



Using Mathematical Modeling to Predict the Spread of Epidemics

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ABSTRACT

In this paper, we give a brief overview of the advances in mathematical modelling applied to epidemiology and the achievements that have been made in epidemiological research using mathematical models. Since the early 1900s when the well-known susceptible–infected–recovered model was proposed, mathematical treatments have played an important role in epidemiology. We introduce the deterministic SIR model and explain the value of computational tools, mathematical modelling and statistical analysis for the understanding of the development of disease and the size of emerging outbreaks. These are issues that are of major concern in everyday life and public health. With the emergence of the novel coronavirus in recent times, it has become evident that mathematical modeling along with computational and statistical tools are extremely relevant. Hence, this study explains the mathematical modelling in Epidemiology and demonstrates the advancement of the discipline over the years.

Keywords: Epidemic ▪ Mathematical modeling ▪ Influenza ▪ SIR model ▪ Disease spread

1. INTRODUCTION

Everyone is concerned about health and health is one of the main issues that is dominating the media these days all over the world. The COVID-19 pandemic is one such epidemic outbreak that had affected numerous countries and made this worry evident. Besides, new types of harmful chemicals in the environment have been found and it is necessary to intervene and take effective steps to reduce their effects. Epidemic is a disease which spreads rapidly among a population. It has been a threat to the life of human beings, societies and even national economies throughout history. There is therefore a need to adopt a variety of strategies to control and contain the spread of epidemics. Mathematical modelling in epidemiology provides a way for scientists to develop principles and rules that can explain and predict the dynamics of disease and how it may spread in the future. Through mathematical models, epidemiological equations and computational simulations, researchers can simulate the

spread of disease and formulate suitable solutions and strategies for implementing informed decisions about public health worldwide [1, 2, 3].

2. ADVANCES IN MATHEMATICAL MODELLING

Mathematical modelling has played an important role in enhancing infectious-disease management in underserved regions. However, heavy reliance on deterministic models reduces the flexibility needed to address changing epidemiological conditions. Furthermore, limitations in data accuracy and availability negatively affect the robustness of modeling results. Future research should therefore emphasize the development of more diverse modelling frameworks, improvement of data-collection systems, and inclusion of a wider spectrum of infectious diseases. These outcomes may contribute to public-health policy by enabling evidence-based decision-making, optimizing resource distribution, and strengthening the incorporation of modelling techniques into epidemic

preparedness and response efforts in underserved communities [4, 5].

Throughout history, humanity has coexisted with many epidemics and pandemics that have caused numerous individual and mass deaths, as well as social and economic disruption. Predicting how a disease spreads between individuals is therefore crucial to mitigating its impact. In this research, we prepare a mathematical model called the SIR model, which helps reduce the spread of infectious diseases by identifying the fundamentals of modelling [6]. One of the most important parts of the model is the division of people into three categories [7]:

- Susceptible (S),
- Infected (I), and
- Recovered (R).

The principal parameters controlling disease spread include the infection rate β , the recovery rate λ , and the basic reproduction number R_0 , which determines the severity of the disease.

2.1 Mathematical Equations

Ordinary or partial differential equations describe the changes that occur in the affected population over time [7, 8]. The purposes of modeling include predicting the number of infections and evaluating vaccines.

3. EPIDEMIC MODEL

How can the dynamic development of a disease be modeled, and how can its growth be reduced? An epidemic usually begins with a single infected individual, called patient zero, who is the first person infected by the virus. Here, the SIR model is used to investigate this dynamic. The SIR model is widely used in epidemiology because, although simple, it predicts a fundamental feature of epidemics: it distinguishes a disease-free scenario from a scenario involving a large number of infected individuals. Many more complex models exist, but almost all are based on SIR principles that describe pandemic dynamics well. We first investigate this successful model using a deterministic approach and then implement the model on networks using a random framework [2, 4].

3.1 The SIR Model

The transmission of infectious diseases can be represented mathematically by classifying a population into categories, each of which represents a specific epidemiological state associated with the disease. The model then studies the interactions and transitions between these groups over time. Let the total population at the initial time $t = 0$ be denoted by N_0 , where N_0 is a positive integer. This population is partitioned into three principal categories: infected individuals I_0 , susceptible individuals S_0 , and individuals who have either recovered from the infection or been removed from the disease-transmission dynamics, R_0 [6, 9]. Thus,

$$S_0 + I_0 + R_0 = N_0. \quad (1)$$

The spread of infectious diseases can be modeled using ordinary differential equations (ODEs). The total population is divided into three epidemiological compartments:

- $S(t)$: susceptible individuals,

- $I(t)$: infected individuals, and
- $R(t)$: recovered (or removed) individuals.

