



THE MATHEMATICAL MODEL OF CONTAGIOUS DISEASE

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Abstract

Mathematical modelling of contagious disease outbreaks is discussed with the help of the SIR (susceptible, infected and recovered) model of the epidemic. In the analysis, governing equations of the SIR model are solved by a numerical technique called Euler's method and physical interpretations are exhibited through tables and graphs. It is found that a disease outbreak is sudden and infection reached its peak in 13 days and consequence 78 percent of the total population is infected with the disease. This mathematical modelling is useful for predicting the disease outbreak caused by contagious diseases such as SARS, Zika, Flu, Covid-19, and monkeypox etc.

Keywords: SIR model, Euler method, Infectious disease, SARS-Cov-2, Epidemic.

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Introduction

The analysis of infectious diseases, their prevention and the remedial solution is a serious concern for medical science for the last century. It is also the fact that transmissible diseases (such as plague, influenza etc.) are one of the reasons for the destruction of many old civilizations [1,2]. There are several infectious diseases which affected individuals, but it is worth mentioning that the first pandemic of the 20th century is called the Spanish flu. It spread due to the H1N1 influenza virus from Spain during the first world war[3,4], In this pandemic, around 50 million people died and almost 500 million population got infected worldwide. This happened due to insufficient medical facilities and a lack of awareness about the disease. Later, during 1957-1958 the influenza epidemic happened. It is also known as Asian flu (H2N2 influenza virus). It originated in China in 1957. Subsequently, it spread rapidly in Europe and Asia. However, it appeared sporadically in Britain. Ultimately it was gone by November 1958. But during this short period, it affected around 12 million people. Further, almost sixteen thousand people died [5].

From the analysis of various epidemic reports of the early 13th and 14th centuries, it is noticed that the epidemic outbreak used to occur at intervals of every 25 years. This pattern of the epidemic continued till 1940. Most of the epidemics occurred only due to the influenza virus. In the series of epidemics, a new epidemic due to the influenza virus H3N2 occurred in 1968. It was known as the Hongkong flu. The first case of this flu was noticed in China, and later it covered Singapore, Hongkong, Australia, the United Kingdom, the United States of America, and Europe. Thus, it was considered a serious pandemic at that time. It caused around one million deaths worldwide [6]. The Hong Kong flu was known as the first severe pandemic of the modern age. Due to this pandemic, a systematic vaccination programme was initiated across the countries. It was the time when public health care schemes were introduced globally to overcome new disease outbreaks.

After the Hong Kong flu pandemic, new disease outbreaks such as HIV (1981), SARS (2002), Swine flu (2009), MERS (2012), Ebola (2014) and Covid-19 (2019) occurred. The SARS-Cov-2 (Severe Acute Respiratory Syndrome) or Covid-19 first occurred in 2019 in the Hubei province of China. Later it spread to other countries. In January 2020, it was declared a medical emergency globally. This particularly severe pandemic led to 538,321,874 confirmed cases with 6,320,599

deaths globally till 20 June 2022. The Covid-19 pandemic has challenged the medical facilities and healthcare systems in the world which were developed in the last three decades [7,8]. The severity of attack has deeply shaken the global population. Therefore, huge attempts are globally on a model such as epidemics. This is where the primary scope of the present work evolves.

In fact, the relevant literature describes the various mathematical models of infectious diseases [9–12]. These models are used to investigate and understand the biological and physical phenomenon of the disease. In 1766, Swiss mathematician and physicist Daniel Bernoulli discussed the first mathematical model for infectious disease [10,11]. Following his remarkable work in the epidemiology field, several advanced, new techniques and mathematical models were developed for dealing with different transmissible diseases to save the life of people. Although diverse mathematical models of infectious disease are used, but SIR (susceptible, infected, recovered) model is the fundamental mathematical model of epidemiology, which explain the characteristics of disease outbreak patterns. It is perceived that the SIR model is useful for the analysis of Avian Influenza, SARS, Cholera, Plague, Ebola, Yellow Fever, MERS Influenza, Zika, Leptospirosis and Covid-19 [14–20] etc.

In view of the disease outbreaks of the last few years, we are motivated to discuss the SIR mathematical model for these kinds of contagious diseases. Since the SIR model is valid for real and hypothetical data, therefore dynamics of transmissible disease are explained for the small size of the population, for instance, a small town or a village. The set of equations that describe the SIR model is derived and solved with the help of numerical technique (Euler's method)/ Thereafter, for the susceptible, infected and recovered/removed populations physical interpretation are explained through tables and figures. Thus, the SIR model is the traditional and simplest model in the epidemiology field, which is used for the study of transmittable diseases such as Avian Influenza, SARS, Cholera, Plague, Ebola, Yellow Fever, MERS Influenza, Zika, Leptospirosis, COVID-19, Monkey Pox and other related infectious diseases etc. [18,19,20]

