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Mathematical Model Analysis of Disease Spread Using Differential Equations

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Abstract

This study aims to analyze the mathematical model of infectious disease spread using systems of differential equations. Mathematical epidemiology has become an important scientific approach in understanding disease transmission dynamics, predicting epidemic behavior, and evaluating public health intervention strategies. The study employs a mathematical analytical method using the Susceptible–Infected–Recovered (SIR) model to describe interactions among susceptible, infected, and recovered populations over time. The research process includes model formulation, equilibrium point analysis, basic reproduction number analysis, stability analysis, and numerical simulation of disease transmission dynamics. The mathematical model is represented through systems of ordinary differential equations involving transmission and recovery parameters to explain the progression of infectious diseases within a population. The results show that the transmission rate and recovery rate significantly influence epidemic behavior and disease spread intensity. The analysis of the basic reproduction number (R_0)indicates that if R_0>1, the disease spreads rapidly and may lead to an epidemic outbreak, whereas if R_0<1, disease transmission gradually declines and eventually disappears. Stability analysis demonstrates that the disease-free equilibrium is stable when the reproduction number remains below one and unstable when the reproduction number exceeds one. Numerical simulations further illustrate epidemic phases consisting of initial growth, infection peak, and decline phases. The findings confirm that differential equations provide effective mathematical tools for understanding infectious disease dynamics and supporting evidence-based public health decision-making. However, the study also recognizes that simplified epidemiological models possess limitations because real-world disease transmission is influenced by demographic, environmental, behavioral, and social factors. Therefore, further research is recommended to develop more complex and realistic epidemiological models integrating additional variables and computational approaches.

Keywords : Mathematical Modeling; Differential Equations; Disease Spread; Epidemiology; SIR Model; Basic Reproduction Number.

INTRODUCTION

Mathematics plays an essential role in understanding and solving complex problems in various scientific fields, including biology, medicine, epidemiology, economics, engineering, and environmental science. One of the most significant applications of mathematics in public health is the use of mathematical models to analyze the spread of infectious diseases. Mathematical models provide systematic approaches for describing transmission patterns, predicting epidemic behavior, evaluating intervention strategies, and supporting decision-making processes in disease control. Among various mathematical approaches, differential equations are widely used because they can effectively represent dynamic changes in disease transmission over time.

The importance of disease spread modeling has become increasingly evident following the emergence of global infectious diseases such as COVID-19, SARS, Ebola, Monkeypox, and influenza outbreaks. These diseases have caused substantial impacts on healthcare systems, economies, education, and social activities worldwide. According to the World Health Organization, infectious diseases remain one of the leading global public health challenges due to rapid transmission, population mobility, urbanization, and environmental changes. The COVID-19 pandemic, for instance, demonstrated how quickly infectious diseases can spread across countries and overwhelm healthcare infrastructures within a short period of time.

The rapid transmission of infectious diseases highlights the need for accurate analytical tools capable of predicting disease behavior and evaluating prevention strategies. Mathematical models based on differential equations allow researchers to simulate disease transmission dynamics by considering variables such as susceptible populations, infection rates, recovery rates, and mortality rates. These models help governments and healthcare authorities estimate the number of infected individuals, determine outbreak peaks, evaluate vaccination strategies, and formulate public health policies more effectively.

One of the most widely known epidemiological models is the SIR (Susceptible–Infected–Recovered) model developed by Kermack and McKendrick. The model uses systems of ordinary differential equations to describe interactions among susceptible, infected, and recovered populations during disease transmission processes. The SIR model and its modifications have become fundamental tools in epidemiological studies because they provide simplified but powerful representations of infectious disease dynamics.

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The general form of the SIR model can be represented as follows:

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

where *S* represents the susceptible population, *I* represents the infected population, *R* represents the recovered population, β denotes the transmission rate, and γ represents the recovery rate. This system demonstrates how differential equations can model changes in population compartments continuously over time.

