

# *Mathematical Model for Corona Virus Disease (COVID-19) and Finding the Effect of Isolation in Disease Spread*



A Project Report for Mathematical Modelling And Simulation  
CSM 321

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## **Abstract:**

*Since the Coronavirus spread started in China, scientists and Mathematicians around the globe have been trying to predict its nature so that they can come up with the most efficient method to handle this epidemic. As this virus mutates to different variants with different spreading rates, tracking its behavior is a matter of concern. As many countries are imposing lockdowns and promoting social distancing, we have proposed a mathematical model which will help in understanding the effect of isolation in preventing the spread. We made the model and presented its stability by finding the reproductive factor,  $R_0$ . For numeration, we have used script.integrate library on python which is based on the explicit Runge–Kutta method. Finally, we plotted susceptible, recovered, infective, exposed for different values of the isolation factor and observed the nature of the system.*

## **Introduction:**

Mathematical models can be an efficient tool to study the spread of a pandemic. Covid 19 has been a matter of concern around the globe; with very high transmission rates, the virus mutates itself to new variants, making it difficult to track.

Although the exact origin of the virus is still unknown,[\[1\]](#) the first outbreak started in Wuhan, Hubei, China, in November 2019. Since then, scientists and researchers have been trying to prepare mathematical models for the compelling study of the pandemic. Now we know the spread of the disease occurs as follows:

- According to the current evidence, the virus spreads mainly between people who are in close contact, around 1 meter (short-range). The infection can happen when aerosols or droplets containing the virus are inhaled or directly contact the eyes, nose, or mouth.
- Poorly ventilated, crowded indoor settings where people spend long periods of time also become the site where the virus can spread. The reason for this is that the aerosols remain suspended in the air or travel farther than 1 meter (long-range).[\[2\]](#)

Thus, people's exposure to the virus has an integral role in spreading the disease. And thus, this exposure can be reduced by isolation and social distancing. We have also seen people who do not have any symptoms but are covid positive; they are exposed to the virus without being infected.

The result can be seen as countries' governments putting lockdowns on the state and promoting masks and social distancing. However, many complicated models have been built to simulate and study the spread. In this project, we provide a model that will help us understand the importance of isolation in the disease spread. This mathematical model is based on the SIR model but with a modification that takes count of the exposed and the isolated population. Our model is currently based on some assumptions and uses hypothetical initial data to do this.

As the virus contacts the susceptible class, they can either be exposed (infected without symptoms) or can be infected. Then a section of them gets quarantined. That is, they will not spread the disease further. With time the quarantined people will recover and be added to the recovered class. As covid can infect a person again [3], the recovered people are again added to the susceptible population.

Our findings, mathematically, show that human-to-human contact has a severe role in spreading the disease, and it can be controlled by isolation and social distancing. Further improvements to this project can be made by up-to-date data and using more complicated mathematical tools.

In this model, we assume that the total population is divided into five categories: susceptible, exposed, infected, isolated (quarantined), and recovered.

In the next section, the model is built, and in the 3rd section, the calculation of Equilibrium point and stability will be discussed. Then, the numeration is done by the Runge-Kutta method in Python with the help of libraries in the 4th section. And finally, we have conclusions in the 5th section

### **Model Formulation:**

A hypothetical situation is taken to study the spread of the disease and its effect of isolation. The case is, in a city of population 15,000, two exposed people come from outside. The values of the constants and the parameters are not exact but are taken manually to get an idea of the effect of isolation.

**Table 1: List Of Variables**

$s$	Fraction of Population Susceptible
$e$	Fraction of Population Exposed
$i$	Fraction of Population Infected
$q$	Fraction of Population Isolated
$r$	Fraction of Population Recovered

**Table 2: List Of Constants and their description**

$N$	Total Population	1000
$e_0$	Initial Fraction Of Population Exposed	$2/N$
$s_0$	Initial Fraction Of Population Susceptible	0
$i_0$	Initial Fraction Of Population infected	0
$q_0$	Initial Fraction Of Population isolated	0
$r_0$	Initial Fraction Of Population recovered	0

<b>Table 3: Parameters and Their Description</b>
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$t_{sie}$	Rate by which susceptible population is being infected and exposed	0.0004
$t_{ei}$	Rate by which exposed population is being infected	0.1
$t_{eq}$	Rate by which exposed population is being quarantined	varying
$t_{iq}$	Rate by which infected population is being quarantined	0.9
$t_{qr}$	Rate by which quarantined population is being recovered	0.08
$t_{ndd}$	Natural + disease death rate	0.03
$t_{ir}$	Rate by which infected population is being recovered	0.08
$t_{er}$	Rate by which exposed population is being recovered	0.03
$t_{rs}$	Rate by which recovered population is being susceptible	0.02

This mathematical model is based on the variables given in Table 1. The assumptions which lead to the IVP are as follows:

- As the disease spreads the infected and exposed people infect the susceptibles.

