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Term Paper

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*SIR processes Ref: (A Contribution to the Mathematical Theory of Epidemics. ,
Kermack, W. O. and McKendrick)*

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Overview

SIR Model is a mathematical model of a spread of a disease explained by Kermack and McKendrick that showed that a population of N people can be divided into three components as S (Susceptible), I (Infected) and R (Recovered) which may vary as a function of time t .

- $S(t)$ are those susceptible but not yet infected with the disease
- $I(t)$ is the number of infected individuals. These people at the time of their Infection has the capability of infecting others.
- $R(t)$ are those who have recovered from the disease or are removed from network as they die.

SIR Model uses two main parameters namely :

- β is defined as the chance of contact with an infected individual times the probability of disease transmission. It is seen as

$$\beta = c * b$$

where c is the average number of contacts between infected and susceptible individuals and b is the probability at which an infected person will be able to transmit the disease to a susceptible person when they come in contact.

- γ is defined as the recovery rate at which one recovers from the disease once infected. $\frac{1}{\gamma}$ is the mean period during which an infected individual can pass it on to another person.

In the paper they also ask the question, when does Termination Occur?

- Is it when there are no susceptible individuals left?
- Is it when Infectivity, Recovery, Mortality can affect while many susceptible people are still left. The virulence of causative organisms has decreased?

The equations that define the model are:

$$\begin{aligned}\dot{S} &= \frac{\beta SI}{N} \\ \dot{I} &= \frac{\beta SI}{N} - \gamma I \\ \dot{R} &= \gamma I\end{aligned}$$

The total number of individuals remain constant in the network.

$$S(t) + I(t) + R(t) = N$$

The equation can be simplified as follows:

$$\begin{aligned}\dot{S} &= -\beta S \dot{R} \frac{1}{\gamma} \\ S &= S_0 e^{-\frac{\beta}{\gamma} R} \\ \dot{R} &= \gamma(1 - R - S_0 e^{-\frac{\beta}{\gamma} R})\end{aligned}$$

(1) The integrated solution turns out to be:

$$t = \frac{1}{\gamma} \int_0^R \frac{dR}{1 - R - S_0 e^{-\frac{\beta}{\gamma} R}}$$

These equations can be simply integrated to see the SIR Model. Taking for example, $N = 1000$ and parameters $\beta = 0.2$ and $\gamma = 0.1$ and initial number of Infected individuals is 0. The subsequent plot is:

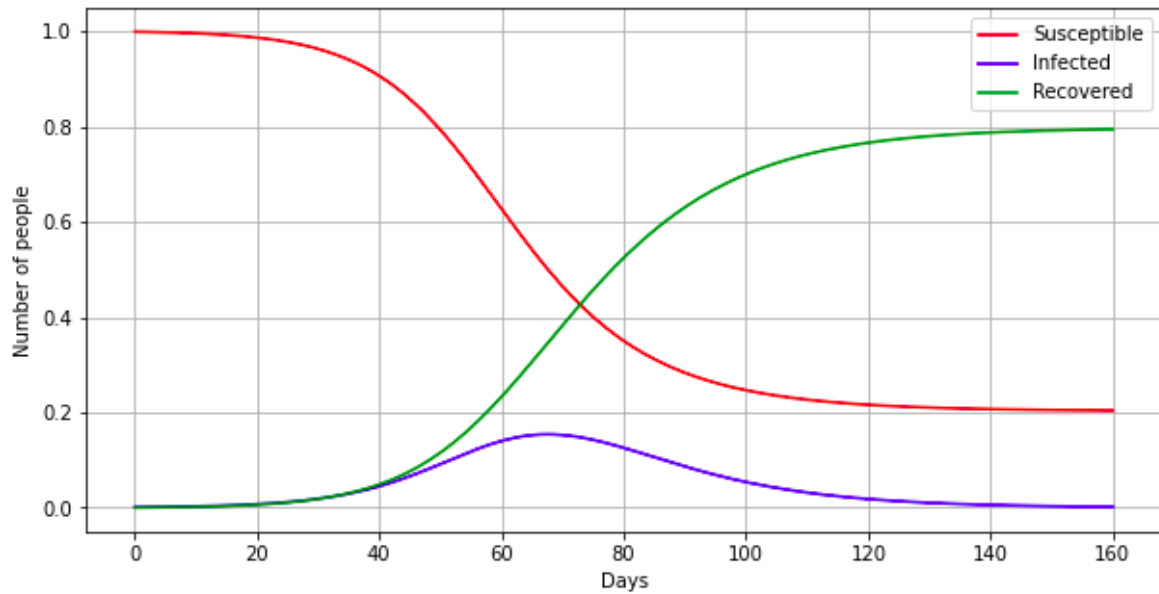


Figure 1: SIR Model

The Equation is simplified taking $t \rightarrow \infty$, the number of recovered people will come to a constant later. Therefore we have $\dot{R} = 0$.

