

Impact Of Control Strategies On Infectious Disease Dynamics: A Differential Equation Modelling And Simulation Approach

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Abstract

Global public health is still severely hampered by infectious diseases, which highlights the necessity for efficient control and intervention measures. Understanding the mechanisms of disease transmission and assessing the efficacy of control measures prior to their practical application depend heavily on mathematical models. A compartmental differential equation-based infectious illness model that incorporates important control techniques like immunisation, therapy, and preventive measures is presented in this paper. To establish threshold conditions for disease persistence or eradication, the fundamental reproduction number is calculated. To evaluate long-term system behaviour, stability analysis of endemic and disease-free equilibria is performed. The influence of changing control settings on disease dynamics is examined by numerical simulations employing the fourth-order Runge-Kutta method. According to simulation studies, effective control measures greatly shorten the duration of outbreaks and the prevalence of infections. The results offer policymakers and public health planners important information for creating successful disease control initiatives.

Keywords: Infectious disease modelling, differential equations, control strategies, stability analysis, numerical simulation.

1. Introduction

A chronic global public health concern, infectious diseases cause substantial morbidity, mortality, and economical disruption in both developed and developing nations. The far-reaching effects of unchecked disease transmission have been eloquently demonstrated by historical and current outbreaks, such as influenza pandemics, COVID-19, Ebola virus disease, TB, and other new and re-emerging illnesses. Such outbreaks have negative effects on social stability, economic activity, and healthcare systems in addition to their direct health effects. Modern socioeconomic conditions include greater population mobility, fast urbanisation, high population density, globalisation of trade and travel, and frequent social interactions all contribute to the rapid spread of infectious agents. These interrelated difficulties underscore the pressing need for

efficient, timely, and long-lasting approaches to disease prevention, mitigation, and control.

In order to track illness patterns and guide public health responses, traditional epidemiological procedures that rely on disease surveillance, clinical investigations, and statistical analysis are essential. However, these methods are frequently limited by issues with incomplete or inaccurate data, high operating expenses, time delays in data gathering, and the moral dilemmas raised by extensive human population testing. Complementary approaches that might get beyond these restrictions and offer a more thorough understanding of disease dynamics are therefore becoming more and more necessary. In this sense, mathematical modelling has become a potent and methodical tool for researching the transmission of infectious diseases. Models allow researchers to investigate transmission mechanisms, model outbreak scenarios, and evaluate the possible results of different intervention techniques in a controlled and economical way by converting biological and epidemiological processes into mathematical formulations.

Differential equation-based compartmental models are one of the most often used modelling techniques in epidemiological research. In order to clearly depict the paths by which diseases are transmitted, these models usually divide the population into discrete compartments, such as susceptible, infected, and recovered individuals. Their adaptable design makes it easier to implement important control measures including immunisation, therapy, isolation, quarantine, and behavioural changes. These models offer important qualitative insights into disease persistence and eradication settings through analytical methods like equilibrium analysis, fundamental reproduction number estimation, and stability analysis. Additionally, by providing quantitative forecasts and visual depictions of illness progression under various epidemiological and intervention scenarios, numerical simulations enhance analytical results.

This study examines how control techniques affect the dynamics of infectious diseases using a deterministic compartmental modelling framework based on systems of differential equations. To determine the threshold conditions that control the persistence or eradication of a disease, a thorough

stability study is carried out, with special attention to the function of the basic reproduction number. The temporal progression of the disease under different levels of intervention and parameter values is then shown using numerical simulations. Combining analytical and simulation-based methods improves knowledge of how control measures affect the spread of illness and gives public health officials and policymakers a strong tool for making decisions. In the end, the suggested modelling framework aids in the creation of well-informed, empirically supported policies for efficient disease control and long-term eradication.

1.1. Global Burden of Infectious Diseases

Global public health is still heavily burdened by infectious diseases, which cause millions of illnesses and fatalities annually in a variety of geographical areas. Infectious diseases continue to be a major source of morbidity and mortality, especially in low- and middle-income nations, despite tremendous advancements in medical knowledge, immunisation programs, and public health infrastructure. The ongoing occurrence of both endemic and epidemic illnesses highlights how intricate and dynamic disease transmission is in a society growing more interconnected by the day.

Large-scale epidemics like smallpox, cholera, plague, and influenza pandemics have historically had a significant impact on society development and population health. Infectious diseases such as COVID-19, Ebola virus disease, Zika virus infection, SARS, MERS, and tuberculosis have emerged and re-emerged in recent decades, reinforcing the susceptibility of populations around the world to infectious threats. In addition to causing a large number of fatalities, these outbreaks have shown flaws in emergency planning, healthcare systems, and disease tracking systems.