At any time t , the total population is assumed constant:

$$S(t) + I(t) + R(t) = N. \quad (2)$$

3.2 Model Assumptions

The SIR model is based on the following assumptions:

- The population is closed, with no births, deaths, or migration.
- The population mixes homogeneously.
- Infection occurs through contact between susceptible and infected individuals.
- The infectious period follows an exponential distribution with rate $\gamma > 0$.
- The incubation period is negligible; therefore, there is no exposed class [6, 3].

3.3 Transmission

The incidence of new infections is proportional to the numbers of susceptible and infected individuals:

$$\frac{\beta S(t)I(t)}{N}, \quad \beta > 0, \quad (3)$$

where β is the transmission rate.

3.4 Model Equations

The dynamics of the system are governed by the following ODEs [9]:

$$\frac{dS}{dt} = -\frac{\beta S(t)I(t)}{N}, \quad (4)$$

$$\frac{dI}{dt} = \beta S(t)I(t) - \gamma I(t), \quad (5)$$

$$\frac{dR}{dt} = \gamma I(t). \quad (6)$$

Here, $S(t)$, $I(t)$, and $R(t)$ denote the susceptible, infected, and recovered populations, respectively; β is the transmission rate; γ is the recovery rate; and t is time. The derivative dS/dt is the rate of change of susceptible individuals and decreases because of infection; dI/dt is the rate of change of infected individuals and increases through infection while decreasing through recovery; and dR/dt is the rate of change of recovered individuals [5]. Figure 1 illustrates these transitions.

3.5 Flu Disease Modeling

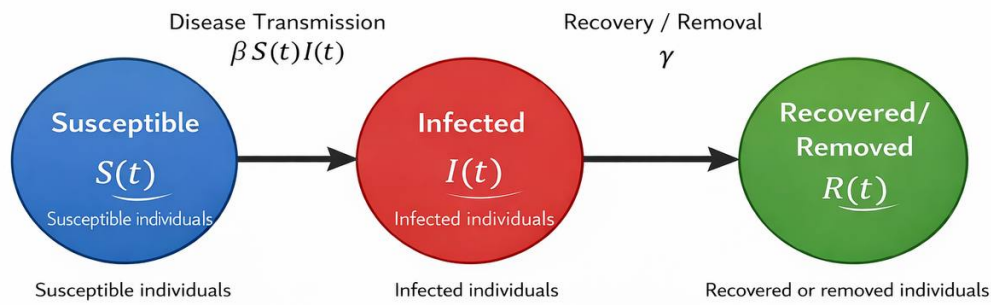
This subsection presents a practical example that models the spread of an influenza epidemic using the SIR model [1, 5]. Consider a city of 1,000 people with five cases of influenza:

$$S(0) = 995, \quad I(0) = 5, \quad R(0) = 0.$$

Suppose that each infected person transmits the infection to 0.3 people per day. Then,

$$\beta = 0.3 \div 1000 = 0.0003. \quad (7)$$

SIR Epidemiological Model



Changes over time:

$$\begin{aligned}\frac{dS}{dt} &= -\beta S(t)I(t) \\ \frac{dI}{dt} &= \beta S(t)I(t) - \gamma I(t) \quad \text{— (Infection / Recovery)} \\ \frac{dR}{dt} &= \gamma I(t)\end{aligned}$$

Figure 1. SIR epidemiological model.

The average illness duration is seven days, so

$$\gamma = 1 \div 7 \approx 0.143. \quad (8)$$

The numerical approximation of the model variables can be expressed as

$$S(t + \Delta t) = S(t) + \frac{dS}{dt} \Delta t, \quad (9)$$

$$I(t + \Delta t) = I(t) + \frac{dI}{dt} \Delta t, \quad (10)$$

$$R(t + \Delta t) = R(t) + \frac{dR}{dt} \Delta t. \quad (11)$$

Here, Δt is the time step and is often selected as one day in epidemiological studies to track disease progression day by day.

Calculating the rates of change at the initial time gives

$$\frac{dS}{dt} = -0.0003 \times 995 \times 5 \approx -1.49, \quad (12)$$

$$\frac{dI}{dt} - \gamma I = 0.0003 \times 995 \times 5 - 0.143 \times 5 \approx 1.49 - 0, \quad (13)$$

$$\frac{dR}{dt} = \gamma I = 0.143 \times 5 = 0.775. \quad (14)$$

Using the Euler formula with a one-day time step ($\Delta t = 1$), the approximate values after the first day are

$$S(1) \approx 995 - 1.49 = 993.51, \quad (15)$$

$$I(1) \approx 5 + 0.775 = 5.775, \quad (16)$$

$$R(1) \approx 0 + 0.715 = 0.715. \quad (17)$$

These results indicate a slight decrease in the number of susceptible individuals, accompanied by a gradual increase in the numbers of infected and recovered individuals one day after the disease begins to spread. This calculation can be

repeated for several successive time steps to obtain the temporal trajectory of the epidemic. Epidemic curves can then be plotted to illustrate the dynamics of the three population compartments.

