EXISTENCE AND UNIQUENESS OF ENDEMIC STATES FOR AN EPIDEMIC MODEL WITH EXTERNAL FORCE OF INFECTION

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ABSTRACT. The existence and uniqueness of steady states for the age structured S-I-R epidemic model is considered. Intercohort form with external force is considered for the force of infection. Existence is obtained for nonvanishing external force of infection. Uniqueness is shown for the case where there is no vertical transmission of the disease.

1. Introduction

In this paper we study the existence and uniqueness of steady states of an age-structured S-I-R type epidemic model.

In studying the propagation of a disease through a population, it is frequently assumed that the population is structured into three disjoint classes according to disease status: susceptibles (those who are not infected with the disease but may become infected later), infecteds, and removeds (those who are removed from the dynamics of the disease transmission either through immune or through death caused by the disease). Based on these three classes, a frequently used family of models for disease propagation is called S-I-R [1, 4, 5, 6, 9, 10] (In S-I-S model, recovery always takes place without immunity [2, 3, 8], while in S-I model, recovery does not take place at all [7]).

Age structured S-I-R models are suitable for most common childhood diseases (measles, chickenpox, rubella), as well as for many sexually transmitted diseases which impart immunity (syphilis, chlamydia), and also for those diseases, like HIV/AIDS or mad cow disease, which lead to definitive isolation or death.

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Even if infection of the human disease mainly occurs between humans through physical contacts, there are lots of other ways of infection. For instance, one can be infected with HIV/AIDS through blood transfusion.

Mad cow disease is another good example. Although there is still no evidence that indicates the recently emerged human form of mad cow disease, it is believed that potentially a lot of people are affected by that disease. Lots of countries have banned the import of beef or meat-related processed foodstuffs from Britain and other European nations. It seems that mad cow disease appears to have jumped the species barrier from cattle to humans, which means infected animals can be the main source of the infection.

In fact, other than infected human individuals, there are still a lot of sources of infection. We call them *external force of infection*. Thus our model is an S-I-R model with external force of infection.

Even though most of existing S-I-R related literature only deals with the force of infection without external force, which is not a small thing to ignore but an important thing to investigate.

So we consider the following system of integro-differential initialboundary value problem.

(1.1)
$$\begin{cases} \frac{\partial s}{\partial t} + \frac{\partial s}{\partial a} + \mu(a)s = -\lambda(a, t)s, \\ \frac{\partial i}{\partial t} + \frac{\partial i}{\partial a} + \mu(a)i = \lambda(a, t)s - \gamma(a)i, \\ \frac{\partial r}{\partial t} + \frac{\partial r}{\partial a} + \mu(a)r = \gamma(a)i, \\ s(0, t) = \int_0^{a_{\dagger}} \beta(a) \left(s(a, t) + r(a, t) + (1 - q)i(a, t)\right) da, \\ i(0, t) = q \int_0^{a_{\dagger}} \beta(a)i(a, t) da, \\ r(0, t) = 0, \\ i(a, 0) = i_0(a), \quad s(a, 0) = s_0(a), \quad r(a, 0) = r_0(a). \end{cases}$$

Here a is the age of individuals, and t is the time. Also, s(a,t), i(a,t) and r(a,t), respectively, denotes the age-specific density of susceptible, infected, and removed individuals.

 $\beta(a)$ is the birth rate and $\mu(a)$ is the death rate of the population. $q \in [0,1]$ is the vertical transmission parameter, i.e. the probability that

the disease be transmitted from parent to newborn, $\gamma(\cdot)$ is the removal rate of infected individuals, and $\lambda(a,t)$ is the force of infection. Note that since we assume the condition r(0,t)=0, our model assumes that there is no vertical transmission of immunity.

Our main concern is the existence and uniqueness of an *endemic* state of the model. Endemic state is a steady state solution of the model for which the density of infected individuals does not vanish identically. Our main results will be give in section 3 (Theorem 3.3 and theorem 3.4).

Summing the equations in (1.1) we obtain the following problem for the population density p(a,t) = s(a,t) + i(a,t) + r(a,t),

(1.2)
$$\begin{cases} \frac{\partial p}{\partial t} + \frac{\partial p}{\partial a} + \mu(a)p = 0, \\ p(0,t) = \int_0^{a_{\dagger}} \beta(a)p(a,t)da, \\ p(a,0) = p_0(a). \end{cases}$$

This is the standard McKendrick-Von Foester equation. We make the following usual hypotheses for this problem,

(1.3)
$$\beta(\cdot) \in L^{\infty}([0, a_{\dagger})), \qquad \beta(a) \ge 0 \text{ in } [0, a_{\dagger}),$$

(1.4)
$$\mu(\cdot) \in L^1_{loc}([0, a_{\dagger})), \quad \mu(a) \ge 0 \text{ in } [0, a_{\dagger}),$$

(1.5)
$$\int_0^{a_{\dagger}} \mu(a) d\sigma = \infty.$$

Here a_{\dagger} is the maximum age an individual of the population may reach and it may be either finite or infinite. If $a_{\dagger} = \infty$, we also assume that

(1.6) there exists
$$A > 0$$
 such that $\beta(a) = 0$ for $a \ge A$.

