

THE ROLE OF SEXUALLY ABSTAINED GROUPS IN TWO-SEX DEMOGRAPHIC AND EPIDEMIC LOGISTIC MODELS WITH NON-LINEAR MORTALITY

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ABSTRACT. We describe several gender structured population models governed by logistic growth with non-linear death rate. We extend these models to include groups of people isolated from sexual activity and individuals exposed to a mild and long-lasting sexually transmitted disease. i.e. without disease-induced mortality and recovery. The transmission of the disease is modeled through formation/separation of heterosexual couples assuming that one infected individual automatically infects his/her partner. We are interested in how the non-reproductive class may change the demographic tendencies in the general population and whether they can curb the growth of the infected group while keeping the healthy one at acceptable levels. A comparison of the equilibrium total population size in the presence and the absence of the isolated class is also provided.

1. INTRODUCTION

The long term dynamics of a population depends on the long-term changes in fertility and mortality rates and much less on their temporary changes. For this reason epidemic models usually ignore the demographic factors since the questions they address are usually about short lived phenomena related to the infectious outbreaks. This is especially true when the infection and recovery times are fast or if the disease induced mortality is big enough to the point where the natural birth and death rate will not affect the outcome too much. There are, however, infectious diseases which, by their own nature, or due to the progress in medical treatment, tend to stay in the population for a very long time. One typical example is given by the Herpes Simplex type 2 virus (HSV-2). In this case the disease is not lethal and, in fact it is symptom free most of the time, yet there is no known cure and it is safe to say that the virus, once acquired, it will never disappear completely. In other cases the advances in medical treatment will increase the life expectancy for the patients with otherwise lethal infections to the point where the demographic parameters become important. Several examples are given by the impact of Highly Active Anti-Retroviral Therapy (HAART) for HIV patients or by the introduction of a new vaccine against the strains of Human Papillomavirus (HPV) responsible for causing cervical cancer in the infected women.

1991 *Mathematics Subject Classification.* 92D30.

Key words and phrases. sexually transmitted diseases, isolation, population models.

All these justify a detailed study of the interplay between the demographic and epidemiological factors that influence the long term evolution of a population. One of the demographic factors that we study here is the impact of isolation from reproduction in general and from sexual activity, in particular, of portions of a general reproductive population exposed to a mild and long-lasting sexually transmitted disease (without recovery and additional mortality).

We mention that we are not going to propose a model for a specific disease since it is, in general, difficult to measure the correlation between demographic factors and infectious diseases trends, especially in the context of a mild and non-lethal STD which is, for most of the time, without symptoms. However, at least in the case of Herpes Simplex type 2, such correlation is implied by various reports of the World Health Organization. While the number of new HSV-2 cases is increasing, even in developed countries, there are notable exceptions such as Japan where the prevalence of herpes is actually declining. At the same time, Japan is confronted with a serious demographic problem with a significant proportion of individuals living alone being *de facto* non-reproductive and, possibly, sexually inactive (three out of five women and almost half the men in their twenties and early thirties are single). The main question that we address is: how much and in what form isolation from sexual contact by some proportion of individuals may affect two important aspects of a real population with a sexually transmitted disease: its growth as a population and the spread of the disease. Previous work addressed this question from a demographic perspective only [6] and from an epidemiological one using $S - I$ type exponential and logistic one-sex models [8].

In this paper we attempt to analyze both the demographic and epidemiological aspects of the problem by using two-sex logistic models with non-linear mortality. The importance of considering gender-structured model is obvious in the context of sexually transmitted diseases. One reason, as mentioned by Hadelar et al.[9], is that faithful healthy couples are temporarily shielded from the infection. On the other hand the pair formation/separation itself may be the underlying mechanism of disease transmission. As we will see later on this leads to different theoretical predictions on the total population size which further emphasizes the importance of using gender structured models in the dynamics of STD's. On the other hand the problem of establishing a logistic two-sex model is not trivial. In the one-sex case one can rely on the well-known logistic equation due to Verhulst [1]:

$$P'(t) = r \left[1 - \frac{P}{K} \right] P,$$

where the K is the carrying capacity. The solution of this equation can be computed explicitly and it satisfies

$$P(t) \rightarrow K \quad \text{as } t \rightarrow \infty \quad \text{whenever } P(0) = P_0 > 0.$$

A similar result is sought in the case of two-sex models where we must find conditions on the parameters that ensure the population always approaches

a positive bounded steady state. Due to the complicated form taken by the pair formation function this is not trivial. The first work was done by Castillo-Chavez and Huang [3] who introduced a two-sex logistic model with non-linear births and separation rates. Our model considers all parameters constant except the mortality which is assumed linearly dependent on the total population P .

This paper is structured as follows: section 2 gives a brief description of the work done on two-sex homogeneous models by Hadeler et al. [2] and on the two-sex logistic model developed by Castillo-Chavez and Huang [3]. In section 3 we introduce a logistic model with non-linear mortality that includes two classes of people isolated from sexual activity and derive an extinction threshold due to the isolation from reproduction. Section 4 is devoted to the full model that includes also the three infected classes, females, males and couples and two additional isolated from sexual contact classes coming from the infected females and males. We also compute and analyze the epidemic reproductive number in the presence and in the absence of the abstained classes and show how the disease can be eliminated by the isolated class and also how the total population size can settle at higher levels than the one in the absence of the non-reproductive groups. In section 5 we treat the symmetric case of equal vital parameters for both men and women and analyze the threshold derived before in the context of a population whose social behavior is not changed in the presence of the disease. Finally, we conclude in section 6 with some thoughts and directions for future research.