Applying the Euler method for ten consecutive days produces the results in Table 1. The table shows the evolution of susceptible (S), infected (I), and recovered (R) individuals. The data illustrate a gradual decline in the susceptible population, an increase in infected cases during the early stages, and a steady increase in recoveries [5, 9].

Table 1. Time progression of influenza over 10 days.

Day (t)	$S(t)$	$I(t)$	$R(t)$
0	995.000	5.000	0.000
1	993.508	5.777	0.715
2	991.786	6.673	1.541
3	989.801	7.704	2.495
4	987.514	8.889	3.597
5	984.882	10.248	4.870
6	981.855	11.805	6.340
7	978.379	13.585	8.036
8	974.392	15.615	9.993
9	969.827	17.924	12.249
10	964.610	20.544	14.846

4. DISCUSSION OF RESULTS USING MATLAB

The results of the SIR model obtained using MATLAB show the temporal evolution of the three population groups: susceptible (S), infected (I), and recovered (R) individuals.

The susceptible-population curve gradually decreases over time because infection is transmitted from infected individuals to others who are vulnerable to infection. In contrast, the number of infected individuals initially increases during the

early stages of the outbreak as the disease spreads through the population.

Eventually, the infected population reaches its highest value, representing the epidemic peak, and then gradually decreases as infected individuals recover. At the same time, the number of recovered individuals increases continuously throughout the simulation, indicating an accumulation of individuals who have recovered and gained immunity. The results therefore demonstrate the dynamic nature of infectious-disease transmission and highlight the initial growth phase, epidemic peak, and final decrease in the number of infected individuals. These dynamics are shown in Figure 2.

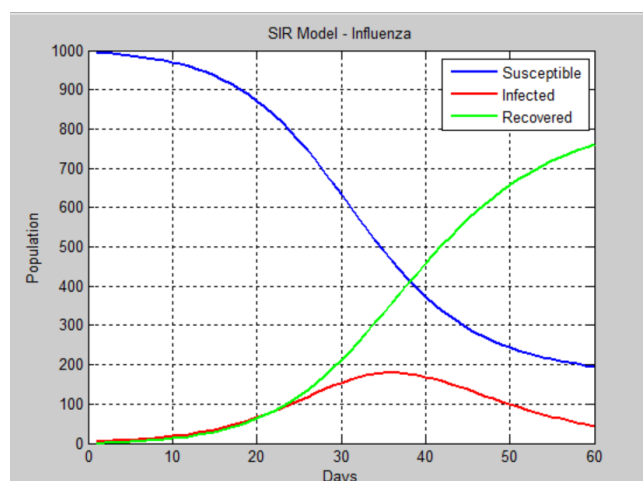


Figure 2. SIR epidemiological model for influenza.

4.1 Analysis and Impact of Interventions

Beyond predicting epidemic trajectories, mathematical models provide a powerful framework for sensitivity analysis, which assesses how variations in model parameters influence outcomes. For the SIR model, the key parameters include the transmission rate β and recovery rate γ . By systematically varying these parameters, their effects on critical epidemiological metrics—such as the epidemic peak, total number of infected individuals, and outbreak duration—can be quantified.

For example, reducing the transmission rate β through public-health interventions such as social distancing, mask wearing, or lockdowns directly lowers R_0 . Consequently, it flattens the epidemic curve, reduces the peak number of infections, and delays the occurrence of the peak. Conversely, increasing the recovery rate γ , perhaps through improved medical treatments or widespread vaccination leading to faster recovery, also lowers R_0 and contributes to a quicker resolution of the epidemic.

This analytical approach provides valuable insights for policymakers, enabling them to evaluate the potential effectiveness of intervention strategies before implementation. It helps optimize resource allocation and design targeted public-health campaigns to mitigate the spread of infectious diseases effectively.

5. CONCLUSION

The ability to model the spread of infectious diseases mathematically has become one of the most critical tools in understanding and predicting their spread. A study was undertaken to provide an explanation of the use of SIR model to describe

the epidemic dynamics of the population by groups into susceptible, infected, and recovered. Theoretical analysis and a numerical approximation showed how the disease transmission evolves and how the major epidemiological parameters like the transmission rate β and the recovery rate γ influence the spread of the disease.

The reported results confirm that the mathematical models do not only provide predictions of the spread of epidemics, but can also be used for the assessment of intervention strategies and health-related decisions. The model employed here is simple yet gives clear insights into the behaviour of outbreaks and is the foundation for more complex epidemiological models.

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