$$1 - r_{\infty} = S_0 e^{-\frac{\beta}{\gamma} r_{\infty}}$$

$$R_{\infty} = 1 + e^{-R_0 r_{\infty}}$$

On differentiating it is seen that the critical value of R_0 is 1. R_0 is another important number in this model called the basic reproductive number. It indicates the average number of infected people by an infectious individual in a totally susceptible population. R_0 should be lesser than 1 for the epidemic to slow down. R_0 is got from the previous parameters:

$$R_0 = \frac{\beta}{\gamma}$$

The authors had taken the Bombay Plague Dataset to validate their Model. I have assumed here a Barabasi Model that follows a Power Law Node Distribution with 1000 individuals to see the results. The adjacency Matrix of the same has been generated to evaluate the ODEs and plot the S, I, R percentages of nodes over the time period. The model is as follows: The value of $\beta = 0.3$

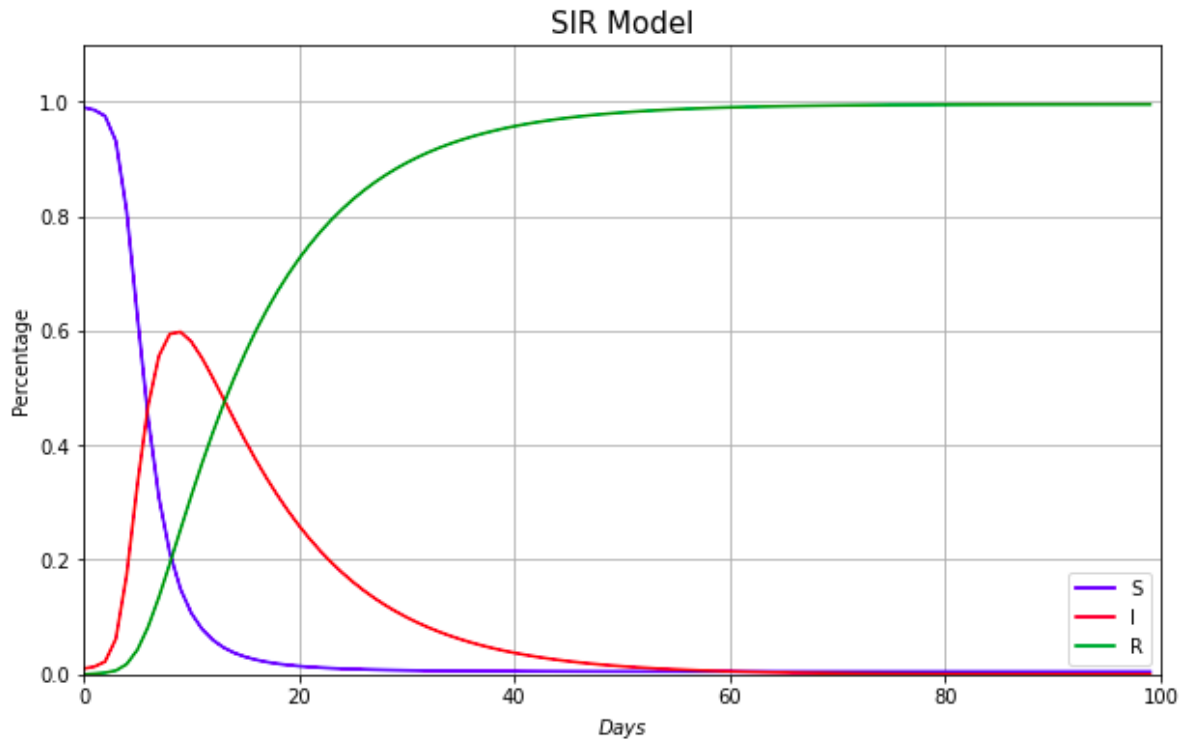


Figure 2: SIR Model for a Barabasi Node Distribution

and $\gamma = 0.2$ gives the above. However if R_0 is brought down below 1, the following is obtained with a $\beta = 0.1$ and $\gamma = 0.6$:

