



Project on Modeling Epidemics using SIR Model

Subject

ENGINEERING ANALYSIS (ENCS 6021)

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ABSTRACT

It has been more than a year since the COVID-19 pandemic hit the world and is still in a recovering state. A pandemic involves the worldwide spread of a new disease, while an epidemic remains limited to a particular region, city or country. These take place when infection due to virus or bacteria can spread widely and rapidly. These can be studied using Mathematical models and one among these is the SIR (Susceptible-Infected- Removed). This was developed by Kermack and McKendrick in 1927 which provides a theoretical approach to look into the spread of the virus by looking at all possible scenarios. The SIR model divides the population into three categories Susceptible Individuals (S), Infected individuals (I), and Removed individuals (R) and these variables are considered moreover as a dependent. There are variables like Time (t), Contacts (b), and Recovered people (k) that fall under the category of independent variables. The advancement of the SIR model has developed analytical solutions providing us with both the vision and perception of the spread of the disease. Thus, making things like lockdown and its lifting interventions possible to test as there holds a way to the arbitrary time dependence of the infection rate. Hence presenting this simple analytical approximation for the rate and a cumulative number of new infections. In this project, the basic SIR model was used to simulate the pandemic. In this model, the infection rate can be neglected to get S (considering the natural mortality and fertility rate of the general population, the susceptibility has increased, and in this improved model, one of the assumptions is that the fertility rate and the mortality rate are the same. The original SIR equation does not have an exact solution, many assumptions and simplifications need to be done. By comparing the numerical method and the analytical solutions.

Modeling Epidemics using SIR Model.

INTRODUCTION:

Now a days we live in a modern world where the development has been very vast over the years.so the air travel is one of the important reasons for spread of diseases from one part of the world to the other part in lesser period. in some cases, the spread of diseases will be increased rapidly to some set of population. There are some diseases which spread to some set of people by a sneeze. The spread has become more infectious by these problems that are happening some say this as epidemic. This epidemic spread in large area and then the spread is more and more globally it's a pandemic. The Spanish flue in 1918 is a pandemic because at that time there are more than 50 million people who lost their lives. Then one more main problem for these viruses is that the mutation that occurs in it depending on the climatic conditions. Influenza virus has mutated into new strain and by this some more new strains are occurring by this. in recent times covid-19 is also a pandemic there are so many people who lost their Lives in this. There are so many people who are getting infected by this, and the recovery rate is also getting better day by day. But the mutations are the only problem now as the virus is getting mutated depending on the climatic conditions of the country. Each country has new variant of this virus which is because of mutations. So, this is becoming harder for researchers to produce vaccinations.

The advancement in the technology and science helps to face any kind of epidemic. There are lot of virologists and researchers who are working hard to fight against a virus by working on producing the vaccines. There are some epidemiologists who turn themselves in to mathematicians to develop a mathematical model which shows the predictions of the progress of the epidemic. These models are helpful for predicting the upcoming rate of spread of disease so by this model the necessary precautions can be taken. Depending on the mathematical model stats. By these precautions we can reduce the spread of disease.

These mathematical models are helpful for the researchers to know the spreading rate in those days when influenzas' virus attacked to so many people. These mathematical models are

also helpful to study how the virus would have developed into a pandemic. This helps in informing the health authorities about the intervention option. In the basic model SIR, which was developed by Kermack and McKendrick (1) in 1927, the population (N) is divided into three categories: susceptible individuals (S), infected individuals (I) and distant individuals (R).

Susceptible individuals are the people who are not infected by the disease but there is a chance for them to get infected. Once they are infected then the susceptible individual can become an infected individual. So, these infected individuals can spread the disease to susceptible individuals. So once these infected individuals are recovered from the disease then they can become the removed individuals. The removed individuals are those who can not infect the susceptible individuals. So, they are recovered individuals who have recovered from the disease. So, these recovered individuals are immune to the disease and they are not having the ability to infect the susceptible individuals. For this model to function, there are some assumptions that need to be done. The total population cannot change, hence there are no births or no natural deaths. The total population (N) = S+I+R. The recovery rate, death rate and infection rate are the same for all individuals, and they are positive in magnitude.

