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Global analysis of an SEIR model with varying population size and vaccination

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ABSTRACT

An SEIR model with varying population size and vaccination strategy is investigated. Three threshold parameters $\mathcal{R}_0, \widehat{\mathcal{R}}_0, \overline{\mathcal{R}}_0$ and $\widetilde{\mathcal{R}}_0$ are obtained to govern the disease eradication, which involve the total number of infectives and their proportion in the population. Parameter conditions on the uniform persistence, the global stability of the disease – "free" equilibrium and the "endemic" equilibrium are derived. The global dynamics of model in population size are studied. The correlations of the two systems in terms of disease eradication, endemicity and disease explosion are summarized and compared. We conjecture that substantially low product of vaccination rate and low vaccine efficacy may lead to complicated dynamics for the system in question.

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1. Introduction

Mathematical modeling for disease transmission in host population is of great practical value in predicting and controlling disease spread (West Nile virus in North America 1990s, Avian influenza worldwide 2000s, SARS in Asia 2003, etc.). The battle between infectious diseases and humans was heavily lopsided for much of the history. Since the pioneering work of Edward Jenner (a doctor, who worked in Gloucestershire, UK, noticed that individuals who had contracted cowpox rarely caught smallpox) on smallpox [1], the process of protecting individuals from infection by vaccination has become routine, with substantial historical success in reducing both morbidity and mortality (see [2,3] and references cited therein). In this paper, we will incorporate a vaccination strategy for disease control into a single host population.

Typically, after the initial infection, the host remains in a latent stage for a period of time before becoming infectious. For some diseases, the latent period is neither short nor negligible comparing with the infectious period (scarlet fever: 1–2 days versus 14–21 days [4]; measles: 4–12 days versus 17–31 days [5]). Distinguished by the evolution history of disease, the heterogeneous population is partitioned into four homogeneous classes: the susceptible $S(t)$, the exposed (in the latent period) $E(t)$, the infective $I(t)$, and the recovered $R(t)$. The total number of population $N(t)$ is denoted by $N(t) = S(t) + E(t) + I(t) + R(t)$, where $N(t)$ is assumed to vary with time since individuals enter and leave the population either through migration, demographics or the disease-induced death, which imbalances the inflows and outflows of a given population. The disease transmission flow is depicted in Fig. 1.

Here the disease is assumed to transmit horizontally, which can occur either by direct contact (licking, touching, biting), or indirect contact (vectors or fomites) with no physical contact. All the offsprings at birth are assumed susceptible to the disease (Cholera, Polio and Hepatitis A are of this case).

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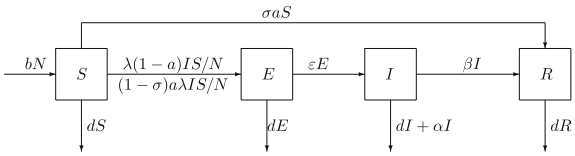

Fig. 1. A schematic representation of the flow of individuals between epidemiological class.

Parameters b and d are the inflow rate (including birth and immigration) and outflow rate (including natural death and emigration), respectively. And α is the constant rate of disease-related death. The proportionate mixing incidence rate is $\lambda IS/N$, i.e., standard incidence, where λ is the effective per capita contact rate of infectious individuals, and I/N is the proportion of contacts between susceptibles and infectives, that is, random mixing is assumed. We assume that susceptible individuals are vaccinated at a constant per capita rate $a(0 \leqslant a < 1)$ (i.e., vaccine coverage rate). Due to the partial efficiency of the vaccine, only $\sigma(0 \leqslant \sigma \leqslant 1)$ fraction of the vaccinated susceptibles goes to the recovered class (i.e., σ is the vaccine efficacy). The remained $1-\sigma$ fraction of the vaccinated susceptibles has no immunity at all and goes to the exposed class after infected by contact with the infectives. When $\sigma = 0$, it means the vaccine has no effect at all, and when $\sigma = 1$, the vaccine is perfectly effective. The parameter ε is the constant rate, at which the exposed individuals become infectious. and $1/\varepsilon$ is then the mean latent period. In the limit when $\varepsilon \to \infty$, the latent period is negligible, and the SEIR model can reduce to an SIR model (see [2,6,7]). Parameter β is the constant rate, at which the infectious individuals recover with acquire permanent immunity. Hence, there is no transfer from class S. R back to class $1/\beta$ is the mean infectious period. When $\beta = 0$, the mean infectious period goes to infinity, which implies that there is no recovery from the disease. The SEIR model then reduces to an SEI model (for example, HIV [8,9]). All the parameters (except the non-negative a, σ) here are assumed positive.

Using these definitions, assumptions and Fig. 1, we derive the following general SEIR model with vaccination and varying population size in a homogeneously mixing population.

$$\begin{aligned} S' &= bN - \lambda(1-a)IS/N - (1-\sigma)a\lambda IS/N - (\sigma a + d)S, \\ E' &= \lambda(1-a)IS/N + (1-\sigma)a\lambda IS/N - (d+\varepsilon)E, \\ I' &= \varepsilon E - (\alpha + \beta + d)I, \\ R' &= \sigma aS + \beta I - dR, \end{aligned} \tag{1}$$

where the derivative d/dt is denoted by $'$.

Moreover, the differential equation of total population size $N(t)$ takes the form:

$$N' = (b-d)N - \alpha I, \tag{2}$$

which is derived by adding the four equations in (1).

The global stability of an SEIR model with nonlinear incidence rates is studied by Sun et al. [10]. Feng [11] give out the final and peak epidemic sizes for SEIR models with quarantine and isolation. Li and Wang [12] systematically analyze the global dynamics of the SEIR model with constant recruitment, and with disease vertical transmission and incorporating perfect vaccination strategy, respectively. Arino et al. [13] consider the vaccine efficacy and waning in an SIRS model and present the occurrence of backward bifurcation leading to bi-stability. The latent time delay is incorporated into the SEIR model by Yan and Liu [14]. All the models above are with constant population size. Busenberg–van den Driessche [15], and Li et al. [16] investigate an SIRS model and an SEIR model with varying population size, respectively. As far as we know, this paper is very novel in analyzing the SEIR model with varying population size and vaccination strategy. The paper is organized in the following manner: We give some well-posed preliminary results and the stability properties of disease-"free" equilibrium of the model in Section 2. Section 3 devotes to the uniform persistence, the existence, local and global stability of the "endemic" equilibrium for the reduced proportional system. In Section 4, we determine the dynamic behaviors of original population model, and obtain the correlation between the original and the reduced models from the perspective of epidemiology. The paper ends up with a discussion.

Remark 1. We have to point out here that there have two distinct concepts of disease eradication and persistence which involve the total number of infectives and their proportion in the population. The quotation marks in disease-"free" and "endemic" only refer to the latter, and however, it can not guarantee the same outcomes happening to the total number of infectives.

2. Disease "eradication"

2.1. Preliminary results

In the situation that the total population size $N(t)$ is not constant, it is often necessary to consider the proportions of individuals in four epidemiological classes, namely,

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