This SIR mathematical modelling is also useful in forecasting the disease outbreak for the large-scale population such as states and countries. Therefore, it may help the authorities to frame the guidelines and protocols (such as social distancing, lockdown,

vaccination time intervals etc.). In addition, the choice of hypothetical data/population size gives us the freedom to discuss the pattern of disease outbreak, choice of infection rate, recovery rate etc. Further, it also helps us to identify the physical condition and parameters that may decrease or control the disease outbreak. Furthermore, due to its simplicity, the SIR epidemic model is easy to use for any contagious disease. Moreover, it does not require any expensive computational software package. It seems plausible to argue that the modelling of the contagious disease may also help us to analyze and predict the disease outbreak pattern of a new unknown disease. In such a scenario, it becomes often very helpful for advancement in public health care policies, and other related sectors.

Therefore, the major objective of the current work is to develop the mathematical model of severe contagious diseases e.g., Covid-19. The present study is divided into five sections. Section 1 highlights the disease outbreaks that occurred in the last few years. Section 2 presents the SIR Model of contagious disease outbreaks based on the patterns as outlined in Section 1. Section 3 elaborates the

numerical solution of the SIR model for the desired population size. Section 4 presents the results and discussion. Finally, section 5 summarizes the concluding remarks of the present work.

Mathematical Modelling of Contagious Disease

The SIR mathematical model predicts the nature of an epidemic caused by an infectious disease. It also helps us to identify the infection rate i.e., how slow/fast the disease spread in the healthy population, the peak time of disease spread, epidemic control and estimation of the total number of deaths, infected population, recovered population, social distancing and vaccination interval (single, double and booster dose) etc. [21]. In SIR mathematical model, the whole population (N) is divided into three categories such as S, I, and R. Here, S represents the susceptible population (healthy people, who may get infected easily). Next, I represents the infected population (the susceptible population, who have been infected with the disease and converted to the infected population). Finally, R represents the removed population (population, who have recovered or died due to disease).

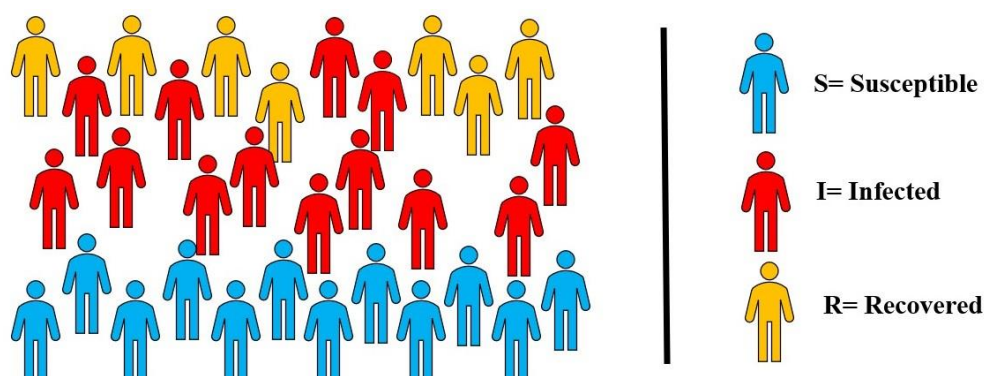


Fig. 01: Schematic view of the SIR Model

In the SIR model, a set of mathematical equations (ordinary differential equations) are solved with the help of analytical methods (direct or homotopy perturbation method, perturbation etc.) as well as numerical methods (Euler's method, Runge Kutta Method etc.), and due to this reason, high computational software or tools are not required. In this mathematical model, it is assumed that the susceptible population will decrease with time,

because the susceptible population is the healthy population, and as they come in contact with the infected population, the total number of susceptible people will reduce and the infected population will increase, and later infected population will recover or die, and this process keeps repeating until the disease dies out. The flow chart of the statement is given as:

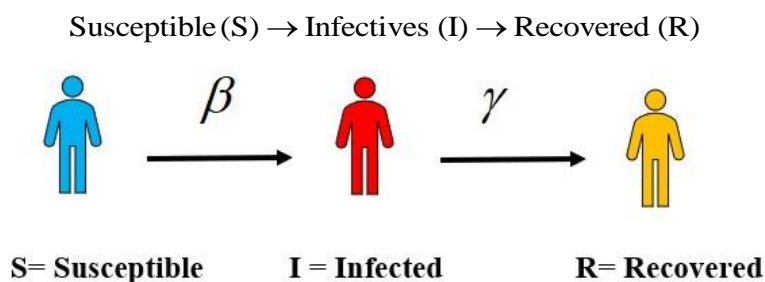


Fig. 02: Schematic view of population distribution

As mentioned earlier, here, S, I and R represent the total number of susceptible, infected and recovered people from infectious diseases. In this processing, the total population is N, which is considered constant and fixed, i.e., no birth or death is considered during the time of disease prediction, and the sum of the total population is given as:

$$N = \text{Susceptible } S(t) + \text{Infectives } I(t) + \text{Recovered } R(t)$$

For instance, N=1.393 billion (2021) of India's population. For the mathematical calculation of COVID-19 spread in India, we have total 5 inputs, susceptible S(t), Infected I(t), Recovered R(t) population, infection constant β and recovery constant γ at time t (t=0), and we are to predict the pattern of the epidemic at the particular time frame such as at t=0 to t=90 days. Here, t=0 means the first day of study.

