

The Analysis of Epidemic Diffusion Models

Suning Sun

School of management, Shanghai University, Shanghai 200444, China

suning_sun@163.com

Abstract

The struggle between human beings and infectious diseases has a long history, such as SARS, H1N1, and Ebola, infectious diseases do more harm to human beings than all wars combined. An epidemic is the rapid spread of an infectious disease within a population. However, infectious disease is exclusive and variable. In order to depict the dynamic diffusion of infectious disease, many scholars have studied the epidemic diffusion models. In this paper, we provide a literature of these research. Meanwhile, we will introduce SEIR models in detail.

Keywords

Infectious Disease; Epidemic Diffusion Models; SEIR.

1. Introduction

In the Regulations on Emergency Response to Public Health Emergencies promulgated by the State Council in May 2003, a public health emergency is defined as "major epidemics of infectious diseases, mass unexplained diseases, major food and occupational poisoning and other events affecting public health that occur suddenly and cause or may cause serious damage to public health, major food and occupational poisoning and other events affecting public health". Among these public health emergencies, major infectious diseases epidemics pose a particularly serious threat to public health safety.

The struggle between human beings and infectious diseases has a long history, such as SARS, H1N1, and Ebola, infectious diseases do more harm to human beings than all wars combined. An epidemic is the rapid spread of an infectious disease within a population, producing many infected individuals in a short period of time [1]. Due to increased social contact, accessibility of transportation, changes in wildlife trade and consumption, the frequency of epidemic has increased over the past century [2]. To date, six global public health emergencies have been classified as PHEIC. Examples of PHEIC include the 2009 H1N1 influenza, the 2014 Ebola virus in West Africa, the 2014 wild poliovirus, the 2015-2016 Zika virus, the 2018 Ebola virus in Congo and the 2019 coronavirus (COVID-19) in China. The epidemic diffusion model is applied to describe the spread of infectious disease and predict the its future trends. This information is essential for controlling the spread of an epidemic [1]. For example, epidemic diffusion models can be used to estimate several effects of epidemics, such as the total number of infected individuals, the demand of medical resources, and the effects of possible prevention measures (social distance, immunization or isolation) [3].

2. Literature Review of Epidemic Diffusion Models

With international trade and population movements brought about by globalisation, when public health emergencies of the infectious disease type occur, epidemics gradually spread. During the epidemic cycle of an infectious disease, the number of infected patients changes constantly, leading to a corresponding change in the demand for healthcare resources. Considering the dynamic time-

sensitive characteristics of infectious diseases, a model to describe the spread of infectious diseases quantitatively can provide an effective basis for infectious disease assessment and response [4].

Considering the characteristics of different infectious diseases, most scholars have designed different models of infectious disease dynamics based on infectious disease theory. Kermack and McKendrick [5], in their study of the Black Death, classified the population in the study area into three categories, Susceptible, Infective and Recoverer, and proposed the well-known The SIR compartment model was developed for infectious diseases transmitted by viruses. Subsequently, Kermack et al [6] created the SIS model based on the SIR compartment model. Kermack et al [6] then created the SIS compartment model based on the SIR compartment model and proposed the well-known threshold theorem. However, considering that many infectious diseases are usually preceded by an incubation period of However, considering that many infectious diseases usually have an incubation period of a certain length of time before the onset of the disease, e.g. AIDS has an incubation period of 2 to 12 years and rabies has an incubation period of 1-3 months, later studies have built on the SIR model. The SIR model has been refined to include a new group of infectious diseases, namely the Exposed, and the SEIR model has been developed. SEIR model. In recent years, many scholars have used the SEIR model to describe the trend of infectious diseases with latency period. For example, Sun and Hsieh[7] examined a SEIR model with different population scales and vaccination tactics. Liu et al. [8] described the medical resource allocation problem during an epidemic outbreak based on the SEIR model, and developed a multi-stage integer planning model with time-varying demand. For COVID-19, Yang et al. [9] developed an extended SEIR model based on the population inflow and outflow data of Wuhan province. Simultaneously, they predicted the spread trend and peak of COVID-19 by combining the training method with data from SARS epidemic in 2003

