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Vertical transmission in epidemic models of sexually transmitted diseases with isolation from reproduction

Daniel Maxin, Timothy Olson and Adam Shull

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We describe a population logistic model exposed to a mild life-long sexually transmitted disease, that is, without significant increased mortality among infected individuals and providing no immunity/recovery. We then modify this model to include groups isolated from sexual contact and analyze their potential effect on the dynamics of the population. We are interested in how the isolated class may curb the growth of the infected group while keeping the healthy population at acceptable levels. In particular, we analyze the connection between vertical transmission and isolation from reproduction on the long term behavior of the disease. A comparison with similar effects caused by vaccination and quarantine is also provided.

1. Introduction

The dynamics of a population depends on the relation between reproduction and mortality. One factor that we analyze in this paper is the long-term effect on the population growth caused by the segregation of portions of the general (reproductive) population into a nonreproductive class that really consists of individuals of two very different kinds: *sexually active but nonprocreating*, such as infertile individuals, and *sexually inactive*, consisting of individuals who by choice or medical reasons refrain from sexual contact for life. The influence of the nonreproductive group on general population dynamics has been analyzed for several exponential and logistic models in [Milner 2005]. It has been shown that the nonreproductive group can indeed alter the population trend and may even make an exponentially increasing population stagnate or decline. A similar result holds for logistic models. Maxin and Milner [2007] extended these models to incorporate a sexually transmitted disease (STD) without recovery that does not increase mortality. It has been

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shown that the abstaining groups have the ability to induce a stable disease-free equilibrium (DFE) in an endemic situation. This is quite different from quarantine since the sexually isolated individuals do not reproduce and, by this, the number of susceptibles decreases since no vertical transmission is assumed.

In this paper we extend the logistic model from [Maxin and Milner 2007] — a reference we henceforth abbreviate as [MM 2007] — to include vertical transmission which assumes that the newborn can acquire the disease from an infected mother. It is intuitively obvious that, with vertical transmission, there is a new source of newly infected individuals in the population and the conditions for disease clearance will become more restrictive. Our goal in this paper is to show that, even in this case, a stable, disease-free steady state is possible and may be caused primarily by isolation from reproduction.

The paper is structured as follows. In Section 2, we introduce the model and analyze the extinction and the disease-free equilibrium, and correlate these results with the ones obtained in [MM 2007]. We then compute a threshold condition on the nonreproductive rates that describes how the isolated class induces a disease-free equilibrium in an endemic situation caused by vertical transmission. In Section 3, we analyze a particular model that assumes total vertical transmission when all the newborn from infected people are infected at birth and that leads to the existence of a *total endemic* steady state when the entire healthy population vanishes. While this is not realistic for known diseases, the stability condition of the endemic equilibrium suggests that, contrary to what might be expected, a higher isolation rate of infected leads to an endemic equilibrium (where healthy and infected individuals coexist) regardless of how big the infection rate may be. We conclude in Section 4 with a brief comparison between our model and a similar S-I type model with vaccination and quarantine to show that the previous result may not be possible in the absence of isolation from reproduction. We conclude our paper with several thoughts on further avenues of research.

2. The logistic model with abstaining groups and vertical transmission

Maxin and Milner [MM 2007] introduced several exponential and logistic STD models that incorporate an abstaining class A of people who are isolated from sexual contact. Here we consider their model with logistic mortality and assume that each newborn from an infected individual has a probability ϵ of being healthy at birth. Thus, if β is the per capita birth rate and I is the infected class, the rate at which individuals are born already infected is $\beta(1-\epsilon)I$. The system becomes

$$\begin{cases} S' = \beta S + \beta\epsilon I - \lambda SI - \bar{\mu} S - \nu_1 S, \\ I' = \beta(1-\epsilon)I + \lambda SI - \bar{\mu} I - \nu_2 I, \\ A' = \nu_1 S + \nu_2 I - \bar{\mu} A, \end{cases} \tag{1}$$

where $\bar{\mu} = \mu + bP$ with $P = S + I + A$.