2. THE TWO-SEX HOMOGENEOUS MODEL AND ITS LOGISTIC VERSION WITH NON-LINEAR FERTILITY

Hadeler et al. [2] gave a complete analysis of the pair-formation model with constant vital parameters using their work in homogeneous models. Their model is an extension of the one introduced by Kendall [4] and Keyfitz [5]:

$$(1) \quad \begin{cases} F' &= -\mu_f F + (\beta\gamma_f + \delta + \mu_m)C - \mathcal{M}(F, M), \\ M' &= -\mu_m M + (\beta\gamma_m + \delta + \mu_f)C - \mathcal{M}(F, M), \\ C' &= \mathcal{M}(F, M) - (\delta + \mu_f + \mu_m)C. \end{cases}$$

F and M denote the single females and males and C the couples. β represents the birth rate while γ_f and γ_m are the probabilities that a newborn is female or a male respectively ($\gamma_f + \gamma_m = 1$). Finally, μ_f and μ_m are the death rates for both genders and δ is the couple separation rate. Notice that a pair can also disappear due to the death of one partner which results in a newly single opposite gender. There are different choices for the marriage function \mathcal{M} and there is no definite agreement as to which one best resembles the reality. It is agreed however that this function should satisfy several basic properties:

$$\begin{aligned} \mathcal{M}(F, M) &\geq 0, \\ \mathcal{M}(0, M) &= \mathcal{M}(F, 0) = 0, \end{aligned}$$

$$\mathcal{M}(F + F', M + M') \geq \mathcal{M}(F, M),$$

$$\mathcal{M}(aF, aM) = a\mathcal{M}(F, M),$$

for all positive F , M , F' and M' .

These assumptions are required in order to avoid biologically incorrect predictions. For example, the homogeneity condition on \mathcal{M} says that if both female and male sizes increase with the same rate we should expect a similar rate increase in the number of couples. That is the reason why one cannot model pair formation using mass action kinetics since that will lead to unrealistically large number of couples for a small increase in the population of singles. Examples of marriage functions are:

$$\min(F, M), \quad \rho F^\alpha M^{1-\alpha} \text{ with } \alpha \in (0, 1), \quad 2\rho \frac{FM}{F + M}$$

In [2], Hadeler et al. used a transformation that reduces the original system to one that admits stationary solutions. They proved that every stationary solution of the reduced system is associated with an exponential solution with an exponent λ given by the following eigenvalue problem:

$$(2) \quad \mathcal{M} \left(\frac{\beta\gamma_f}{\mu_f + \lambda} - 1, \frac{\beta\gamma_m}{\mu_m + \lambda} - 1 \right) = \mu_f + \mu_m + \delta + \lambda.$$

Moreover, they also proved the global stability of these stationary solutions whenever they exists. Consequently λ determines whether the total population grows exponentially or decays to zero.

The equation (2) can be used to prove the extinction threshold for the logistic two-sex model introduced by Castillo-Chavez and Huang in [3] and for our own logistic model with non-linear mortality without isolation discussed later on.

The first logistic version of the pair formation model was introduced by Castillo-Chavez and Huang in their 1995 paper [3]. The model contains the same classes of people but it has non-linear births and separations. Consequently β and δ are now functions of the total population P with the following properties:

$$\frac{d\beta(P)}{dP} < 0, \quad \lim_{P \rightarrow \infty} \beta(P) = 0 \quad \text{and} \quad \frac{d\delta(P)}{dP} \geq 0.$$

The main result of their model is given below in the form of three propositions:

PROPOSITION 2.1. *If*

$$\min \left\{ \frac{\beta(0)\gamma_f}{\mu_f}, \frac{\beta(0)\gamma_m}{\mu_m} \right\} \leq 1$$

or

$$\mu_f + \mu_m + \delta(0) \geq \mathcal{M} \left(\frac{\beta(0)\gamma_f}{\mu_f} - 1, \frac{\beta(0)\gamma_m}{\mu_m} - 1 \right)$$

then

$$\lim_{t \rightarrow \infty} P(t) = 0.$$

PROPOSITION 2.2. *If*

$$\min \left\{ \frac{\beta(0)\gamma_f}{\mu_f}, \frac{\beta(0)\gamma_m}{\mu_m} \right\} > 1$$

and

$$\mu_f + \mu_m + \delta(0) < \mathcal{M} \left(\frac{\beta(0)\gamma_f}{\mu_f} - 1, \frac{\beta(0)\gamma_m}{\mu_m} - 1 \right)$$

then the trivial solution $(0, 0, 0)$ is unstable.

PROPOSITION 2.3. *If*

$$\min \left\{ \frac{\beta(0)\gamma_f}{\mu_f}, \frac{\beta(0)\gamma_m}{\mu_m} \right\} > 1$$

and

$$\mu_f + \mu_m + \delta(0) < \mathcal{M} \left(\frac{\beta(0)\gamma_f}{\mu_f} - 1, \frac{\beta(0)\gamma_m}{\mu_m} - 1 \right)$$

then there exist a unique positive steady state (F^*, M^*, C^*) locally- and conjectured globally-asymptotically stable.