Infectious diseases have serious social and economic repercussions in addition to their direct effects on health. Increased healthcare costs, lower worker productivity, and long-term financial losses at the national and international levels are all consequences of high illness incidence. The disproportionate impact on vulnerable groups, such as children, the elderly, and people with impaired immune systems, exacerbates health disparities. Furthermore, outbreaks of infectious diseases frequently cause disruptions in social relations, trade, education, and travel, which adds to the instability of society as a whole.

Modern variables like rapid urbanisation, population expansion, greater international travel, climate change, and shifting human-environment interactions all contribute to the worldwide burden of infectious illnesses. These elements promote the development of new diseases and quicken the international spread of already-existing ones. When

taken as a whole, these difficulties show how urgently strong, proactive, and scientifically based methods are needed to comprehend disease dynamics and lessen their effects on global public health.

2. Review Of Literature

Alqahtani (2021) designed a fractional-order SIR epidemic model to analyse the kinetics of COVID-19 transmission. Classical integer-order models frequently overlook memory and genetic effects inherent in disease transmission mechanisms; this work used fractional derivatives to address this. The influence of fractional orders on the spread of disease was demonstrated using numerical simulations and stability analysis of equilibrium points. In comparison to more conventional models, the results showed that fractional models accurately reflected actual epidemic data and offered more flexibility.

Keimer and Pflug (2020) developed an integro-differential equation-based framework for modeling infectious disease dynamics, with particular emphasis on COVID-19. Their work incorporated time-delay effects and cumulative infection history into the modeling process. The authors formulated optimal control strategies to support policy decision-making and analyzed the effectiveness of interventions such as social distancing and lockdown measures. The study highlighted the importance of advanced mathematical models in designing efficient and timely public health policies.

Ivorra et al. (2015) provided the mathematical framework known as the Be-Codis model to forecast the global transmission of infectious diseases affecting humans via networks of global mobility. The model accounted for population movement between countries and was validated using real epidemiological data from the 2014–2015 Ebola virus disease outbreak. The results showed that the model could effectively identify high-risk regions and forecast disease propagation patterns. This work demonstrated the usefulness of mathematical modeling in global epidemic preparedness and risk assessment.

Beira and Sebastião (2021) performed a differential equation-based model-fitting analysis to study multi-wave COVID-19 dynamics using real epidemiological data. Their approach focused on parameter estimation and data-driven calibration of compartmental models to explain successive infection waves. The study revealed that changes in transmission rates, behavioral responses, and intervention measures significantly influenced the emergence of multiple waves. The findings emphasized the importance of continuous model updating and data integration in accurately capturing complex epidemic trends.

3. Mathematical Model Formulation

Based on illness state, the entire population at any given time is divided into three different epidemiological compartments: susceptible $S(t)$, infected $I(t)$, and recovered $R(t)$. Those who have not yet acquired the illness but are susceptible to infection through interaction with infectious individuals make up the susceptible compartment. People who are currently infected and have the potential to infect others are included in the infected compartment. The recovered compartment stands for those who have effectively recovered from the illness and are thought to have developed immunity, which means they are no longer involved in the spread of the disease.

The model also incorporates crucial control measures meant to slow the spread of disease. By putting susceptible people straight into the recovered class, vaccination lowers the number of people who can spread the infection. Infected people receive treatment to hasten healing, limit the infectious time, and lessen the severity of the sickness. The framework enables a methodical assessment of how public health interventions impact disease dynamics and aid in infection control and ultimately disease eradication by integrating these control measures into the model structure.

The governing system of nonlinear ordinary differential equations is given by:

$$\begin{aligned}\frac{dS}{dt} &= \Lambda - \beta SI - \mu S - u_1 S \\ \frac{dI}{dt} &= \beta SI - (\gamma + \mu + u_2) I \\ \frac{dR}{dt} &= \gamma I + u_1 S + u_2 I - \mu R\end{aligned}$$

4. Basic Reproduction Number

The fundamental copy number in a totally susceptible population, the average number of secondary infections caused by a single infected individual is quantified by R_0 , a fundamental epidemiological threshold value. It is a crucial measure of the community's susceptibility to the spread of infectious diseases. A decrease in disease transmission and eventual eradication of the infection from the population occurs when $R_0 < 1$, since each diseased individual typically does not transmit more than one new infection. But when $R_0 > 1$, the illness can spread across the population and cause an epidemic or long-term transmission. R_0 for the suggested model is obtained by applying the next-generation matrix method as:

$$R_0 = \frac{\beta \Lambda}{(\mu + u_1)(\gamma + \mu + u_2)}$$

If $R_0 < 1$, the disease will die out; if $R_0 > 1$, the disease persists in the population.

