

Mathematical Modelling of Infectious Disease Dynamics Using Nonlinear Differential Equations and Stability Analysis

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ABSTRACT

Mathematical modelling is essential in controlling and understanding the spread of infectious diseases. This study involves mathematical modelling of nonlinear in-contact disease dynamics using nonlinear differential equations and a stability study. The interactions of different groups of people through time are modelled using classical compartmental models, including the Susceptible-Infected-Recovered (SIR) framework. The nonlinear character of the governing equations represents real transmission mechanisms, recovery mechanisms and population dynamics. The model's equilibrium points, such as the disease-free and endemic equilibria, are established and analyzed to understand the disease's long-run behaviour better. Stability analysis is a mathematical method that employs linearization and eigenvalue analysis to determine whether a disease will die out or persist in the population. The basic reproduction number R_0 is a critical threshold parameter for the dynamics of disease spread. $R_0 < 1$ Local asymptotic stability of disease-free equilibrium, whereas R_0 appears to be unstable, and an endemic state arises. The analytical conclusions and the effects of model parameters on disease development are demonstrated through numerical simulations. The paper focuses on the utility of nonlinear differential equation models for forecasting outbreak patterns and evaluating control strategies, such as vaccination and treatment. These lessons can be used to make sounder choices regarding the planning of community health and the prevention of illness.

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1. Introduction

Many infectious disease outbreaks have emerged in recent decades. The severity of these outbreaks directly affects the health of people in the affected areas. Some infectious diseases have a history of wiping out entire nations due to their severity. In the early 1900s, during the influenza pandemic, nearly 40 million people worldwide died. Every year, a large number of people are affected by different types of infectious diseases, such as AIDS and influenza. The death rate among people affected by these severe forms of infectious agents is increasing rapidly. The UNAIDS report suggests that in 2010, almost thirty-four million people worldwide, including children, were affected by HIV, and deaths due to this pandemic in 2010 were almost 2 million. Infectious diseases emerge in different forms each year. Handling these changing infectious agents is a major task for government health organizations (Ezekiel et al., 2025). Health-related sectors are advancing with modern technology-based systems to detect infectious diseases at an early stage. Technological advances have helped the health sector better understand the causes behind the spread of infectious diseases. At the global level, numerous efforts have been made to understand the molecular behaviours of infectious agents in order to develop vaccines against them. Developing a drug against a viral agent is a complex task. A virus changes its shape and molecular structure across hosts, making it difficult to develop a universal drug that treats all viral variants. This problem is addressed first by studying the virus's molecular mechanism and then by developing a universal drug against it. To develop a good vaccine, mathematical models are employed in healthcare computational systems (Hoang & Ehrhardt, 2025). These models aid decision-making in the health sector.

Dealing with infectious diseases using mathematical modelling techniques requires great expertise. In the past, various scientists have used mathematical modelling to predict the severity of viral agents and the likelihood of their outbreak as pandemics. Rapidly assessing an agent's infectiousness is critical. Through mathematical modelling, assessing

infectious agents has become easier. Mathematical models predict different parameters using the SIR model (Huang et al., 2025). This model explains the susceptibility to infection (S), the number of infected individuals (I), and the number of individuals recovered from the disease (R). These dynamics are readily captured by the SIR model. Additionally, these mathematical models are developed to estimate the viral reproductive number in an infected individual. Mathematical models of infectious diseases identify the most suitable strategies for use during a pandemic outbreak of an infectious agent. Mathematical models provide two types of outcomes. The first is deterministic, in which these models accurately predict the outcome. The second type is stochastic, in which the model prediction is completely random (Khan et al., 2025).

Mathematical models used for infectious disease predictions are mainly of two types. The first is a linear model that explains the direct relationship among variables that cause infectious outbreaks. At the same time, nonlinear models are used to explain the complex interactions among variables responsible for the spread of infectious diseases (Mannan et al., 2025). In a nonlinear mathematical model, variables are not proportional; therefore, predicting infection outcomes in people is possible. Nonlinear mathematical models are designed to capture the dynamics of infectious diseases accurately. Intervention methods for disease control are evaluated using nonlinear models. Nonlinear models are used at the population level because they provide realistic predictions of disease spread (Muthu & Modak, 2025). Nonlinear models elucidate the complexities of health systems in detecting infectious diseases in the population. After detecting potential disease complexity, this model provides feedback on disease severity and type. Disease outcomes can be predicted using nonlinear mathematical models. The advantages of nonlinear models make their use highly suitable for predicting the long-term outcomes of infectious disease pandemics.