The proposition says that the population goes extinct whenever the reproductive number of each genders is below 1 and when there are not enough marriages to compensate for the initial separation rate of the couples. Otherwise the total population approaches a non-trivial bounded equilibrium. These are in fact the basic features of a logistic model. While proving 2.3 can be done using the classic Routh-Hurwitz criterion, this is no longer true for the extinction steady state $(0, 0, 0)$ since the marriage function fails to be differentiable at that point. In order to prove 2.1 and 2.2, Castillo-Chavez and Huang used an equivalent system that follows the dynamics of the total females and males $x = F + C$ and $y = M + C$. For the global stability of the extinction steady state they considered the following continuous and, in general, not differentiable function:

$$\eta(t) = \max \left\{ \frac{\mu_f x(t)}{\beta(0)\gamma_f}, \frac{\mu_m y(t)}{\beta(0)\gamma_m}, C(t) \right\}$$

and showed that

$$D^+ \eta(t) = \limsup_{\epsilon \rightarrow 0^+} \frac{\eta(t + \epsilon) - \eta(t)}{\epsilon} < 0.$$

However just by itself this condition does not imply that $\eta(t) \rightarrow 0$ as desired. Instead, we propose using a homogeneous two-sex system that bounds above the two-sex logistic one and show that the corresponding non-linear eigenvalue problem (2) has only negative roots. This argument is provided below.

The system in x , y and C is as follows:

$$(3) \quad \begin{cases} x' &= -\mu_f x + \beta(P)\gamma_f C, \\ y' &= -\mu_m y + \beta(P)\gamma_m C, \\ C' &= \mathcal{M}(x - C, y - C) - (\delta(P) + \mu_f + \mu_m)C, \end{cases}$$

where $P = x + y$.

First notice that the biological meaningful domain for this system is

$$\Omega = \{(x, y, C) : x \geq 0, y \geq 0, C \geq 0, x > C, y > C\}$$

and one can show, using standard methods, that it is invariant.

If either

$$\frac{\beta(0)\gamma_f}{\mu_f} < 1 \quad \text{or} \quad \frac{\beta(0)\gamma_m}{\mu_m} < 1$$

then

$$x' < (-\mu_f + \beta(0)\gamma_f)x \quad \text{or} \quad y' < (-\mu_m + \beta(0)\gamma_m)y$$

meaning that $x(t)$ or $y(t)$ is bounded above by an exponential with negative rate, hence $x(t) \rightarrow 0$ or $y(t) \rightarrow 0$ and, consequently, $P(t) \rightarrow 0$. Suppose now that both female and male reproductive numbers are greater than 1 but there are not enough marriages initially, i.e.

$$\mathcal{M} \left(\frac{\beta(0)\gamma_f}{\mu_f} - 1, \frac{\beta(0)\gamma_m}{\mu_m} - 1 \right) \leq \mu_f + \mu_m + \delta(0).$$

We can construct a homogeneous system obtained from (3) by replacing $\beta(P)$ and $\delta(P)$ with the constants $\beta(0)$ and $\delta(0)$. The solution of this system is greater than the one of the original logistic system since $\beta(P) < \beta(0)$ and $\delta(P) > \delta(0)$ for every $P > 0$. The non-linear eigenvalue problem associated with this system is, according to (2)

$$\mathcal{M} \left(\frac{\beta(0)\gamma_f}{\mu_f + \lambda} - 1, \frac{\beta(0)\gamma_m}{\mu_m + \lambda} - 1 \right) = \mu_f + \mu_m + \delta(0) + \lambda$$

It is clear that the equation cannot have a positive root in the condition of Proposition 2.1 since for positive λ the left hand side decreases and the right hand side increases. So if there are not enough marriages as stated in the proposition, the non-linear eigenvalue problem yields a negative root and therefore the solution of the homogeneous system—and, consequently, of the logistic one—declines to zero.

The proof of Proposition 2.2 uses a function similar to η . First we notice that due to the assumptions of 2.2 there exists a strictly positive P_0 such that

$$\mu_f + \mu_m + \delta(P_0) < \mathcal{M} \left(\frac{\beta(P_0)\gamma_f}{\mu_f} - 1, \frac{\beta(P_0)\gamma_m}{\mu_m} - 1 \right).$$

Then, it is shown in [3], that for any initial condition $x_0 + y_0 < P_0$, the function

$$\xi(t) = \min \left\{ \frac{\mu_f x(t)}{\beta(P_0)\gamma_f}, \frac{\mu_m y(t)}{\beta(P_0)\gamma_m}, C(t) \right\}$$

has the following property:

$$D^+ \xi(t) = \liminf_{\epsilon \rightarrow 0^+} \frac{\xi(t + \epsilon) - \xi(t)}{\epsilon} > 0$$

as long as $x(t) + y(t) < P_0$ and this indeed shows that $(0, 0, 0)$ is unstable.

In the next sections we will use a similar approach, with some modifications, to establish the logistic behavior in the two-sex logistic models with non-linear mortality and with non-reproductive groups.

3. THE TWO-SEX LOGISTIC EQUATION WITH NON-LINEAR MORTALITY AND NON-REPRODUCTIVE GROUPS

The purpose of this section is to study the demographic role of the non-reproductive groups in the context of a two-sex logistic model with non-linear mortality. The first work was done by Milner [6] on one-sex exponential and logistic demographic models as well as on two-sex homogeneous models with constant birth and death rate. The models were modified to include groups of non-reproductive people and threshold values were computed for ν_f and ν_m —the transition rates into the female and male non-reproductive classes—that would stop the exponential growth and result in stagnant population.