The set of equations that describe the SIR model [21,22] are ordinary differential equations of the first order and first degree and are given as:

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

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

$$\frac{dR}{dt} = \gamma I(t) \quad (3)$$

from the above relation, we have

$$1 = \frac{S(t)}{N} + \frac{I(t)}{N} + \frac{R(t)}{N} \Rightarrow 1 = S(t) + I(t) + R(t)$$

Here, equation (1) is referred to the rate of change of the susceptible population over time, and it explains how the susceptible population will change with time. The total number of (S) susceptible people (healthy people) decreases and convert into the infected population (I). Similarly, one can predict the infected population, and how the infected population varies with time. It is a fact that the susceptible population converts into an infected one and therefore infected population keeps increasing and the susceptible population keep decreasing unless effective disease control parameters or protocols are not considered.

It is also assumed that the infected population will be recovered or may have died over time, and therefore the rate of change of the infected population is given by equation (2). After time t, the infected person either recovered, got immunity or in severe cases may have died. Thus, the mathematical expression of the rate of change of recovery with time is given by equation (3). The concept of the SIR model is in vogue, due to its simplicity.

On the right-hand side of equations (1) to (3), we have two variables/constants β and γ . The numerical value of β ($\beta > 0$) stands for the infection or contact rate of the susceptible population with the infected population. Further, γ represents the recovery rate of infections, and its numerical value is $\gamma > 0$. Physically, it explains how infected people are died or recovered. The incubation period λ ($\gamma = 1/\lambda$) is also an important factor in the epidemiology field that reveals the symptoms of the diseases in an individual or group of people [23].

Incubation periods may vary and depends on the type of viruses, such as for flu it is very short i.e., 1 to 4 days as confirmed by the CDC (Centers for Disease Controls and Prevention), whereas the incubation periods for Mononucleosis (Mononucleosis is also popular as kissing diseases, which spreads through saliva during sharing the same glass of drink, food utensils, and often possible due to kissing a partner who is suffering from Epstein-Barr virus) ranges from 4 to 6 weeks, and similarly incubation periods is 60 to 150 days for hepatitis B case. The incubation period of the severe acute respiratory syndrome (SARS) caused by a novel coronavirus in Asia Pacific regions (8000 cases were reported) was reported to be around 6.4 days [24] from 2002-to 2003, while it was around 14 days in COVID-19 (SARS-CoV-2) pandemic time as confirmed by govt officials and WHO.

In the mathematical modelling of infectious diseases, there are some other parameters together with incubation period λ , infections rate β , and recovery rate γ , which are needed to be discussed for the well understanding, prevention and control of the disease. A basic reproduction number \mathfrak{R}_0 ($\mathfrak{R}_0 = \beta/\gamma$) is a dimensionless number which is used in the biomedical and epidemiology field [23,25]. The numerical strength \mathfrak{R}_0 explains the new case

of the disease appearance i.e., how a healthy person may get infected when he/she comes in contact with an infected person, and it will be easy to say that a higher value of \mathfrak{R}_0 ($\mathfrak{R}_0 > 1$) will spread the disease repeatedly[23] and it reduces when \mathfrak{R}_0 ($\mathfrak{R}_0 < 1$) is small. The value of \mathfrak{R}_0 only depends on the parameters; β and γ , and detailed analysis is given in Table1 [26].

Table 1 Threshold number/ Basic Reproduction Number and Epidemic conditions

Epidemic/Pandemic outbreak condition	Epidemic/Pandemic outbreak die-out condition
Increment in infected population over time $\frac{dI}{dt} > 0 \Rightarrow \beta I(t)S(t) - \gamma I(t) > 0$ $\Rightarrow \beta S(t) > \gamma$ $\Rightarrow \frac{\beta S(t)}{\gamma} > 1 \Rightarrow \frac{\beta S(t)}{\gamma N} > 1$ initial $t = 0, N(0) \cong S(0) \Rightarrow N \cong S$ $\Rightarrow \mathfrak{R}_0 > 1$,	Decrement in infected population over time $\frac{dI}{dt} < 0 \Rightarrow \beta I(t)S(t) - \gamma I(t) < 0$ $\Rightarrow \beta S(t) < \gamma$ $\Rightarrow \frac{\beta S(t)}{\gamma} < 1 \Rightarrow \frac{\beta S(t)}{\gamma N} < 1$ initial $t = 0, N(0) \cong S(0) \Rightarrow N \cong S$ $\Rightarrow \mathfrak{R}_0 < 1$

\mathfrak{R}_0 can minimize with the appropriate change in recovery or infection rate. The recovery rate γ increases when the Standard Operating Procedures (SOP's) of disease control (COVID-19) like social distancing, compulsory use of face mask in public places, complete or partial lockdown, shutdown of schools and universities, restriction of gathering in marriage and other public events are considered until the complete vaccinations and herd immunity are not achieved at large scale of the population [22,23].