- Exposed people can either be infected, dead, quarantined, or recovered, all at a rate proportional to the fraction of the exposed population.
- The infected population can either die, quarantine, or recover, all at a rate proportional to the fraction of the infected population.
- The quarantine population can either die or can be recovered both at a rate proportional to the fraction of the quarantined population.
- The rate at which the population is recovering will also increase the rate of change of susceptibles by the same value.

The above assumptions lead to the following IVP with Initial conditions in Table 2.

$$\begin{aligned}
 \frac{ds}{dt} &= tndd - tndd * s - tsie * N * s * (e + i) + tqr * q - tndd * r + ter * e + tir * i \\
 \frac{de}{dt} &= tsie * N * s * (e + i) - tei * e - (tndd + teq) * e - ter * e \\
 \frac{di}{dt} &= tei * e - tiq * i - tndd * i - tir * i \\
 \frac{dq}{dt} &= teq * e + tiq * i - tqr * q - tndd * q \\
 \frac{dr}{dt} &= tqr * q - tndd * r + ter * e + tir * i
 \end{aligned} \tag{1}$$

## Basic Reproductive Number and Equilibrium Point of the model:

Basic Reproductive Number, mathematically represented as  $R_0$ , is defined as the number of secondary infections caused by an infected person in a susceptible population. Hence, we can deduce that if:

$R_0 < 1$ , the disease won't spread and will eventually die out.

$R_0 = 1$ , the disease will spread but not in a fatal manner (Endemic)

$R_0 > 1$ , the disease will spread and become an epidemic

So, the existence of unique positive equilibrium and stability of system (1) depends on the basic reproductive number  $R_0$  on free equilibrium point (FEP)  $C_0$ , which is determined with the help of the next-generation matrix method[4]. Now, for the Disease Free equilibrium (DFE), we assume that:

$$e=i=q=0$$

And,  $C_0 = (s, e, i, q)$

We have:

$$S' = t_{n_{dd}} - t_{n_{dd}} \times S = 0$$

So, we get:  $S = 1$ . Hence,  $C_0 = (1, 0, 0, 0)$

Now,  $F$  is the matrix that contains terms that include secondary infections.  $V$  is the matrix that contains terms that do not include secondary infections. Let us now see the matrices:  $F$  and  $V$ :

$$F = \begin{pmatrix} t_{sie} \times N \times S \times (e + i) \\ 0 \end{pmatrix} \quad V = \begin{pmatrix} t_{ei}e + (t_{n_{dd}} + t_{eq})e + t_{er}e \\ -t_{ei}e + t_{iq}i + t_{n_{dd}}i + t_{ir}i \end{pmatrix}$$



Next, we will find the Jacobian of  $F$  and  $V$  at  $C_0$ . According to the definition, we have:

$$F = \begin{pmatrix} \frac{\partial f}{\partial e} & \frac{\partial f}{\partial i} \\ \frac{\partial g}{\partial e} & \frac{\partial g}{\partial i} \end{pmatrix}$$

$$\text{where, } f = t_{sie} * N * S * (e + i) \\ g = 0$$

$$V = \begin{pmatrix} \frac{\partial f}{\partial e} & \frac{\partial f}{\partial i} \\ \frac{\partial g}{\partial e} & \frac{\partial g}{\partial i} \end{pmatrix}$$

$$\text{where, } f = (t_{ei} + t_{n_{dd}} + t_{eq} + t_{er}) * e \\ g = -t_{ei} * e + (t_{iq} + t_{n_{dd}} + t_{ir}) * i$$