In this paper we consider a constant birth rate β and two logistic mortality terms for each gender as functions of the total population P :

$$\mu_f + b_f P \quad \text{and} \quad \mu_m + b_m P$$

The assumption is that the linear coefficients b_f and b_m are much smaller than the corresponding natural mortality, i.e.

$$\mu_f \gg b_f \quad \text{and} \quad \mu_m \gg b_m,$$

otherwise there would be an unrealistic increase in the death rate for rather small increases in the total population P .

This particular form of the death rate is also justified by the well established logistic model introduced by Verhulst in [1] and it represents a first approximation of a more realistic population dynamics than that of the one exhibited by the exponential two-sex model in [2].

Remark 3.1. *Another argument for taking non-linear mortality and constant birth rate is that in general the natural factors that impose a limit on the population size are more prevalent on the number of deaths rather than births. In fact crowding should increase the number of contact between people and therefore the number of births per unit of time. What changes is the survivability of the individuals. There are however situations when human intervention is clearly acted on the fertility and is correlated with the total population size justifying taking β as a decreasing function. One such example is given by China and its demographic laws that limit the number of offspring a family can have.*

The two-sex model becomes

$$(4) \quad \begin{cases} F' &= -(\mu_f + b_f P)F + (\beta\gamma_f + \delta + \mu_m + b_m P)C - \mathcal{M}(F, M), \\ M' &= -(\mu_m + b_m P)M + (\beta\gamma_m + \delta + \mu_f + b_f P)C - \mathcal{M}(F, M), \\ C' &= \mathcal{M}(F, M) - (\delta + \mu_f + \mu_m + (b_f + b_m)P)C. \end{cases}$$

The equivalent system that follows the dynamics of the total females and males is

$$(5) \quad \begin{cases} x' &= -(\mu_f + b_f P)x + \beta\gamma_f C, \\ y' &= -(\mu_m + b_m P)y + \beta\gamma_m C, \\ C' &= \mathcal{M}(x - C, y - C) - (\delta + \mu_f + \mu_m + (b_f + b_m)P)C. \end{cases}$$

Before we include the non-reproductive groups we will show that this model exhibits a similar threshold condition on the parameters as the one derived by Castillo-Chavez and Huang [3].

PROPOSITION 3.1. *If*

$$\min \left\{ \frac{\beta\gamma_f}{\mu_f}, \frac{\beta\gamma_m}{\mu_m} \right\} \leq 1$$

or

$$\mu_f + \mu_m + \delta \geq \mathcal{M} \left(\frac{\beta\gamma_f}{\mu_f} - 1, \frac{\beta\gamma_m}{\mu_m} - 1 \right)$$

then

$$\lim_{t \rightarrow \infty} P(t) = 0.$$

Otherwise the trivial solution is unstable and there exist a positive interior steady state (F^*, M^*, C^*) that is locally asymptotically stable.

Proof. The argument for the stability and non-stability of the extinction equilibrium mirrors the one we used for Castillo-Chavez and Huang's model. Using the fact that the death rate is an increasing function of P we can neglect the logistic terms $b_f P$ and $b_m P$ in (5) and obtain a homogeneous bounding system whose solution exponentially declines to zero and attracts all other solutions. Furthermore, a function similar to ξ and an analogous argument shows that the trivial solution is unstable. We proceed now to show the existence and the stability of the interior steady state whenever

$$\frac{\beta\gamma_f}{\mu_f} > 1, \quad \frac{\beta\gamma_m}{\mu_m} > 1 \quad \text{and} \quad \mu_f + \mu_m + \delta < \mathcal{M} \left(\frac{\beta\gamma_f}{\mu_f} - 1, \frac{\beta\gamma_m}{\mu_m} - 1 \right).$$

First notice that, as it is expected, the total population is always bounded. Namely,

$$x' < (\beta\gamma_f - \mu_f - b_f x)x \quad \text{implies} \quad x(t) \leq \max \left\{ x(0), \frac{\beta\gamma_f - \mu_f}{b_f} \right\}.$$

Similarly,

$$y(t) \leq \max \left\{ y(0), \frac{\beta\gamma_m - \mu_m}{b_m} \right\}.$$

Substituting x and y from the first two equations into the third one we obtain the equation that gives the steady state for the total population $P = x + y$ i.e

$$(6) \quad \mathcal{M} \left(\frac{\beta\gamma_f}{\mu_f + b_f P} - 1, \frac{\beta\gamma_m}{\mu_m + b_m P} - 1 \right) = \delta + \mu_f + \mu_m + (b_f + b_m)P$$

denote

$$H(P) = \mathcal{M} \left(\frac{\beta\gamma_f}{\mu_f + b_f P} - 1, \frac{\beta\gamma_m}{\mu_m + b_m P} - 1 \right) - (\delta + \mu_f + \mu_m + (b_f + b_m)P)$$

It is easy to see that H is a decreasing function in $P > 0$.
Moreover $H(0) > 0$ since this is equivalent to

$$\mathcal{M}\left(\frac{\beta\gamma_f}{\mu_f} - 1, \frac{\beta\gamma_m}{\mu_m} - 1\right) > \delta + \mu_f + \mu_m,$$

which is true by assumption. Also, taking into account that

$$\mathcal{M}(0, y) = \mathcal{M}(x, 0) = 0 \quad \text{for every } x, y \geq 0,$$

we have that

$$H\left(\frac{\beta\gamma_f - \mu_f}{b_f}\right) < 0 \quad \text{and} \quad H\left(\frac{\beta\gamma_m - \mu_m}{b_m}\right) < 0$$

Hence there exist a unique positive steady state denoted by $P^* = x^* + y^*$

$$0 < P^* < \min\left\{\frac{\beta\gamma_f - \mu_f}{b_f}, \frac{\beta\gamma_m - \mu_m}{b_m}\right\}.$$

Notice that

$$C^* = \frac{P^*}{\frac{\beta\gamma_f}{\mu_f + b_f P^*} + \frac{\beta\gamma_m}{\mu_m + b_m P^*}}$$

and

$$x^* = \frac{\beta\gamma_f}{\mu_f + b_f P^*} C^*, \quad y^* = \frac{\beta\gamma_m}{\mu_m + b_m P^*} C^*.$$

In order to prove the stability of the interior steady state we linearize the system around (x^*, y^*, P^*) and use the Routh-Hurwitz criterion to show that all roots of the characteristic polynomial have negative real part.