Furthermore, in order to deal with a steady state population, we assume that the net reproductive rate of the population is equal to 1 and that the total population is at an equilibrium. This means that

(1.7)
$$\int_0^{a_{\dagger}} \beta(a) e^{-\int_0^a \mu(\sigma) d\sigma} da = 1, \qquad p(a,t) = p_{\infty}(a) = b_0 \pi(a),$$

where

(1.8)
$$\pi(a) = e^{-\int_0^a \mu(\sigma)d\sigma}.$$

Note that the function $\pi(a)$ is the probability that an individual at age 0 can survive until age a. Since no individual may live past age a_{\dagger} , (1.5) is needed.

Clearly, we have to take initial data such that

$$s_0(a) \ge 0, \quad i_0(a) \ge 0, \quad r_0(a) \ge 0, \quad s_0(a) + i_0(a) + r_0(a) = p_{\infty}(a),$$

which gives

$$(1.10) b_0 = \frac{\int_0^{a_{\dagger}} s_0(a) da + \int_0^{a_{\dagger}} i_0(a) da + \int_0^{a_{\dagger}} r_0(a) da}{\int_0^{a_{\dagger}} \pi(a) da}.$$

We assume that

(1.11)
$$\gamma(\cdot) \in L^{\infty}([0, a_{\dagger})), \qquad \gamma(a) \ge 0 \text{ in } [0, a_{\dagger})$$

and consider the following form for the force of infection:

(1.12)
$$\lambda(a,t) = \kappa(a) \int_0^{a_{\dagger}} h(\sigma)i(\sigma,t) \, d\sigma + g(a),$$

where h is the age-specific infectiousness, κ the age-specific contagion rate, and g is the *external* force of infection. They satisfy the following conditions:

(1.13)
$$h, \kappa, g \in L^{\infty}([0, a_{\dagger})) \text{ and } h, \kappa, g \geq 0 \text{ on } [0, a_{\dagger}).$$

We also assume that none of $\beta(\cdot)$, $\mu(\cdot)$, $\gamma(\cdot)$, $h(\cdot)$, $\kappa(\cdot)$, $g(\cdot)$ is identically zero.

We note that by assumption (1.7), the fourth equation in (1.1) becomes

(1.14)
$$s(0,t) = \int_0^{a_{\dagger}} \beta(a) \, p_{\infty}(a) \, da - q \, \int_0^{a_{\dagger}} \beta(a) \, i(a,t) \, da$$
$$= b_0 - q \, \int_0^{a_{\dagger}} \beta(a) \, i(a,t) \, da,$$

so that the equations involving the variable r(a,t) in (1.1) can be disregarded since s(a,t) and i(a,t) are sufficient to determine the evolution

of the whole system. Thus, in the rest of the paper, we will be concerned with the following reduced system derived from (1.1) and (1.7):

$$(1.15) \begin{cases} \frac{\partial s}{\partial t}(a,t) + \frac{\partial s}{\partial a}(a,t) + \mu(a)s(a,t) = -\lambda(a,t)s(a,t), \\ \frac{\partial i}{\partial t}(a,t) + \frac{\partial i}{\partial a}(a,t) + \mu(a)i(a,t) = \lambda(a,t)s(a,t) - \gamma(a)i(a,t), \\ s(0,t) = b_0 - i(0,t), \\ i(0,t) = q \int_0^{a_t} \beta(a)i(a,t)da, \\ i(a,0) = i_0(a), \quad s(a,0) = s_0(a). \end{cases}$$

This problem is also intimately associated with the study of long-time behavior of solutions of the model, which has some important epidemiological consequences such as determining whether an outbreak of a particular disease may result in an endemic situation or the infection will die out.

We shall use the techniques developed in [4]; however, we modify them so as to apply to our case. So, in the next section we shall reduce the problem of finding non-trivial steady states to that of finding the zeros of a real function. Then, in sections 3 we shall prove that the non-trivial equilibria always exist unless external force g is identically zero, and give uniqueness result if there is no vertical transmission of the disease.

