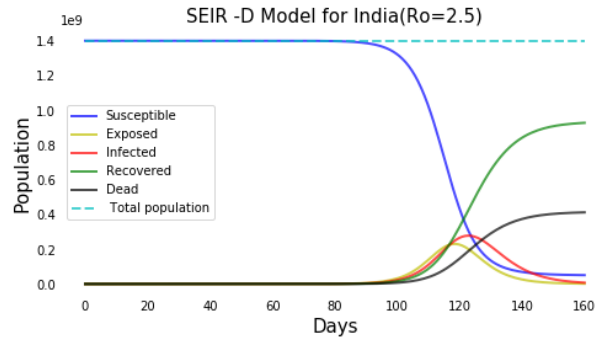


Fig. 8 Temporal evolution for SEIR-D(for R<sub>0</sub>=2.5) model

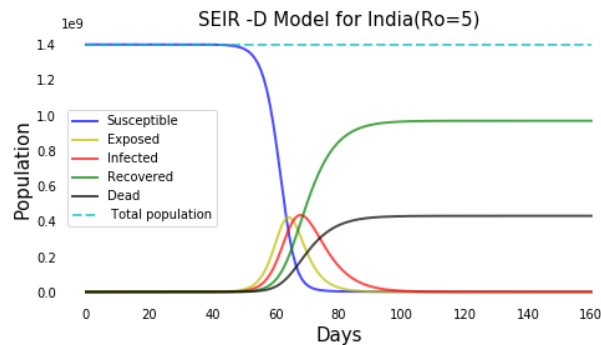


Fig. 9 Temporal evolution for SEIR-D(for R<sub>0</sub>=5) model

### 3 LIMITATIONS

Similarly as with every other model, our own also has certain restrictions. For simplicity of modelling, we have accepted homogenous appropriation of the Indian population that doesn't includes varieties in population thickness or the urban-provincial variations.

### 4 CONCLUSION

In this paper we have discussed the four mathematical models out of these models last three SIR, SEIR, SEIR-D models are suitable for COVID-19 like disease. Although SIR model simplifies the way in which a contagious disease can be transmitted in a group of people, and it has even been coded in a programming language, python, the results obtained, as depicted in Fig. 5, did not represent exact COVID-19 scenario. So, we modify this basic model by including other "compartments" like Recovered (R), Exposed (E) and dead (D). As we can see the plots of SEIR for R<sub>0</sub>=2.5 and 5 in the Fig. 6 and 7 respectively and concludes that if R<sub>0</sub> =5 rate of infected people will decreased after 65 days and for R<sub>0</sub> =2.5 peak of infected people will be on 125 day and for SEIR-D model, from Fig. 8 it is clear that death rate will increase after 100<sup>th</sup> day and susceptible population curve also get down after 100<sup>th</sup> day but for R<sub>0</sub> =5, scenario would be different as we can see from the Fig. 9, as the R<sub>0</sub> increases situation became worst in between 60-70<sup>th</sup> days. From Fig. 5-10, for all models we have used parameters values  $\alpha = 0.5$ ,  $\beta = R_0 \cdot \gamma$ ,  $\gamma = 2.5$ ,  $R_0 = 2.5, 5$ ,  $N =$  approximate population of India. Here RK 4<sup>th</sup> order method is applied to get the solution of all four methods. Calculations also shows that reproduction number R<sub>0</sub>, is a key parameter to describe the rate of infection of covid-19. No model, can serve as a magic box to forecast what is going to happen in the near future, but these models or set of models

can shed light on aspects of the pandemic that might be otherwise unknowable. In the last we conclude that the recovery from this pandemic may last for many months, and authorities and administration in every state will need to make specific choices about how to handle with COVID-19 in India.

## 5 DISCLAIMER

We are not an epidemiologist and these analyses are based on assumptions, implemented on number of mathematical models. The plots and results patterns discussed in this paper based on the past data and on some assumptions. These results should not be considered for any administrative decisions.

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