The independent variable in this model is time (t). Thus, S, I and R are all functions of t and we can express them as R(t), I(t) and S(t). The dependent variable can be divided by the total population (N), the variables become a fraction of the total population and they can still be represented by the same letters S(t), I(t) and R(t).

In this project, basic SIR model will be used to simulate a pandemic. In this model, the infection rate will be negligible, to keep S (susceptible improved by considering the natural rate death and birth rate in the overall population, while at the same time incorporating vaccination). In this improved model, one of the assumptions is that the birth rate and death rate are equal.

1. Basic SIR model

$$\frac{dS}{dt} = -\beta SI$$

$$\frac{dI}{dt} = \beta SI - \gamma I - \omega I$$

$$\frac{dR}{dt} = \gamma I + \omega I$$

β is the rate of infection, γ is the rate of recovery and ω is the death rate coefficient.

The SIR model is a nonlinear system of ordinary differential equation that does not have analytic solution. For this reason, we can make assumptions and simplification to make the model a linear system that can be solved analytically and its solution can be compared to its solutions using numerical methods,



Table 1. Table of parameters

Independent Variable	Dependent Variable	Constants
Time (t)	Infected Individuals ($I(t)$)	Recovery coefficient (γ)
	Susceptible Individuals ($S(t)$)	Infection coefficient (β)
	Removed Individuals ($R(t)$)	Death rate coefficient (ω)

The main aim of this project is to obtain a simulation using numerical methods and analytical methods that can predict an epidemic.

3. Analytical Derivation of Mathematical Model with Differential Equations

The purpose of this section is to determine a solution of the mathematical model that was presented. In order to simplify the model composed of three unknown differential equations, we would only solve for $I(t)$ and for $S(t)$, the proportion of the removed individuals would not be taken into account in this SIR mathematical model. The model solved instead is the SI model, which considers the entry of recovered individuals with no immunity ($+\gamma$) and the exit of susceptible individuals that have gained immunity without ever being infected ($-\gamma s(t)$) from the change of susceptible individuals per time ($\frac{ds}{dt}$). The difference between this model and the original SIR model is that, the change of susceptible individual is also dependent on the recovery coefficient (2) (3).

The mathematical model is going to be represented by these equations:

$$\frac{dS}{dt} = -\beta S(t)I(t) - \gamma s(t) + \gamma \quad (1)$$

$$\frac{dI}{dt} = \beta S(t)I(t) - \gamma I(t) \quad (2)$$

By addition of equations (1) and (2), we get:

$$\frac{dI}{dt} + \frac{dS}{dt} = -\gamma(I(t) + s(t)) + \gamma$$

Integration of the equation

$$\begin{aligned} \frac{dI}{dt} + \frac{dS}{dt} &= -\gamma(I(t) + s(t)) + \gamma \\ \ln(I(t) + s(t) - 1) &= \gamma t \\ e^{\ln(I(t) + s(t) - 1)} &= Ce^{\gamma t} \\ S(t) &= 1 + Ce^{\gamma t} - I(t) \end{aligned} \quad (3)$$

Where C is the integration constant

Substituting this final equation with equation (2).

$$\begin{aligned} \frac{dI}{dt} &= \beta I(t)(1 + Ce^{\gamma t} - I(t)) - \gamma I(t) \\ &= \beta I(t) + \beta I(t)Ce^{\gamma t} - \beta I(t)^2 - \gamma I(t) \end{aligned}$$

By integrating and substituting u= 1/I(t)

$$\begin{aligned} \frac{duI^2}{dt} &= \frac{1}{u}(\beta + \beta Ce^{\gamma t} - \beta \frac{1}{u} - \gamma) \\ u e^{(\beta-\gamma)t - (\frac{\beta C}{\gamma})e^{-\gamma t}} &= \int \beta e^{(\beta-\gamma)t - (\frac{\beta C}{\gamma})e^{-\gamma t}} dt + C_1 \end{aligned}$$