2. Formal reduction of the model

We now consider the problem of existence of steady states of system (1.15). Consequently, we are concerned with the problem:

(2.1)
$$\begin{cases} i) & \frac{\partial s}{\partial a} + \mu(a)s(a) = -\left(J\kappa(a) + g(a)\right)s(a), \\ ii) & \frac{\partial i}{\partial a} + \mu(a)i(a) = \left(J\kappa(a) + g(a)\right)s(a) - \gamma(a)i(a), \\ iii) & J = \int_0^{a_\dagger} h(a)i(a)da, \\ iv) & s(0) = b_0 - i(0), \\ v) & i(0) = q \int_0^{a_\dagger} \beta(a)i(a)da. \end{cases}$$

It is easy to see that the problem admits the disease-free equilibrium $s^*(a) = p_{\infty}(a)$, $i^*(a) \equiv 0$, if and only if $g(a) \equiv 0$. Since we are assuming that g is not identically zero, we have to concentrate on the search of endemic states, that is nonnegative solutions for which $i^*(a)$ does not vanish identically. To investigate the existence of such solutions, we modify problem (2.1) by taking the following new variables, the age profiles respectively of infecteds and susceptibles:

(2.2)
$$u(a) = \frac{i(a)}{p_{\infty}(a)}; \qquad v(a) = \frac{s(a)}{p_{\infty}(a)}.$$

With these definitions, problem (2.1) becomes

(2.3)
$$\begin{cases} i) & \frac{dv}{da} = -\left(J\kappa(a) + g(a)\right)v(a), \\ ii) & \frac{du}{da} = \left(J\kappa(a) + g(a)\right)v(a) - \gamma(a)u(a), \\ iii) & J = b_0 \int_0^{a_\dagger} h(\sigma)\pi(\sigma)u(\sigma)d\sigma, \\ iv) & v(0) = 1 - X, \\ v) & X = q \int_0^{a_\dagger} \beta(\sigma)\pi(\sigma)u(\sigma)d\sigma. \end{cases}$$

Our aim in this section is to reduce the solution of this problem to that of solving a system of equations on the scalar variables X and J. For this purpose, we first note that integration of (2.3.i) gives

(2.4)
$$v(a) = (1 - X)e^{-\int_0^a (J\kappa(\sigma) + g(\sigma))d\sigma}.$$

Then, substituting (2.4) into (2.3.ii) and integrating the equation we have

$$(2.5)$$

$$u(a) = Xe^{-\int_0^a \gamma(\sigma)d\sigma} + (1 - X) \int_0^a \left(J\kappa(\sigma) + g(\sigma)\right) e^{-\int_\sigma^a \gamma(s)ds - \int_0^\sigma (J\kappa(s) + g(s))ds} d\sigma.$$

Substituting (2.4) and (2.5) into (2.3.iii) and (2.3.v) we are led to the following relations,

(2.6)
$$\begin{cases} J = XG + (1 - X)(JM(J) + D(J)), \\ X = XR + (1 - X)(JL(J) + C(J)), \end{cases}$$

where we have introduced the following notation:

(2.7)
$$G = b_0 \int_0^{a_{\dagger}} h(a) \pi(a) \Gamma(a) da,$$

(2.8)
$$R = q \int_0^{a_{\dagger}} \beta(a) \pi(a) \Gamma(a) da,$$

(2.9)
$$M(J) = b_0 \int_0^{a_{\dagger}} h(a) \, \pi(a) \, F(a, J) \, da,$$

(2.10)
$$L(J) = q \int_0^{a_{\dagger}} \beta(a) \, \pi(a) \, F(a, J) \, da,$$

(2.11)
$$D(J) = b_0 \int_0^{a_{\dagger}} h(a) \, \pi(a) \, H(a, J) \, da,$$

(2.12)
$$C(J) = q \int_0^{a_{\dagger}} \beta(a) \, \pi(a) \, H(a, J) \, da,$$

(2.13)
$$\Gamma(a) = e^{-\int_0^a \gamma(\sigma)d\sigma},$$

$$(2.14) F(a,J) = \int_0^a \kappa(\sigma) e^{-\int_\sigma^a \gamma(s)ds - \int_0^\sigma (J\kappa(s) + g(s))ds} d\sigma,$$

$$(2.15) H(a,J) = \int_0^a g(\sigma)e^{-\int_\sigma^a \gamma(s)ds - \int_0^\sigma (J\kappa(s) + g(s))ds} d\sigma.$$

We seek solutions of (2.6) such that $J \ge 0$ and $0 \le X \le 1$. (Note that X = u(0) and $0 \le u(0) \le 1$.) In fact, any such a pair (X^*, J^*) provides a nonnegative solution of (2.3) via (2.4) and (2.5).