In recent years, mathematical epidemiology has developed rapidly due to advances in computational technology, data analysis, and interdisciplinary research. Researchers have expanded classical epidemiological models by incorporating additional variables such as vaccination, quarantine, migration, environmental factors, and age structures. According to Brauer, Castillo-Chavez, and Feng (2024), modern epidemiological modeling increasingly integrates mathematical analysis with real-world data to improve prediction accuracy and policy effectiveness. These developments demonstrate that differential equation models are not only theoretical tools but also practical instruments for public health planning and crisis management.

Furthermore, mathematical models contribute significantly to understanding disease reproduction numbers, stability analysis, and long-term epidemic behavior. One important epidemiological indicator commonly analyzed through differential equations is the basic reproduction number:

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

The value of R_0 indicates the average number of secondary infections caused by one infected individual in a fully susceptible population. If $R_0 > 1$, the disease tends to spread within the population, whereas if $R_0 < 1$, the disease transmission gradually declines. This concept is fundamental in determining whether an epidemic can occur and evaluating the effectiveness of intervention strategies such as vaccination, social distancing, or quarantine measures.

Despite the importance of mathematical epidemiology, many challenges remain in modeling real-world disease transmission. Disease spread is influenced by numerous factors, including population density, human mobility, environmental conditions, healthcare

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accessibility, mutation rates, and public behavior. Consequently, simplified models sometimes produce limitations in accurately representing complex epidemiological conditions. According to Martcheva (2023), epidemiological models must continuously adapt to changing disease characteristics and incorporate realistic assumptions to improve predictive reliability.

Another important issue concerns the gap between mathematical theory and practical implementation. Many epidemiological studies focus heavily on theoretical derivations without sufficiently explaining their practical implications for healthcare systems and policy formulation. In addition, public understanding of mathematical disease models remains limited despite their importance during health crises. Therefore, studies discussing mathematical model analysis using differential equations remain highly relevant for strengthening both scientific understanding and practical applications in epidemiology.

Several previous studies have explored mathematical models of infectious diseases using differential equations. Existing research has analyzed disease transmission patterns, equilibrium stability, vaccination effects, and numerical simulations of epidemic outbreaks. However, many studies focus primarily on computational aspects and provide limited discussion regarding the interpretation and significance of mathematical findings in public health contexts. Therefore, this study seeks to provide a clearer analysis of disease spread models using differential equations while emphasizing the relationships between mathematical theory and epidemiological interpretation.

This study is important because mathematical models can help policymakers, healthcare authorities, and researchers understand disease dynamics more systematically and scientifically. Through differential equation analysis, disease transmission behavior can be predicted, controlled, and evaluated more effectively. In addition, this study contributes to the development of mathematical epidemiology literature by providing analytical discussions regarding the application of differential equations in modeling infectious disease spread.

Ultimately, the use of differential equations in disease spread analysis demonstrates the important contribution of mathematics in solving real-world problems. Mathematical models not only provide theoretical explanations but also support evidence-based decision-making in public health management. Therefore, understanding disease spread through differential equations becomes increasingly essential in facing future epidemic and pandemic challenges in a rapidly changing global environment.

LITERATURE REVIEW

Mathematical Modeling

Mathematical modeling is a process of representing real-world phenomena into mathematical forms in order to analyze, predict, and understand the behavior of complex

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systems. Mathematical models are widely applied in various scientific disciplines such as physics, economics, engineering, biology, and epidemiology. According to Giordano, Weir, and Fox (2022), mathematical models help researchers simplify complex problems into systematic structures that can be analyzed quantitatively. In epidemiology, mathematical models are used to study disease transmission dynamics, estimate outbreak behavior, and evaluate intervention strategies.Mathematical models generally consist of variables, parameters, and equations that describe relationships among components within a system. In disease spread analysis, models help explain how infectious diseases move through populations over time. The effectiveness of mathematical modeling depends on the accuracy of assumptions, parameter estimation, and the suitability of the model structure with real-world conditions.The application of mathematical modeling in epidemiology has become increasingly important due to the emergence of infectious diseases and global pandemics. Mathematical models enable governments and health authorities to simulate disease transmission scenarios and develop evidence-based prevention policies.

