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Stability analysis of a novel epidemics model with vaccination and nonlinear infectious rate

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ABSTRACT

In this paper, by considering pathogen evolution and human interventions behaviors with vaccines or drugs, we build up a novel SEIRW model with the vaccination to the newborn children. The stability of the SEIRW model with time-varying perturbation to predict the evolution tendency of the disease is analyzed. Furthermore, we introduce a time-varying delay into the susceptible and infective stages in the model and give some global exponential stability criteria for the time-varying delay system. Finally, numerical simulations are presented to verify the results.

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1. Introduction

Infectious diseases result in 14.7 million deaths, 26% of global mortality in accordance with WHO estimates in 2001 [1]. Mathematical analysis and modeling operation of infectious diseases are critical to study virus spreading dynamics which can state clearly the origination and evolution of viruses. In recent years, many mathematical models have been proposed for the transmission dynamics of infectious diseases [2–9] such as, SI (susceptible–infective), SIR (susceptible–infective–removed), SEIR (susceptible–exposure–infective–recovered), SEI (susceptible–exposure–infective), SIRS (susceptible–infective–removed–susceptible), SEIS (susceptible–exposure–infective–susceptible). The development of such models is aimed at exploring the transmission dynamics of epidemic virus, investigating the evolution of resistance to antibiotics and the evolutionary cost of resistance, and designing the programs for disease control. However, a model's ability to achieve the above goals depends greatly on whether the assumptions made in the modeling process are consistent with the actual evolution of the epidemic diseases. Understanding and predicting the actual transmission dynamics of the epidemic diseases is, therefore, an important pursuit in mathematical epidemiology, which is one of our motivations for this work.

At the same time, the stability analysis of epidemic models has also attracted much attention of biologists, mathematicians and ecologists. The underlying reason behind such attention is that through stability analysis for the epidemic models, the tendency of the infectious diseases can be found by the basic reproductive number R_0 (the average number of secondary cases produced by a typical primary case in an entirely susceptible population) and the generation time (the average time from symptom onset in a primary case to symptom onset in a secondary case), which determine to a large extent the speed of epidemic outbreaks. Based on the stability principles, the conditions of the infectious diseases persistence or extinction were obtained [10–15].

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Huang [3] presented an SEIR model, which is suitable for the eradication of diseases by mass vaccination or the control of diseases by case isolation combined with contact tracing, incorporating the vaccine efficacy or the control efficacy into the model. An SIRC model with a fourth class, i.e., the cross-immune individuals, was proposed [9]. Via bifurcation analysis of the model, they discussed the effect of seasonality on the epidemiological regimes. In this model, the incubation period of virus is not considered, nevertheless, a majority of infectious diseases have incubation period. Buonomo et al. [16] studied the global behavior of a non-linear SIR epidemic model with a non-bilinear feedback mechanism, which describes the influences of information and information-related delays on a vaccination campaign. Wan and Cui [17] proposed an SEIS epidemic model to study the effect of transport-related infection on the spread and control of infectious disease. Furthermore, through stability analysis, they found that it is very essential to strengthen restrictions of passengers once infectious diseases appearance is known. In [18], McCluskey studied the complete global stability for the SIR models with distributed delay and with discrete delay. Lahrouz et al. [19] analyzed the complete global stability for an SIRS epidemic model with generalized nonlinear incidence and vaccination. In [20], Kuniya studied the global asymptotic stability for an age-structured multigroup SIR epidemic model with a discretization approach. Muroya et al. [21] investigated the global asymptotic stability of a disease transmission model of SIRS type with latent period and the specific non-monotone incidence rate. The results of these studies, however, do not take into account the whole process of the epidemic diseases such as the exposed fraction and the partial immunity individuals, which are to a great extent owing to deficiency of the genetic variation behavior of the virus and the epidemiology theory. Consequently, they are limited on reflecting the actual transmission dynamics of the epidemic diseases and offering the practical proposal for government to draw up the policy.

On the other hand, human interference behaviors such as enhancing the host's immune system with drugs or vaccines that alter pathogen genetic diversity, carrying out public health educational campaigns and vaccination in adolescents have been incorporated into the epidemic diseases models [22–25]. Mathematical models for the spread of infectious diseases are an important tool for investigating and quantifying such effects of these behaviors. However, few efforts have been made to quantify and capture the effects in a systematic way.

In this paper, to overcome the disadvantages above, by considering more complete processes of the epidemic diseases, we first build a novel susceptible–exposed–infective–recovered–partial immunity (SEIRW) model, which incorporates pathogen evolution and human interventions behaviors with vaccines or drugs that alter pathogen genetic diversity, aiming to reflect the transmission dynamics of infectious diseases more realistically. Our model differs from the existing ones in [17–21] in the following respect: (i) our model additionally takes into account the exposed fraction and the partial immunity individuals; (ii) our model is coupled with evolutionary–epidemic strategy and human interference behaviors such as vaccination to a proportion of all newborn children; (iii) in particular, the force of infection of the infectious disease in the existing work is multiplied by a constant such as survival probability while in this paper, it is governed by a nonlinear time-varying growing curve of pathogens, which reflects the viruses' evolution. Subsequently, we transform the SEIRW model into the ordinary differential equation with time-varying perturbation. Then we carry out a complete stability analysis of the transformed SEIRW model and establish its stability criteria. Furthermore, we introduce the time-varying delay into the susceptible and infective stages of the SEIRW model and provide the globally exponential stability criteria for the SEIRW model with the time-varying delay. Finally, the numerical simulations verify the results. One of our purposes for this work is to investigate the effect of the treatment on the long term dynamics of the disease, and show that the treatment or rational immunization to prolong the susceptible or infective stages can hasten the disease dying out. To the best of our knowledge, this work is the first one that builds a novel SEIRW model by considering pathogen evolution and human interference behaviors, and further establishes sufficient conditions for the asymptotic stability of the model with time-varying perturbation and the global exponential stability of the model with time-varying delay.

The rest of this paper is organized as follows: in Section 2, the infectious rate function of pathogens is obtained. The SEIRW model is provided in Section 3. In Section 4, the stability of the SEIRW model with time-varying perturbation is analyzed. In Section 5, we discuss the global stability of the SEIRW model with time-varying delay by means of suitable Lyapunov functionals. Simulation to verify analysis for the model is gained in Section 6, concluding remarks. Section 7 concludes this work.

2. The infectious rate function of pathogens

Mathematical modeling of the evolution of pathogens responding to the viruses' genetic variation plays an important role in clinical epidemiology and statistics of infectious diseases. In the existing literatures, the mathematical descriptions of the contact rate which implies the infectivity depend on the analysis for the empirical data. Nevertheless, the contact process described by empirical data could be questionable on account of the incomplete statistical methods, e.g., the methods of the investigation based conversational contacts, which describe the spread of respiratory infections, the routine surveys of travel. Furthermore, the contact rate served as the infectious power cannot reflect the evolution of pathogens, especially the viruses' genetic variation in the available studies.

The growing curve of pathogens indicates the speed of viruses spread as it is the coordinate figure of time-viruses number. The one-step growth curves, which reflect pathogen genetic diversity under the condition of interpretation of interventions with drugs or vaccines, have been studied by many biologists [26–29]. Usually, the viruses' growth simulating the viruses' growth curve is expressed by:

$$y = k/(1 + be^{-at}), \quad a, b, k > 0. \tag{1a}$$

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