Mathematical Model of Infectious Disease Transmission

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Abstract: A mathematical model of biological processes has helped us better understand and anticipate how life works in the actual world. Because they provide real-time decision assistance, mathematical techniques have had a tremendous impact on research into illness and emerging epidemics all over the world. Control and prevention of infectious illness transmission need a full knowledge of the elements that influence their occurrence. There are several aspects of infectious disease transmission that are particularly relevant to public health experts, and this article provides an overview of the most important ones. This paper also goes over some of the fundamentals of diagnosing, treating, and preventing infectious diseases.

Keywords: Mathematical Model of Biological Processes, Control and Prevention of Infectious Illness, Infectious Disease Transmission.

I. Introduction

It is possible to describe an infectious disease as an ailment caused by a pathogen or its toxic product, which is transmitted from an infected human, an infected animal, or a contaminated inanimate item to a vulnerable host. Globally, infectious illnesses place a heavy strain on public health systems and economy, disproportionately harming the most disadvantaged. A total of 45 million years of disability and 9 million deaths were attributed to infectious illnesses in 2013. There are many health problems that may cause death across the world. Among the most common are infections of the lower respiratory tract, diarrheal illnesses, HIV/AIDS, malaria, and tuberculosis (TB). Emerging infectious illnesses, such as Middle East Respiratory Syndrome (MERS), or drug-resistant tuberculosis (XDR TB) and the Zika virus, have also been included in the category of infectious diseases. Control and prevention of infectious illness transmission need a full knowledge of the elements that influence their occurrence. Some of the most important aspects of infectious disease transmission are discussed in this article, including the role played by the illness's agent, host, and environmental factors.

II. Literature Review

Wang et al. (2019), A stochastic epidemic mathematical model is developed in this paper to represent two separate viral illnesses that spread concurrently by both horizontal and vertical transmissions, taking into account the influence of environmental disruption. In order to demonstrate that our model is well-posed and of biological importance, we establish the existence and uniqueness of a positive solution. As a result of applying Ito's formula and Chebyshev's inequality, we also establish the necessary conditions for stochastic ultimate boundedness by constructing suitable Lyapunov functions (which can prove the stability of a certain fixed point in dynamical system or autonomous differential equation). Furthermore, we show stochastic permanence when certain key parameters and all of the stochastically perturbed intensities meet a certain connection. For the system to survive, the perturbed intensities must not exceed a specific positive value that is up-bounded by certain system parameters. To further demonstrate the validity of theoretical conclusions, numerical simulations are used. Lastly, in the discussion section, we posed two crucial and intriguing topics that need more research.

Miller et al. (2012), Kermack & McKendrick's mass action susceptible–infected–recovered model is the most important tool for forecasting infectious disease transmission and therapeutic success. Despite its simplicity, it presupposes that all people have the same contact rate and that all relationships are short-lived, which is not the case. We eliminate these assumptions in our work through the use of edge-based compartmental modelling. Models that capture social heterogeneity (heterogeneous contact rates) while explicitly incorporating the influence of relationship time have been developed. An easy-to-understand graphical description of the model is introduced and we concentrate on applying it under various assumptions about how contact rates are distributed and how long relationships survive.

Ciaran et al. (2013), The construction of a global monitoring network to battle emerging and re-emerging infectious disease pandemics has accelerated in recent years due to a concerted global effort. In order to rapidly examine potentially critical circumstances involving many different disciplines, including medical and molecular biology as well as computer science and applied mathematics, a group of scientists has come together. Attempts to forecast, analyse, and restrict the spread of disease rely heavily on mathematical modelling to help achieve this goal. Numerous variables, from the micro-host-pathogen level to host-to-host interactions, as well as prevalent global ecological, social, economic, and demographic aspects, must be researched and carefully studied in order to better understand and predict contagious dynamics. In this section, we show and discuss the most common methods used to monitor and simulate the dynamics of infectious diseases. For each area, we provide an annotated list of exemplary works, and we explain the key principles driving their implementation and practise.

SM Jenness et al. (2018), Package EpiModel is a set of tools for creating, executing, and evaluating mathematical models of infectious disease transmission in R. Models of epidemic spread are provided in this programme, but the distinctive feature is a stochastic framework for simulating epidemic transmission on networks. It is possible to root epidemic modelling on real data on contacts that potentially transmit illness using recent improvements in statistical approaches for network analysis (temporal exponential random graph models). An overview of EpiModel's modelling tools and its application programming interface for extending the package is provided in this article. The modelling tools are intended to help students who are new to modelling learn the basics, while the API is intended to help advanced modellers explore new research questions.

Chisholm et al. (2018), While certain hosts may contain and spread diseases such as Staphylococcus aureus and Streptococcus pneumoniae, they may not show any symptoms themselves. As long as these asymptomatic carriers remain unrecognised, they continue to transmit illness unchecked. A better understanding of how illness spreads and how carriers spread it is critical to designing effective prevention and control measures. Infectious illness mathematical models are widely employed to influence control choices and, as a result, should appropriately describe the role performed by asymptomatic carriers in the disease. Due to the lack of concrete data, it is difficult to include asymptomatic carriers into models. As a result of the lack of data, model parameters and the model structure itself are subject to ambiguity. A novel model of disease transmission with asymptomatic carriage has been proposed in order to explore the consequences of this ambiguity. It is possible to draw various conclusions regarding disease transmission and control using alternative assumptions about the function of asymptomatic carriers. Even if parameters are accurately assessed, using an unsuitable model structure might lead to over or under estimations of intervention efficacy. It's critical to appropriately account for carriers in models used to make control choices regarding illness, since our findings demonstrate the necessity of doing so.