To simplify the computation we are going to use the following notations and substitutions:

$$\bar{\mu}_f = \mu_f + b_f P^*, \quad \bar{\mu}_m = \mu_m + b_m P^*, \quad b = b_f + b_m, \quad \beta\gamma_f = \bar{\mu}_f \frac{x^*}{C^*}, \quad \beta\gamma_m = \bar{\mu}_m \frac{y^*}{C^*},$$

$$\mathcal{M}_x = \frac{\partial \mathcal{M}}{\partial F}(x^* - C^*, y^* - C^*) \quad \text{and} \quad \mathcal{M}_y = \frac{\partial \mathcal{M}}{\partial M}(x^* - C^*, y^* - C^*).$$

It follows then,

$$\frac{\partial}{\partial C} [\mathcal{M}(x^* - C^*, y^* - C^*)]_{C=C^*} = -\mathcal{M}_x - \mathcal{M}_y$$

From [3] we can also use the following identity due to the homogeneity of \mathcal{M} :

$$\delta + \bar{\mu}_f + \bar{\mu}_m + \mathcal{M}_x + \mathcal{M}_y = \frac{1}{C^*} (x^* \mathcal{M}_x + y^* \mathcal{M}_y)$$

This is obtained by differentiating the following identity with respect to α and evaluated at $\alpha = 1$:

$$\mathcal{M}[\alpha(x^* - C^*), \alpha(y^* - C^*)] = \alpha \mathcal{M}(x^* - C^*, y^* - C^*).$$

Having these, the Jacobian computed at the interior steady state is

$$A = \begin{pmatrix} -\bar{\mu}_f - b_f x^* & -b_f x^* & \bar{\mu}_f \frac{x^*}{C^*} \\ -b_m y^* & -\bar{\mu}_m - b_m y^* & \bar{\mu}_m \frac{y^*}{C^*} \\ \mathcal{M}_x - bC^* & \mathcal{M}_y - bC^* & -\frac{1}{C^*} (x^* \mathcal{M}_x + y^* \mathcal{M}_y) \end{pmatrix}.$$

If we denote by $\lambda^3 + p_1\lambda^2 + p_2\lambda + p_3 = 0$ the corresponding characteristic equation then a straightforward computation shows:

$$\begin{aligned}
p_1 &= -Tr(A) = \bar{\mu}_f + \bar{\mu}_m + b_fx^* + b_my^* + \frac{1}{C^*}(x^*\mathcal{M}_x + y^*\mathcal{M}_y) > 0 \\
p_2 &= [(\bar{\mu}_f + b_fx^*)(\bar{\mu}_m + b_my^*) - b_fb_mx^*y^*] + \\
&+ \left[\frac{1}{C^*}(\bar{\mu}_f + b_fx^*)(x^*\mathcal{M}_x + y^*\mathcal{M}_y) - \frac{1}{C^*}\bar{\mu}_fx^*\mathcal{M}_x + b\bar{\mu}_fx^* \right] + \\
&+ \left[\frac{1}{C^*}(\bar{\mu}_m + b_my^*)(x^*\mathcal{M}_x + y^*\mathcal{M}_y) - \frac{1}{C^*}\bar{\mu}_my^*\mathcal{M}_y + b\bar{\mu}_my^* \right] = \\
&= \bar{\mu}_f\bar{\mu}_m + b_m\bar{\mu}_fy^* + b_f\bar{\mu}_mx^* + b(\bar{\mu}_fx^* + \bar{\mu}_my^*) + \frac{1}{C^*}(\bar{\mu}_mx^*\mathcal{M}_x + \bar{\mu}_fy^*\mathcal{M}_y) + \\
&+ \frac{1}{C^*}(b_fx^* + b_my^*)(x^*\mathcal{M}_x + y^*\mathcal{M}_y) > 0 \\
p_3 &= -Det[A] = \left(b - \frac{\mathcal{M}_x}{C^*} \right) [x^*y^*(b_m\bar{\mu}_f - b_f\bar{\mu}_m) + x^*\bar{\mu}_f\bar{\mu}_m] + \\
&+ \left(b - \frac{\mathcal{M}_y}{C^*} \right) [x^*y^*(b_f\bar{\mu}_m - b_m\bar{\mu}_f) + y^*\bar{\mu}_f\bar{\mu}_m] + \\
&+ \frac{1}{C^*}(x^*\mathcal{M}_x + y^*\mathcal{M}_y)[(\bar{\mu}_f + b_fx^*)(\bar{\mu}_m + b_my^*) - b_fb_mx^*y^*] = \\
&= (x^* + y^*) \left(b\bar{\mu}_f\bar{\mu}_m + b_f\bar{\mu}_mx^*\frac{\mathcal{M}_x}{C^*} + b_m\bar{\mu}_fy^*\frac{\mathcal{M}_y}{C^*} \right) > 0
\end{aligned}$$

Similarly, a lengthy computation shows also that $p_1p_2 > p_3$ and it is easy to see, in fact, that p_3 appears entirely as part of p_1p_2 with additional non-negative terms. \square

In all likelihood the interior steady state is globally stable. If we assume that we have the same parameters for both genders the marriage function becomes linear and the system can be reduced to two dimensions. We can prove in this case the global stability of the interior steady state using the Poincare-Bendixson theory for planar systems.