Studies of typhoid fever using nonlinear mathematical models help predict the impact of infectious diseases on the population (Pandey & Ghosh, 2025). The model assessed two states. In the first state, the virus was absent from any contaminated state. In the second state, typhoid was detected in a contaminated environment. The analysis of both states indicates that the incidence of typhoid fever is associated with environmental factors. Additionally, disease transmission within the population contributed to the spread of typhoid. The stability of contaminated and non-contaminated states determines whether the typhoid virus spreads or is removed from the population (Prakash Raj et al., 2025). Studies have shown that the dynamics of typhoid are nonlinear, making its persistence in the population highly complex. The complex behaviour of typhoid fever, as modelled nonlinearly, makes it difficult to eliminate the disease using available interventions. The persistence of typhoid virus in the population, even after its complete eradication, indicates that it can remain at low levels due to its complex nature. However, proper hygiene and preventive measures help in reducing the spread of the typhoid virus in the population.

Using various mathematical models to study infectious diseases helps elucidate the nature of disease outbreaks in populations. Different mathematical models used in the health sector include statistical and machine learning models. These models help in evaluating the possibility of disease outbreak, its severity and its complexity (Raza et al., 2025). Many health organizations are working around the globe to develop mathematical models that aid in eliminating the possibility of outbreaks of infectious diseases. Various policies are developed to assess the molecular behaviour of infectious diseases and to predict their treatment. The mathematical models utilized by health organizations explain the possibility of diseases spreading or elimination using stability analysis (Sanni, 2025). Theoretical analysis aids in predicting the potential outcomes of infectious diseases across different populations. Moreover, mathematical models explain that small parametric changes affect the behavioral activity of infectious agents. These small parameters are then responsible for causing pandemic or epidemic outbreaks. Controlling these parameters through appropriate government health policies reduces the risk of disease outbreaks. Additionally, health agencies are developing mathematical models based on health policies to minimize the incidence of infectious diseases. Many health organizations are educating youth about the importance of mathematical models for assessing the possibility of infectious disease outbreaks in the near future.

1.1 Research Objectives

This research paper provides insight into the importance of mathematical models in predicting disease complexity. Additionally, it assesses the significance of nonlinear models in addressing the diverse dynamics of infectious diseases in the population.

2. Literature Review

Researchers claim that co-infection of diphtheria with HIV is a deadly infectious disease that badly impacts the health of people in the population. The HIV infected individual is likely to infect other individuals, and thus the rate of spread of the infectious disease increases. To study infection dynamics, a Mathematical Compartmental Deterministic Model was applied in a population co-infected with diphtheria along with HIV. This nonlinear model predicted that when the reproduction number of infection reduces to one, then the chances of co-infection minimize (Abah et al., 2026). Studies suggest that world health is declining due to outbreaks of deadly infectious diseases. Investigating the nature of the infectious agent requires proper modelling systems. The Fractional Differential Model provides information on the

probability of reinfection with the poliovirus in the population. This model serves as a tool for early prediction of epidemics caused by the polio virus (Abbas et al., 2026). Scholars predict that, in humans, the spread of infectious diseases is governed by the SEIR mathematical model. This model has two expressions that help in predicting outcomes. The first is a nonlinear form of expression, and the second is a simplified linear expression. Both expressions are used mathematically to assess the likelihood of the spread of infectious diseases in any population (Al-Jebouri & Kaki, 2025). Studies suggest that a viral dynamics model can predict the incidence of infectious diseases in a population when incorporated with an antibody-based immune response to capture the complexity of infections. The model predicts that some viral cells are latent, whereas others are actively dividing. The behaviour of viral cells predicted by these models is highly realistic. The model's results are then analyzed theoretically using computerized systems (Alade & Al Rahbi, 2026). Studies show that pine wilt disease is assessed using mathematical models that use Fractal Equations. These models are based on six nonlinear equations that estimate the numbers of infected and exposed individuals in the population. The Fractal-Fractional Equations provide insight into the dynamics of pine wilt infection (Aldwoah et al., 2025). Scholars explain that the spread of measles infections is caused by numerous factors. One major factor influencing the spread of the deadly measles virus is social factors. The SEIR model is used to predict the number of people affected by measles. This model uses the fractional derivative to assess the dynamics of the measles virus (Alshammari et al., 2025). Scholars have shown that infectious diseases can be modelled using SEIR and SEIRS models.