Mathematical Solution for SIR Model

For the numerical study of contagious diseases, the SIR model is considered which is valid for real data (I.e., the data retrieved from WHO and other official sites) and hypothetical data. In the present scenario, the hypothetical data is considered that give us the freedom to analyze the disease spread pattern, choice of selecting infection rate, recovery rate and basic reproduction number etc. The hypothetical study of contagious disease helps us to identify the physical conditions and parameters that may help to decrease or control the disease. In the SIR model of contagious disease, we generally deal with infection rate β , recovery rate γ and basic reproduction number \mathfrak{R}_0 , and their mathematical expression is given as:

- Infection rate (β) = $\frac{\text{Infected population}}{\text{Susceptible population}} \times K$.

- Recovery rate (γ) = $\frac{1}{\lambda}$.
- Basic reproduction number (\mathfrak{R}_0) = $\frac{\text{Infection rate}}{\text{Recovery rate}} = \frac{\beta}{\gamma}$.

Assumed Data for Numerical Interpretation

Mathematical calculation at the initial time of disease spread in a town
 Total population of town (N) = 1,00,000 =1 unit
 Total infected population (I_0) =700 =0.007 unit
 Total susceptible population (S_0) =1,00,000-700=99300=0.993 unit and K is the constant, which shows the “standard population and time period for interpretation of the rate” as explained by [26]. In general, the assigned values of K are 100, 1000, and so on.

In the present case K=100, we get

Infection rate (β) = $\frac{700}{99300} \times 100 = 0.70$.

Incubation period $\lambda = 20$ [26], and recovery rate (γ) = $\frac{1}{\lambda} = \frac{1}{20} = 0.05$

Basic reproduction number

(\mathfrak{R}_0) = $\frac{\text{Infection rate}}{\text{Recovery rate}} = \frac{\beta}{\gamma} = \frac{0.70}{0.05} = 14$.

This value of \mathfrak{R}_0 shows that one person infected from the contagious disease will spread the virus among 14 persons, and therefore it is a sign of an epidemic. Thus, the data in Table 2 are given here

for detailed insight of \mathfrak{R}_0 with different outbreaks that occurred between 1918-2020.

Table 2 Threshold Number/ Basic Reproduction Number and Outbreaks

Name of Disease	Location	Year	\mathfrak{R}_0
Spanish flu pandemic	Geneva (Switzerland)	1918-1919	1.49
Poliomyelitis	Europe	1955-1960	6.0
H2N2 influenza pandemic	USA	1957	1.68
Measles	Ghana	1960-1968	14.5
Smallpox	Indian subcontinent	1968-1973	4.50
Ebola	Guinea	2004	1.51
H1N1 influenza	South Africa	2009	1.33
Zika	South Africa	2015-2016	2.06
Covid-19 pandemic	India	2-8 March 2020	3.20

Numerical Method and Algorithm

The set of equations (1)-(3) that describe the SIR model are ordinary differential equations (ODEs) of the first order and first degree. It is an initial value problem (IVP). Therefore, these can be solved by appropriate numerical techniques of IVP. In the present analysis, we have used Euler's method for ODEs of the SIR model [24,25]. The detailed algorithm is given as:

Change in the susceptible population

$$\frac{dS}{dt} = S'(t) = -\frac{\beta IS}{N}, \quad (4)$$

Change in the infected population

$$\frac{dI}{dt} = I'(t) = \frac{\beta IS}{N} - \gamma I, \quad (5)$$

Change in recovered/removed population

$$\frac{dR}{dt} = R'(t) = \gamma I, \quad (6)$$

Initial condition

For step size $h = \Delta t = 1$ and $t_0 \leq t \leq t_n$, with $t_i = t_0 + ih$, the associated initial conditions are as:

$$S(t_0) = S_0 \Rightarrow S(0) = 0, \quad I(t_0) = I_0 \Rightarrow I(0) = 0, \quad \text{and} \\ R(t_0) = R_0 \Rightarrow R(0) = 0. \quad (7)$$

