Mathematical Model on Epidemiology

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Abstract: There has never been a time in human history when communicable illnesses haven't played a significant role. Epidemics have plagued societies from the beginning of recorded history, causing many fatalities before dissipating, potentially returning years later, and possibly reducing in intensity as people get more used to the illness. Some infectious organisms cause many fatalities before vanishing, while others resurface years later in populations that have developed some degree of tolerance from previous exposure to the same or similar diseases. This paper analysis the mathematical model for epidemiology.

Key Word: Epidemiology, Mathematical model, Infectious Disease

I. Introduction

Epidemiology is a scientific discipline that focuses on studying the spread of illness and its origins among large groups of people. Individuals are considered as part of a larger community in epidemiology. Health-related states and events (not just illnesses) are studied in epidemiology, which is defined as the study of the distribution, patterns, and causes (causes) of health-related states and occurrences (not just diseases) (neighbourhood, school, city, state, country, global). Furthermore, this study's applicability to the control of health issues is equally important. Infectious disease epidemics may be predicted using mathematical models, which can assist guide public health and plant health measures. Assumptions are made about various infectious illnesses, and these assumptions are used with gathered data and mathematics to quantify the consequences of various treatments, including mass vaccination campaigns. Modeling may aid in making decisions on which interventions to avoid and which to try, or it can forecast future development trends, etc. The notion that infectious illness transmission and dissemination may be explained mathematically is a venerable one. Mathematical life table analysis was used by Daniel Bernoulli to study smallpox variation and its impact on life expectancy in 1766. It wasn't until the twentieth century that infectious illness transmission patterns were finally recognised. An epidemic's ferocity may have changed throughout the course of the outbreak, which may explain why it terminated before all of its victims had been infected, in the early 1900s. Hamer (1906) was one of the first to realise that the epidemic could be brought to a stop only if the number of people who were vulnerable to the disease decreased. Nobel Prize-winning malaria researcher Sir Ronald Ross employed mathematical modelling to test potential interventions for the disease, which he discovered in 1902 and was awarded the Nobel Prize for in 1902.

In a series of studies published in 1927, Kermack and McKendrick used a set of differential equations to explain the dynamics of disease transmission. To distinguish between distinct dynamic regimes, they developed the idea of a threshold quantity. An infectious illness may only spread to a vulnerable population if the so-called basic reproduction number is greater than a certain threshold value. As a result, the notion of herd immunity, which states that it is not essential to vaccinate the whole population in order to eradicate an infectious illness, is born. When smallpox was eradicated in the 1970s, this hypothesis came into its own. In conjunction with ring vaccination, immunisation coverage of roughly 80% globally was adequate to eradicate this virus. Epidemiologists collect and analyse data as a first step in responding to a public health emergency or as part of routine monitoring. In order to identify a pathogen (when it is unknown) behind an observed illness epidemic or to design or execute policies to mitigate its effect, researchers employ data, observations, science, and theory. When it comes to anticipating or minimising the effect on populations at risk, knowing the origins and routes of transmission of each illness is very essential. Both short-term and long-term planning for disease management has been greatly aided by the use of mathematical models. In epidemiology and public health policy, mathematical models have played an important role. To better understand illness dynamics and control, we'll go through a variety of models and techniques. Researchers in the disciplines of epidemiology, public health, and allied subjects will benefit from this book's methodology for using modelling and computational techniques to better understand how diseases spread and regulate their spread.

II. Literature Review

Kovesdy (2016), More than 800 million people worldwide are affected with chronic kidney disease, which is a degenerative disorder that affects more than 10% of the general population. Chronic kidney disease is more common in the elderly, women, persons with diabetes, and those with high blood pressure. The burden of chronic kidney disease is disproportionately heavy in nations with low and intermediate incomes, where resources are scarcest to address the problem. One of the few non-communicable illnesses to have seen a rise in the number of fatalities connected with it over the last two decades is chronic renal disease, which is now one of the top causes of death globally. As chronic kidney disease affects a large number of people and has a substantial negative effect, more efforts should be made to prevent and cure it.

