

Mathematical Model for Coronavirus Using R Program

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ABSTRACT

An SIR model mutually exclusive compartment (susceptible – infected – removed) is presented to describe a reality. A mathematical model is developed to present dynamical behavior of corona virus using R program for the year 2022. Calculated a population data to analyze the spread of disease for the district Coimbatore. Formulation of the model is represented. Then graphical output is presented. Our finding shows that human to human contact is potential cause of outbreaks of corona virus. Therefore, isolating an infected human overall can reduce the most significant problem occur in the future.

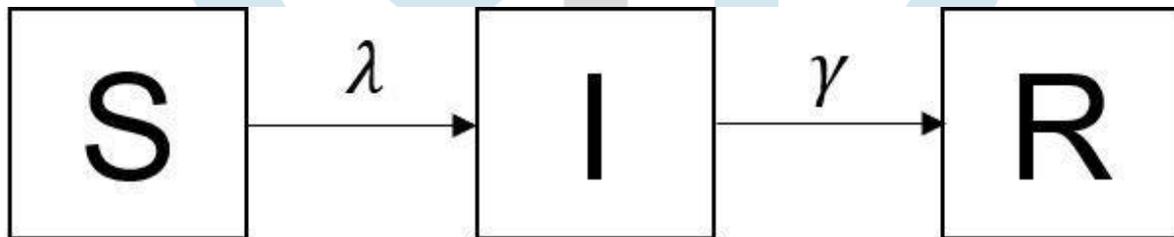
Keywords: Corona virus, SIR model, suspected individuals, infected individuals, removable individuals.

INTRODUCTION TO SIR MODEL

Mathematical models such as the **Susceptible, Infectious, and Recovered** (SIR) model are used to predict different scenarios related to epidemiologic factors and possible outcomes to assess epidemic spread. The SIR model configure the keystone for transmissible diseases modeling. This model is a compartmentalized model where the individuals belong to one of the three categories:

- Susceptible (S)
- Infected (I)
- Recovered (R)

It's a **population-based model** in the sense that each compartment models the behavior of an average individual in each compartment can be obtained. Even though, it's an oversimplification of the real-life scenario it is possible to build more complex models depending on this.



An SIR model is a contagious model which calculates the theoretical number of affected people with a communicable illness in a closed community in a certain time. The name of this class of models is derived from the fact that they involve coupled equations relating the count of susceptible people (S), count of people infected (I), and the count of people who have recovered (R). Kermack-McKendrick model is one of the simplest SIR models. Our SIR model is given by the simple system of three ordinary differential equations (ODEs). The classic SIR model can be used to gain a better understanding of the spreading of COVID-19 virus within communities of variable populations in time, including the possibility of surges in the susceptible populations. Thus, the SIR model here is depicted to remove many of the complexities associated with the real-time evolution of the spread of the virus, in a way that is useful both quantitatively and qualitatively. It is a dynamical system the time evolution of the following three populations is given by three coupled ODEs.

SUSCEPTIBLE INDIVIDUALS, S(T):

Susceptible individuals are those who are not infected, but susceptible individual may become infected or remain susceptible. The susceptible population will increase for a period of time (surge period) as the virus spreads from its source or new sources occur, more individuals will become infected.

INFECTED INDIVIDUALS, I(T):

These individuals are those who have already been infected by the virus and will transmit to susceptible individuals. An infected individual can be removed from the infected population to recover or die and may remain infected.

REMOVED INDIVIDUALS, R_m(T):

Those individuals who have been recovered from the virus are assumed to be immune, $R_m(t)$ or have died, $D(t)$.

As the time scale of the SIR model is short enough so that births and deaths can be neglected. The number of deaths from the virus is small compared with the living population. Depending on these assumptions and concepts, the rates of change of the three populations are governed by the following system of ODEs constitutes SIR model used in our study.

CLASSICAL MODEL OF DISEASE TRANSMISSION

The SIR model is a classical model of disease transmission within a population. It can be modified to account for several important population dynamics, such as death rate, immigration or birth rate, recovery, and immunity - but even the most basic model has powerful public health applications. The spreading of disease depends on population size; infection is instantaneous; at the beginning no one is resistant to the disease when immunity is gained, is permanent; and that the disease is non-infectious.

SIR MODEL WORKS

In SIR model all individuals in the population are placed into one of three classes at any given time: individuals susceptible to disease, infected individuals, and "removed" individuals. The removed class includes those individuals who are not infected and not susceptible.

Fundamental Equation relation of the SIR model is the following:

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

Where, N is the total population size, taken to be constant; S(t) is the size of the susceptible population; I(t) is the size of the infected population; R(t) is the size of the removed population.