Where C1= is the integration constant

An assumption can be done to simplify this equation. The term $e^{-\gamma t}$ approaches 0 as $t \rightarrow \infty$, taking a series of expansion of this term, the result is $= 1 - \gamma t$. Then the equation becomes

$$\begin{aligned} u e^{(\beta-\gamma)t - (\frac{\beta C}{\gamma})(1-\gamma t)} &= \int \beta e^{(\beta-\gamma)t - (\frac{\beta C}{\gamma})(1-\gamma t)} dt + C_1 \\ u &= \frac{\beta}{\beta - \gamma + \beta C} + C_1 e^{-(\beta - \gamma + \beta C)t} e^{\frac{\beta C}{\gamma}} \end{aligned}$$

Since we substituted u= 1/I, we can plug 1/I back into the equation

$$I(t) = \frac{\beta - \gamma + \beta C}{\beta + (\beta - \gamma + \beta C)C_1 e^{-(\beta - \gamma + \beta C)t} e^{\frac{\beta C}{\gamma}}}$$

To determine the integration constants, we can use our initial conditions with initial conditions $I(0) = I_0$ and $S(0) = S_0$.

$$C_1 = \frac{(\beta - \gamma + \beta C) - I_0\beta}{(\beta - \gamma + \beta C)I_0 e^{\frac{\beta C}{\gamma}}}$$

$$C = S_0 + I_0 - 1$$

Then the $S(t)$ equation can be determined by substituting $I(t)$ in equation (3). Reminding that we are using $(1-\gamma t)$ instead of $e^{\gamma t}$

$$S(t) = 1 + C(1 - \gamma t) - \frac{\beta - \gamma + \beta C}{\beta + (\beta - \gamma + \beta C)C_1 e^{-(\beta - \gamma + \beta C)t} e^{\frac{\beta C}{\gamma}}}$$

Finally, the differential equations representing this model were solved, making some assumptions. In fact, the real SIR model cannot be solved analytically.

4. Numerical Solution of SIR Model

The solution can be solved numerically using Fourth Order Runge-Kutta Method.

The method has the form of

$$y_{r+1} = y_r + \frac{1}{6}(k_1 + 2k_2 + 2k_3 + k_4)$$

With $k_1 = hf(x_r, y_r)$

$$k_2 = hf\left(x_r + \frac{1}{2}h, y_r + \frac{1}{2}k_1\right)$$

$$k_3 = hf\left(x_r + \frac{1}{2}h, y_r + \frac{1}{2}k_2\right)$$

$$k_4 = hf(x_r + h, y_r + k_3)$$

This method was selected based upon the fact that, it has better accuracy and relatively easy to program with minimal rounding error.

Using the above numerical method, the SIR model can as a set of ordinary differential equations are in the form as follows

$$\frac{dS}{dt} = f(t, S, I, R) = -\beta SI$$

$$\frac{dI}{dt} = g(t, S, I, R) = \beta SI - \gamma I - \omega I$$

$$\frac{dR}{dt} = i(t, S, I, R) = \gamma I + \omega I$$

The above equations are solved using the fourth-order Runge-Kutta method as

$$S_{r+1} = S_r + \frac{1}{6}(k_1 + 2k_2 + 2k_3 + k_4)$$

$$I_{r+1} = I_r + \frac{1}{6}(l_1 + 2l_2 + 2l_3 + l_4)$$

$$R_{r+1} = R_r + \frac{1}{6}(m_1 + 2m_2 + 2m_3 + m_4)$$

Where,

$$k_1 = -\beta S_r I_r$$

$$l_1 = \beta S_r I_r - \gamma I_r - \omega I_r$$

$$m_1 = \gamma I_r + \omega I_r$$

$$k_2 = -\beta(S_r + k_1 \frac{1}{2}h)(I_r + l_1 \frac{1}{2}h)$$

$$l_2 = \beta(S_r + k_1 \frac{1}{2}h)(I_r + l_1 \frac{1}{2}h) - \gamma(I_r + l_1 \frac{1}{2}h) - \omega(I_r + l_1 \frac{1}{2}h)$$