The flow of infectious diseases like HIV and AIDS from one person to another is explained by these mathematical models. SEIRS models are widely used to analyze the stability of infectious diseases (Anjapuli et al., 2026). Scholars suggest that compartmental nonlinear models can be used to determine the effect of vaccination dose on COVID-19-infected patients. Models suggest that increasing the number of vaccination doses reduces the likelihood of infection spread. Additionally, information on the effectiveness of COVID-19 vaccination is obtained using the Variational Iteration Equation (Ghani et al., 2026). Scholar's studies reveal that NVD is a disease in which the viral agent affects the patient's intestine. It is a contagious disease that spreads through infected utensils of an NVD patient. Stability analysis models are used in the healthcare sector to manage the spread of NVD (Ibrar et al., 2026). Studies have shown that nonlinear fractional models help predict the transmission dynamics of the coronavirus. The impact of vaccination on COVID-19 patients is also assessed through the nonlinear mathematical model (Jajarmi et al., 2026). Studies show that COVID-19-related uncertainty is addressed using interval-based methods. The Runge-Kutta method is used to solve the uncertain COVID-19 parameters (Karanakar et al., 2025). Scholars suggest that the digitalization of the healthcare sector has created numerous challenges. These challenges are tackled using nonlinear mathematical equations. The Lotka-Volterra framework was employed in the digital health sector. This framework revealed that the use of digitized systems in the health sector makes it more sustainable (Krawczyk et al., 2025). Scholar's studies determine that using mathematical models to predict the dynamics of behaviors of symptomatic and asymptomatic patients was used to investigate the transmission rate of HIV infection (Morani et al., 2025). Studies suggest that employing a nonlinear model of Exhumated Arteritis provides insight into the disease's complexity. This model uses three equations to explain the disease dynamics (Nasresfahani & Eslahchi, 2026). Researchers explain that the stochastic Ebola virus model is a mathematical model that analyses disease prevalence across different cases. Mathematical equations provide information about the parameters that drive disease persistence. Effective preventive strategies help minimize the risk of Ebola virus infection (Nasrin & Rajivganthi, 2025). Studies show that the factorial-fractional derivative equation provides information on the hereditary properties underlying disease persistence in individuals co-infected with tuberculosis and diabetes mellitus. The model's results predict that vaccination reduces the likelihood of disease spread (Nawaz et al., 2026). Scholar studies explain that a large portion of the world's population is facing the chronic diabetes mellitus problem. Managing diabetes mellitus in a large population is a critical task. Clinical interventions, along with proper disease management strategies, are required for its management. Mathematical models are developed for implementing intervention strategies. Mathematical models are cost-effective methods for managing diabetes mellitus. Additionally, NSFD is used in mathematical models to optimize them and to provide immediate solutions for the management of diabetes mellitus (Nivetha & Ghosh, 2026). Scholar's studies explain that infection in CD4+ cells results in HIV. Understanding the complexity of CD4 cell binding provides insight into disease dynamics, and mathematical modelling offers solutions for controlling the spread of infection. The bifurcation models also predict about two states of HIV patients. The first stage is disease-free, and the second stage is infected. Both states are managed using a Bifurcation Analysis Model (Prakash et al., 2025). Studies determine that different states of HIV patients are explained using a fractional order model. This model predicts parameters that either facilitate or impede the spread of infection. Fractional values are directly related to viral load. A low fractional value indicates a stabilized system, whereas a high value indicates disease progression (Sardar et al., 2025). Scholars' studies indicate that epidemic models are solved using appropriate numerical methods. These models then predict the spread of infection under different conditions. The SEIR model explains the dynamics of infectious diseases and offers potential solutions for their complete eradication. Public health care sectors are planning to improve the quality of their health services by using SEIR-based models for disease management (Yousuf & Alshakhoury, 2026).

3. Methodology

The nonlinear differential equations and stability analysis are used to model infectious disease dynamics in this paper. It is largely theoretical research with numerical simulations being used to confirm analytical findings. It employs a compartmental modelling approach that can be decomposed into a few epidemiological classes, each representing the entire population by disease state. As the basis model, the conventional Susceptible-Infected-Recovered (SIR) framework is selected because it is useful in the transmission and recovery processes modelling. It is assumed that the population is closed and homogeneous, with no age- or spatial-distribution changes. People move in and out of compartments at an agreed rate.