The derivative of this equation articulates that, given a constant population size, the rates of change of the three sub-classes must cancel each other out.

$$\frac{ds}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0$$

LAW OF MASS ACTION

The SIR model assumes that individuals within the population follow the law of mass action, that is, they come into contact with one another randomly.

The likelihood at which an infected individual comes into contact with any other members of the population is described by the fixed parameter c. The likelihood that the disease is actually transmitted is described by the parameter a. By multiplying a and c, we can collapse these two constants into a single constant disease transmission rate r. It is important to note the separate components of r when it comes to disease spread. More generally the law of mass action assumes that the transmission of disease is based on the size of the population.

APPLICATION OF SIR MODEL

The reality is described by the simplest epidemiologic model composed by mutually exclusive compartments SIR (susceptible-infected-susceptible). The basic transmission model is analyzed, as well as simple tools that allow us to extract a great deal of information about possible solutions. A set of applications - traditional and new ones - is described to show the importance of this model best used in the medical field.

CORONAVIRUS USING R PROGRAM

COVID-19, **coronavirus disease (2019)**, is caused by a severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), which hit the globe with a bang. The first outbreak was noticed in Hubei province, Wuhan, China on December 2019.

The World Health Organization (WHO) revealed COVID-19 to be a public health emergency on 30 January, 2020 and identified it as a pandemic on 11 March, 2020. The symptoms of COVID-19 are not specific, it includes fatigue, muscle and joint pain, respiratory sputum production (phlegm), sore throat, loss of the sense of smell, headache or chills, and the shortness of breath. The majority of the cases have two common symptoms which include dry cough (68%) and fever (88%). But many cases showed that an infected person might be asymptomatic.

The growth of this infection will proceed to acute respiratory distress syndrome, severe pneumonia, and death.

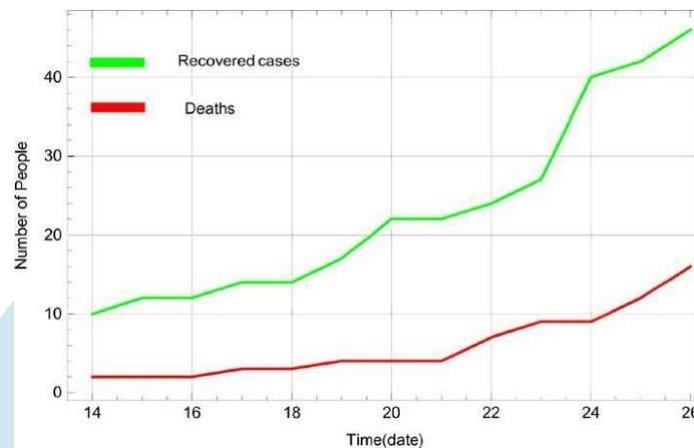
The COVID-19 virus spreads to large extent between people within approximately 2 m in close contact with each other. The common incubation period ranges from 1 to 14 days. The concealment of physical contact in working environments, schools and other open circles are the preventive measures.

Timeline And Data Analyses The first case of COVID-19 was announced in India on 30 January, 2020. The nation exposed its initial three cases in Kerala, all were students who had a travel history from Wuhan, China. The transmission escalated within March when many reported cases throughout the country were found to be connected to the people having travel history to the countries which were affected by COVID-19. On 11 March, 2020, the Indian government started to revoke all visas to India from 13 March, 2020 till 15 April, 2020. The first victim of disease in the country was a 76-year-old man who had returned from Saudi Arabia on 12 March, 2020. 100 cases were confirmed on 15 March, 2020, but this number increased to 1,000 on 28 March, 2020 and then 2,000 on 2 April, 2020. The Indian government has imposed high measures for a moderate outbreak. On 22 March, 2020 a day-long countrywide public curfew was observed in India. On 24 March, 2020 countrywide lockdown was announced by the Prime Minister of India, for 21 days.

14 MARCH, 2020 TILL 26 MARCH, 2020 ANALYSE The reported cases of SARS-CoV-2, from 14 March, 2020 till 26 March, 2020, was greater compared to initial period. We summarize the actual reported data in the country as shown in the following.

CONFIRMED CASES OF COVID-19 IN INDIA OF GRAPHICAL FORMAT

Figure:



R PROGRAMMING

R programming is a free software developed in 1993 by Ross Ihaka and Robert Gentleman. R owns a diligent schedule of machine learning algorithms, simple and linear regression, statistics, applied mathematics and graphical strategies. Most of the R libraries are written in R, except for serious machine tasks, C, C++.

Data analysis with R can be performed in the following order: programming, transforming, discovering, modeling, and communicating the results. Tutors are available for assistance with R programming homework or assignment.