The meaning of the remaining parameters is as follows:

- S and A denote the susceptible and the abstaining class. Note that, since the abstaining individuals do not reproduce and do not participate in the infection process, we can include both the infected and healthy isolated people into a single group A in order to keep the dimension of the system as small as possible. Whenever the disease is cleared (such as in the case of a stable disease-free equilibrium) A will contain healthy isolated individuals only.
- $\bar{\mu}$ is the logistic death rate and b is the logistic linear coefficient that captures the total population effect on the death rate.
- λ represents the infection rate using the mass-action law corresponding to a homogeneous population.
- ν_1 and ν_2 represent the transition rates from susceptibles and infected into the isolated class A.
- P will denote, throughout this paper, the total population.

When $\epsilon = 1$, this system is identical with the one analyzed in [MM 2007].

It is reasonable to assume that the isolation rate of infected individuals is greater, since some infected individuals may choose to quarantine themselves in order to avoid spreading the disease. Thus, we will assume throughout this paper that

$$\nu_1 < \nu_2.$$

The model always admits an extinction equilibrium $(0, 0, 0)$.

If $\beta - \mu - \nu_1 > 0$ there is also a disease-free equilibrium (S_*, I_*, A_*) where

$$\begin{cases} S_* = \Big(K - \dfrac{\nu_1}{b}\Big)\Big(1 - \dfrac{\nu_1}{\beta}\Big) = \Big(\dfrac{\beta - \mu - \nu_1}{b}\Big)\Big(1 - \dfrac{\nu_1}{\beta}\Big), \\ I_* = 0, \\ A_* = \Big(K - \dfrac{\nu_1}{b}\Big)\dfrac{\nu_1}{\beta} = \Big(\dfrac{\beta - \mu - \nu_1}{b}\Big)\dfrac{\nu_1}{\beta}, \end{cases} \tag{2}$$

with $K = (\beta - \mu)/b$. The endemic equilibrium will be analyzed in the context of complete vertical transmission in the following section.

Theorem 1 (stability of the boundary steady states). *The extinction equilibrium is locally asymptotically stable if*

$$\beta - \mu - \nu_1 < 0.$$

The disease-free equilibrium (S_*, I_*, A_*) *is locally asymptotically stable if*

$$\beta - \mu - \nu_1 > 0 \quad \textit{and} \quad \lambda < \frac{\beta\epsilon - \nu_1 + \nu_2}{\Big(1 - \dfrac{\nu_1}{\beta}\Big)\Big(K - \dfrac{\nu_1}{b}\Big)}.$$

Proof. The Jacobian of (1) is

$$J = \begin{pmatrix} \beta-\lambda I-\bar{\mu}-bS-\nu_1 & \beta\epsilon-\lambda S-bS & -bS \\ \lambda I-bI & \beta(1-\epsilon)+\lambda S-\bar{\mu}-bI-\nu_2 & -bI \\ \nu_1-bA & \nu_2-bA & -\bar{\mu}-bA \end{pmatrix}.$$

Evaluated at $(0, 0, 0)$ this is

$$J(0,0,0) = \begin{pmatrix} \beta-\mu-\nu_1 & \beta\epsilon & 0 \\ 0 & \beta(1-\epsilon)-\mu-\nu_2 & 0 \\ \nu_1 & \nu_2 & -\mu \end{pmatrix}.$$

It follows that the extinction equilibrium is locally asymptotically stable if

$$\beta-\mu-\nu_1<0 \quad \text{and} \quad \beta(1-\epsilon)-\mu-\nu_2<0.$$

However, the second inequality follows from the first, since $0<\epsilon<1$ and $\nu_1<\nu_2$:

$$\beta(1-\epsilon)<\beta<\mu+\nu_1<\mu+\nu_2.$$

Assuming now that $\beta-\mu-\nu_1>0$, and denoting

$$P_* = S_* + A_* = K - \frac{\nu_1}{b} = \frac{\beta-\mu-\nu_1}{b} > 0,$$

the Jacobian J evaluated at (S_*, I_*, A_*) is

$$\begin{pmatrix} \beta-\mu-bP_*-bS_*-\nu_1 & \beta\epsilon-\lambda S_*-bS_* & -bS_* \\ 0 & \beta(1-\epsilon)+\lambda S_*-\mu-bP_*-\nu_2 & 0 \\ \nu_1-bA_* & \nu_2-bA_* & -\mu-bP_*-bA_* \end{pmatrix}.$$

The eigenvalues are $\beta(1-\epsilon)+\lambda S_*-\mu-bP_*-\nu_2$ (this being the single nonzero entry on its row) together with the eigenvalues of the complementary minor,

$$M = \begin{pmatrix} \beta-\mu-bP_*-bS_*-\nu_1 & -bS_* \\ \nu_1-bA_* & -\mu-bP_*-bA_* \end{pmatrix}.$$