PROPOSITION 3.2. *Assuming that*

$$\mu = \mu_f = \mu_m, \quad b = b_f = b_m, \quad \gamma_f = \gamma_m = \frac{1}{2}$$

and

$$\frac{\beta}{2\mu} > \frac{\delta + 2\mu}{\mathcal{M}(1, 1)} + 1$$

the interior equilibrium (x^*, y^*, C^*) is globally asymptotically stable.

Proof. The last condition in the proposition essentially combines the hypothesis of the general case stating that there should be enough births and enough marriages in order for the population to avoid extinction. Taking into account that \mathcal{M} is homogeneous and that $x(t) = y(t)$ —provided $x(0) = y(0)$ —the system (5) reduces to

$$(7) \quad \begin{cases} x' &= -(\mu + 2bx)x + \frac{\beta}{2}C & := \bar{f}(x, C), \\ C' &= (x - C)\mathcal{M}(1, 1) - (\delta + 2\mu + 4bx)C & := \bar{g}(x, C). \end{cases}$$

By applying the Dulac's criterion we can exclude the possibility of periodic solutions since

$$\begin{aligned} & \frac{\partial}{\partial x} \left[\frac{1}{xC} \bar{f}(x, C) \right] + \frac{\partial}{\partial C} \left[\frac{1}{xC} \bar{g}(x, C) \right] = \\ &= -\frac{1}{xC} \left[2bx + \mathcal{M}(1, 1) \frac{x}{C} + \frac{\beta}{2} \frac{C}{x} \right] < 0 \end{aligned}$$

in the positive quadrant. Furthermore, the extinction equilibrium is unstable whenever the interior one exists by Proposition 3.1. From this and the fact that the solution is bounded for all time we conclude the global stability result stated above. \square

We introduce now two classes of individuals, A_f and A_m representing the number of females and males who become sexually abstained for life by any reason, either social or medical. The modified two-sex logistic model is

$$(8) \quad \begin{cases} F' &= -(\mu_f + b_f P)F + (\beta\gamma_f + \delta + \mu_m + b_m P)C - \mathcal{M}(F, M) - \nu_f F, \\ M' &= -(\mu_m + b_m P)M + (\beta\gamma_m + \delta + \mu_f + b_f P)C - \mathcal{M}(F, M) - \nu_m M, \\ C' &= \mathcal{M}(F, M) - [\delta + \mu_f + \mu_m + (b_f + b_m)P]C, \\ A'_f &= \nu_f F - (\mu_f + b_f P)A_f, \\ A'_m &= \nu_m M - (\mu_m + b_m P)A_m. \end{cases}$$

The corresponding system in x, y, C, A_f, A_m is

$$(9) \quad \begin{cases} x' &= -(\mu_f + \nu_f + b_f P)x + (\beta\gamma_f + \nu_f)C, \\ y' &= -(\mu_m + \nu_m + b_m P)y + (\beta\gamma_m + \nu_m)C, \\ C' &= \mathcal{M}(x - C, y - C) - [\delta + \mu_f + \mu_m + (b_f + b_m)P]C, \\ A'_f &= \nu_f(x - C) - (\mu_f + b_f P)A_f, \\ A'_m &= \nu_m(y - C) - (\mu_m + b_m P)A_m. \end{cases}$$

Notice that in this case x and y denotes the total number of reproductive females and males, hence

$$P(t) = x(t) + y(t) + A_f(t) + A_m(t).$$

The next proposition establishes a similar condition as the one for the model without isolation from reproduction that ensure the logistic behavior of our model. This will also provide a threshold condition on the isolation rates ν_f and ν_m that will cause an otherwise stable positive population to decline to zero. Thus we will give an answer for the question about the demographic influence of the non-reproductive groups. As we mentioned before, this was done in [6] for the homogeneous two-sex models.

PROPOSITION 3.3. *If*

$$\min \left\{ \frac{\beta\gamma_f}{\mu_f}, \frac{\beta\gamma_m}{\mu_m} \right\} \leq 1$$

or

$$\mu_f + \mu_m + \delta \geq \mathcal{M} \left(\frac{\beta\gamma_f + \nu_f}{\mu_f + \nu_f} - 1, \frac{\beta\gamma_m + \nu_m}{\mu_m + \nu_m} - 1 \right)$$

then

$$\lim_{t \rightarrow \infty} P(t) = 0$$

Proof. First notice that ν_f and ν_m have no influence on the first condition since

$$x' < (-\mu_f - \nu_f + \beta\gamma_f + \nu_f)x = (-\mu_f + \beta\gamma_f)x$$

and

$$y' < (-\mu_m - \nu_m + \beta\gamma_m + \nu_m)y = (-\mu_m + \beta\gamma_m)y.$$

Therefore

$$\frac{\beta\gamma_f}{\mu_f} < 1 \quad \text{or} \quad \frac{\beta\gamma_m}{\mu_m} < 1 \quad \text{implies} \quad x(t) \rightarrow 0 \quad \text{or} \quad y(t) \rightarrow 0$$

and then $P(t) \rightarrow 0$.

