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Global analysis of a model of differential susceptibility induced by genetics

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ABSTRACT

This paper is concerned with global analysis of an SIS epidemiological model in a population of varying size with two dissimilar groups of susceptible individuals. We prove that this system has no periodic solutions and use the Poincaré index theorem to determine the number of rest points and their stability properties. It has been shown that multiple equilibria (bistability) occurs for suitable values of parameters. We also give some numerical examples of all possible bifurcations of this system.

1. Introduction

Most of the epidemiological models are multigroup models. Groups can be geographical such as communities, cities and countries, behavioral such as different patterns of contact and high risk groups or epidemiological, to incorporate differential infectivity, vertical transmission and co-infection of multiple strains of the disease agent [1]. In the differential infectivity models, the infective individuals are divided into some groups according to their different levels of infectivity [2]. Medical evidences show that it is reasonable to incorporate differential susceptibility as well [1,3–5].

Genetic variation of susceptible individuals and the active effect of vaccination may lead to the differentiation of susceptibility on infection. In some diseases vaccinated individuals may still contract the disease, but it varies from one individual to the other one. The differential susceptibility has been investigated in the immune system too [6–8]. The results of research on some specific diseases have shown significant differentiation of susceptibility among individuals [9,10]. For example, through their surface expression of CD38, $CD4^+$ T cells have shown differential susceptibility to M- and T-tropic HIV-1 infection. The $CD4^+CD38^-$ and $CD4^+CD45RA^-$ subsets have higher susceptibility to infection with the M-tropic Ba-L strain of HIV-1, and the $CD4^+CD38^+$ subset has higher susceptibility to infection with the T-tropic (LAI) strain of HIV-1 [7].

Hyman et al. in [11] introduced a differential infectivity model with dissimilar groups of infective individuals. In [12] a compartmental differential susceptibility, susceptible-infective-removed (SIR), has been modeled by dividing the susceptible population into multiple subgroups according to the susceptibility of individuals. There are some models which combine differential infectivity and susceptibility [13]. In [14] a couple of SIS and SIR models with differential infectivity and differential susceptibility have been considered and the equilibria, their stabilities and the reproductive number have been determined for these models. Some models are constructed by the combination of differential susceptibility and staged progression [15,16]. A disease transmission model with two groups of infectives has been analyzed in [17]. Multiple

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equilibria for a differential infectivity model with two dissimilar groups of infective individuals has been reported in [18]. In this paper, we show that differential susceptibility may lead to multiple equilibria too. The existence of multiple equilibria and limit cycles has been shown for more complicated systems [19–26].

In this paper, we examine an SIS model of disease transmission in a population of varying size with a homogeneous infective group and two dissimilar groups of susceptible individuals. In our model, the incidence function is of proportionate mixing type introduced by Nold [27]. We assume that the newborns of each susceptible groups have the same properties of susceptibility as their parents. This assumption is plausible for differential susceptibility caused by genetic variation of susceptible individuals. Our model includes vertical transmission and disease-induced mortality.

In Section 2, we first introduce our model equations which is a homogeneous system of degree one. For such a system, it is more convenient to consider the proportions system. In Section 3, we state a result concerning the nonexistence of certain types of the solutions for the proportions system [28]. This result helps us to show that every solution in the feasibility region tends to a rest point. The rest of this paper is mainly concerned with the discussion of existence and stability of equilibria. The technique used here is the Poincaré index theorem which is based on a careful choice of Jordan curves and counting the number of rest points inside them. This technique has no hard analysis and can be easily applied to other similar problems [18,29]. In Section 4, we reduce our system to a planar one to examine its local analysis. In Section 5, we first study the degenerate rest points which determine the bifurcations of the system. Then we state the main theorems of this paper which explore the possible behaviors of the system and then give a set of examples for each of these behaviors. In Section 6, some numerical examples of the bifurcations of the planar system have been established.

2. The model

In order to derive our model, we divide the population into three groups: infective individuals and two groups of susceptible individuals, the size of each of these groups at time t is denoted by $I(t)$, $S_1(t)$ and $S_2(t)$, respectively. Let $N = S_1 + S_2 + I$ be the total size of the population which is assumed to be varying in this paper. The groups S_1 and S_2 have different parameters according to their different properties of susceptibility. We also assume that the newborns of each susceptible groups have the same properties of susceptibility as their parents. The following parameters appear in our model:

b_i : per capita birth rate of S_i;
b'_i : per capita birth rate of I entering S_i;
b'_0 : per capita birth rate of I entering I;
d : per capita disease free death rate;
ε : excess per capita death rate of infectives;
λ_i : effective per capita contact rate of S_i;
γ_i : per capita recovery rate of infectives entering S_i;

where $i \in \{1, 2\}$. All the parameters are assumed to be positive unless otherwise specified. These hypotheses lead to the following system of differential equations in $\mathbb{R}^3_+$, where "′" denotes the derivatives with respect to time, t:

$$\begin{cases} S_1' = b_1 S_1 + b'_1 I - dS_1 + \gamma_1 I - \lambda_1 \dfrac{IS_1}{N}, & \text{(a)} \\ S_2' = b_2 S_2 + b'_2 I - dS_2 + \gamma_2 I - \lambda_2 \dfrac{IS_2}{N}, & \text{(b)} \\ I' = (b'_0 - d - \varepsilon - \gamma) I + \lambda_1 \dfrac{IS_1}{N} + \lambda_2 \dfrac{IS_2}{N}, & \text{(c)} \end{cases} \tag{2.1}$$

where $\frac{\lambda_j I S_j}{N}$ is of the proportionate (or random) mixing type [27,30] and $\gamma := \gamma_1 + \gamma_2$. The total population equation is obtained by the sum of the above three equations:

$$N' = b_1 S_1 + b_2 S_2 + (b' - \varepsilon) I - dN,$$

where $b' = b'_0 + b'_1 + b'_2$.

Since the above system is homogeneous of degree one, it is more convenient to consider the proportions of the population, $s_1 = \frac{S_1}{N}$, $s_2 = \frac{S_2}{N}$ and $i = \frac{I}{N}$. The dynamics of s_1, s_2 and i are governed by the following system of equations:

$$\begin{cases} s_1' = b_1 s_1 + (b'_1 + \gamma_1) i - s_1 (b_1 s_1 + b_2 s_2 + (b' + \lambda_1 - \varepsilon) i), & \text{(a)} \\ s_2' = b_2 s_2 + (b'_2 + \gamma_2) i - s_2 (b_1 s_1 + b_2 s_2 + (b' + \lambda_2 - \varepsilon) i), & \text{(b)} \\ i' = i(b'_0 - \varepsilon - \gamma + (\lambda_1 - b_1) s_1 + (\lambda_2 - b_2) s_2 - (b' - \varepsilon) i). & \text{(c)} \end{cases} \tag{2.1′}$$

In this paper, we investigate the dynamics of the proportions system in the feasibility region:

$$D = \{(s_1, s_2, i) : s_1 + s_2 + i = 1, s_1 \geq 0, s_2 \geq 0, i \geq 0\}.$$