Since $\operatorname{Tr}(M) = -\mu-2bP_*<0$ and $\det M = b\beta S_*>0$, the eigenvalues of M have negative real parts. Thus local asymptotic stability holds for (S_*, I_*, A_*) if

$$\beta(1-\epsilon)+\lambda S_*-\mu-bP_*-\nu_2<0,$$

which is equivalent to

$$\lambda < \frac{\beta\epsilon-\nu_1+\nu_2}{\left(1-\frac{\nu_1}{\beta}\right)\left(K-\frac{\nu_1}{b}\right)}.$$

□

From [MM 2007] we know that, in the absence of the isolated class A, the disease is endemic if $\beta/K<\lambda$. Similarly, with vertical transmission, if there is no isolation from reproduction, the disease is endemic provided that $\beta\epsilon/K<\lambda$. The

double inequality below indicates the range of the infection rate λ that would cause an endemic situation in the absence of the isolated class A and a stable disease-free equilibrium in the presence of it:

$$\frac{\beta\epsilon}{K} < \lambda < \frac{\beta\epsilon - \nu_1 + \nu_2}{\left(1 - \frac{\nu_1}{\beta}\right)\left(K - \frac{\nu_1}{b}\right)}. \tag{3}$$

This condition resembles the similar one obtained in [MM 2007], with $\epsilon = 1$ (no vertical transmission):

$$\frac{\beta}{K} < \lambda < \frac{\beta - \nu_1 + \nu_2}{\left(1 - \frac{\nu_1}{\beta}\right)\left(K - \frac{\nu_1}{b}\right)}.$$

This means that the isolated class A, represented by the two isolation rates ν_1 and ν_2, has the ability to induce stability to the disease-free equilibrium in an otherwise endemic situation. With the addition of vertical transmission we notice another threshold effect which suggests that the vertical transmission alone can induce an endemic situation even in the case where the abstaining class satisfies the condition in [MM 2007]. This happens if the infection rate satisfies

$$\frac{\beta\epsilon - \nu_1 + \nu_2}{\left(1 - \frac{\nu_1}{\beta}\right)\left(K - \frac{\nu_1}{b}\right)} < \lambda < \frac{\beta - \nu_1 + \nu_2}{\left(1 - \frac{\nu_1}{\beta}\right)\left(K - \frac{\nu_1}{b}\right)}.$$

To summarize, the vertical transmission reduces the disease-free stability range of λ, which is to be expected with the additional infected newborns in the model.

In Figure 1 we plot two numerical examples to illustrate Theorem 1. The birth

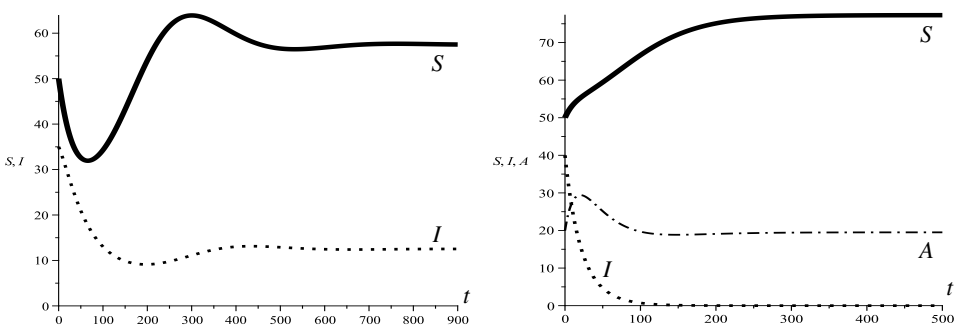

Figure 1. Example equilibria: endemic equilibrium (left) in the absence of abstainers ($\nu_1 = \nu_2 = 0$) and disease-free equilibrium (right) in their presence ($\nu_1 = 0.01$, $\nu_2 = 0.04$). In both cases, $\beta = 0.04962$, $\mu = 0.02026$, $\epsilon = 0.7$, $b = 0.0002$, and $\lambda = 0.0004$. The first inequality in (3) is satisfied in the first case, and both are in the second.

and death rates are those given in the *CIA World Factbook* for Niger in 2008, but all other parameter values are for illustration purposes only and do not reflect real data.