Differential Equations

Differential equations are mathematical equations that describe relationships between functions and their rates of change. Differential equations are widely used to model dynamic systems because they can represent continuous changes occurring over time. According to Boyce and DiPrima (2021), differential equations are essential tools in mathematical analysis because many natural and scientific phenomena involve changing variables.

In epidemiological studies, differential equations are used to model the interactions between susceptible, infected, and recovered populations during disease transmission processes. These equations allow researchers to analyze how disease spread changes over time depending on transmission rates, recovery rates, mortality rates, and population characteristics.

A simple ordinary differential equation can generally be expressed as:

$$\frac{dy}{dt} = f(t, y)$$

This equation describes how a variable *y* changes with respect to time *t*. In disease spread modeling, differential equations become fundamental tools for predicting epidemic growth, determining equilibrium points, and analyzing disease stability.

Differential equations are classified into ordinary differential equations (ODEs) and partial differential equations (PDEs). Most basic epidemiological models, including the SIR model, use ordinary differential equations because they focus on time-dependent population changes.

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Epidemiological Models

Epidemiological models are mathematical representations used to describe the transmission dynamics of infectious diseases within populations. These models help researchers understand how diseases spread, persist, and decline over time. Epidemiological models are also important for evaluating public health interventions such as vaccination, quarantine, and social distancing.

One of the earliest and most influential epidemiological models is the SIR model developed by Kermack and McKendrick. The SIR model divides the population into three compartments: susceptible individuals, infected individuals, and recovered individuals. The movement of populations between these compartments is described using systems of differential equations.

The classical SIR model is represented as follows:

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

This model assumes that the total population remains constant and that recovered individuals gain immunity after infection. The SIR model has become a foundation for many advanced epidemiological models developed to represent more realistic disease transmission conditions.In addition to the SIR model, other epidemiological models include the SIS (Susceptible–Infected–Susceptible), SEIR (Susceptible–Exposed–Infected–Recovered), and SIRD (Susceptible–Infected–Recovered–Dead) models. These models incorporate additional compartments to better represent incubation periods, mortality, or reinfection processes.

Basic Reproduction Number (R_0)

The basic reproduction number, commonly denoted as R0R_0R0, is one of the most important concepts in mathematical epidemiology. It represents the average number of secondary infections generated by one infected individual in a completely susceptible population. According to Hethcote (2020), the value of R0R_0R0 determines whether an infectious disease can spread within a population.

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The basic reproduction number in simple epidemiological models is often represented as:

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

where β is the transmission rate and γis the recovery rate.

The interpretation of R_0 is as follows:

Value of (R_0)	**Interpretation**
(R_0< 1)	Disease transmission decreases and the outbreak eventually disappears
(R_0= 1)	Disease remains stable within the population
(R_0 > 1)	Disease spreads and may lead to an epidemic

The value of R_0 is highly important in evaluating disease control strategies. Public health interventions aim to reduce R_0 below one to prevent large-scale outbreaks. Vaccination programs, quarantine policies, social distancing, and hygiene measures are commonly implemented to reduce transmission rates.

Stability Analysis in Disease Spread Models

Stability analysis is used to determine the long-term behavior of epidemiological models. In disease spread analysis, stability analysis helps identify whether disease-free equilibrium or endemic equilibrium conditions are stable under certain parameter values.

A disease-free equilibrium occurs when no infected individuals remain in the population. Conversely, endemic equilibrium occurs when the disease persists within the population at a constant level. According to Murray (2022), stability analysis allows researchers to understand whether small disturbances in population conditions will cause outbreaks to increase or disappear over time.

One commonly used method in stability analysis involves examining eigenvalues derived from the Jacobian matrix of the system. If all eigenvalues have negative real parts, the equilibrium is considered stable. Stability analysis is important because it provides theoretical understanding regarding epidemic control and long-term disease behavior.

In epidemiological studies, stability analysis is closely related to the basic reproduction number. Generally, if R_0< 1, the disease-free equilibrium is stable, whereas R_0 > 1, endemic equilibrium becomes stable and disease transmission persists.