3.1 Data Measurements

A system of nonlinear ordinary differential equations is constructed to describe the time dependence of the rate of change of each compartment. The disease-transmission term is primarily responsible for nonlinearity, modelled as the product of the susceptible and infected populations, reflecting the true dynamics of contact. Normal epidemiological assumptions and existing literature are used to determine the model parameters, including transmission rate, recovery rate and natural elimination rate. All parameters are assumed to be positive and remain constant throughout the simulation. The model equations are first analyzed to note that the solutions are positive and bounded, thereby demonstrating the biological feasibility of the system. In order to obtain the equilibrium locations of the model, we equate the time derivatives to zero. It is known that there are both disease-free and endemic equilibrium states. The next-generation matrix method is used to compute the fundamental reproduction number (R_0) and is used as a threshold parameter to test the persistence/eradication of a disease. The stability of equilibria in a nonlinear system is studied by linearizing the system about the equilibria. Jacobian is constructed, and an analysis based on eigenvalues is performed to obtain the stability criteria. Numerical simulations are also conducted to complement the results of the analysis using the standard computing methods used to solve ordinary differential equations. The time-dependent behaviour of the system is simulated as the system parameters are varied, and the results can support theoretical predictions of stability and threshold behaviour. Graphical products are made to depict changes in population groups over time. In general, this scientific method is based on nonlinear modelling, analysis of analytical stability, and numerical experimentation to offer a complete insight into infectious disease dynamics and the factors that determine the spread and control of the disease (Figure 1).



Figure 1: Infectious Disease Dynamics

3.2 Equational Analysis

To analyze the dynamics of infectious disease transmission, a nonlinear compartmental model is formulated using ordinary differential equations. The total population at the time t , denoted by $N(t)$, is divided into three epidemiological compartments: susceptible $S(t)$, infected $I(t)$, and recovered $R(t)$. Thus,

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

The model assumes a closed population with no immigration or emigration, and disease transmission occurs through effective contact between susceptible and infected individuals. The following system of nonlinear differential equations governs the flow of individuals between compartments:

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

where β represents the transmission rate of the disease, and γ denotes the recovery rate of infected individuals. The nonlinear term βSI captures the interaction between susceptible and infected populations, reflecting realistic disease spread

The above result shown in table 1 demonstrates that the ANOVA table reports the sum of squares, the mean square, the F statistic, and the significance of each model. The regression model indicates that the sum of squares is 2.279 and the mean square is 1.139. The F-statistic is 3.353, and the p-value is 0.043, indicating a 4% significance level. The residual model accounts for 16.309 of the sums of squares, and the mean square error is 0.340.

3.6 Nonlinear Equational Analysis

Table 2: Results of Coefficients^a

		Coefficients ^a			t	Sig.
Model		Unstandardized Coefficients		Standardized Coefficients		
		B	Std. Error	Beta		
1	(Constant)	1.348	.328		4.107	.000
	Mathematical Modeling	-.103	.129	-.108	-.800	.427
	Stability Analysis	.332	.137	.328	2.424	.019

a. Dependent Variable: Infectious Disease Dynamics

The above result shown in table 2 demonstrates that the nonlinear regression analysis yields unstandardized coefficient estimates, including the beta coefficient and its standard error. The result is also the t-statistic, which indicates the significance of each model. The mathematical modelling indicates that the beta value is -0.103, the t-statistic is -0.800, and the significance level is 0.427, indicating a negative but 42% significant association with infection disease dynamics. The stability analysis also shows a t-statistic of 2.424 ($p = 0.019$), indicating a 19% difference between them (Figure 3).

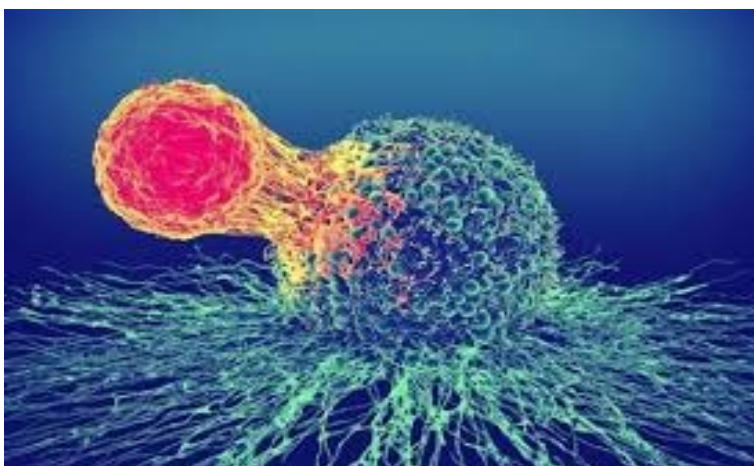


Figure 3: Infected Cell Proliferation

4. Applications of Mathematical Modelling in Infectious Disease Dynamics

Using nonlinear differential equations in mathematical modelling has many applications in monitoring, predicting and controlling outbreaks of infectious diseases. The models provide a conceptual system used to explore the pathways of disease transmission, evaluate the intervention activities, and make evidence-based health decisions in the population. The analysis of stability is a way of extending their usefulness in indicating the conditions in which diseases become extinct or persist in a population.