A major difference from the model treated in [MM 2007] appears when the vertical transmission rate is very high. Although not realistic, for theoretical purposes we will assume the extreme case, $\epsilon = 0$, which indicates 100% vertical transmission. We treat this case in greater detail in the following section.

3. Complete vertical transmission

Setting $\epsilon = 0$ in (1), we obtain:

$$\begin{cases} S' = \beta S - \lambda SI - \bar{\mu} S - \nu_1 S, \\ I' = \beta I + \lambda SI - \bar{\mu} I - \nu_2 I, \\ A' = \nu_1 S + \nu_2 I - \bar{\mu} A. \end{cases} \tag{4}$$

The system, in this form, allows us to explicitly compute the endemic equilibrium (a nontrivial task if $\epsilon \neq 0$):

$$S^* = \frac{\mu^* + \nu_2 - \beta}{\lambda}, \quad I^* = \frac{\beta - \mu^* - \nu_1}{\lambda}, \quad A^* = \frac{(\nu_2 - \nu_1)(\beta - \mu^*)}{\lambda \mu^*},$$

where $\mu^* = \mu + bP^*$. Adding the equations for S^*, I^*, and A^* together gives us

$$P^* = \frac{(\nu_2 - \nu_1)\beta}{\lambda \mu^*}.$$

For a biologically meaningful endemic equilibrium (EE) to exist (i.e., positive values) we need

$$\nu_1 < \beta - \mu^* < \nu_2,$$

or

$$\frac{\beta}{\mu^* + \nu_1} > 1 \quad \text{and} \quad \frac{\beta}{\mu^* + \nu_2} < 1.$$

This translates to a requirement that the reproductive number of the susceptibles must be greater than one, while the reproductive number of the infected population must be less than one.

In addition to the disease-free and endemic equilibria, (4) admits a third steady state in which the entire healthy population vanishes. We call this the susceptible extinction equilibrium (SEE):

$$\bar{S} = 0, \quad \bar{I} = \left(1 - \frac{\nu_2}{\beta}\right)\bar{P}, \quad \bar{A} = \frac{\nu_2}{\beta}\bar{P},$$

where $\bar{P} = (\beta - \mu - \nu_2)/b$.

We see that, for a positive SEE equilibrium, we need $\beta - \mu - \nu_2 > 0$.

Theorem 2 (existence and local stability conditions for EE and SEE). *If either*

$$\frac{\nu_2-\nu_1}{\left(1-\frac{\nu_1}{\beta}\right)\left(K-\frac{\nu_1}{b}\right)}<\lambda<\frac{\nu_2-\nu_1}{\left(1-\frac{\nu_2}{\beta}\right)\left(K-\frac{\nu_2}{b}\right)} \tag{5}$$

or

$$\frac{\nu_2-\nu_1}{\left(1-\frac{\nu_1}{\beta}\right)\left(K-\frac{\nu_1}{b}\right)}<\lambda \quad \textit{and} \quad \beta<\frac{\mu}{2}+\nu_2, \tag{6}$$

the endemic equilibrium (S^*, I^*, A^*) *exists and is locally asymptotically stable. If*

$$\beta>\mu+\nu_2 \quad \textit{and} \quad \lambda>\frac{\nu_2-\nu_1}{\left(1-\frac{\nu_2}{\beta}\right)\left(K-\frac{\nu_2}{b}\right)}, \tag{7}$$

the susceptible extinction equilibrium $(\bar{S}, \bar{I}, \bar{A})$ *exists and is locally asymptotically stable.*

Proof. First we show that the EE is stable whenever it exists. The Jacobian of (4), evaluated at (S^*, I^*, A^*), is

$$J(S^*, I^*, A^*)=\begin{pmatrix} -bS^* & -\lambda S^*-bS^* & -bS^* \\ \lambda I^*-bI^* & -bI^* & -bI^* \\ \nu_1-bA^* & \nu_2-bA^* & -\mu^*-bA^* \end{pmatrix}.$$

If the characteristic equation of this matrix is $x^3+p_1x^2+p_2x+p_3=0$, then

$$\begin{aligned} p_1 &= -\operatorname{Tr}(J)=\mu^*+bP^*, \\ p_2 &= \left(b^2S^*I^*+(\lambda^2-b^2)S^*I^*\right)+\left(bS^*(\mu^*+bA^*)+bS^*(\nu_1-bA^*)\right) \\ &\qquad +\left(bI^*(\mu^*+bA^*)+bI^*(\nu_2-bA^*)\right) \\ &= \lambda^2I^*S^*+b\nu_1S^*+b\nu_2I^*+b\mu^*(S^*+I^*), \\ p_3 &= -\operatorname{Det}(J)=\lambda S^*I^*(b\nu_2-b\nu_1+\lambda\mu^*+\lambda bA^*). \end{aligned}$$

Clearly $p_1>0$, $p_2>0$ and $p_3>0$, since $\nu_2>\nu_1$.