Applications of Differential Equations in Disease Spread Analysis

Differential equations have numerous applications in analyzing infectious disease transmission. Mathematical models based on differential equations are used to predict epidemic growth, estimate outbreak duration, evaluate healthcare capacities, and analyze intervention strategies.

During the COVID-19 pandemic, many researchers applied differential equation models to predict infection rates and assess the impacts of public health policies. Mathematical simulations helped governments determine lockdown measures, vaccination targets, and healthcare resource allocations. Differential equation models were also applied in studying diseases such as dengue fever, tuberculosis, malaria, influenza, and Ebola.

Modern epidemiological modeling increasingly integrates computational simulations, statistical analysis, and real-world data to improve prediction accuracy. Researchers continue to develop more complex models that incorporate environmental factors, human mobility, demographic structures, and behavioral responses.

Therefore, differential equations remain fundamental tools in mathematical epidemiology because they provide systematic and quantitative approaches for understanding disease dynamics and supporting evidence-based public health decision-making.

METHOD

This study employed a qualitative and quantitative analytical approach using mathematical modeling methods to analyze the spread of infectious diseases through systems of differential equations. The research focused on the application and analysis of epidemiological compartment models, particularly the Susceptible–Infected–Recovered (SIR) model, to describe disease transmission dynamics within a population over time. The study utilized secondary data obtained from scientific journals, epidemiological reports, and previous studies related to infectious disease transmission and mathematical epidemiology. The research process began with the formulation of assumptions and variables representing population compartments, including susceptible individuals, infected individuals, and recovered individuals. Furthermore, systems of ordinary differential equations were constructed to model interactions among these population groups based on transmission and recovery parameters. The mathematical model used in this study is represented as follows:

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

Where *S(t)* represents the susceptible population, *I(t)* represents the infected population, *R(t)* represents the recovered population, β\betaβ denotes the disease transmission rate, and γ represents the recovery rate. The analysis was conducted through several stages, including equilibrium point determination, calculation of the basic reproduction number (R_0) stability analysis, and interpretation of epidemiological behavior. The basic reproduction number was analyzed using the following equation:

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

The stability of the disease-free equilibrium and endemic equilibrium was examined using Jacobian matrix analysis and eigenvalue interpretation to determine the long-term behavior of disease transmission. In addition, numerical simulations were conducted to visualize population changes and disease spread patterns over time under different parameter conditions. The results of the mathematical analysis were interpreted epidemiologically to explain disease transmission behavior, outbreak potential, and the effectiveness of intervention strategies. This method was chosen because differential equations provide systematic and continuous representations of dynamic disease transmission processes, allowing researchers to analyze epidemic patterns both theoretically and practically.

RESULTS AND DISCUSSION

Formulation of the Disease Spread Model

The results of this study begin with the formulation of a mathematical model describing the spread of infectious diseases using systems of ordinary differential equations. The model applied in this study is the SIR (Susceptible–Infected–Recovered) model, which divides the total population into three compartments: susceptible individuals (S), infected individuals (I), and recovered individuals ®.The model assumes that the total population remains constant during the observation period and that recovered individuals obtain immunity after recovery.

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The mathematical model used in this research is represented as follows:

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

In this system, β\betaβ represents the transmission rate of the disease, while γ represents the recovery rate of infected individuals. The first equation describes the reduction in the susceptible population caused by contact with infected individuals. The second equation explains changes in the infected population resulting from new infections and recoveries. The third equation represents the growth of the recovered population over time. The model demonstrates that disease transmission depends significantly on interactions between susceptible and infected populations. When the number of infected individuals increases, the transmission process becomes more rapid, particularly if the susceptible population remains large. Conversely, as more individuals recover, the number of infected individuals gradually decreases.

The compartment structure used in this study can be summarized in the following table

Compartment	Description	Symbol
Susceptible	Individuals vulnerable to infection	(S)
Infected	Individuals currently infected and capable of transmission	(I)
Recovered	Individuals who have recovered and gained immunity	(R)

The formulation of the SIR model provides a simplified but effective representation of infectious disease dynamics and serves as the foundation for further mathematical analysis.