Vytla et al. (2018), There is a pressing need for accurate mathematical models to anticipate the spread of novel Coronavirus (Covid-19). Non-pharmaceutical interventions, medical resources, and risk variables are all affected by the outcomes of these models. Predictive power, practical validity, assumptions and limitations are all taken into account while evaluating popular mathematical models. The emphasis of this study is on widely used methods for Covid-19 pandemic forecasting. These methodologies, as well as the most recent developments in -SEIHRD, are discussed in the study.

Olivares & Staffetti (2017), In this research, a mathematical model of the SARS-CoV-2 viral transmission dynamics with mass vaccination method has been analysed for uncertainty quantification and sensitivity analysis. To be more precise, a compartmental epidemic model has been examined, in which vaccination, social distance measurements, and testing of vulnerable people have all been taken into account Because there is a degree of uncertainty associated with the use of these mitigation measures (social distance and testing of susceptible persons), the consequences of this uncertainty on the disease transmission have been evaluated, under the premise of mass vaccination. The polynomial chaos expansion of the output random variables has been used to depict the uncertainty propagation via the epidemic model. Statistically moment-based polynomial chaos expansion has been implemented, providing a substitute model for compartments of an epidemic simulation model and allowing statistical estimations to be made, as well as a sensitivity analysis to be carried out on interest-producing output variables of the simulation model at a given time instant. Sensitivity analysis is a method for determining which model parameters have the greatest impact on the model's output random variable at a particular time interval. When it comes to healthcare resource planning, a number of numerical experiments have shown that the suggested spectrum approach to the measurement of uncertainty and sensitivity analysis of epidemic models is a helpful tool.

Widyaningsih et al. (2018), The diabetes complication (DC) model was used to develop a mathematical model for estimating the prevalence of diabetics. Uncomplicated diabetics (D) and complicated diabetics (C) were the two categories of diabetics in the DC model (C). Diabetes is a condition that may be influenced by both genetics and one's diet and exercise habits. A person who is predisposed to developing diabetes has a poor quality of life. Risky social interactions have a significant impact on a person's unhealthy lifestyle. Diabetic genetic condition is caused by a combination of hereditary and environmental factors. As a result of these considerations, the DC model was transformed into an SDC model. Risky contacts were calculated with the participation of vulnerable persons. It is a nonlinear differential equation of the first order. The solution to this model reveals the number of people and the rate of change in each section. Diabetic prevalence in the U.S. is examined in this study using a model called the SDC. Thus, the SDC model is capable of predicting the prevalence.

Perasso (2018), Introduction of R0 in mathematical epidemiology is presented in this paper. Next, we explain how to calculate its mathematical definition in epidemic models defined by ordinary differential equations after providing a historical recall of the processes leading up to it (ODEs). An infectious load-structured PDE model and four ODE examples are used to demonstrate the R0's applicability to biological and mathematical problems.

Ndii, & Supriatna, (2017), The dynamics of disease transmission may be studied using a stochastic epidemic model. A major difficulty in stochastic epidemic modelling is the determination of illness persistence or extinguishment. A recent study examines the impact of parameter sensitivity on extinction probability using stochastic epidemic models. Simple epidemic models with direct transmission, vaccinations, and vector-borne illnesses are the focus of this research. Deterministic and stochastic epidemic models are described, together with the likelihood of extinction. In this paper, we report fresh findings on how several characteristics affect the likelihood of extinction.

Kretzschmar & Wallinga, (2009), The notion that infectious illness transmission and dissemination may be explained mathematically is a venerable one. Mathematical life table analysis was used by Daniel Bernoulli to study smallpox variation and its impact on life expectancy in 1766. It wasn't until the twentieth century that infectious illness transmission patterns were finally recognised. An epidemic's ferocity may have changed throughout the course of the outbreak, which may explain why it terminated before all of its victims had been infected, in the early 1900s.

Perelman et al. (2004) This study is dedicated to the building of the mathematical model of the TB morbidity dynamics. The model takes into consideration the characteristics of morbidity epidemiology and its management. The model is tuned to the data obtained in the Orlovskaya oblast. The findings acquired will be utilized for the study of the epidemiological situation and devising the effective strategy of TB control.

Brauer (2009) A short account of the relevance of communicable illnesses in history and the development of mathematical models of disease transmission is presented. This comprises reasons for mathematical modelling, the history of mathematical modelling from the foundations set in the late nineteenth century to the present, some of the successes of mathematical modelling, and some problems for the future. Our objective is to highlight the usefulness of mathematical modelling for the study and control of infectious disease transmission.