Replacing S^*, I^*, A^* and P^* with their corresponding values computed above, we also see that $p_1p_2>p_3$ since

$$p_1p_2-p_3=\frac{b\beta(\nu_2-\nu_1)\left(\lambda(\mu^*)^2+b\beta(\nu_2-\nu_1)\right)}{\lambda^2\mu^*}>0.$$

Hence, according to the Routh–Hurwitz criterion, the interior equilibrium is always stable whenever it exists. It remains now to interpret the positivity condition $\nu_1<\beta-\mu^*<\nu_2$ in terms of the original parameters.

To this end, we solve for μ^* using the following equation:

$$P^* = \frac{\mu^* - \mu}{b} = \frac{\beta(\nu_2 - \nu_1)}{\lambda\mu^*}.$$

There is a unique positive solution

$$\mu^* = \frac{\mu\lambda + \sqrt{\mu^2\lambda^2 + 4b\beta\lambda(\nu_2 - \nu_1)}}{2\lambda},$$

and the existence condition above becomes

$$2(\beta - \nu_2) - \mu < \frac{1}{\lambda}\sqrt{\mu^2\lambda^2 + 4b\beta\lambda(\nu_2 - \nu_1)} < 2(\beta - \nu_1) - \mu. \tag{8}$$

Consider the second inequality first. Its right side is positive, since our standing assumption is that $\beta > \mu + \nu_1$, to avoid total population extinction. Therefore squaring both sides leads to an equivalent inequality,

$$\frac{1}{\lambda^2}\big(\mu^2\lambda^2 + 4b\beta\lambda(\nu_2 - \nu_1)\big) < 4(\beta - \nu_1)^2 + \mu^2 - 4\mu(\beta - \nu_1),$$

which after simplification becomes, in terms of $K = \dfrac{\beta - \mu}{b}$, the condition

$$\lambda > \frac{\nu_2 - \nu_1}{\left(1 - \frac{\nu_1}{\beta}\right)\left(K - \frac{\nu_1}{b}\right)}.$$

Thus the second inequality in (8) amounts to precisely the opposite of the condition for disease-free stability at the end of the statement of Theorem 1, in the case $\epsilon = 0$.

There remains to study the first inequality in (8). It is certainly satisfied if its left side is negative, that is, if

$$\beta < \frac{\mu}{2} + \nu_2.$$

In the opposite case, $\beta \geq \dfrac{\mu}{2} + \nu_2$, we can square both sides to obtain the equivalent condition

$$\lambda < \frac{\nu_2 - \nu_1}{\left(1 - \frac{\nu_2}{\beta}\right)\left(K - \frac{\nu_2}{b}\right)}. \tag{9}$$

In other words, the endemic equilibrium exists and it is stable if conditions (5) and (6) are satisfied.

The Jacobian of (4) evaluated at $(\bar{S}, \bar{I}, \bar{A})$ is

$$\begin{pmatrix} -\lambda\bar{I} + \nu_2 - \nu_1 & 0 & 0 \\ (\lambda - b)\bar{I} & -b\bar{I} & -b\bar{I} \\ \nu_1 - b\bar{A} & \nu_2 - b\bar{A} & -\bar{\mu} - b\bar{A} \end{pmatrix},$$

where $\bar{\mu}$ here denotes $\mu + b(\bar{S} + \bar{I} + \bar{A})$.