Nonlinear infectious disease models are frequently applied to predict the spread of an epidemic. These are simulation models that can be used to estimate the peaks of infections, the length of an outbreak, and long-term trends as they interact between the susceptible, infected, and recovered populations. Models that incorporate differential equations enable researchers to examine the effects of small changes in transmission or recovery rates on disease spread. This predictive capability is particularly effective in the case of booming epidemics, when authorities can predict the demand for healthcare and effectively manage the resources.

Mathematical models: would be important in assessing the effectiveness of the public health activities such as vaccinations, isolation, quarantine and treatment programs. By modifying the model parameters, the researchers can simulate the action of different control methods on the dynamics of the disease. Stability analysis can be used to determine whether an intervention can be effective in reducing the basic reproduction number to a critical level. This would help policymakers to compare methods and pick the most efficient and cost-effective methods of controlling disease.

Policy Design and Optimization Vaccination: Vaccination policy design and optimisation usually designed using

nonlinear models. Bringing the vaccination rates into the compartmental models allows the researchers to determine the minimum level of coverage in terms of vaccination needed to achieve herd immunity. Disease-free equilibrium stability analysis assesses whether immunization can control the disease. These programs are particularly applicable to the design of mass immunization campaigns and pandemic control measures for available vaccines.

Theory of Threshold Behavior and Disease Persistence: The concept of threshold behaviours very important in mathematical modelling and is defined by the basic reproduction number R_0 . Nonlinear differential equations can be used to determine whether infectious diseases survive or disappear. Stability analysis enables scholars to examine the impact of parameter changes on equilibrium stability. This knowledge is essential for the management of long-term disease, especially endemic diseases that require long-term intervention strategies rather than immediate solutions.

Planning and Allocation of Resources in the Health System: The mathematical models assist healthcare organizations in managing the limited resources, such as hospital beds, staff, and treatment facilities. The models help authorities to plan depending on the rise in patient volume, since it predicts the trends and the peak season of the infection. This initiative would play a key role in avoiding overload in the healthcare system in the case of a massive outbreak. The stability analysis is used to make the decision-makers aware of the long-term sustainability of healthcare responses.

Comparative Analysis of Infectious Diseases: The framework of nonlinear modelling allows a comparison of infectious diseases by changing factors that are associated with transmission, recovery, and immunity. This program helps researchers understand why some diseases spread rapidly, whereas others are localized. In stability situations, models can predict disease-specific factors that contribute to persistence and control. These comparisons are applicable to the concentration of research and treatment on several disorders.

The process of policy formation and the Evidence-Based Decision Making: Many governments and public health agencies use mathematical modelling as an informational tool to guide policy making. The model results provide quantitative information to implement or relax the interventions of public health. The stability analysis gives a scientific basis for when the discontinuation of therapies can be safely done without the relapse of the disease. Such applications substitute transparency and accountability in the process of health decisions by the population.

Training and Education on Epidemiology: Mathematical models play an important role in applied mathematics, epidemiology and public health. They apply analytical and numerical techniques in order to make students and professionals understand the complex disease processes. To encourage critical thinking, nonlinear differential equations and stability analysis, as well as exposure to real-world health data analysis. This teaching tool is useful in producing professional employees capable of addressing emerging health issues.

Endorsement of Global Disease Surveillance Systems: The combination of epidemiological and mathematical models to invent infectious disease models enhances global disease surveillance. Through these applications, it is possible to identify the outbreaks early and evaluate cross-border transmission issues. The stability analysis will help to define the areas susceptible to long-term transmission, therefore, support international cooperation and reaction strategies.

Improvements in the Interdisciplinary Research: The application of nonlinear differential equations in the modelling of infectious diseases stimulates interdisciplinary research in the fields of mathematics, biology, medicine, and community health. This form of cooperation enhances model realism and the accuracy of the forecast. The stability analysis bridges the gap between theoretical and practical parts of mathematics and promotes the creation of scientific innovations and superior methods of treatment of disease (Figure 4).