$$m_2 = \gamma(I_r + l_1 \frac{1}{2}h) + \omega(I_r + l_1 \frac{1}{2}h)$$

$$k_3 = -\beta(S_r + k_2 \frac{1}{2}h)(I_r + l_2 \frac{1}{2}h)$$

$$l_3 = \beta(S_r + k_2 \frac{1}{2}h)(I_r + l_2 \frac{1}{2}h) - \gamma(I_r + l_2 \frac{1}{2}h) - \omega(I_r + l_2 \frac{1}{2}h)$$

$$m_3 = \gamma(I_r + l_2 \frac{1}{2}h) + \omega(I_r + l_2 \frac{1}{2}h)$$

$$k_4 = -\beta(S_r + k_3 h)(I_r + l_3 h)$$

$$l_4 = \beta(S_r + k_3 h)(I_r + l_3 h) - \gamma(I_r + l_3 h) - \omega(I_r + l_3 h)$$

$$m_4 = \gamma(I_r + l_2 h) + \omega(I_r + l_2 h)$$

5. Modelling Parameters

The initial values and parameters used for the SIR model presented above are taken from one particular case in Kota Makassar, for which the data is obtained from the Division of Disease Prevention and Environmental Health of Makassar City Health office, from the year 2013.

The initial conditions and parameters are as follows

Initial Condition of SIR Model		
Variable/Parameter	Description	Value
N	Total Population	1449401
S (0)	No. of Individuals initially vulnerable	$\frac{1446093}{1449401}$
I (0)	No. of Individuals initially infected	$\frac{1885}{1449401}$
R (0)	No. of individuals initially recovered	$\frac{1423}{1449401}$
β	Rate of infection	$\frac{1}{2} = 0.5 /month$
γ	Rate of recovery	$\frac{1}{9} = 0.111111 /month$
ω	Rate of death	$\frac{1}{71.41 * 12} = 0.001167 /month$

6. RESULTS

6.1 Using Numerical Method (RK4)

Before looking at the results from the SIR model with the above specified model, the first iteration of is presented for $r = 0$, to get be able to see how the numerical method works.

As we know

$$S_{r+1} = S_r + \frac{1}{6}(k_1 + 2k_2 + 2k_3 + k_4)$$

$$I_{r+1} = I_r + \frac{1}{6}(l_1 + 2l_2 + 2l_3 + l_4)$$

$$R_{r+1} = R_r + \frac{1}{6}(m_1 + 2m_2 + 2m_3 + m_4)$$

For $r = 0$

$$S_1 = S_0 + \frac{1}{6}(k_1 + 2k_2 + 2k_3 + k_4)$$

$$I_1 = I_0 + \frac{1}{6}(l_1 + 2l_2 + 2l_3 + l_4)$$

$$R_1 = R_0 + \frac{1}{6}(m_1 + 2m_2 + 2m_3 + m_4)$$

Where

$$k_1 = -\beta S_0 I_0$$

$$l_1 = \beta S_0 I_0 - \gamma I_0 - \omega I_0$$

$$m_1 = \gamma I_0 + \omega I_0$$

$$k_2 = -\beta(S_0 + k_1 \frac{1}{2}h)(I_0 + l_1 \frac{1}{2}h)$$

$$l_2 = \beta(S_0 + k_1 \frac{1}{2}h)(I_0 + l_1 \frac{1}{2}h) - \gamma(I_0 + l_1 \frac{1}{2}h) - \omega(I_0 + l_1 \frac{1}{2}h)$$

$$m_2 = \gamma(I_0 + l_1 \frac{1}{2}h) + \omega(I_0 + l_1 \frac{1}{2}h)$$

$$k_3 = -\beta(S_0 + k_2 \frac{1}{2}h)(I_0 + l_2 \frac{1}{2}h)$$

$$l_3 = \beta(S_0 + k_2 \frac{1}{2}h)(I_0 + l_2 \frac{1}{2}h) - \gamma(I_0 + l_2 \frac{1}{2}h) - \omega(I_0 + l_2 \frac{1}{2}h)$$

$$m_3 = \gamma(I_0 + l_2 \frac{1}{2}h) + \omega(I_0 + l_2 \frac{1}{2}h)$$

$$k_4 = -\beta(S_0 + k_3 h)(I_0 + l_3 h)$$

$$l_4 = \beta(S_0 + k_3 h)(I_0 + l_3 h) - \gamma(I_0 + l_3 h) - \omega(I_0 + l_3 h)$$