Iteration schemes for equations (4) to (6) with Euler's method are given as:

$$S_{i+1} = S_i - h \left(\frac{\beta I_i S_i}{N} \right), \quad (8)$$

$$I_{i+1} = I_i + h \left(\frac{\beta I_i S_i}{N} - \gamma I_i \right), \quad (9)$$

$$R_{i+1} = R_i + h(\gamma I_i), \quad (10)$$

where subscript i ($i = 0, 1, 2, 3, \dots$) is given for iteration i.e., $i = 0$ presents the first iteration and in this case, equations (8) to (10) are converted as:

$$S_1 = S_0 - h \left(\frac{\beta I_0 S_0}{N} \right) \quad (12)$$

$$\Rightarrow S(1) = S(0) - h \left(\frac{\beta I(0) S(0)}{N} \right),$$

$$I_1 = I_0 + h \left(\frac{\beta I_0 S_0}{N} - \gamma I_0 \right) \quad (13)$$

$$\Rightarrow I(1) = I(0) + h \left(\frac{\beta I(0) S(0)}{N} - \gamma I(0) \right),$$

$$R_1 = R_0 + h\gamma I_0 \Rightarrow R(1) = R(0) + h\gamma I(0), \quad (14)$$

here

$$S_0 = S(0), \quad S_1 = S(1), \quad I_0 = I(0), \quad I_1 = I(1), \quad R_0 = R(0), \\ R_1 = R(1).$$

The iterative solution of these equations is not given here for the sake of brevity, but on the basis of the result obtained by the equations, complete physical interpretation among the pertained parameters is described below in the result and discussion section.

Results and Discussion

The SIR (Susceptible, Infected and Recovered) epidemic model is discussed for prediction, numerical discussion and physical interpretation of any transmissible disease (like Covid-19, Measles, smallpox, Ebola etc.). The epidemic model equations are solved by a numerical iterative scheme called Euler's method as mentioned above, and the prediction of the population from $t = 0$ days to $t > 0$ days is given in Table 3 and the graphical representation is given in Fig 3 to 6 when infection constant (β) = 0.70, recovery rate (γ) = 0.05, basis reproduction number $\mathfrak{R}_0 = 14$, and total population $N = 1$ unit are considered.

Table 3 Prediction of Population (Susceptible, Infected and Recovered) size at different times.