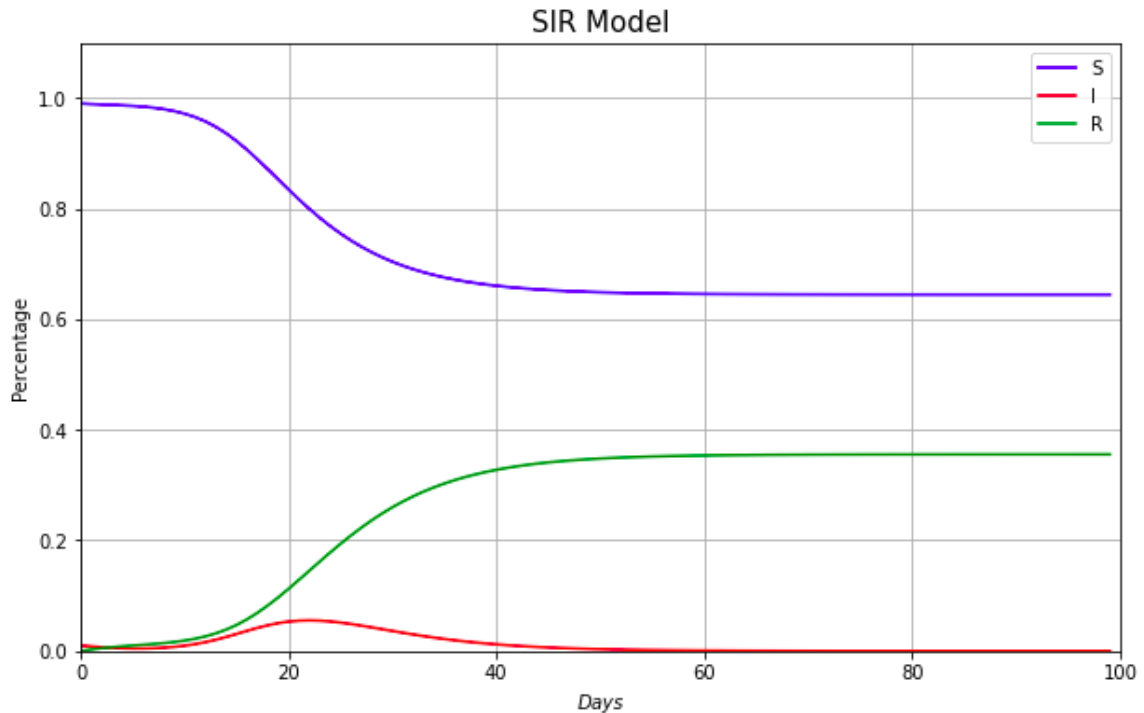


Figure 3: SIR Model for different R_0 value

The results from the Graph obtained are:

- The Susceptible members will only decrease and the Recovered members will only increase. The number of Infected people has to reach its peak before it can decrease and the epidemic dies.
- The value of R_0 is really important while checking for the termination of the epidemic.

Code

Solving the ODEs

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

def SIRmodel(y,t,N,beta,gamma):
    S, I, R = y
    Sdot = -beta * S * I/N
    Idot = beta * S * I/N - gamma * I
    Rdot = gamma * I
    return Sdot, Idot, Rdot

def SIR(N, IO , R0, beta , gamma):
    # N is the total population
```

```

# IO is the number of infected individuals
# R0 is the number of recovered individuals
# S0 is the initial number susceptible to infection
# beta is the contact rate
# gamma is the recovery rate

t = np.linspace(0,160,160) # Number of days
S0 = N - IO - R0
y0 = S0, IO, R0

sol = odeint(SIRmodel , y0, t, args =(N, beta, gamma))
S, I, R = sol.T
return S, I, R, t

def plotSIR(S, I, R, t):
    fig = plt.figure(figsize = ([10,5]))
    plt.plot(t, S/1000 , 'r', label = 'Susceptible')
    plt.plot(t, I/1000 , 'b', label = 'Infected')
    plt.plot(t, R/1000 , 'g', label = 'Recovered')

    plt.xlabel('Days')
    plt.ylabel('Number of people')
    plt.grid()
    plt.legend()
    plt.show()

S, I , R , t = SIR(1000, 1, 0 , 0.2, 1./10)

plotSIR(S, I , R, t)

```

With Barabasi Model

```

import numpy as np
import scipy as sp
import networkx as nx
import matplotlib.pyplot as plt
from numpy.linalg import eig
from scipy.integrate import odeint

n = 500
G = nx.barabasi_albert_graph(n, 3) # Follows a Power Law
A = np.array(nx.adjacency_matrix(G).todense()) # Adjacency Matrix
beta = 0.3
gamma = 0.2

t = np.arange(0,50,0.5)

# Initial state
idx = np.random.choice(range(n), 1)

```

```

i0 = np.zeros((n,))
i0[idx] = 5
z0 = np.concatenate((1-i0,i0,np.zeros((n,))))

# System of ODEs
def sir(z, t, A, n, beta, gamma):
    return np.concatenate((
        -beta * z[0:n] * A.dot(z[n:2*n]),
        beta * z[0:n] * A.dot(z[n:2*n]) - gamma * z[n:2*n],
        gamma * z[n:2*n]))

z = odeint(sir, z0, t, (A, n, beta, gamma))

S = np.average(z[:,0:n], axis =1)
I = np.average(z[:,n:2*n], axis = 1)
R = np.average(z[:,2*n:3*n], axis = 1)
plt.figure(figsize=[10,6])
plt.plot(S,color = 'blue', label = 'S')
plt.plot(I,color = 'red', label = 'I')
plt.plot(R,color = 'green', label = "R")
plt.xlabel('$ Days $')
plt.ylabel('Percentage')
plt.legend()
plt.grid()
plt.xlim(0,100)
plt.ylim(0,1.1)
plt.title('SIR Model', fontsize = 15)

```