$$m_4 = \gamma(I_0 + l_2 h) + \omega(I_0 + l_2 h)$$

Calculating the values of $k_1, k_2, k_3, k_4, l_1, l_2, l_3, l_4, m_1, m_2, m_3, m_4$, manually with hand, using afore mentioned initial conditions and parameters with a step size of $h=1$ month we get

k_1	-0.000648505
l_1	0.0005025436
m_1	0.0001459614
k_2	-0.0007736004356
l_2	0.000599267404
m_2	0.0001741736952
k_3	-0.0007976679029
l_3	0.0006180642301
m_3	0.0001796036728
k_4	-0.000956061352
l_4	0.0007407049364
m_4	0.0002153564156

Therefore, for the above calculated values of $k_1, k_2, k_3, k_4, l_1, l_2, l_3, l_4, m_1, m_2, m_3, m_4$

$$S_1 = 0.9969088162$$

$$I_1 = 0.001912985301$$

$$R_1 = 0.001158145425$$

Repeating the same steps, the results for S_2, I_2, R_2, S_3, I_3 and R_3 are tabulated as follows

h	S(h)	I(h)	R(h)
0	0.9977	0.0013	0.00098
1	0.9969088162	0.001912985301	0.001158145425
2	0.995783473	0.002784778	0.001411749
3	0.994148016	0.004051181	0.001780804

From the above table for 3 iterations a crude trend can be seen for the SIR model as the time progresses per month. It can be seen that the number of suspected individuals $S(h)$ begins to decrease, as the number of infected individuals $I(h)$ begins to increase, so does the number of individuals recovered, $R(h)$.

The complete numerical solution of the SIR model is simulated using the basic Microsoft Excel package. The figure below shows the results for the proposed model.

