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Simulation of SIR Deterministic Epidemic Model in Infectious Disease Prediction using R Programming

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Abstract— Mathematical models and the statistical models are at present the fundamental elements in planning control and mitigation measures against any future epidemic of an infectious disease. These models allow us to decide from current information about the state and progress of an outbreak, to predict the future, and, most importantly, to quantify the uncertainty in these predictions. In this research paper, we consider a deterministic Susceptible-Infected-Recovered (SIR) epidemic model to disclose a simulation method, and a mathematical model was implemented in the R software environment that allows simulating the spread of infectious disease. Through the aid of the SIR model, data on a wide range of infectious diseases have been analyzed. SIR stands for Susceptible, Infected, and Recovered and indicates the three possible states of the members of the population affected by a contagious disease. SIR model is one of the most effective models which can predict the spreading rate of the virus. We have validated the SIR model with the current spreading rate. The findings of the SIR model can be used to forecast transmission and avoid the disease outbreak. The graphical interface shown in this paper is performed using the R software version 3.4.4.

Keywords— Epidemiology, R Programming, Deterministic SIR

INTRODUCTION

Epidemic infectious diseases may be considered as the effect of disasters of another type such as tropical cyclones, floods, earthquakes, and droughts [1]. Infectious diseases are caused by pathogenic microorganisms such as bacteria, viruses, parasites, or fungi [5]. The diseases can be spread directly or indirectly from one person to another. Microorganisms capable of causing disease or pathogens usually enter our human bodies through the eyes, mouth, nose, or urogenital openings or through wounds, bites that breach the skin barrier [7]. Therefore, the threat of emerging and re- emerging infectious diseases to global population health

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remains significantly enormous and the pandemic and epidemic preparedness capabilities are necessary to confront such threats must be of greater potency.

There are two types of epidemic models: stochastic and deterministic [3]. The word stochastic means “having a random variable”. Stochastic models generally depend on the chance variations in risk exposure, disease and other illness dynamics. On the other hand, while dealing with large populations as in the case of COVID-19 like infectious diseases, deterministic model can be used. It is otherwise also called as “compartmental” mathematical model [2]. The transition rates from one class to another class are mathematically expressed as derivatives; and therefore the model is formulated using differential equations. When building such models, it must be assumed that the population size in a compartment is differentiable with respect time and that the epidemic process is deterministic [4].

There are many basic deterministic models available. They are SIS model, SIR model and SIRS model [16]. If the individual recovers with permanent immunity, then SIR model is appropriate. And, if individuals recover with temporary immunity so that they sooner or later become susceptible again, then SIRS model is appropriate. Similarly, if the recovery does not give immunity to the individuals, then SIS model would be appropriate. SIS model can be applicable for some epidemic bacterial diseases like Chikungunya, Cholera, Ebola virus, Hendra virus, Corona virus, Influenza, Marburg and many more.

Thus, the SIR model aims to predict the number of individuals who are susceptible to infection, are actively infected or have recovered from infection at any given time. In the deterministic epidemic model, various subgroups or compartments are allocated to individuals in the population and these compartments are specified concerning the epidemic's disease status. We have considered an epidemic model in this proposed study which was developed in 1927 by Kermack and McKendrick. This epidemic model is also known as the epidemic model SIR (Susceptible, Infective, and Recover / Removed) [17].

The number of confirmed cases varies from country to country because of variations in epidemiological monitoring and detection capacities. This can however be said that as of today the disease has spread across the world. Since there is no method of treatment for this form of the virus yet known, it requires careful preparation of the health system and facilities where the risk of spread of disease can be managed. For this purpose, it is important to predict the total reported cases and potential new cases in the future to handle and guide demand to the health system.

To cope with the outbreak, mathematical and statistical modelling methods that can be used to make short and long- term case predictions are required to schedule the number of additional materials and resources. Estimating the projected burden of disease is important for public health authorities to coordinate medical services and other resources that are required to resolve the epidemic efficiently and in time. These estimates can also guide the strength and form of interventions needed to ease the outbreak. For this analysis, we presumed from the time of spread to India the impact of social distancing interventions, lockdown, and face cover.

Many infectious outbreaks such as avian influenza, cholera, SARS, Aids, Plague, Yellow Fever, Meningitis, MERS, influenza, Zika, Rift Valley Fever, Lassa fever, Leptospirosis have also been widely used in this model. The SIR model is very useful for future prediction,

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ending, and the peak of infectious disease and other outbreak-related activity.

The simplest model, which was described by Kermack and McKendrick in 1927, consists of three compartments: susceptible (S), infected (I), and recovered (R).

Susceptible (S):-People who have never had the disease and can catch it.