Now we have to state some facts about the functions and the constants defined above. We shall find the following parameters useful in the sequel. Let

$$a_{\beta}^{+} = \inf\{A : \beta(a) = 0 \text{ a.e. in } [A, a_{\dagger})\},$$

 $a_{h}^{+} = \inf\{A : h(a) = 0 \text{ a.e. in } [A, a_{\dagger})\},$
 $a_{g}^{-} = \sup\{A : g(a) = 0 \text{ a.e. in } [0, A]\},$
 $a_{\kappa}^{-} = \sup\{A : \kappa(a) = 0 \text{ a.e. in } [0, A]\},$
 $a_{\kappa}^{-} = \sup\{A : \gamma(a) = 0 \text{ a.e. in } [0, A]\}.$

Then, it is easy to obtain the following results.

LEMMA 2.1.
$$R = 1$$
 if and only if

$$(2.16) q = 1 and a_{\beta}^{+} \leq a_{\gamma}^{-}.$$

LEMMA 2.2. If q > 0, the function $C(\cdot)$ vanishes identically if and only if

$$a_{\beta}^{+} \leq a_{g}^{-}.$$

Otherwise, it is positive and decreasing.

LEMMA 2.3. The function $L(\cdot)$ vanishes identically if and only if

$$a_{\beta}^{+} \leq a_{\kappa}^{-}.$$

Otherwise, it is positive and decreasing.

LEMMA 2.4. The function $D(\cdot)$ vanishes identically if and only if

$$(2.19) a_h^+ \le a_g^-.$$

Otherwise, it is positive and decreasing.

LEMMA 2.5. The function $M(\cdot)$ vanishes identically if and only if

$$(2.20) a_h^+ \le a_\kappa^-.$$

Otherwise, it is positive and decreasing.

Note that if the following conditions are satisfied, then (2.6) reduces to a single equation with two unknowns J and X:

(2.21)
$$R = 1$$
 and $L(J) = C(J) = 0$ for all J .

Note also that (2.21) is equivalent to the following:

(2.22)
$$q = 1, \quad a_{\beta}^{+} \le a_{\gamma}^{-}, \quad a_{\beta}^{+} \le a_{\kappa}^{-}, \quad \text{and} \quad a_{\beta}^{+} \le a_{g}^{-}.$$

These results lead us to consider the following very special case.

LEMMA 2.6. Assume (2.22) holds. Then problem (2.3) has a continuum of nontrivial solutions.

PROOF. Under our assumptions, the system (2.6) reduces to

$$J = XG + (1 - X)(JM(J) + D(J)).$$

That is,

$$J(1 - (1 - X)M(J)) = XG + (1 - X)D(J).$$

Now, for every fixed $X \in [0,1]$ this equation has exactly one solution in the variable J. In fact, the left-hand side

$$J(1-(1-X)M(J))$$

vanishes at J=0, is increasing when nonnegative, and tends to ∞ as $J\to\infty$, while the right-hand side is monotone decreasing and converging to the nonnegative value XG. Thus, we have a solution (J,X) for any choice of $X\in[0,1]$ and, consequently, a solution of (2.3) via (2.4) and (2.5).

Thus if (2.22) is satisfied, (2.6) has infinitely many solutions and it is not desired to our model. Since we want to rule out such a pathological case, the following assumption is required in the rest of the paper.

(2.23) All the relations in (2.22) do not hold simultaneously.

Under the assumption (2.23) we can further reduce the system (2.6) to a single equation. In fact, solving the second equation for X we obtain

(2.24)
$$X = \frac{JL(J) + C(J)}{1 - R + JL(J) + C(J)},$$

which, when substituted into the other equation yields:

$$(2.25) \quad (1-R)(J-JM(J)-D(J)) + (J-G)(JL(J)+C(J)) = 0.$$

Thus, we need to study this equation. Note that any solution $J^* \ge 0$ of (2.25) provides a solution of (2.6) with $X^* \in [0, 1]$ given by (2.24).

In order to study equation (2.25), we will consider the continuous function

$$(2.26) \ \phi(J) = (1 - R)(J - JM(J) - D(J)) + (J - G)(JL(J) + C(J))$$

and we shall analyze its behavior in the interval $[0, \infty)$. This will be done in the next section as we consider conditions on the model parameters that allows us to determine this behavior.

3. Existence and uniqueness of endemic states

We begin with the following two lemmas.