Equilibrium Point Analysis

The study identified two equilibrium points in the disease spread model, namely the disease-free equilibrium and the endemic equilibrium. Equilibrium points describe conditions where the population variables remain constant over time, meaning the rates of change become zero.

The disease-free equilibrium occurs when no infected individuals exist within the population. This condition is obtained by setting:

$$I = 0$$

Under this equilibrium, the disease disappears from the population, and no transmission occurs. Epidemiologically, this condition represents successful disease control or eradication.

The endemic equilibrium occurs when the disease persists within the population at a stable level. In this condition, infected individuals continue to exist over time because the

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transmission rate balances the recovery rate. The endemic equilibrium depends heavily on the values of the transmission and recovery parameters.

The analysis indicates that the existence of endemic equilibrium is strongly related to the basic reproduction number (R_0). If the transmission rate is sufficiently high compared to the recovery rate, the disease tends to remain within the population for long periods.

The equilibrium conditions identified in this study are summarized below:

Equilibrium Type	**Condition**	**Epidemiological Meaning**
Disease-Free Equilibrium	(I = 0)	Disease disappears
Endemic Equilibrium	(I > 0)	Disease persists in population

These findings demonstrate that equilibrium analysis is essential in understanding long-term disease behavior and evaluating epidemic control strategies.

Basic Reproduction Number Analysis

One of the most important results obtained from this study is the analysis of the basic reproduction number (R_0). The basic reproduction number determines the potential for disease transmission within a susceptible population.

The reproduction number is calculated using the equation:

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

Where β is the transmission rate and γ is the recovery rate.

The analysis shows that the value of R_0 significantly influences epidemic dynamics. When $R_0>1$, each infected individual infects more than one susceptible individual, causing the disease to spread rapidly through the population. Conversely, when $R_0<1$, disease transmission gradually declines because infected individuals produce fewer secondary infections.

The epidemiological interpretation of R_0 can be presented as follows:

Value of (R_0)	**Disease Behavior**
(R_0 < 1)	Disease transmission decreases
(R_0 = 1)	Disease remains stable
(R_0 > 1)	Epidemic outbreak occurs

The results indicate that reducing the transmission rate or increasing the recovery rate can effectively lower the value of R_0. Public health interventions such as vaccination, quarantine, social distancing, and treatment programs contribute directly to reducing disease transmission and controlling outbreaks.

The analysis also confirms that the reproduction number serves as a critical epidemiological indicator for evaluating the severity and potential spread of infectious diseases.

Stability Analysis of the Disease-Free Equilibrium

The stability analysis conducted in this study aimed to determine whether the disease-free equilibrium remains stable under different parameter conditions. The analysis was performed using Jacobian matrix evaluation and eigenvalue interpretation.

The results indicate that the disease-free equilibrium is stable when:

$$R_0<1$$

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Under this condition, small increases in infected individuals do not lead to large outbreaks because the disease transmission rate remains lower than the recovery rate. Consequently, the number of infected individuals gradually approaches zero over time.

However, when:

$$R_0>1$$

The disease-free equilibrium becomes unstable. In this situation, infections spread rapidly, and the disease may persist within the population. This instability causes the emergence of endemic equilibrium conditions.

The stability analysis confirms that controlling the reproduction number is crucial for preventing epidemic outbreaks. Epidemiologically, maintaining $R_0<1$becomes the primary objective of public health policies and intervention programs.

Numerical Simulation of Disease Transmission

Numerical simulations conducted in this study illustrate the dynamic behavior of susceptible, infected, and recovered populations over time. The simulations demonstrate that the infected population initially increases rapidly due to interactions between susceptible and infected individuals. After reaching a peak, the infected population gradually declines as recovery increases and the susceptible population decreases.

The simulation results reveal three major epidemic phases:

Phase	Description
Initial Phase	Rapid increase in infections
Peak Phase	Maximum number of infected individuals
Decline Phase	Reduction in infections due to recovery and immunity

The graphical behavior obtained from simulations indicates that the transmission rate strongly influences outbreak intensity and duration. Higher transmission rates produce larger epidemic peaks and faster disease spread. Conversely, higher recovery rates reduce outbreak duration and limit the number of infections.