Infected (I):-People that are infectious and have the disease.

Recovered (R):-People that still have the disease and are resistant to it.

So, the total population (N) = (S) + (I) +(R).

The SIR model is easily written using ordinary differential equations (ODEs), which imply a deterministic model with continuous time. In this paper, we consider a SIR epidemic model with non-monotonic incidence rate proposed by [4] with the initial conditions: $S(0) = S_0$, $I(t) = I_0$ and $R(0) = R_0$.

The deterministic SIR model is simulated in R programming environment. R is a programming language and open source software. It possesses an extensive catalogue of statistical and graphical methods. That is, R allows the students and research scholars to practice a wide variety of statistical and graphical techniques like linear and non-linear modelling, time-series analysis, classification, classical statistical tests, clustering and many more. Moreover, it is a highly extensible and easy to learn language and fosters an environment for statistical computing and graphics.

R software provides exemplary support for data wrangling. It has a vast array of packages with over 10,000 packages in CRAN repository and since it is open source, the number is constantly growing. It is highly compatible and can also be paired with many other programming environments like C, C++, Java, and Python. It can also be integrated with many other technologies like Hadoop and various popular database management systems. Since, it is a cross-platform programming language (platform-independent), it can be executed easily on Windows, Linux and Mac operating systems.

Using R packages like Shiny and Markdown, statistical analysis report can be easily done. Furthermore, R also provides various facilities for carrying out machine learning operations like classification, regression and also provides packages support for developing artificial neural networks. Consequently, R software programming environment is prominently known as the popular language for statistical researchers (lingua franca of statistics) [17].

I. METHODOLOGY OF SIR EPIDEMIC MODEL

We have considered an epidemic model in this proposed study which was developed in 1927 by Kermack and McKendrick. This epidemic model is also known as the epidemic model SIR (Susceptible, Infective, and Recover / Removed). Many infectious outbreaks such as avian influenza, cholera, SARS, Aids, Plague, Yellow Fever, Meningitis, MERS, influenza, Zika, Rift Valley Fever, Lassa Fever, Leptospirosis have also been widely used in this model [6].

The SIR model is very useful for future prediction, ending, and the peak of infectious

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disease and other outbreak-related activity. Unlike most diseases, this model does not recognize infectious disease growth. In comparison, however, my proposed SIR model seen in Figure 2 takes into account the nature of the infectious disease outbreak.

This model also predicts high growth in India from the infectious disease outbreak. This model also predicts maximum growth in India from the epidemic outbreak. Figure 2 highlights the definition of the SIR model for recovered re- tuning as susceptible since an epidemic outbreak has developed into one that can re-infect.

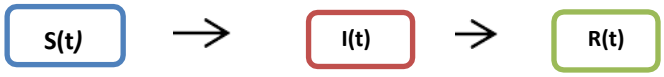

Figure 1: Description of the SIR model not considering the epidemic outbreak virus evolution

Figure 2: Description of the SIR model considering the epidemic outbreak virus evolution.

Let's find the following three differential equations being used for disease outbreak experimental studies and experimental debate. The definition is given below for these three differential equations:

$S'(t) = -\beta SI$ (1)
$I'(t) = \beta SI - \gamma I$ (2)
$R'(t) = \gamma I$ (3)

The parameters β and γ of the above differential equations are known as infection rate and recovery/removal rate. These numerical β and γ values are very useful in the initial stage for resolving the three differential outbreak equations.

The three differential equations (1), (2), and (3) of the proposed epidemic SIR model for epidemic outbreak can also be written as :

$\frac{dS}{dt} = -\beta SI$ (4)
$\frac{dI}{dt} = \beta SI - \gamma I$ (5)
$\frac{dR}{dt} = \gamma I$ (6)

The parameters β and γ of the above differential equations are known as the infection rate recovery / removal rate. These numerical β and γ values are very useful in the initial stage for resolving the three differential outbreak equations.

$$\frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = -\beta SI + \beta SI - \gamma I + \gamma I = 0$$

$$dS + dI + dR = 0 \quad (7)$$

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Using the integration of equation number (7), we can get the following relationship for estimating the total infected population:

S' + I' + R' = N, regarded as the convergence constant comparing the overall population size for infection disease at the original level and after the epidemic. It is a constant

$$S(t) + I(t) + R(t) = N \quad (8)$$

We will take the following initial values of the proposed SIR model, i.e., for the experimental reason for data analysis of the epidemic outbreak.