Figure 4: Global Distribution of Infection Hotspots During an Epidemic

5. Discussion

Mathematical simulation of infectious disease dynamics is performed using nonlinear differential equations, which provide important insights into disease transmission and control. The results of this paper demonstrate that nonlinear compartmental models can be useful to formulate real interactions between susceptible, infected and recovered people. Nonlinear transmission parameters are added to the model, which includes realistic patterns of contact, which are essential in epidemiological growth and decay. The analysis of the equilibrium points proves the importance of threshold behavior in the dynamics of infectious diseases. The disease-free equilibrium refers to a balanced state of public health whereby infection has been eliminated in the population. It can be shown by a stability analysis that this equilibrium is locally asymptotically stable when the basic reproduction number R_0 is less than unity. This result corresponds to the classical theory of epidemiology and highlights the necessity of a decrease in transmission rates or an increase in recovery rates in the eradication of disease. When R_0 is greater than one, a disease-free equilibrium is not maintained, and an endemic equilibrium is formed, where the infection is maintained throughout the population. This conclusion is important because it highlights how hard it is to control highly transmissible diseases without long-term intervention methods. The results also indicate that even small shifts in some such critical parameters as transmission and recovery rates can affect the long-term behavior of the system significantly. This sensitivity shows the need for proper parameter estimation and continuous monitoring of epidemiology data.

The analytical simulations are supplemented by numerical simulations that demonstrate the model's behaviour over time. The simulations show clear peaks of epidemics and thereafter stabilization which confirm the theoretical predictions of the stability analysis. These results are evidence in favour of the use of nonlinear differential equations as a model to approximate real outbreak patterns and the success of interventions. Although the virtues may be associated with the modelling approach, there are some limits. Homogeneous mixing and constant parameter assumptions may not be a good representation of the actual populations, which are often heterogeneous and influenced by social, demographic and environmental factors. Moreover, the model lacks stochastic effects that minimize the capability of the model to duplicate the random fluctuations in the actual outbreaks. Initial studies can expand on this framework by incorporating age structure, geographical dynamics, or stochastic to be more realistic in future studies. All in all, the talk shown above illustrates the fact that nonlinear mathematical models with stability analysis present a powerful and systematic approach to the dynamics of infectious diseases. These models provide theoretical and practical assistance to the development of effective disease control and prevention strategies.

6. Conclusion

This publication employed nonlinear differential equations and stability analysis to demonstrate that mathematical modelling is useful in the study of the dynamics of infectious diseases. The study provides a structured and quantitative description of the ways of disease propagation, recovery, and population dynamics by creating a compartmental structure. The nonlinearity of this model gives the opportunity to describe the spread of the virus realistically, including the most important epidemiological peculiarities typical of the real-life outbreak. Equilibrium point analysis plays an important role in analyzing the long-term dynamics of infectious diseases. The identification of disease-free and endemic equilibria allows for a precise understanding of the circumstances in which diseases are eliminated or persist in a given population. Studies on the stability indicate that the basic reproduction number is an important threshold parameter that affects the dynamics of disease. When this threshold is maintained below unity, the disease-free equilibrium is maintained, leading to the ultimate eradication of the disease. The values above the threshold, in their turn, lead to instability and long-term spread, which underlines the challenges of curbing really contagious diseases. Numerical simulations further support the analytical conclusions because they reveal the dynamic development of disease outbreaks in different parameter conditions. These simulations demonstrate the influence of variation in transmission and recovery rates on epidemic peaks and long-term impacts. The fact that theoretical outcomes are correct compared with numerical data enhances confidence in the validity and helpfulness of nonlinear models of the various forms of differential equations in epidemiological research. Even though the suggested modelling method can provide some valuable insights, it is imperative to remember the limitations of the method. Reduced assumptions, e.g., homogenous population mixing and homogeneous parameters, might not be able to reflect the complexity of the real populations.

However, the assumptions allow the analytical tractability and give a fundamental understanding of the behaviour of the disease. This paradigm can be developed further by considering other factors like population heterogeneity, regional organization, and time-dependent factors as an addition to enhance the realism of the models in the future. In short, nonlinear mathematical models combined with stability analysis can be viewed as an effective and versatile instrument to study the dynamics of infectious diseases. This study contributes to the growing literature that favours the application of mathematical modelling in the field of public health planning and the control of diseases. Such models can be used to elicit

effective intervention and evidence-based decision-making that can lead to the reduction of infectious disease burden by providing insights into the mechanism of transmission and threshold behavior.

7. Recommendations

7.1 Model Extension and Enhancement

To enhance the current nonlinear differential equation framework, compartments representing exposed, vaccinated, and asymptomatic individuals should be incorporated in future studies. The model would be made more realistic and closer to application with age structure, spatial distribution and population heterogeneity. Such changes would allow scientists to model more complex dynamic disease processes better and reflect a more realistic transmission process.

7.2 Integrating Real-Time Data

It is recommended that mathematical models should be used in conjunction with the real-time epidemiological data to enhance the accuracy of the parameter estimates and predictions. Calibration processes of data can be used to narrow down the transmission and recovery rates, enhancing the policy and planning reliability of models. The application of current surveillance data will also enable the timely evaluation of the severity of the outbreak and the effectiveness of the implementation.