Suppose now that both female and male reproductive numbers are positive but we have

$$a_1 := \mu_f + \mu_m + \delta - \mathcal{M} \left(\frac{\beta\gamma_f + \nu_f}{\mu_f + \nu_f} - 1, \frac{\beta\gamma_m + \nu_m}{\mu_m + \nu_m} - 1 \right) > 0$$

In this case we are no longer able to use the homogeneous bounding system that we mentioned in the model without isolation and in the Proposition 2.1. By doing so, the isolation rates ν_f and ν_m will cancel and we end-up with the same extinction threshold which is too strong and, evidently, does not capture the influence of the non-reproductive groups. Instead, we will use Castillo-Chavez and Huang approach by taking a function similar to η for which we derive a stronger result by taking advantage of our particular form of the death rate.

Consider the forward solution $(x(t), y(t), C(t), A_f(t), A_m(t))$ through an initial point $(x_0, y_0, C_0, A_{f_0}, A_{m_0})$ and the following function, as in [3]:

$$h(t) = \max \left\{ \frac{(\mu_f + \nu_f)x(t)}{\beta\gamma_f + \nu_f}, \frac{(\mu_m + \nu_m)y(t)}{\beta\gamma_m + \nu_m}, C(t) \right\}$$

For any $t > 0$ fixed one of the following holds:

- $h(t) = C(t)$. In this case we have

$$\begin{aligned} C' &= C \left[\mathcal{M} \left(\frac{x}{C} - 1, \frac{y}{C} - 1 \right) - (\delta + \mu_f + \mu_m + (b_f + b_m)P) \right] < \\ &< C \left[\mathcal{M} \left(\frac{\beta\gamma_f + \nu_f}{\mu_f + \nu_f} - 1, \frac{\beta\gamma_m + \nu_m}{\mu_m + \nu_m} - 1 \right) - (\delta + \mu_f + \mu_m) \right] < -a_1 C. \end{aligned}$$

- $h(t) = \frac{(\mu_f + \nu_f)x(t)}{\beta\gamma_f + \nu_f}$. This implies that

$$x' = \left[(\beta\gamma_f + \nu_f) \frac{C}{x} - \mu_f - \nu_f - b_f P \right] x < -b_f x^2.$$

- Similarly if $h(t) = \frac{(\mu_m + \nu_m)y(t)}{\beta\gamma_m + \nu_m}$ we have $y' < -b_m y^2$.

This means that if we denote

$$D^+ h(t) = \limsup_{\epsilon \rightarrow 0^+} \frac{h(t + \epsilon) - h(t)}{\epsilon}$$

we have

$$D^+ h(t) < -a_1 h(t) \quad \text{or} \quad D^+ h(t) < -a_2 h^2(t),$$

where

$$a_2 = \min \left\{ \frac{b_f(\beta\gamma_f + \nu_f)}{\mu_f + \nu_f}, \frac{b_m(\beta\gamma_m + \nu_m)}{\mu_m + \nu_m} \right\}.$$

While $h(t)$ is a continuous function one cannot in general assume that it is differentiable so we can't use the Riemann integral nor the fundamental theorem of calculus to integrate the inequalities above. We can use, however, the following weaker version of the theorem of calculus:

THEOREM 3.1. *Let f be an increasing real-valued function on the interval $[a, b]$. Then f is differentiable almost everywhere. The derivative f' is measurable and*

$$\int_a^b f'(x) dx \leq f(b) - f(a).$$

Consider now $T > 0$ a fixed time. On the compact $[0, T]$, $h(t)$ is continuous and decreasing. Therefore $-\ln(h(t))$ and $\frac{1}{h(t)}$ are increasing. We define now the following sets:

$$A = \{t \in [0, T], D^+ h(t) < -a_1 h(t)\}$$

and

$$B = \{t \in [0, T], D^+ h(t) < -a_2 h^2(t)\}$$

These are clearly measurable with respect with the usual real Lebesgue measure denoted by l . Hence

$$l(A) + l(B) \geq T.$$

Since both $-\ln h(t)$ and $\frac{1}{h(t)}$ are differentiable almost everywhere on $[0, T]$ we can consider the Lebesgue integral of their derivatives:

$$\int_A [-\ln h(t)]' dt < \int_0^T [-\ln h(t)]' dt \leq -\ln h(T) + \ln h(0).$$

However on A we also have

$$\int_A [-\ln h(t)]' dt = \int_A \frac{-h'(t)}{h(t)} dt > \int_A a_1 dt = a_1 l(A).$$

Similarly,

$$\int_B \left[\frac{1}{h(t)} \right]' dt < \int_0^T \left[\frac{1}{h(t)} \right]' dt \leq \frac{1}{h(T)} - \frac{1}{h(0)}$$

and

$$\int_B \left[\frac{1}{h(t)} \right]' dt = \int_B \left[-\frac{h'(t)}{h^2(t)} \right] dt > \int_B a_2 dt = a_2 l(B).$$

Combining these inequalities and denoting $a = \min\{a_1, a_2\}$ we obtain

$$\frac{1}{h(T)} - \frac{1}{h(0)} + \ln \frac{h(0)}{h(T)} > a[l(A) + l(B)] \geq aT.$$

As $h(T)$ is decreasing in T and bounded below it must be convergent but since the right hand side of the above inequality goes to ∞ then we must have $h(T) \rightarrow 0^+$ as $T \rightarrow \infty$ and therefore $P(t) \rightarrow 0$ as claimed. \square

Notice that this provides a threshold phenomenon regarding the segregation rates of the healthy group

If

$$\mathcal{M} \left(\frac{\beta\gamma_f - \mu_f}{\mu_f + \nu_f}, \frac{\beta\gamma_m - \mu_m}{\mu_m + \nu_m} \right) < \delta + \mu_f + \mu_m < \mathcal{M} \left(\frac{\beta\gamma_f}{\mu_f} - 1, \frac{\beta\gamma_m}{\mu_m} - 1 \right)$$

then the total population goes to zero due to the non-reproductive rates of healthy people.