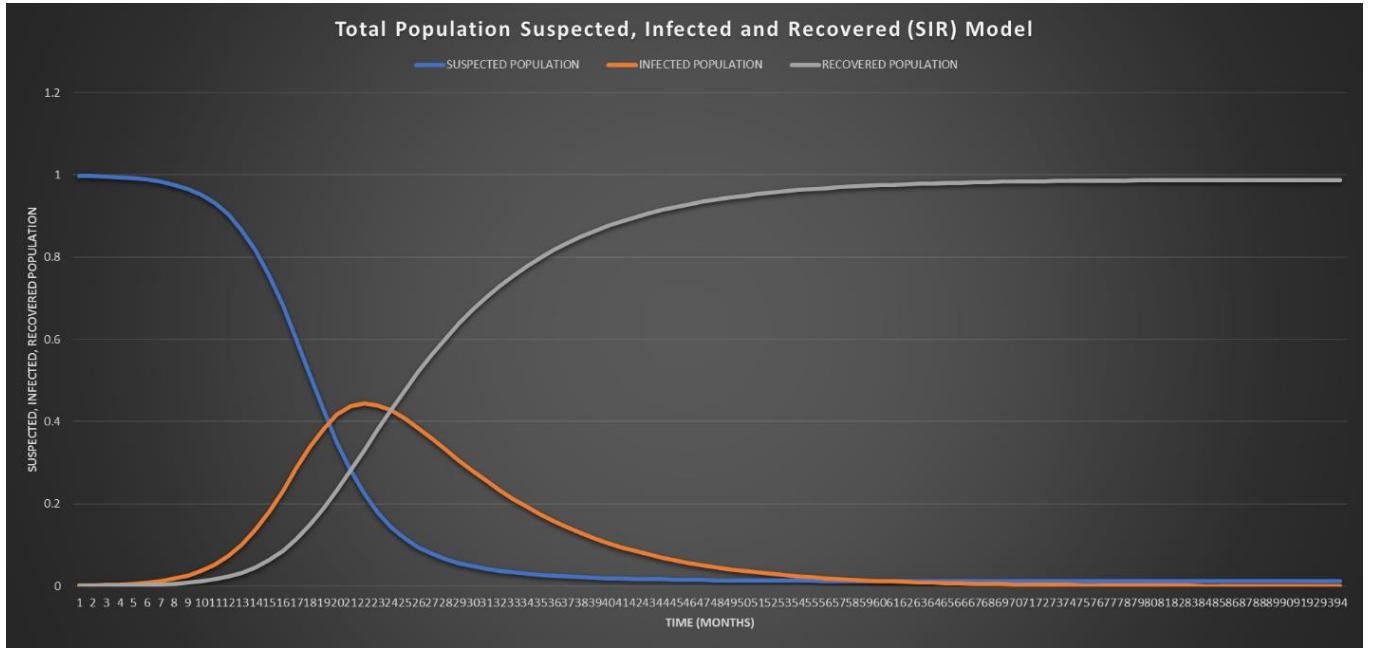


Figure 1. Numerical Solution plot using Excel

It can be seen that, the number of infected individuals is high around 22nd month and the entire population is recovered within a span of around 50 months, this is without any external interference like vaccination etc.

6.2 Using Analytical Solution

The table below shows the results of the SIR model using the analytical solution of the set of ordinary differential equations that form the SIR model as discussed above in Section 3, with the same initial conditions and parameters as for the numerical method.

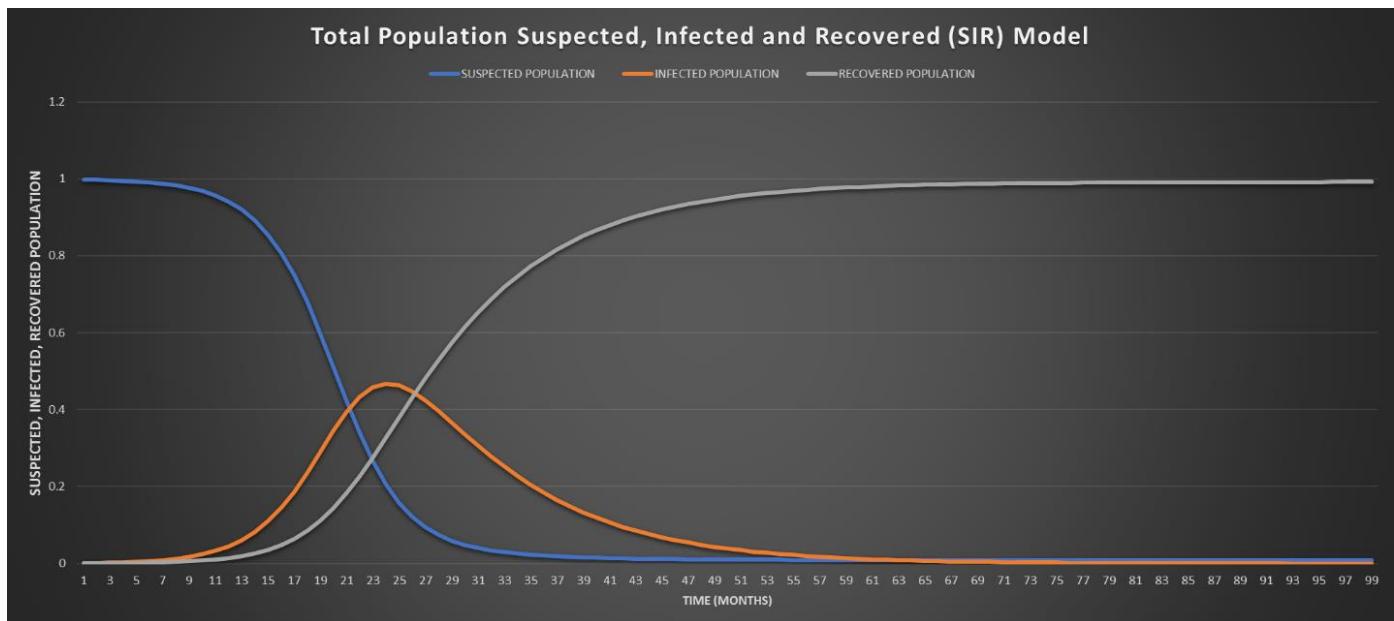


Figure 2. Analytical solution plot using Excel.