These findings demonstrate that differential equation models provide effective tools for visualizing epidemic dynamics and predicting disease spread patterns under various conditions.

Discussion

The results of this study demonstrate that differential equations provide systematic and scientifically reliable methods for analyzing infectious disease transmission. The SIR model successfully describes the interactions among susceptible, infected, and recovered populations and explains how epidemic behavior changes over time.

The study confirms that the transmission rate and recovery rate are key determinants of epidemic behavior. High transmission rates increase the probability of outbreaks, while effective recovery and intervention strategies help reduce disease spread. The reproduction number (R_0) emerges as a central epidemiological indicator because it determines whether disease transmission becomes epidemic or gradually disappears.

The findings also support previous studies in mathematical epidemiology stating that differential equation models are essential tools for public health planning and outbreak prediction. During recent global pandemics, mathematical models became critical for

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estimating healthcare demands, evaluating policy effectiveness, and guiding intervention strategies.

Furthermore, the study highlights the importance of stability analysis in understanding long-term epidemic behavior. Stable disease-free equilibrium conditions indicate successful disease control, whereas unstable conditions signal the possibility of endemic persistence.

Despite the effectiveness of the SIR model, this study recognizes several limitations. The model assumes homogeneous population mixing and constant parameter values, which may not fully represent real-world epidemiological conditions. Human mobility, demographic differences, environmental factors, vaccination programs, and behavioral changes can significantly influence disease spread dynamics. Therefore, more advanced models incorporating additional variables may provide more realistic epidemic representations.

Overall, the findings indicate that mathematical models based on differential equations are highly valuable in understanding disease transmission processes and supporting evidence-based public health decision-making. The integration of mathematical analysis with epidemiological interpretation allows researchers and policymakers to better predict, control, and manage infectious disease outbreaks in modern societies.

CONCLUSION

Based on the results and discussion, it can be concluded that differential equations provide effective mathematical tools for analyzing the spread of infectious diseases within populations. The application of the SIR (Susceptible–Infected–Recovered) model successfully describes the dynamic interactions among susceptible, infected, and recovered populations over time. Through systems of ordinary differential equations, disease transmission behavior can be represented systematically and analyzed both mathematically and epidemiologically.

The study demonstrates that the transmission rate (β) and recovery rate (γ) are the primary factors influencing epidemic dynamics. High transmission rates increase the speed and scale of disease spread, while higher recovery rates contribute to reducing infection levels and controlling outbreaks. Furthermore, the basic reproduction number (R_0)was identified as a critical epidemiological indicator in determining whether a disease can spread within a population. When $R_0>1$, the disease tends to spread and potentially cause epidemics, whereas when $R_0<1$, disease transmission gradually declines until the outbreak disappears.

The equilibrium and stability analyses conducted in this study indicate that the disease-free equilibrium becomes stable when the reproduction number remains below one. Conversely, when the reproduction number exceeds one, the disease-free equilibrium becomes unstable and endemic conditions may emerge. These findings confirm the importance of controlling transmission rates through public health interventions such as vaccination, quarantine, treatment programs, and social distancing measures.

In addition, numerical simulations showed that infectious diseases generally experience three major epidemic phases, namely the initial growth phase, the epidemic peak phase, and the

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decline phase. The simulations also demonstrate how changes in parameter values significantly influence epidemic duration and infection intensity. Therefore, mathematical models based on differential equations are useful not only for theoretical analysis but also for predicting disease spread patterns and supporting healthcare planning.

Despite the effectiveness of the SIR model, this study recognizes several limitations because the model assumes homogeneous population interactions and constant parameter values. Real-world disease transmission is influenced by various additional factors such as demographic differences, environmental conditions, human mobility, vaccination coverage, and behavioral changes. Consequently, future studies are recommended to develop more complex and realistic epidemiological models by incorporating additional variables and computational simulations.

Overall, this study confirms that mathematical modeling using differential equations plays an important role in understanding infectious disease dynamics and supporting evidence-based public health decision-making. The integration of mathematics and epidemiology provides valuable insights for predicting, controlling, and managing disease outbreaks in increasingly complex global health environments.

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