7.3 Stochastic Effects

Stochastic features in deterministic models should be incorporated in future research to overcome the ambiguity in the transmission of diseases. The random changes and unforeseeable variations that arise in the course of a real epidemic can be better reflected in the stochastic modelling. This would enhance the capacity of the model to aid the risk assessment and early alarms.

7.4 To Policy and Decision Support

Policymakers and the public health authorities can make informed decisions with the help of mathematical modelling and stability analysis. The results of the models can be used to develop targeted intervention programs, including the level of vaccine coverage and the allocation of resources. The involvement of modelling knowledge in population health planning would enhance preparedness and response operations.

7.5 Apply Sophisticated Computer Software

Software tools such as MATLAB, Python, or Mathematica may be used by researchers in numerical simulation and sensitivity analysis. These technologies allow for analyzing complicated models fast and exploring numerous situations. Utilization of improved calculation methods can be developed in visualization and, interpretation and presentation of modelling findings.

7.6 Interdisciplinary Collaboration

It is strongly recommended that mathematicians, epidemiologists, healthcare practitioners, and policymakers collaborate. Interdisciplinary methods can enhance the validity of the model and ensure that mathematical findings are implemented in viable and effective public health regulations.

8. References

- Abah, E., Acheneje, G. O., Omede, B. I., Afere, B. A. E., & Bolaji, B. (2026). A new compartmental epidemiological model governed by a system of non-linear differential equations for the control of co-infection between diphtheria and HIV. *Modeling Earth Systems and Environment*, 12(1), 14.
- Abbas, A., Rahman, G. u., Arif, M. S., Abodayeh, K., & Asif, M. (2026). Dynamical aspects of poliomyelitis disease via non-singular fractional differential equations: mathematical and biological aspects. *Boundary Value Problems*, 2026(1), 1.
- Al-Jebouri, M. M., & Kaki, M. N. M. (2025). Application of Matrices Modelling for Infectious Diseases of Humans. *Open Journal of Applied Sciences*, 15(9), 2733-2758.
- Alade, T. O., & Al Rahbi, Y. (2026). Mathematical Modeling and Analysis of Virus Dynamics: Integrating Immune Response and Multitarget Cells. In *Nonlinear Dynamical Control, Computer Simulation and Optimization Systems: Theory and*

Applications (pp. 147-161). World Scientific.