From the above graph we can see that the analytical and numerical methods give fairly the same results.

Using python, a simulation was performed using the original SIR model. The resulting graph has a similar shape than the numerical and analytical method.

SIR model simulation using python.

APPENDIX

Python Code

```
import matplotlib.pyplot as plt
from scipy.integrate import odeint
import numpy as np

N = 195843
S = N - 1
I = 1
R = 0
beta = 0.8 # infection rate
gamma = 0.1 # recovery rate

# differential equatinons
def diff(sir, t):
    # sir[0] - S, sir[1] - I, sir[2] - R
    dsdt = - (beta * sir[0] * sir[1])/N
    didt = (beta * sir[0] * sir[1])/N - gamma * sir[1]
    drdt = gamma * sir[1]
    print (dsdt + didt + drdt)
    dsirdt = [dsdt, didt, drdt]
    return dsirdt

# initial conditions
sir0 = (S, I, R)

# time points
t = np.linspace(0, 100)

# solve ODE
```

```

# the parameters are, the equations, initial conditions,
# and time steps (between 0 and 100)

sir = odeint(diff, sir0, t)

plt.plot(t, sir[:, 0], label='S(t)')
plt.plot(t, sir[:, 1], label='I(t)')
plt.plot(t, sir[:, 2], label='R(t)')

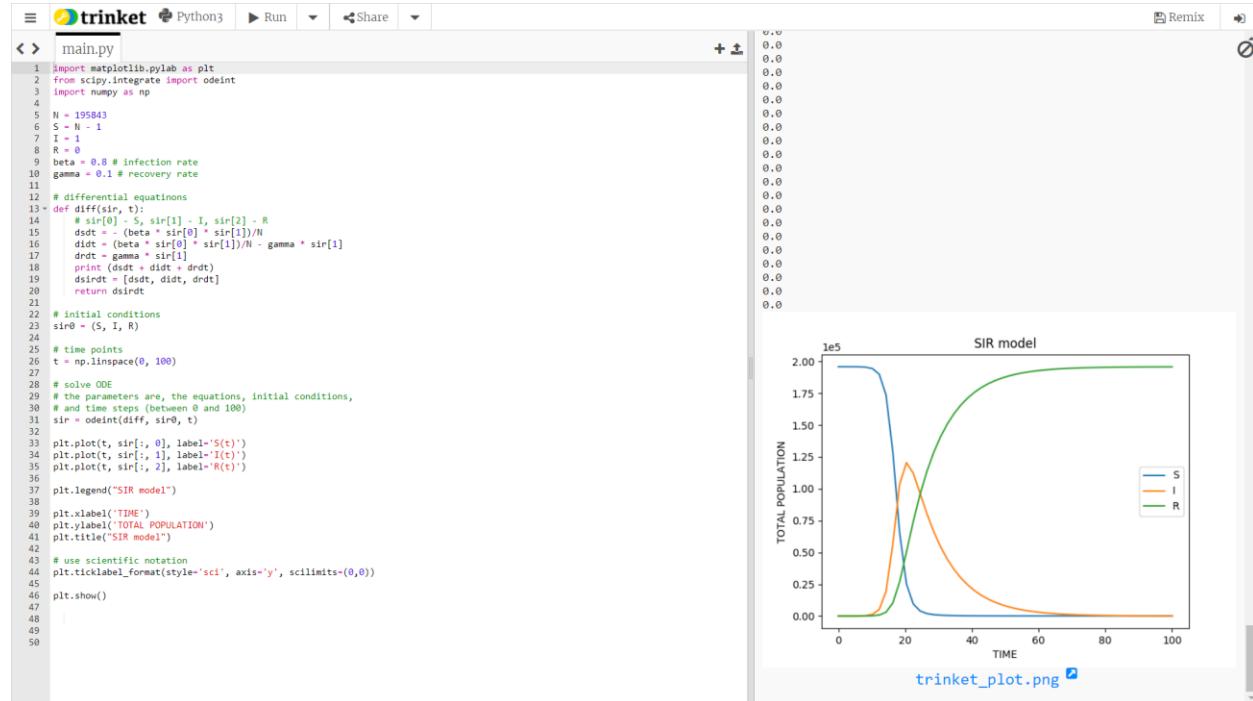
plt.legend("SIR model")

plt.xlabel('TIME')
plt.ylabel('TOTAL POPULATION')
plt.title("SIR model")

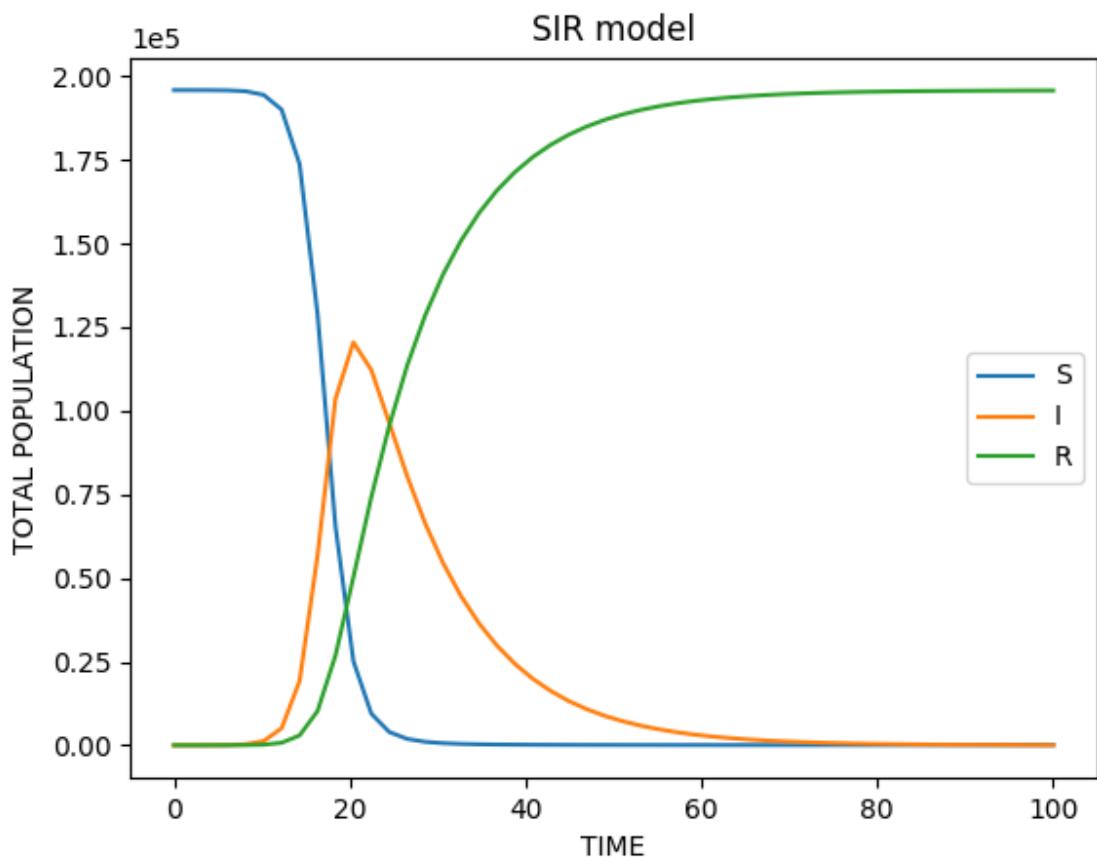
# use scientific notation
plt.ticklabel_format(style='sci', axis='y', scilimits=(0,0))

plt.show()

```



<https://trinket.io/python3/f2f27095cc>



SIR model simulation using python figure.

Conclusion:

As mentioned, the mathematical model for infectious diseases, SIR, is greatly important for epidemiologists to help understand the dynamics of an epidemic. The original SIR equation does not have an exact solution, many assumptions and simplifications need to be done. By comparing the numerical method and the analytical solutions, it can be seen that they are identical. Thus, it can be said that the two methods can be used to solve the equation. In addition, the use of computational analysis can help us in the analysis of the model with more ease.

References:

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5. compile used for running the python code: <https://trinket.io/>