Using these definitions, Jacobian[5] of  $F$  and  $V$  at  $C_0$  is obtained as follows:

$$F = \begin{pmatrix} t_{sie} * N & t_{sie} * N \\ 0 & 0 \end{pmatrix}$$

$$V = \begin{pmatrix} (t_{ei} + t_{n_{dd}} + t_{eq} + t_{er}) & 0 \\ -t_{ei} & (t_{iq} + t_{n_{dd}} + t_{ir}) \end{pmatrix}$$

$R_0$  is given by the dominant eigenvalue of  $FV^{-1}$ . Hence, consider  $V^{-1}$  as follows:

$$V^{-1} = \frac{1}{|V|} \begin{pmatrix} (t_{iq} + t_{n_{dd}} + t_{ir}) & 0 \\ t_{ei} & (t_{ei} + t_{n_{dd}} + t_{eq} + t_{er}) \end{pmatrix}$$

Substituting the value of  $|V|$ , we get:

$$V^{-1} = \begin{pmatrix} \frac{1}{(t_{ei} + t_{n_{dd}} + t_{eq} + t_{er})} & 0 \\ \frac{t_{ei}}{(t_{ei} + t_{n_{dd}} + t_{eq} + t_{er}) * (t_{iq} + t_{n_{dd}} + t_{ir})} & \frac{1}{(t_{iq} + t_{n_{dd}} + t_{ir})} \end{pmatrix}$$

$FV^{-1}$  is obtained as follows:

$$\begin{aligned} FV^{-1} &= \begin{pmatrix} t_{sie} * N & t_{sie} * N \\ 0 & 0 \end{pmatrix} \times \frac{1}{|V|} \begin{pmatrix} (t_{iq} + t_{n_{dd}} + t_{ir}) & 0 \\ t_{ci} & (t_{ci} + t_{n_{dd}} + t_{cq} + t_{cr}) \end{pmatrix} \\ &= \frac{N * t_{sie}}{|V|} \begin{pmatrix} 1 & 1 \\ 0 & 0 \end{pmatrix} \begin{pmatrix} (t_{iq} + t_{n_{dd}} + t_{ir}) & 0 \\ (t_{iq} + t_{n_{dd}} + t_{ir}) & 0 \end{pmatrix} \\ &= \frac{N * t_{sie}}{|V|} \begin{pmatrix} (t_{iq} + t_{n_{dd}} + t_{ir} + t_{ei}) & (t_{ei} + t_{n_{dd}} + t_{eq} + t_{er}) \\ 0 & 0 \end{pmatrix} \end{aligned}$$

To find the eigenvalues of the obtained  $FV^{-1}$ , use the following:

$$|FV^{-1} - \lambda I| = 0$$

$$\begin{vmatrix} \frac{N * t_{sie}}{|V|} * (t_{iq} + t_{n_{dd}} + t_{ir} + t_{ei}) - \lambda & (t_{ei} + t_{n_{dd}} + t_{eq} + t_{er}) \\ 0 & 0 - \lambda \end{vmatrix} = 0$$

$$(-\lambda) \left\{ \frac{N * t_{sie}}{|V|} * (t_{iq} + t_{n_{dd}} + t_{ir} + t_{ei}) - \lambda \right\} = 0$$

Hence,

From these, we obtain 2 eigenvalues:

$$\lambda = \frac{N * t_{sie} * (t_{iq} + t_{n_{dd}} + t_{ir} + t_{ei})}{(t_{ei} + t_{n_{dd}} + t_{eq} + t_{er}) * (t_{iq} + t_{n_{dd}} + t_{ir})}$$

For the value of  $R_0$ , we will use the dominant eigenvalue, hence,  $R_0$  is:

$$\frac{N * t_{sie} * (t_{iq} + t_{n_{dd}} + t_{ir} + t_{ei})}{(t_{ei} + t_{n_{dd}} + t_{eq} + t_{er}) * (t_{iq} + t_{n_{dd}} + t_{ir})}$$

For the local stability at  $C_0$ , we will find the Jacobian for the system of equations (1). We get:

$$J = \begin{pmatrix} -t_{n_{dd}} & -t_{sie} * N + t_{er} & -t_{sie} * N + t_{ir} & t_{qr} \\ 0 & t_{sie} * N - t_{ei} - t_{n_{dd}} - t_{eq} & t_{sie} * N & 0 \\ 0 & t_{ei} & -(t_{iq} + t_{n_{dd}} + t_{ir}) & 0 \\ 0 & t_{eq} & t_{iq} & -(t_{qr} + t_{n_{dd}}) \end{pmatrix}$$

*After analyzing the matrix we can conclude that,  $\lambda_2 < 0$ ,  $\lambda_3 < 0$ , and  $\lambda_4 < 0$  for  $R_0 < 1$ . Therefore, system (1) is locally stable related to virus-free*

equilibrium point  $C_o$ , if  $R_o < 1$  and unstable if  $R_o > 1$ . We can also conclusively, using the Lyapunov [\[6\]](#) function, say that for  $R_o$ , the system is globally stable.