USES OF R PROGRAMMING

Necessity of R language in real-world applications because of the following reasons:

- 1. Important for data science:** As R is an interpreted language, we can run code without any compiler which is essential in data science. Since R language is a vector language it is powerful and faster than another language. R is used in biology, genetics as well as in statistics.
- 2. Open-Source:** R language is an open-source language. There is no restriction in the usage of R because it is issued under the General Public License (GNU).
- 3. Popularity:** R programming language has become the most popular programming language in the technological world. With the emersion of data science, the requirement for R in industries has been increased.

Robust visualization library: Graphical plots to the users are provided by R language libraries like ggplot2, plot. R is mostly acknowledged for its astonishing visualizations which is very important in data science programming language.

- 4. Used to develop web apps:** R provides the ability to build web applications. Using the R package, we can create develop interactive applications using the console of your R IDE.
- 5. Platform independent:** R language can work on any system irrespective of whether it is Windows, Linux, and Mac because it is a platform-independent language.
- 6. Used in machine learning:** R programming helps to carry out machine learning operations like classification, regression and also provides features for artificial intelligence and neural networks.

SOME SPECIAL FEATURES OF R PROGRAMMING

Due to availability of large number of packages, there are many other adjustable features as well:

R doesn't require looping as it performs operations directly on vectors.

R can procure data from APIs, servers, SPSS files, and many other formats.

R is utilized for web harvesting.

R can perform various complicated arithmetical operations by a single command.

As R plays a vital role in research and statistical calculations, innovative ideas and technologies emerge in the R at first.

MODEL FORMULATION & ANALYSIS

In this project, R program is used to formalize and analyze the corona virus data of Coimbatore in 2022. Here comes the model

formulation for deriving a mathematical description of individual analyse in growth, survival and reproduction based on the environment conditions.

DATA ANALYSIS

DISTRICT : COIMBATORE
SOFTWARE : R STUDIO
DATA YEAR : 2022
TOTAL POPULATION 2935000

SIR MODEL CODING IN R PROGRAM

```
{
Io<-3 P<-
2935
gamma=0.5
alpha<-5/(Io*(2985-Io)) SIR<-
function(NUM,ch){ S<-
rep(NA,NUM)
I<-rep(NA,NUM) R<-
rep(NA,NUM) S[1]<-
P-Io
I[1]<-Io
R[1]<-Io*gamma
for(j in 1:NUM){
S[j+1]<-S[j]-alpha*S[j]*I[j]
I[j+1]<-I[j]+alpha*S[j]*I[j]-gamma*I[j]
R[j+1]<-R[j]+gamma*I[j]
}
if(ch=="s"){
return(S)}
else if(ch=="i"){
return(I)}
else{
return(R)}
}
}

S<-SIR(NUM=30,ch="s") I<-
SIR(NUM=30,ch="i") R<-
SIR(NUM=30,ch="r") X<-
c(0:30)
plot(X,S,type="l",col=1,main="Coimbatore - 2022",xlab="Days",ylab="No
subjects",sub="SIR Model",lwd=2,ylim=c(0,3000))

lines(X,I,type="l",col=2,lwd=4,)
lines(X,R,type="l",col=3,lwd=6)
legend("topright",col=c(1,2,3),border="darkblue",lty=c(1,1,1),bty="o",xjust=0,yjust=0.5,adj=
c(0,0.5),inset=0.001,legend=c("susceptible","infection","recovery"))
}
```