- Aldwoah, K., Ahmed, S., Jahan, S., Touati, A., Eljaneid, N., & Aljaaidi, T. (2025). Fractal-fractional modeling and stability analysis of pine wilt disease dynamics. *PloS one*, 20(2), e0318534.
- Alshammari, N. A., Alharthi, N., Mohammed Saeed, A., Khan, A., & Ganie, A. H. (2025). Numerical solutions of a fractional order SEIR epidemic model of measles under Caputo fractional derivative. *PloS one*, 20(5), e0321089.
- Anjapuli, L. S. S., Patel, B., Banavar, M. K., Tepedelenioglu, C., Spanias, A., Schuckers, S., & Achalla, M. (2026). Stability Analysis of a Modified SEIRS Compartmental Model for Infectious Diseases. *IEEE Access*, 14, 10499-10509.
- Ezekiel, I. D., Iyase, S. A., & Anake, T. A. (2025). Stability and Hopf Bifurcation Analysis of an Infectious Disease Delay Model. *WSEAS Transactions on Mathematics*, 24, 126-143.
- Ghani, U., Ahmad, B., Mahmood, S., Flah, A., Ghatasheh, M., & Pergl, I. (2026). Nonlinear compartmental modeling of COVID-19 with dual dose vaccination using Mason graphs and variational iteration method: U. Ghani et al. *Scientific Reports*.
- Hoang, M. T., & Ehrhardt, M. (2025). Differential equation models for infectious diseases: Mathematical modeling, qualitative analysis, numerical methods and applications: MT Hoang, M. Ehrhardt. *SeMA Journal*, 1-36.
- Huang, L., Anjam, Y. N., Ali, A., Rehman, B., & Tahir, M. A. (2025). Transmission dynamics and stability analysis of fractional HIV and AIDS epidemic model with antiretroviral therapy. *Scientific Reports*, 15(1), 18212.
- Ibrar, M., Ahmad, I., Ali, N., Khan, S., Pamucar, D., Baskonus, H. M., & Ali, Z. (2026). Bifurcation and Stability Analysis of Norovirus Disease. *Nonlinear Analysis and Computer Simulations*, 1(1), 5.
- Jajarmi, A., Baleanu, D., Arshad, S., & Wali, M. (2026). Nonlinear fractional differential equation model analysis and application: A numerical approach and real data validation. In *Recent Developments in Theory and Applications of Fractional Order Systems* (pp. 51-65). Elsevier.
- Karunakar, P., Reddy, K. S., & Chakraverty, S. (2025). Stability analysis and approximate solution of interval mathematical model for the COVID-19 pandemic. *Mathematical Methods in the Applied Sciences*, 48(7), 7641-7650.
- Khan, M., Khan, N., Ullah, I., Shah, K., Abdeljawad, T., & Abdalla, B. (2025). A novel fractal fractional mathematical model for HIV/AIDS transmission stability and sensitivity with numerical analysis. *Scientific Reports*, 15(1), 9291.
- Krawczyk, D., Kolomiiets, S., & Chvankin, Y. (2025). Nonlinear Models of Economic Dynamics as a Tool for Public Health Research. *Health Economics and Management Review*, 6(1), 179-196.
- Mannan, A., Shoket, N., Ul Rahman, J., & Uwitije, R. (2025). Dynamic analysis of ebola virus disease with non-linear incidence rate using morlet wavelet neural networks and hybrid optimization techniques. *Modeling Earth Systems and Environment*, 11(2), 79.
- Morani, A. H., Saeed, M. M., Aslam, M., Mehmoud, A., Shokri, A., & Mukalazi, H. (2025). Local and global stability analysis of HIV/AIDS by using a nonstandard finite difference scheme. *Scientific Reports*, 15(1), 4502.
- Muthu, P., & Modak, B. (2025). Stability of in-host models of dengue virus transmission with linear and nonlinear infection rate. *Differential Equations and Dynamical Systems*, 33(3), 1019-1045.
- Nasresfahani, F., & Eslahchi, M. (2026). Convergence-Focused Numerical Solutions for Nonlinear Moving Boundary Models of Rheumatoid Arthritis. *International Journal of Computational Methods*.
- Nasrin, S. F., & Rajivganthi, C. (2025). Dynamical Analysis of a Stochastic Ebola Model with Nonlinear Incidence Functions. *Journal of Nonlinear Science*, 35(1), 33.
- Nawaz, R., Kainat, S., Long, N. M. A. B. N., Shah, K., & Abdeljawad, T. (2026). Fractal-fractional order mathematical modelling of co-infection dynamics of tuberculosis and diabetes mellitus with vaccination. *Journal of Applied Mathematics and Computing*, 72(2), 60.
- Nivetha, S., & Ghosh, M. (2026). Mathematical modeling and cost-effective intervention strategies for diabetes management: A data-driven and numerical analysis approach. *PloS one*, 21(1), e0339463.
- Pandey, A., & Ghosh, S. (2025). Numerical study of childhood disease model with Lyapunov stability analysis. *Indian Journal of Physics*, 1-16.

- Prakash Raj, M., Venkatesh, A., Arun Kumar, K., & Manivel, M. (2025). Mathematical modeling of the co-infection dynamics of dengue and malaria using delay differential equations. *Advanced Theory and Simulations*, 8(2), 2400609.
- Prakash, S., Umrao, A. K., & Srivastava, P. K. (2025). Bifurcation and stability analysis of within host HIV dynamics with multiple infections and intracellular delay. *Chaos: An Interdisciplinary Journal of Nonlinear Science*, 35(1).
- Raza, A., Ali, K., Sattar, S., Fadugba, S. E., & Jeeva, N. (2025). Mathematical Modeling and Numerical Simulations of Influenza Transmission Dynamics with Structured Infectious Population. *Advanced Theory and Simulations*, e00236.
- Sanni, B. (2025). Mathematical Modeling of Complex Biological Systems Using Nonlinear Differential Equations.
- Sardar, P., Biswas, S., Das, K. P., Sahani, S. K., & Gupta, V. (2025). Stability, sensitivity, and bifurcation analysis of a fractional-order HIV model of CD⁴⁺ T cells with memory and external virus transmission from macrophages. *The European Physical Journal Plus*, 140(2), 1-28.
- Taylor, K. W., Joubert, B. R., Braun, J. M., Dilworth, C., Gennings, C., Hauser, R., Heindel, J. J., Rider, C. V., Webster, T. F., & Carlin, D. J. (2016). Statistical approaches for assessing health effects of environmental chemical mixtures in epidemiology: lessons from an innovative workshop. *Environmental health perspectives*, 124(12), A227-A229.
- Yousuf, M., & Alshakhoury, N. (2026). Stability analysis and numerical simulation of nonlocal extended epidemic models using positivity-preserving scheme. *Scientific Reports*.