## Numerical Methods and Results

**By Runge-Kutta method:**

Runge Kutta method [\[7\]](#) is used for solving an IVP using numeration.

It requires the following inputs,

- An ordinary differential equation that defines the value of  $dy/dx$  in the form of  $x$  and  $y$ .
- Initial value of  $y$ , i.e.,  $y(0)$

We have the system of ODEs described in Eqn(1) with the initial conditions in Table-2.

$$y'(t) = f(t, y), \quad y(0) = y^{(0)}$$

Here  $y'$ ,  $y$ ,  $y(0)$  all will be variable matrices. The solution matrix will be-

$$y(t) = \begin{bmatrix} S(t) \\ e(t) \\ i(t) \\ q(t) \\ r(t) \end{bmatrix}$$

The system of ODEs can in matrix form will be written as:

$$f(t, y) = \begin{bmatrix} S(t, y) \\ e(t, y) \\ i(t, y) \\ q(t, y) \\ r(t, y) \end{bmatrix}, \quad y^{(0)} = \begin{bmatrix} 0 \\ \frac{2}{N} \\ 0 \\ 0 \\ 0 \end{bmatrix}$$

The following slope approximations are used to establish the slope at some time  $t_0$ :

$$k_1 = f(y * t_0, t_0)$$

$$k_2 = f(y * t_0 + k_1 \frac{h}{2}, t_0 + \frac{h}{2})$$

$$k_3 = f(y * t_0 + k_2 \frac{h}{2}, t_0 + \frac{h}{2})$$

$$k_4 = f(y * t_0 + k_3 h, t_0 + h)$$

$$y_{n+1} = y_n + \frac{k_1}{6} + \frac{k_2}{3} + \frac{k_3}{3} + \frac{k_4}{6} + O(h^5)$$

We have solved the equation in python using the odeint function[\[8\]](#) and plotted the graph.

### Code:

```

• import numpy as np
• from scipy.integrate import odeint
• import matplotlib.pyplot as plt
•
• N = 15000 #Total Population
• # initial number of infected, exposed, quarantined, recovered, and
  susceptible individuals
• # s->susceptible
• # e->exposed
• # i->infected
• # q->isolated
• # r->recovered
•
• e0=2/N

```

```

• s0=1-e0
• i0=0
• q0=0
• r0=0
• x0 = [s0,e0,i0,q0,r0]
•
• tsie=0.00004      # susceptible->(infected+exposed)
• tei= 0.05*2      # exposed->infected
• for i in range(0,8):
•
•     teq=0.8-0.1*i # exposed->isolation
•     tiq=0.9      # infected->isolated
•     tqr=0.08     # isolation->recovery
•     tndd=0.01*3   # (natural+diseases)_death rate
•     tir=0.006*3   #infected->recover
•     ter=0.03      #exposed->recover
•     trs=0.02      #recover->susceptible
•
•     def covid(x,t):
•         s,e,i,q,r = x
•         dx = np.zeros(5)
•         dx[0] = tndd*tndd*s-tsie*N*s*(e+i)+tqr*q-tndd*r +ter*e
•         +tir*i# dS/dt equation
•         dx[1] = tsie*N*s*(e+i)-tei*e-(tndd+teq)*e-ter*e# dE/dt
•         equation
•         dx[2] = tei*e-tiq*i-tndd*i-tir*i # dI/dt equation
•         dx[3] = teq*e+tiq*i-tqr*q-tndd*q# dQ/dt equation
•         dx[4]=tqr*q-tndd*r +ter*e +tir*i # dR/dt
•         return dx
•
• t = np.linspace(0, 365, 1000)
• x = odeint(covid,x0,t)