Time (Days) (t _i)	Susceptible S(t _i)	Infected I(t _i)	Recovered R(t _i)	Time (Days) (t _i)	Susceptible S(t _i)	Infected I(t _i)	Recovered R(t _i)
0	0.993	0.007	0	61	1.08864E-07	0.071852709	0.928147183
1	0.9881343	0.0115157	0.00035	62	1.03388E-07	0.068260079	0.931739818
2	0.980168959	0.018905256	0.000925785	63	9.84481E-08	0.06484708	0.935152822
3	0.967197718	0.030931234	0.001871048	64	9.39793E-08	0.06160473	0.938395176
4	0.946256084	0.050326306	0.00341761	65	8.99266E-08	0.058524498	0.941475412
5	0.912920983	0.081145092	0.005933925	66	8.62425E-08	0.055598276	0.944401637
6	0.861065643	0.128943177	0.00991179	67	8.28861E-08	0.052818366	0.947181551
7	0.783345665	0.200215997	0.016438338	68	7.98215E-08	0.050177451	0.949822469
8	0.673558832	0.29999203	0.026449138	69	7.70179E-08	0.047668581	0.952331342
9	0.532115235	0.426436025	0.04144874	70	7.44479E-08	0.045285155	0.954714771
10	0.373276061	0.563953398	0.062770541	71	7.2088E-08	0.043020899	0.956979029
11	0.225918849	0.68311294	0.090968211	72	6.99171E-08	0.040869856	0.959130074
12	0.117889186	0.756986956	0.125123858	73	6.79168E-08	0.038826366	0.961173567
13	0.055420783	0.781606011	0.162973206	74	6.60709E-08	0.036885049	0.963114885
14	0.025098731	0.772847763	0.202053506	75	6.4365E-08	0.035040798	0.964959137
15	0.011520482	0.747783623	0.240695894	76	6.27862E-08	0.03328876	0.966711177
16	0.005490103	0.716424822	0.278085075	77	6.13232E-08	0.031624324	0.968375615
17	0.002736831	0.683356853	0.313906317	78	5.99657E-08	0.030043109	0.969956831
18	0.001427668	0.650498173	0.348074159	79	5.87046E-08	0.028540955	0.971458987
19	0.000777581	0.618623351	0.380599068	80	5.75318E-08	0.027113908	0.972886035
20	0.00044086	0.588028904	0.411530235	81	5.64398E-08	0.025758214	0.97424173
21	0.000259393	0.558808926	0.440931681	82	5.54222E-08	0.024470304	0.975529641
22	0.000157927	0.530969946	0.468872127	83	5.44728E-08	0.02324679	0.976753156
23	9.92291E-05	0.504480147	0.495420624	84	5.35864E-08	0.022084451	0.977915495
24	6.41877E-05	0.479291181	0.520644632	85	5.2758E-08	0.020980229	0.979019718
25	4.26525E-05	0.455348157	0.544609191	86	5.19832E-08	0.019931219	0.980068729
26	2.90573E-05	0.432594344	0.567376598	87	5.12579E-08	0.018934659	0.98106529
27	2.02583E-05	0.410973426	0.589006316	88	5.05785E-08	0.017987926	0.982012023
28	1.44303E-05	0.390430583	0.609554987	89	4.99417E-08	0.017088531	0.982911419
29	1.04865E-05	0.370912997	0.629076516	90	4.93443E-08	0.016234105	0.983765846
30	7.7638E-06	0.35237007	0.647622166	91	4.87835E-08	0.0154224	0.984577551
31	5.84879E-06	0.334753482	0.665240669	92	4.82569E-08	0.014651281	0.985348671
32	4.47826E-06	0.318017178	0.681978344	93	4.7762E-08	0.013918717	0.986081235
33	3.48134E-06	0.302117316	0.697879202	94	4.72966E-08	0.013222782	0.986777171
34	2.7451E-06	0.287012187	0.712985068	95	4.68588E-08	0.012561643	0.98743831
35	2.19359E-06	0.272662129	0.727335678	96	4.64468E-08	0.011933561	0.988066392
36	1.77491E-06	0.259029441	0.740968784	97	4.60588E-08	0.011336884	0.98866307
37	1.45308E-06	0.246078291	0.753920256	98	4.56933E-08	0.01077004	0.989229915
38	1.20278E-06	0.233774627	0.766224171	99	4.53488E-08	0.010231538	0.989768417
39	1.00596E-06	0.222086092	0.777912902	100	4.5024E-08	0.009719962	0.990279993
40	8.49571E-07	0.210981944	0.789017207	101	4.47177E-08	0.009233964	0.990765992
41	7.241E-07	0.200432972	0.799566304	102	4.44286E-08	0.008772266	0.99122769
42	6.22506E-07	0.190411425	0.809587952	103	4.41558E-08	0.008333653	0.991666303
43	5.39534E-07	0.180890937	0.819108524	104	4.38982E-08	0.00791697	0.992082986
44	4.71216E-07	0.171846458	0.82815307	105	4.3655E-08	0.007521122	0.992478834
45	4.14532E-07	0.163254192	0.836745393	106	4.34251E-08	0.007145066	0.99285489
46	3.6716E-07	0.15509153	0.844908103	107	4.32079E-08	0.006787813	0.993212144
47	3.273E-07	0.147336993	0.852662679	108	4.30026E-08	0.006448423	0.993551534
48	2.93544E-07	0.139970177	0.860029529	109	4.28085E-08	0.006126002	0.993873955
49	2.64782E-07	0.132971697	0.867028038	110	4.26249E-08	0.005819702	0.994180255
50	2.40136E-07	0.126323137	0.873676623	111	4.24513E-08	0.005528717	0.994471241
51	2.18902E-07	0.120007001	0.87999278	112	4.2287E-08	0.005252281	0.994747676
52	2.00513E-07	0.11400667	0.88599313	113	4.21315E-08	0.004989667	0.99501029
53	1.84511E-07	0.108306352	0.891693463	114	4.19844E-08	0.004740184	0.995259774
54	1.70523E-07	0.102891049	0.897108781	115	4.18451E-08	0.004503175	0.995496783
55	1.58241E-07	0.097746508	0.902253333	116	4.17132E-08	0.004278016	0.995721942
56	1.47414E-07	0.092859194	0.907140659	117	4.15883E-08	0.004064116	0.995935843
57	1.37832E-07	0.088216244	0.911783618	118	4.14699E-08	0.00386091	0.996139048
58	1.2932E-07	0.08380544	0.916194431	119	4.13579E-08	0.003667865	0.996332094
59	1.21734E-07	0.079615176	0.920384703	120	4.12517E-08	0.003484472	0.996515487
60	1.1495E-07	0.075634424	0.924365461	$\beta = 0.70, \gamma = 0.05, R_0 = 14, N = 1$			

Fig. 3 to Fig. 6 explain the change in susceptible, infected and recovered populations with time $t=0$ day to $t=180$ days. From Fig. 4 it is perceived that the susceptible population decreases with time and converts into an infected one. It is also visible from Fig. 5 that infected individuals achieved the maximum peak on $t = 13$ days and around 78% (also see table 3 for $t=13$ days) of the total population (1,00,000) is infected with the disease, which is undoubtedly an indication of an epidemic. It is the case of a high reproduction number $\mathcal{R}_0 = 14$ which is similar to the measles outbreak of Ghana ($\mathcal{R}_0 = 14.5$) in 1960-1968 [29]. Fig. 5 also suggests how the local authorities could prevent the disease outbreak with the execution of disease prevention guidelines and protocols such as social distancing,

the use of masks, prohibition of social gatherings, the shutdown of public places, schools, colleges and universities etc. and maximize the daily test and vaccination[28,30]. The infected individuals start to recover from the disease with time t as seen in Fig. 6, and it is an important outcome of the study that may be helpful for epidemiologists to predict and calculate the exact time when the disease dies out. Although, the present analysis is focused on a limited population sample size ($N = 1,00,000$) which is enough for the prediction of the infectious disease with time, and may extend with real-time data such as for the COVID-19 case in India, where the population is taken as e.g., 1.39 billion. In this analysis, we intend to explore the SIR model and its use in the future prediction of any transmissible disease with time.