The second stream of research related to simulation methods including computer simulation and numerical methods to characterize the diffusion of infectious diseases. To test the impact of three control strategies (maintaining social distance, rapid case confirmation, and timely prevention), Elizabeth Halloran et al. [10] constructed a stochastic simulation model. The results showed that the timely prevention strategy was more effective. Kim et al. [11] and Liu and Zhang [12] all adopted numerical calculations and computer simulation methods to establish and optimize infectious disease models. In addition, Samsuzzoha et al. [13]proposed a diffuse compartmentalized epidemiological model of vaccination to investigate the effect of vaccination and diffusion on trend in influenza transmission. Most recently, Dasaklis et al. [14] addressed the problem of smallpox outbreak in two modules, one to simulate the disease progression and the other to develop a linear programming model to rationally distribute medical supplies to affected populations.

Another stream of works combined network theory to explain the diffusion of infectious diseases. Network theories commonly used included complex network, random network, scale-free network, small-world networks, etc. For instance, Eames and Keeling [15] proposed a mechanism to forecast the transmission of infection through the contact network, meanwhile, they developed a mathematical framework to tackle the heterogeneity implied within the contact network and those arising due to the infection process. Considering the realistic urban social networks, Eubank et al. [16] analysed the relative strengths of some proposed strategies to mitigate smallpox transmission. The results suggested that targeted vaccination in conjunction with earlier detection could be effective in controlling epidemics. Keeling and Eames [17] reviewed the foundations of epidemiological and network theories (random networks, small-world networks, spatial networks and scale-free networks), and argued that network theory associated with epidemiological modelling could be more effective in preventing epidemics.

3. The Analysis of SEIR Diffusion Model

Infectious disease kinetic models are used to predict the development trend of an epidemic based on the development pattern of infectious diseases and the characteristics of each population, and to characterise the number of patients at each time period, thus providing a basis for epidemic prevention

and control. Currently, the commonly used infectious disease dynamics models include SIR model, SEIR model, SEIAR model, etc. Only the SEIR model is described in detail in this section.

Taking into account the infectious characteristics of infectious diseases, the SEIR model divides the total population into four categories: Susceptible, Exposed, Infected and Removed [12]. Of these, all people located in the infected area are considered susceptible. If a susceptible population comes into contact with an infected person, it becomes a latent population, which is not infectious. When a latent population becomes infectious after an incubation period, it becomes an infected population. A diagram of the SEIR model is shown in Figure 1.

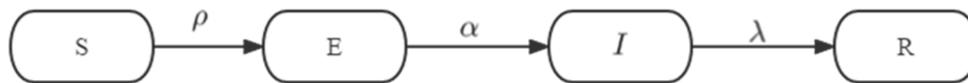


Fig 1. SEIR model

The numbers of the four population groups at time t are denoted by $S(t)$, $E(t)$, $I(t)$, $R(t)$, respectively. The differential equations of the SEIR model are shown in (1)-(5), without considering the birth and death rates and the inflow and outflow of the population.

$$\frac{dS(t)}{dt} = -\rho I(t)S(t)/N \quad (1)$$

$$\frac{dE(t)}{dt} = \frac{\rho I(t)S(t)}{N} - \alpha E(t) \quad (2)$$

$$\frac{dI(t)}{dt} = \alpha E(t) - \lambda I(t) \quad (3)$$

$$dR(t)/dt = \lambda I(t) \quad (4)$$

$$S(0) = S_0, E(0) = E_0, I(0) = I_0, R(0) = R_0 \quad (5)$$

In this model, ρ , α and λ denote the rate of infection from susceptible to latent population, the rate of infection from latent population to infected population and the rate of infected patients to migrated population, respectively. S_0 , E_0 , I_0 and R_0 denote the initial number of people in the four categories, respectively, and N denotes the total number of people in the infected area. Also, $S(0) + E(0) + I(0) + R(0) = N$.

4. Conclusion

In this paper, the researches about the epidemic diffusion models have been reviewed. Meanwhile, we have introduced SEIR diffusion model in detail, which can improve the application of the epidemic diffusion models.

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