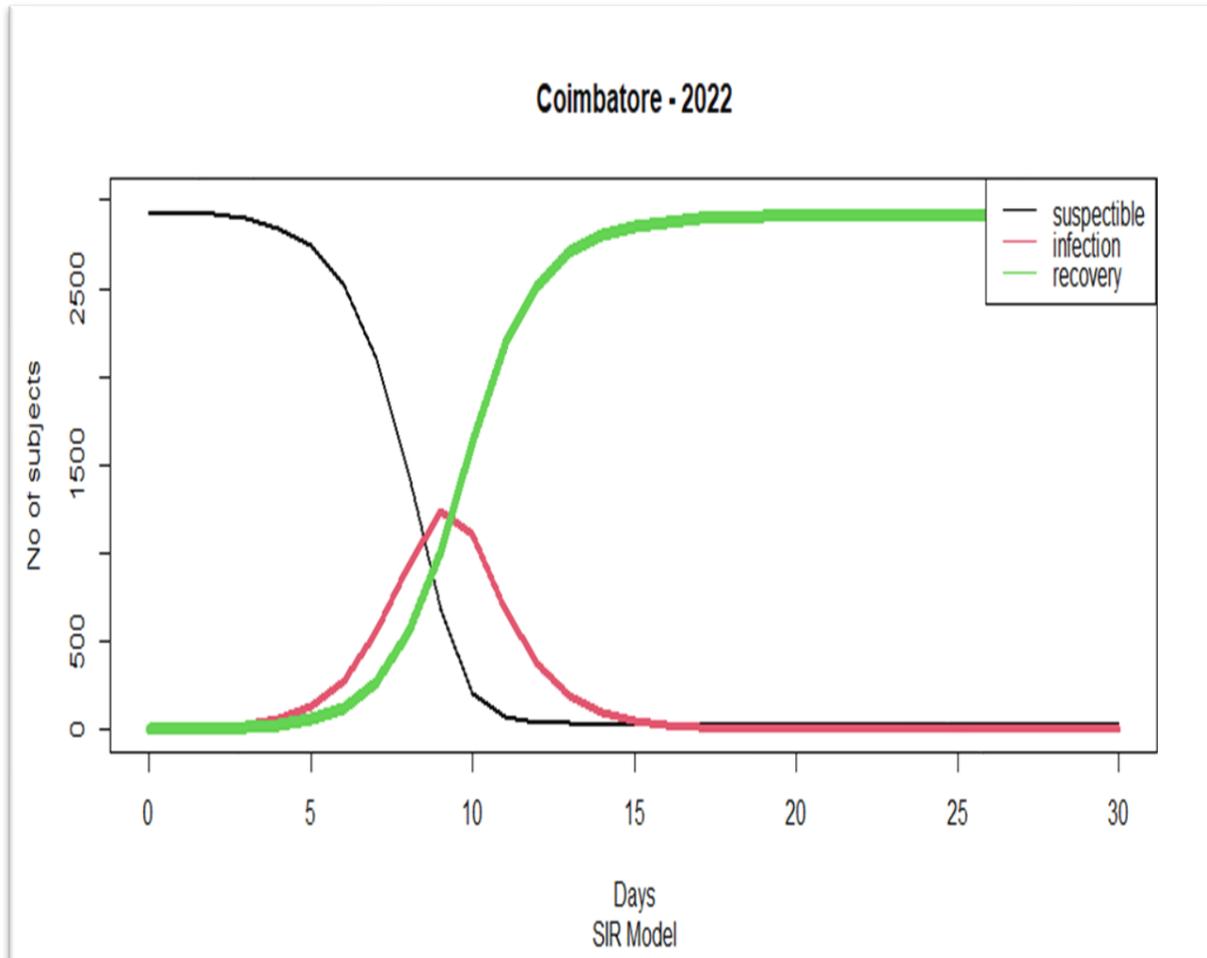
IN THIS CODING, VALUES ARE TAKEN AS:

| | |
|--------------|------------------------------|
| S | Suspectable population |
| I | Infection |
| R | Recovered |
| alpha | Rate of infection - 5 |
| gamma | Rate of Recovery – 0.5 |
| Io | Initial infected persons - 3 |
| P | population – 2935 units |

In this program, SIR model for Coimbatore data is calculated.

- First, I initialised the values for initial infected persons (**I₀**), Population(**P**), Rate of infection(**A**), Rate of Recovery(**g**).
- Second, **SIR** function is defined to calculate the Susceptable population(**S**), Infection(**I**), Recovered(**R**) for the given number of days.
- Finally visualizing the result in graph by plot, line, legend build-in functions of R.

OUTPUT



THE GRAPH SHOWS THE SIR MODEL FOR COIMBATORE DATA:

- where the **BLACK, PINK, GREEN LINE** represented the *Susceptable population(S)*, *Infection(I)*, *Recovered(R)* respectively.
- From graph we can understand that the infection rate of Coimbatore will increase to its peak in 5 to 15, after that we have a smaller number of infections.
- The Recovery rate of Coimbatore will increase gradually and attain its peak after 10 days. Here after it is stable.
- Overall, the graph shows the positive result, the corona cases may be higher from 5 to 15 days where we have to be more consciously follow the government instruction to reduce the infection.
- Since the recovery rate is also increasing gradually from day 5, we have more possibility of recovery even if we get infected. After 15 days we have less infection and high recovery rate.

CONCLUSION

In this project, we provided that the spread of covid19 (corona virus) can be reduced by the isolation of overall infected persons. Our model shows that the coronavirus spread in Coimbatore district of Tamil Nadu, through contact and describes how fast something changes by counting number of people who are infected and likelihood of new infection. Here R programme is used to compute the SIR model, which calculate the spread of Covid19 virus and provided the graphical visualization of it. It showed the impact of interaction of infected people to susceptible population and proved graphically and analytically that if we control this contact rate, the control of the current disease is possible, otherwise. State government have different restriction for every district in places for public gathering. Therefore, citizens need to follow the direction from time to time, to minimize the health

risk.

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