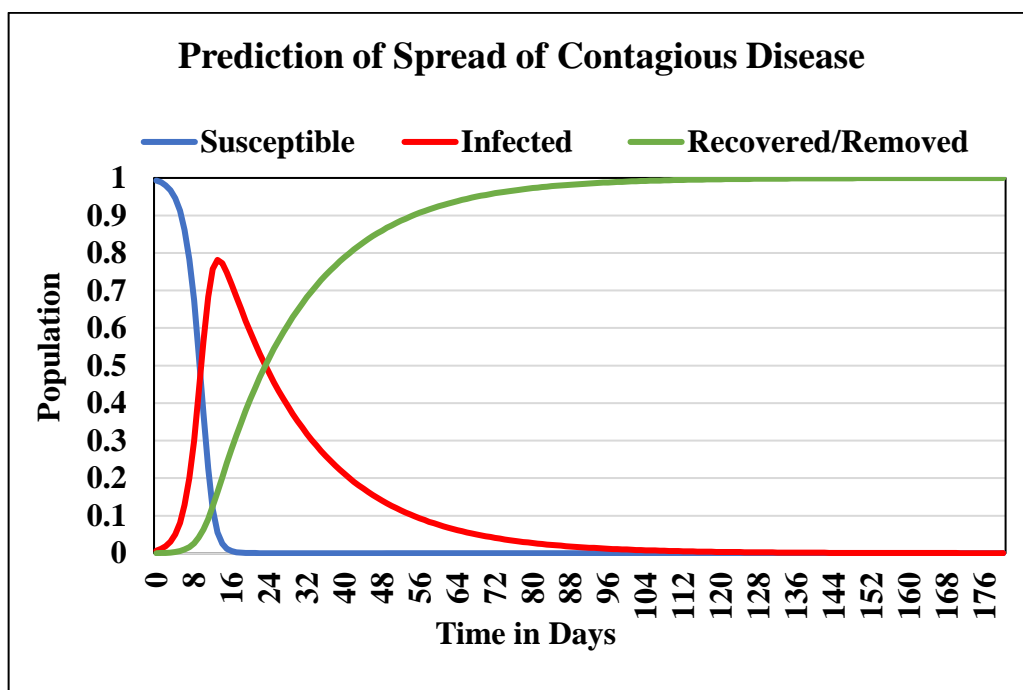


Fig. 3: Prediction of contagious disease with time-dependent SIR model.

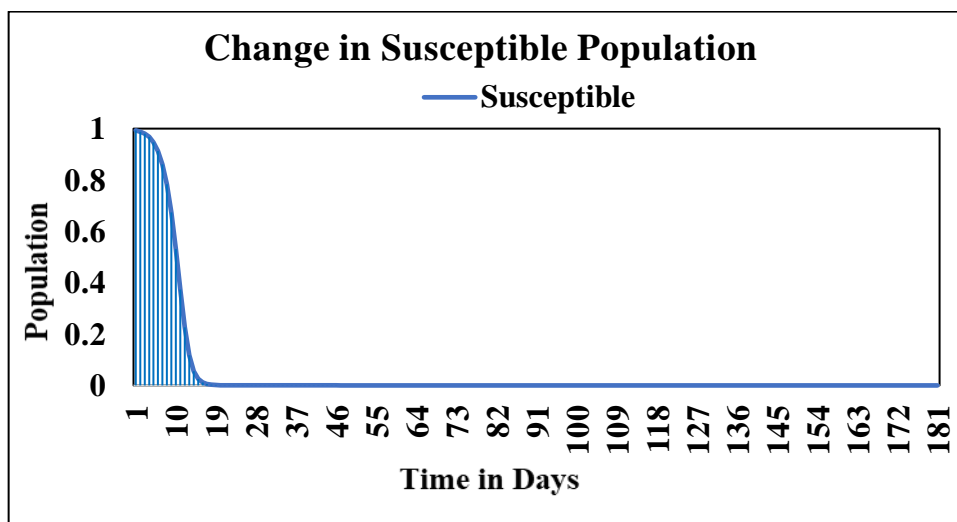


Fig. 4: Prediction of susceptible population with time-dependent SIR model.