Greenhalgh et al. (2015), The influence of public education campaigns on an epidemic of an infectious illness is examined using a mathematical model that we developed and tested. Affected individuals are divided into two groups: those who are conscious of their vulnerability and those who are oblivious of their vulnerability. It's possible for the system to achieve both a disease-free and an endemic equilibrium. From this, it is possible to deduce both the expression for the fundamental reproduction number and the criteria necessary to ensure the stability of equilibrium systems. The model is further improved and studied by including two time-delay components, one for the time lag in memory fading of knowledgeable persons and another for the delay between instances of illness arising and increasing awareness initiatives. Positive bounded solutions exist for the delayed system. A Hopf bifurcation occurs as the time delay increases and we demonstrate that in general the system oscillates in a limit cycle. We demonstrate the system's permanence under certain parameter circumstances. The numerical simulations on the model, utilising genuine Pneumococcus characteristics, are carried out in order to validate our analytical conclusions.

III. Mathematical Modelling

It is possible to approximate the behaviour of an epidemic in a closed system using deterministic infectious disease models, which divide the population into compartments that represent different disease states, and use differential equations appearing as derivatives to describe the movement between these states over time. Assuming a complete population N (equation 1), which is originally located in a compartment termed susceptible (S equation 2), which following the introduction of a disease, progressively travels to the compartment infected (I equation 3), according to the differential equations below:

Equation 1 $N=S+I$, $N=S+I$, where

Equation 2 $dS/st=-\beta+1$,
Equation 3 $dI/dt=\beta SI$.

Figure 1 illustrates the SI model, where the negative sign before the infection rate () shows that S x I declines among the individuals in compartment S while the number of infected persons increases proportionally (on the left side). Because there aren't any more susceptible people to sustain new instances when a system achieves saturation, this model can't accurately depict the natural fall in the number of cases that occurs after infection and exponential rise in the number of cases have occurred. In this regard, the SI model is more suited to infectious disorders such as HIV, which are long-lasting and do not respond to treatment.

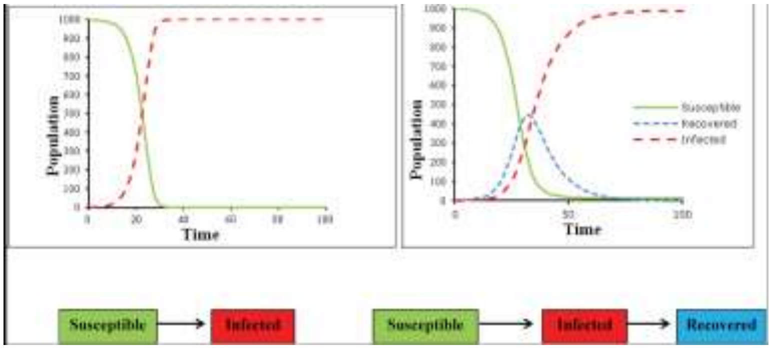

Fig1: infectious disorders such as HIV

Thus, the inclusion of a new compartment capable of capturing the drop in epidemic curves owing to acquired immunity or mortality adds greater realism and application to self-limiting or treated illnesses to the system. R equation 7 emphasises that no matter how many people are infected, the recovered or eliminated (new compartment) amount should rise exponentially with the number of infected multiplied by the recovery constant.

In this case, the system of equations becomes:
Equation 4 $N=S+I+R$,
Equation 5 $dS/dt=-\beta SIN$,
Equation 6 $dI/dt=\beta SIN-\gamma I$,
Equation 7 $dR/dt=\gamma I$.

For infectious diseases, this new compartment makes the graphic representation capable of describing their epidemiological behaviour, as shown in Figure 1 (right): the number of susceptible individuals decreases as the number of infections rises, and the number of recovered people rises when there are fewer infected people. To emphasise, the deterministic models are not limited to a single SI or SIR structure, but rather can incorporate a variety of structures and dynamics into the deterministic systems, resulting in more realistic epidemic representations of infectious diseases, such as the incubation period (E), age stratification, and spatial structures.

IV. Conclusion

The development of a mathematical model of biological processes has assisted us in better understanding and anticipating how life functions in our real world. Throughout the globe, mathematical approaches have had a significant influence on study into sickness and developing epidemics due to the fact that they give real-time decision help. Control and prevention of infectious disease transmission need a thorough understanding of the factors that determine the emergence of infectious diseases. There are various elements of infectious disease transmission that are especially relevant to public health professionals, and this article gives an overview of the most significant of these characteristics for public health professionals. Aspects of diagnosing, treating, and preventing infectious illnesses will also be covered in more depth.

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