It is clear that one of the eigenvalues is negative when $\lambda \bar{I} > \nu_2 - \nu_1$, which is equivalent to the second condition in (7):

$$\lambda > \frac{\nu_2 - \nu_1}{\left(1 - \frac{\nu_2}{\beta}\right)\left(K - \frac{\nu_2}{b}\right)}. \tag{10}$$

Removing the row and column containing that eigenvalue leaves us with a 2×2 matrix whose determinant is always positive ($b\beta\bar{I} > 0$) and whose trace is always negative ($-\bar{\mu} - b\bar{P} < 0$). Thus, the susceptible extinction equilibrium is locally asymptotically stable, with λ satisfying condition (7) . □

Remark 1. Condition (6) has an interesting consequence. First, if $\beta < \mu/2 + \nu_2$, then $\beta < \mu + \nu_2$ also, so the susceptible extinction equilibrium does not exist in this case. This means that if ν_2 is big enough, the susceptible class never goes extinct and the endemic equilibrium is stable *regardless* of how big the infection rate λ may be. This emphasizes the epidemiological role of isolation from reproduction.

Remark 2. If one excludes the fact that the isolated class A does not reproduce, then the model (4) resembles an $S - I$ type model with vaccination (ν_1) and quarantine (ν_2). Thus, in order to sustain the previous remark that the Susceptible Extinction Equilibrium may be eliminated by the isolation from reproduction we need to investigate whether this result holds for a similar model where the vaccinated and quarantined classes do reproduce. In the next section we show that the answer to this question is negative meaning that the result obtained for our original model is indeed primarily due to the isolation from reproduction.

We provide some numerical examples to illustrate Theorem 2. In Figure 2 we

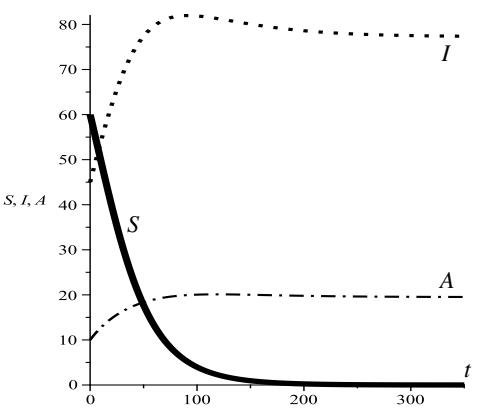

Figure 2. Example of a susceptible extinction equilibrium: $\beta = 0.04962$, $\mu = 0.02026$, $\nu_1 = 0.005$, $\nu_2 = 0.01$, $\epsilon = 0$, $b = 0.0002$, $\lambda = 0.0004$. Inequality (10) is satisfied.

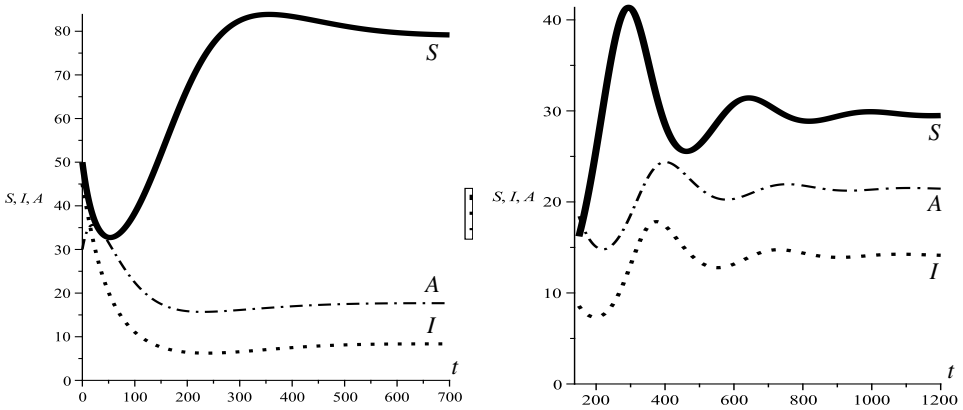

Figure 3. Examples of endemic equilibria: $\beta = 0.04962$, $\mu = 0.02026$, $\nu_1 = 0.005$, $\nu_2 = 0.04$, $\epsilon = 0$, $b = 0.0002$, $\lambda = 0.0004$ (left) or $\lambda = 0.0008$ (right). Inequalities (6) are satisfied.

show an example when the SEE is stable. In Figure 3 we illustrate the case of a stable EE satisfying (6). In Figure 3, right, we double the value of λ while keeping the other parameters the same as in the left half of the figure, to illustrate that under condition (6) the stability of EE is maintained regardless of how big the infection rate is.