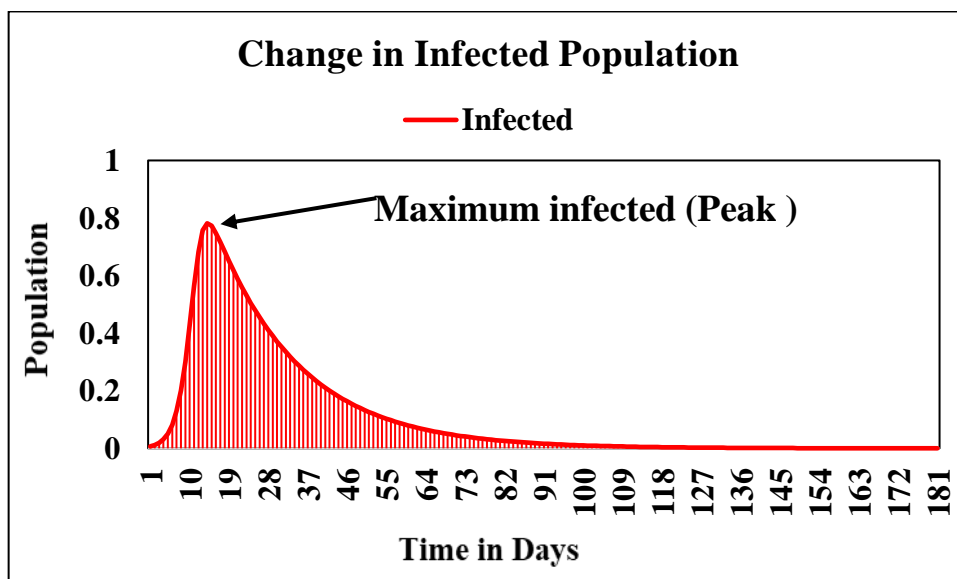


Fig. 5: Prediction of infected population with time-dependent SIR model.

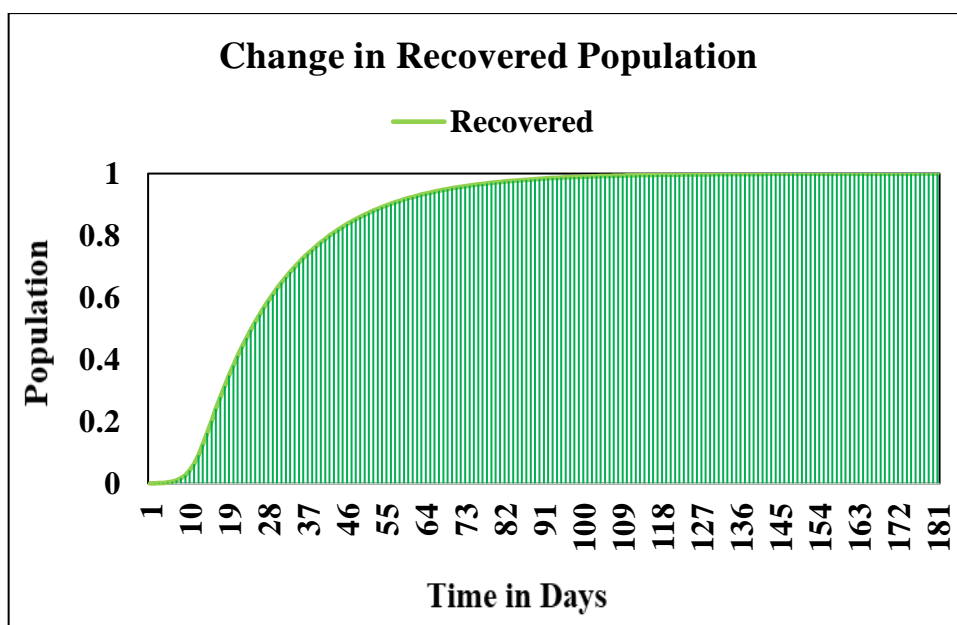


Fig. 6: Prediction of recovered population with time-dependent SIR model.

Conclusion

In the present analysis, the SIR model of the epidemic for the population of small sample size ($N=1,00,000$) is explained with the help of numerical techniques for forecasting the disease outbreak, infection peak time, recovery time, and the disease dies out time. In the analysis, we have observed the following points:

1. Contagious disease outburst is sudden and 78 percent of the population is infected in 13 days, which is due to high reproduction number ($\mathcal{R}_0 = 14$) because the high value of reproduction number leads to the epidemic.
2. It is observed that susceptible populations get infected and convert into infected ones, and this is the main reason for the outbreak of the disease.

3. It is suggested that disease outbreak may control with self-isolation or quarantine of susceptible individuals, because the mixing of susceptible with others always increases the infections, as noticed in the SARS-Cov-2 case in India and other countries, therefore present study also recommends the strict lockdown at infected locations.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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