```

```

s = x[:,0]; e = x[:,1]; i = x[:,2]; r = x[:,4]

# plot the data
plt.figure(figsize=(8,5))

plt.subplot(2,1,1)
plt.title('teq= '+str(round(teq,4))+', Ro = '+str(
round(tsie*N*(tiq+tndd+tir+tei)/((tei+tndd+teq+ter)*(tiq+tndd+tir)
),4))+', max infected= '+str(round(max(i),4)) )
plt.plot(t,s, color='blue', lw=3, label='Susceptible')
plt.plot(t,r, color='red', lw=3, label='Recovered')
plt.ylabel('Fraction')
plt.legend()

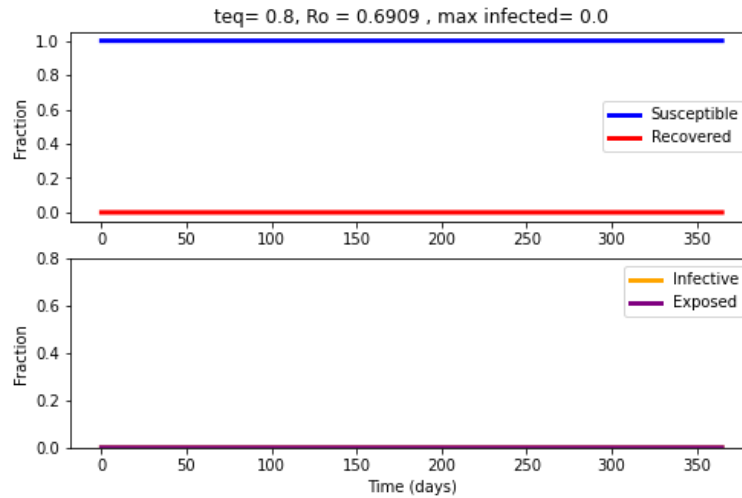
plt.subplot(2,1,2)
plt.plot(t,i, color='orange', lw=3, label='Infective')
plt.plot(t,e, color='purple', lw=3, label='Exposed')
plt.ylim(0, 0.8)
plt.xlabel('Time (days)')
plt.ylabel('Fraction')
plt.legend()

plt.show()

```

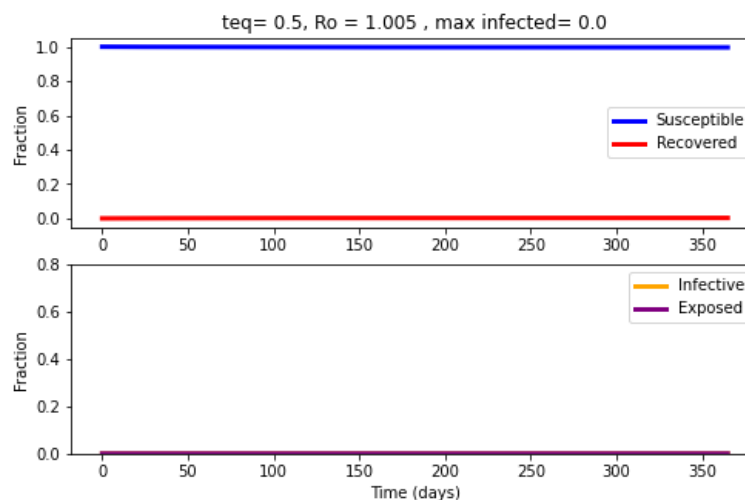
## Graphs:

1. For  $t_{eq} = 0.8$ :



The  $R_0$  is 0.69028, that is the disease won't spread as almost 0 percent of the population is exposed if 80% of the exposed population is quarantined.