Huppert & Katriel (2013) They explore to what degree disease transmission models produce trustworthy predictions. The notion of prediction is outlined as it is understood by modellers, and demonstrated by several classic and modern cases. A requirement for a model to make good predictions is that the assumptions underpinning it match to the reality, but such correlation is always limited—all models are simplifications of reality. A basic principle of the modelling endeavor is what we may term the ‘robustness thesis': a model whose assumptions nearly match to reality will produce predictions that are approximately true. To determine whether of the predictions produced by a model are trustworthy, it is vital to analyze the results of multiple models. Thus, if a very simplified model makes a forecast, and if the same or a very similar prediction is made by a more detailed model that contains certain processes or features that the original model did not, then we gain some confidence that the prediction is resilient. An essential advantage acquired from mathematical modelling activity is that it requires openness and correctness about our assumptions, therefore allowing us to assess our grasp of the disease epidemiology by comparing model findings with actual patterns. Models may also aid in decision-making by producing forecasts about crucial concerns such as intervention-induced changes in the spread of illness.

III. Basic Concepts in Mathematical Modeling

Transmission models, as opposed to statistical models, focus on a mechanical explanation of how an illness spreads from one person to another. With this mechanistic definition, it is feasible to integrate the individual level transmission mechanism with a population-level description of infectious disease incidence and prevalence in mathematical terms. Because of the precision with which these relationships must be mathematically formulated, a thorough examination of all dynamic processes that contribute to disease transmission is required. A mathematical model helps to concentrate on the main processes that shape an infectious disease's epidemiology, and it reveals the factors that are most significant and controllable. When used to fields as diverse as microbiology, sociology, and medicine, mathematical modelling may serve as an integrative tool. Individuals may be characterised as "vulnerable," "infected," or "recovered and immune" for a variety of illnesses, including influenza and smallpox. These are the phases of infection that people who are vulnerable to an epidemic go through (Fig. 1).

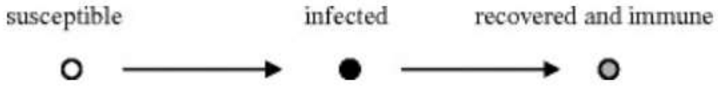

Fig. 1: Transition of an individual through different stages of infection

It's a vital statistic in infectious disease epidemiology: the number of secondary cases that are infected by one infectious person, known as the R-value. An epidemic with a reproduction number of three, R, may be shown to follow a standard pattern (here the generation time equals the duration of infectivity; Fig. 2).

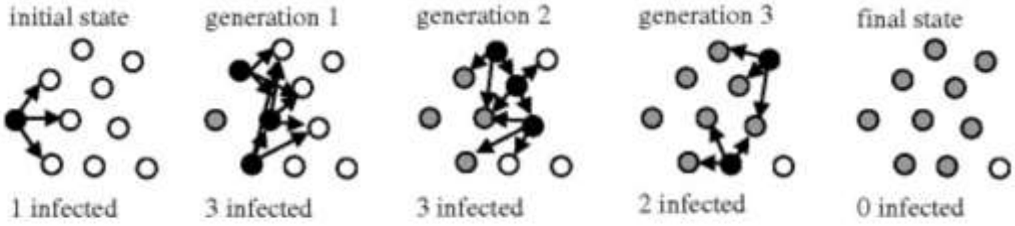

Fig. 2 Propagation of infection through a small population

There is an exponential rise in new infections in Fig. 2 that is proportional to the reproduction number R. In the course of the epidemic, the number of people who are vulnerable to the disease decreases. When the final afflicted individual is no longer able to infect anybody else, the pandemic has come to a close.

IV. Conclusion and Future Work

There has never been a period in human history in which infectious diseases did not play a substantial part in the lives of people. For as long as humans have been recording history, epidemics have afflicted human cultures, producing a large number of deaths before dispersing, sometimes returning years later, and possibly decreasing in severity as people get used to the sickness. Some infectious organisms cause a large number of deaths before disappearing, whilst others reappear years later in populations that have gained some degree of resistance to the same or comparable illnesses as they did before after being exposed to them. This study examines the mathematical model used in epidemiological research.

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