$S(0) = S_0$, $I(t) = I_0$, and $R(0) = R_0$

Here the size of the infected population is constant. We can quantify the recovered infection disease outbreak population, which is given by the following formulation:

$$R(t) = N - (S(t) + I(t)) \quad (9)$$

The three differential equations (4), (5), and (6) above the proposed SIR model can be translated into the number of differential equations (9). Such two differential equations are very difficult to solve and time-intensive. But of these two differential equations, the solution is very important for data analysis of an epidemic outbreak. We have used a quantitative approach in this proposed study to solve these two differential equations of the model SIR.

THE SIR MODEL AS FUNCTION IN R PROGRAMING

When the treatment rate is proportional to the infective so that $0\ 0 < I \leq I$, choose the parameters in the model as follows:
$\beta = 1.4247$, $\gamma = 0.14286 = 0.2$ .The basic reproduction number on above parameters is R = 0.0, I = 1e-6, S = 1-1e-6

```
## Load deSolve package library (deSolve)

## Create an SIR function
sir <- function(time, state, parameters) { with(as.list(c(state,
 parameters)), {
   dS <- -beta * S * I
   dI <- beta * S * I - gamma * I dR <-  gamma  *  I
   return(list(c(dS, dI, dR)))
  })
}

### Set parameters
## Proportion in each compartment: Susceptible 0.999999,
Infected 0.000001, Recovered 0
   init  <- c(S = 1-1e-6, I = 1e-6, R = 0.0)
```

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```
## beta: infection parameter; gamma: recovery parameter parameters <- c(beta = 1.4247, gamma = 0.14286)

## Time frame
times    <- seq(0, 70, by = 1)

## Solve using ode (General Solver for Ordinary Differential Equations)
out <- ode(y = init, times = times, func = sir, parms = parameters)

## change to data frame out <- as.data.frame(out)

## Delete time variable out$time <- NULL

## Show data head(out, 10)

## Plot
matplot(x = times, y = out, type = "l",
     xlab = "Time", ylab = "Susceptible and Recovered", main = "SIR Model",
     lwd = 1, lty = 1, bty = "l", col = 2:4)

## Add legend
legend(40, 0.7, c("Susceptible", "Infected", "Recovered"), pch = 1, col = 2:4, bty = "n")
```

Which yield Figure.3.

RESULTS AND DISCUSSION

Figure 3 displays the SIR model for the disease condition. This proposed research is highly useful for disease outbreak prediction in the future. The new SIR model would accurately predict the number of weekly, bimonthly, monthly, and even year events. Specifically, when this model is simulated in R software, it computes the theoretical number of people infected with a contagious illness in a closed population over time.

Therefore, we might assume that for next week or in the future, the Indian government and doctors should hold a watch on hospital services, the requisite medicines for new patients, medical aid, and isolation.

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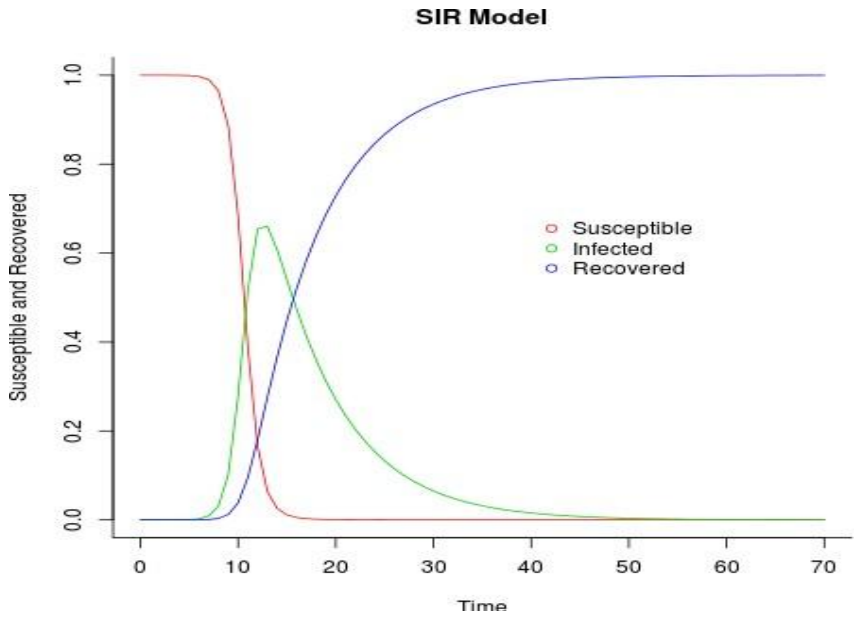

Figure 3 SIR Model Simulation

CONCLUSION

This R programming allows simulating and analyzing the dispersion of a SIR epidemic disease model with different parameters. It is valid for teaching in a simple, affordable, and practical way.

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