5. stability analysis

The suggested model's disease-free equilibrium (DFE) is achieved when the infected population component $I=0$, which represents a condition when the disease is totally absent from the population, is set to 0. When the basic reproduction number $R_0 < 1$, the DFE is found to be asymptotically stable according to the local stability analysis. In this state, the average number of secondary infections caused by an infected person is fewer than one, which means the disease is being progressively eliminated and the control methods are working. On the other hand, when $R_0 > 1$, the DFE starts to fluctuate and an endemic equilibrium forms, which means that the disease is still present in the population.

In order to prove these stability qualities with certainty, we linearize the system of nonlinear differential equations around the equilibrium points and obtain the Jacobian matrix that corresponds to it. In order to learn how solutions, act locally around the equilibria, we examine the eigenvalues of the Jacobian matrix. While the presence of eigenvalues with positive real parts when $R_0 > 1$ indicates instability and sustained disease transmission, the results show that all eigenvalues have negative real parts when $R_0 < 1$, guaranteeing asymptotic stability of the DFE. These results from the analysis show how important control-related factors are for reducing the basic reproduction number and managing the disease's spread, such as treatment rates, prevention initiatives, and transmission reduction.

6. Numerical Simulation

To back up the analytical conclusions obtained from the model, numerical simulations are carried out using the fourth-order Runge-Kutta (RK4) method. The goal is to get approximate solutions of the nonlinear system of differential equations. Because of its effectiveness in solving coupled ordinary differential equations, numerical stability, and high accuracy, the RK4 approach is preferred for epidemiological modelling. By running the simulations under various control conditions, we can see how the susceptible, infected, and recovered populations changed over time.

The starting conditions are chosen to mimic a real-life epidemic, where the majority of people are susceptible although only a tiny percentage of them get sick at first. This model assumes a completely nonexistent recovered population at the outset and sets the vulnerable population at 95% of the overall population, the infected population at 5%, and the recovered population at a trivial amount. The disease is moderately contagious, thus the transmission rate (β) is set at 0.3, while the recovery rate (γ) is set to

0.1. To study the effects of vaccination and treatment rates on illness dynamics, we use them as variable control parameters, u_1 and u_2 , respectively. The simulations examine the effects of various intervention intensities on the peak magnitude of infections, the duration of outbreaks, and the overall success of disease control measures by methodically altering these control rates.

7. Results

The simulation results clearly demonstrate that increasing the rates of vaccination and treatment has a substantial impact on controlling the spread of the infectious disease. As the vaccination rate increases, the number of susceptible individuals declines, which directly limits the potential for new infections and results in a noticeable reduction in the peak number of infected individuals. Similarly, higher treatment rates shorten the infectious period by accelerating recovery, thereby decreasing both the intensity and duration of disease transmission. Together, these effects lead to a significant flattening of the infection curve and a reduction in overall disease burden.

Furthermore, the simulations reveal that stronger and timely implementation of control measures leads to faster disease eradication, with the infected population declining rapidly to zero. In contrast, scenarios with low or delayed control intensity exhibit prolonged outbreaks, characterized by higher infection peaks and extended persistence of the disease within the population. These findings emphasize the importance of adopting combined control strategies rather than relying on a single intervention. The results validate the effectiveness of integrating vaccination and treatment measures, highlighting their critical role in achieving efficient disease control and informing evidence-based public health planning.

8. Conclusion

In order to analyse the dynamics of infectious disease transmission and the effectiveness of different control methods, this work provides a comprehensive mathematical model based on differential equations. To allow for a systematic examination of their influence on the disease's progression, the proposed model incorporates crucial intervention mechanisms and epidemiological markers. To confirm the theoretical results and capture correct disease behaviour throughout time, analytical investigations like stability and equilibrium analysis are employed in conjunction with comprehensive numerical simulations. The results show that infection prevalence can be significantly decreased by putting in place suitable control measures such as immunisation, treatment, isolation, and preventive

awareness. Specifically, the results show that when the fundamental reproduction number is successfully lowered below unity, disease elimination is possible. The established modelling and simulation framework may be easily modified to analyse newly developing and reemerging infectious illnesses under various epidemiological scenarios, and it offers a reliable and adaptable tool for assessing public health intervention efforts.

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