4. A model with complete vertical transmission, vaccination and quarantine

The model proposed in this section is intended to eliminate the ambiguity concerning the epidemiological role of the isolated class A. In other words, we would like to see if the result in the previous section is due to the nonreproduction or perhaps due to vaccination and quarantine (which are other possible interpretations for the transition rates ν_1 and ν_2). To this end, we assume now that the model resembles an S-I type dynamics with vaccination and quarantine. Another main difference is that all individuals reproduce, including the quarantined. Since the isolated classes reproduce and one needs to track the infected and healthy newborns, we must separate the isolated class A into two classes: V, the vaccinated individuals and Q the quarantined infected people. Furthermore, we denote by η the transition rate from vaccinated individuals back to the susceptible class S to account for a possible imperfect vaccine where some individuals loose the acquired immunity.

The model is as follows:

$$\begin{cases} S' = \beta(S+V) - \lambda SI - \bar{\mu}S - \nu_1 S + \eta V, \\ I' = \beta(I+Q) + \lambda SI - \bar{\mu}I - \nu_2 I, \\ V' = \nu_1 S - \bar{\mu}V - \eta V, \\ Q' = \nu_2 I - \bar{\mu}Q, \end{cases} \tag{11}$$

where $\bar{\mu} = \mu + b(S + I + V + Q)$.

Remark 3. In this model we assumed the same reproduction rate for all individuals. A possible interpretation is that, in the case of sexually transmitted diseases, quarantine can be viewed as abstaining from sexual contact with healthy people only. This is true sometimes for diseases such as herpes simplex type 2 (HSV-2) when infected individuals search for partners among groups already infected. In reality, due to these considerations, the quarantined class will always exhibit a certain degree of isolation from reproduction. However, the main purpose of model (11) is to verify the results in the previous sections under the assumption that no isolation from reproduction occurs with transitions from one class to another.

Notice that there is no endemic equilibrium where the healthy and infected individuals coexist as shown below:

Substituting $V = \nu_1 S/(\bar{\mu} + \eta)$ and $Q = \nu_2 I/\bar{\mu}$ into the first two equations, we obtain

$$\lambda I = (\beta - \bar{\mu})\Big(1 + \frac{\nu_1}{\bar{\mu} + \eta}\Big) \quad \text{and} \quad \lambda S = (\bar{\mu} - \beta)\Big(1 + \frac{\nu_2}{\bar{\mu}}\Big).$$

Clearly, it is impossible for both of them to be positive since $\lambda S > 0$ implies $\beta < \bar{\mu}$ which, in turn, implies $\lambda I < 0$.

Adding the equations of (11) we obtain a logistic equation for the total population P:

$$P' = \beta P - \bar{\mu} P = (\beta - \mu - bP)P.$$

Therefore,

$$\lim_{t \to \infty} P(t) = \frac{\beta - \mu}{b} := K,$$

provided that $\beta > \mu$. If $\beta < \mu$ the population declines to zero.

Thus there are three steady states:

- the extinction equilibrium: $(0, 0, 0, 0)$,
- the susceptible extinction equilibrium (SEE):

$$\bar{S} = 0, \quad \bar{I} = \frac{\beta K}{\beta + \nu_2}, \quad \bar{V} = 0, \quad \bar{Q} = \frac{\nu_2 K}{\beta + \nu_2},$$

- the disease-free equilibrium (DFE):

$$S^* = \frac{(\beta + \eta)K}{\beta + \nu_1 + \eta}, \quad \bar{I} = 0, \quad \bar{V} = \frac{\nu_1 K}{\beta + \nu_1 + \eta}, \quad \bar{Q} = 0.$$

Theorem 3. *If $\beta > \mu$, the SEE is locally asymptotically stable and the DFE is unstable* (*whenever it exists*).

Proof. The Jacobian of (11) is

$$J = \begin{pmatrix} \beta-\lambda I-\bar{\mu}-bS-\nu_1 & -(\lambda+b)S & -bS+\beta+\eta & -bS \\ (\lambda-b)I & \beta+\lambda S-\bar{\mu}-bI-\nu_2 & -bI & -bI+\beta \\ \nu_1-bV & -bV & -\bar{\mu}-bV-\eta & -bV \\ -bQ & \nu_2-bQ & -bQ & -\bar{\mu}-bQ \end{pmatrix}.$$

We evaluate first the characteristic polynomial of $J(\bar{S}, \bar{I}, \bar{V}, \bar{Q})$, which is

$$f(x) = \big(x^2 + (b\bar{I} + b\bar{Q} + \beta + \nu_2)x + b(\bar{I} + \bar{Q})(\beta + \nu_2)\big) \times \big(x^2 + (\beta + \nu_1 + \lambda\bar{I} + \eta)x + \lambda\bar{I}(\beta + \eta)\big).$$

Since all its coefficients are positive then the real parts of all eigenvalues are negative and the susceptible extinction equilibrium is locally asymptotically stable whenever it exists.