LEMMA 3.1.

$$(3.1) \quad \lim_{J \to \infty} \left(JM(J) + D(J) \right) = G \quad \text{and} \quad \lim_{J \to \infty} \left(JL(J) + C(J) \right) = R.$$

Proof.

$$\begin{split} JM(J) + D(J) \\ &= b_0 \int_0^{a_\dagger} h(a) \, \pi(a) \\ &\times \int_0^a e^{-\int_\sigma^a \gamma(s) ds} \big(J\kappa(\sigma) + g(\sigma) \big) e^{-\int_0^\sigma (J\kappa(s) + g(s)) ds} d\sigma \, da. \end{split}$$

But

$$\begin{split} &\int_0^a e^{-\int_\sigma^a \gamma(s)ds} \big(J\kappa(\sigma) + g(\sigma)\big) e^{-\int_0^\sigma (J\kappa(s) + g(s))ds} d\sigma \\ &= -\int_0^a e^{-\int_\sigma^a \gamma(s)ds} \frac{d}{d\sigma} e^{-\int_0^\sigma (J\kappa(s) + g(s))ds} d\sigma \\ &= e^{-\int_0^a \gamma(s)ds} - e^{-\int_0^a (J\kappa(s) + g(s))ds} \\ &+ \int_0^a \gamma(\sigma) e^{-\int_\sigma^a \gamma(s)ds - \int_0^\sigma (J\kappa(s) + g(s))ds} d\sigma. \end{split}$$

Hence

$$\lim_{J\to\infty} \big(JM(J)+D(J)\big) = b_0 \int_0^{a_\dagger} h(a)\pi(a)\Gamma(a)\,da = G.$$

Similarly,

$$\lim_{J \to \infty} \left(JL(J) + C(J) \right) = q \int_0^{a_{\dagger}} \beta(a) \pi(a) \Gamma(a) \, da = R. \quad \Box$$

LEMMA 3.2.

$$\lim_{J \to \infty} \phi(J) = \infty.$$

PROOF. Note that $\lim_{J\to\infty}D(J)=0$ and $\lim_{J\to\infty}\left(J-JM(J)-D(J)\right)=\infty$ by Lemma 3.1.

Since $\phi(J) \geq (1-R)(J-JM(J)-D(J))$ for $J \geq G$, we have $\lim_{J\to\infty} \phi(J) = \infty$ if $0 \leq R < 1$.

If R=1, then $\phi(J)=(J-G)\big(JL(J)+C(J)\big)\to\infty$ as $J\to\infty$ by Lemma 3.1.

Now we are ready for the existence theorem.

Theorem 3.3. An endemic state always exists.

PROOF. Note that ϕ is a continuous function of J. Since $\phi(0) = -(1-R)D(0) - GC(0) \le 0$ and $\lim_{J \to \infty} \phi(J) = \infty$, the equation $\phi(J) = 0$ has a nonnegative solution.

Note that if g is identically zero, our model just comes back to usual S-I-R model without external force of infection. In such cases, the existence of endemic states depends on the parameters and lots of threshold results are known for various cases [1, 4, 9].

Now we give the uniqueness result for a special case.

THEOREM 3.4. Assume that (2.19) does not hold. Then the endemic state is unique if there is no vertical transmission of the disease.

PROOF. Since q=0, we know that R=L(J)=C(J)=0 and $\phi(J)=J-JM(J)-D(J)$ for all $J\geq 0$. Also note that $\phi(0)=-D(0)<0$ since we are assuming that (2.19) does not hold.

Since
$$\phi(J) = J\left(1 - M(J) - \frac{D(J)}{J}\right)$$
 for $J > 0$ and each of $M(J)$ and $D(J)/J$ is monotone decreasing, we see that $\phi(J)$ is monotone increasing when nonnegative. Since we also know that $\lim_{J \to \infty} \phi(J) = \infty$, the theorem is proved.

Note that if (2.19) does hold, -D(0) = 0 in the proof of theorem 3.4. Thus we can easily see that the equation $\phi(J) = 0$ has exactly two zeros. However, in biological point of view, (2.19) is too restrictive to hold.

4. Concluding remarks

We have considered an age-structured model of epidemics of S-I-R type with external force of infection.

We obtained the existence result which is quite natural in the sense that the endemic states always exist unless the external force of infection vanishes: in case we do not control the external source of infection, even if we isolate infected individuals from susceptibles, the disease will still remain in our population.

As far as uniqueness is concerned, we have shown only for the case where there is no vertical transmission of the disease (q = 0). This uniqueness result applies to many disease, including most sexually transmitted diseases.

General results concerning uniqueness of endemic states are still open. As a future work, stability analysis might be a reasonable choice, as well as finding more general uniqueness results.

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