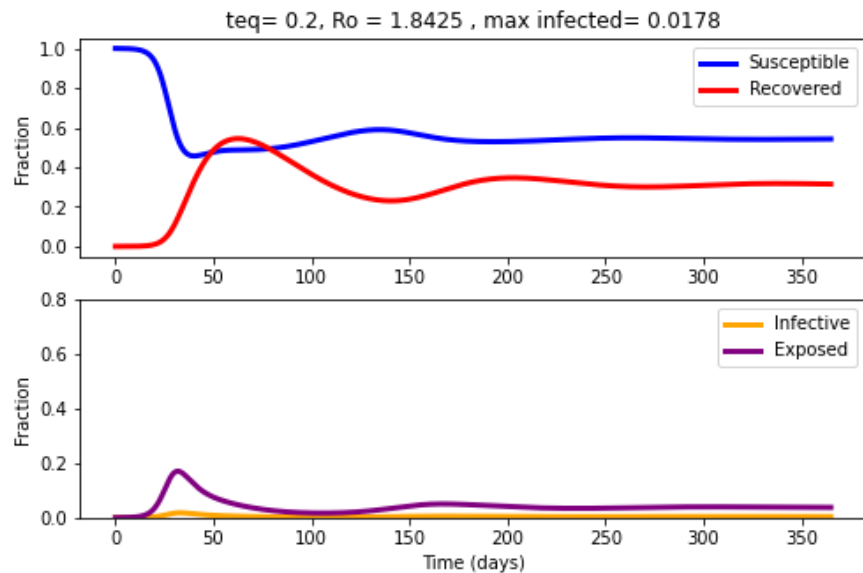
2. For  $t_{eq} = 0.5$ :



The  $R_0$  is 1.005 when 50% of the exposed are quarantined, again the disease spread won't be fatal as it is not spreading in the overall population significantly.

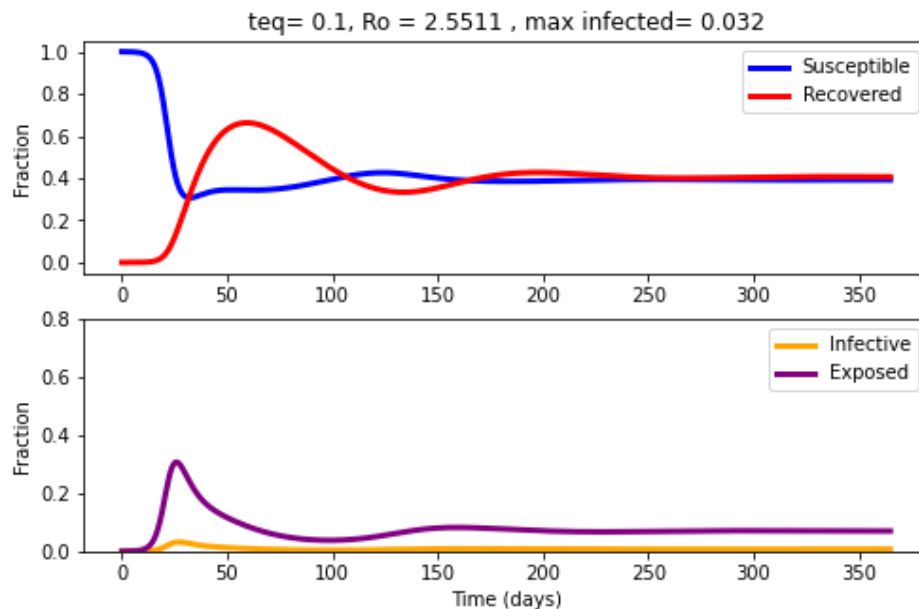


### 3. When $t_{eq}=0.2$ :



That is when 20 percent of the exposed population is quarantined,  $R_0$  comes out to be  $1.8425 > 1$ , the disease spread can be seen as two waves with a maximum of 1.78 percent of the population getting positive on a particular day.

### 4. When $t_{eq}$ is 0.1:



When 10 percent of the exposed population quarantine themselves,  $R_0$  comes out to be 2.5511 which is a large number for any disease spread. And again the spread can be seen in 2 waves with a maximum of 3.2 percent of the entire population getting exposed to it on a particular day, which is a matter of concern.

### **Conclusion:**

In this report, we present a mathematical model to show that the isolation of infected humans can reduce the risk of future Covid-19 spread. We establish a Covid-19 control model based on isolation measures, analyze the effect of centralized diagnosis and treatment, and make predictions about the development of the epidemic. Our model shows that Covid-19 spreads through contact with infected people. We describe how fast the rate of infection changes along with the likelihood of infections. The new infections lead to epidemics. Our model provides better intuitions of the spread of the disease and its future. We have also discussed the reproductive number related stability and the effect of the interaction of infected people to the susceptible. From the graphs, we can finally conclude that when the isolation factor (teq) reduces, the reproductive number increases. Hence, isolation is essential for diseases like COVID-19.

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