On the contrary, for the disease-free equilibrium, the characteristic polynomial of $J(S^*, I^*, V^*, Q^*)$ is

$$g(x) = \big(x^2 + (bS^* + bV^* + \beta + \eta + \nu_1)x + b(S^* + V^*)(\beta + \eta + \nu_1)\big) \times \big(x^2 + (\beta + \nu_2 - \lambda S^*)x - \beta\lambda S^*\big)$$

and the real part of one of its eigenvalues is always positive: from the second quadratic factor of $g(x)$ we see that the product of its roots is given by

$$x_1 x_2 = -\beta\lambda S^* < 0. \qquad \square$$

Thus, the DFE is always unstable and the possibility of eliminating the disease is not possible through quarantine and vaccination alone when the population is faced with complete vertical transmission. In Figure 4 we provide a numerical example using the same parameter values as those in Figure 3 to illustrate that, in the absence of isolation from reproduction, the SEE is stable and the healthy population vanishes.

5. Conclusions

We modified the epidemic model with sexually abstaining groups introduced in [MM 2007] to include vertical transmission. We found that previous results claiming that the isolated class may induce the stability of the disease-free equilibrium in an endemic situation are still valid in the presence of vertical transmission although the range of the infection rate when this is possible is more restrictive.

One major difference appears when the vertical transmission rate is very high, that is, close to 100%. To simplify our analysis we actually considered a complete vertical transmission situation where every newborn from infected parents is infected as well. In this case, under certain conditions on the vital parameters, we

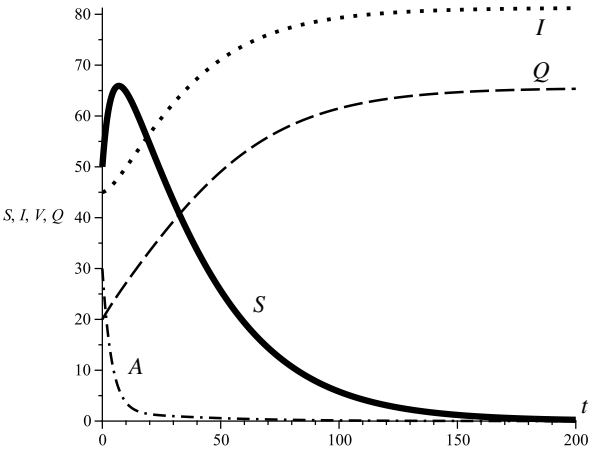

Figure 4. The susceptible extinction equilibrium in the absence of isolation from reproduction. Parameter values: $\beta = 0.04962$, $\mu = 0.02026$, $\nu_1 = 0.005$, $\nu_2 = 0.04$, $\epsilon = 0$, $b = 0.0002$, $\lambda = 0.0004$, $\eta = 0.2$.

found that the model admits a steady state (SEE) when the entire susceptible population vanishes, in addition to the disease-free and interior (endemic) steady states. The local stability analysis for the endemic equilibrium shows that both the infected and the healthy groups may coexist and that the total endemic situation when the healthy population declines to zero can be avoided by isolation from reproduction alone. A comparison with model (11) shows that this result may indeed be due to isolation from reproduction and not due to vaccination or quarantine, which are other possible interpretations for the transition rates ν_1 and ν_2.

One important limitation of our work is given by the use of one-sex models. Since we were interested in showing that there is an important correlation between vertical transmission and isolation from reproduction, we chose the simplest possible model to sustain our argument and to keep the mathematical details as simple as possible. Our next objective related to the present research is to investigate if similar results can be obtained using two-sex models. The influence of sexually abstaining groups on STD dynamics has been analyzed in [Maxin 2009; Maxin and Milner 2009] using a gender structured logistic model. We intend to extend that model to include vertical transmission. This research is currently underway and will be reported later.

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