The equation that gives the interior steady state in the segregated case is

$$(10) \quad \mathcal{M} \left(\frac{\beta\gamma_f + \nu_f}{\mu_f + \nu_f + b_f P} - 1, \frac{\beta\gamma_m + \nu_m}{\mu_m + \nu_m + b_m P} - 1 \right) = \delta + \mu_f + \mu_m + (b_f + b_m)P.$$

which by the same argument as in the case without the non-reproductive groups has a unique positive root denoted by P_s^* . We denote also by F_s^* , M_s^* , C_s^* , $A_{f_s}^*$ and $A_{m_s}^*$ the corresponding interior equilibrium.

Remark 3.2. *The stability of the interior steady state appears to hold whenever it exists according to the simulations. Applying the Routh-Hurwitz criterion is difficult in this case because the 5 dimensional system leads to very large coefficients. In order to check the stability we implemented a numerical algorithm that computes the eigenvalues of the Jacobian of (9) evaluated at the interior steady state for a given set of data. We generated approximately 1000 sets of data assuming that each parameter is uniformly distributed in the interval $[0, 1]$ and in all cases the eigenvalues had a negative real part. We will use this numerical result in the interpretation of the epidemic reproductive number computed in the next section.*

4. THE EPIDEMIC TWO-SEX LOGISTIC MODEL WITH GROUPS ISOLATED FROM SEXUAL ACTIVITY

The two-sex logistic model introduced in the previous section can be extended to an epidemic model where the disease transmission is realized by the pair formation. We assume that once a couple is formed between a healthy person and an infected one then the infection is certain. While this

might be an oversimplification it allows us to keep the dimension of the system as low as possible.

The epidemic model includes 6 classes of individuals: F , M , C as before and the corresponding Φ , X and Γ for the infected females, males and couples.

The pair formation is assumed to be independent of the disease. In other words single individuals enter in relationships without a behavioral change according to whether they are infected or not. We consider from now on that the marriage function is given by the harmonic mean:

$$\mathcal{M}(x, y) = 2\rho \frac{xy}{x + y}.$$

In our model this can be written as follows:

$$\mathcal{M}(F + \Phi, M + X) = \mathcal{P}(F, M) + \mathcal{P}(F, X) + \mathcal{P}(\Phi, M) + \mathcal{P}(\Phi, X)$$

where

$$\mathcal{P}(x, y) = 2\rho \frac{xy}{F + M + \Phi + X}.$$

Using the pair-formation function \mathcal{P} we can track the source of new infections in the model. Notice that this is given by $\mathcal{P}(\Phi, M)$ and $\mathcal{P}(F, X)$. The last term that pairs the sick females and males while it will be a source for infected couples Γ it does not technically constitute new infection since the partners are already infected before entering in the relationship. Finally we will add the 4 classes abstained from sexual activity A_f , A_m , A_φ and A_χ coming from single females and males both healthy and infected with the rates given by ν_f , ν_m , ν_φ and ν_χ . We denote also by δ_i the separation rate of the infected couples. A flow diagram is provided below. The infected classes are emphasized by the red color.

The model equations are:

$$\begin{aligned}
(11) \quad F' &= -(\mu_f + b_f P)F + \beta\gamma_f(C + \Gamma) + (\delta + \mu_m + b_m P)C - \mathcal{P}(F, M) - \mathcal{P}(F, X) - \nu_f F, \\
M' &= -(\mu_m + b_m P)M + \beta\gamma_m(C + \Gamma) + (\delta + \mu_f + b_f P)C - \mathcal{P}(F, M) - \mathcal{P}(\Phi, M) - \nu_m M, \\
C' &= \mathcal{P}(F, M) - (\delta + \mu_f + \mu_m + (b_f + b_m)P)C, \\
\Phi' &= -(\mu_f + b_f P)\Phi + (\delta_i + \mu_m + b_m P)\Gamma - \mathcal{P}(\Phi, M) - \mathcal{P}(\Phi, X) - \nu_\varphi \Phi, \\
X' &= -(\mu_m + b_m P)X + (\delta_i + \mu_f + b_f P)\Gamma - \mathcal{P}(\Phi, X) - \mathcal{P}(F, X) - \nu_\chi X, \\
\Gamma' &= \mathcal{P}(F, X) + \mathcal{P}(\Phi, M) + \mathcal{P}(\Phi, X) - (\delta_i + \mu_f + \mu_m + (b_f + b_m)P)\Gamma, \\
A'_f &= \nu_f F - (\mu_f + b_f P)A_f, \\
A'_m &= \nu_m M - (\mu_m + b_m P)A_m, \\
A'_\varphi &= \nu_\varphi \Phi - (\mu_f + b_f P)A_\varphi, \\
A'_\chi &= \nu_\chi X - (\mu_m + b_m P)A_\chi.
\end{aligned}$$

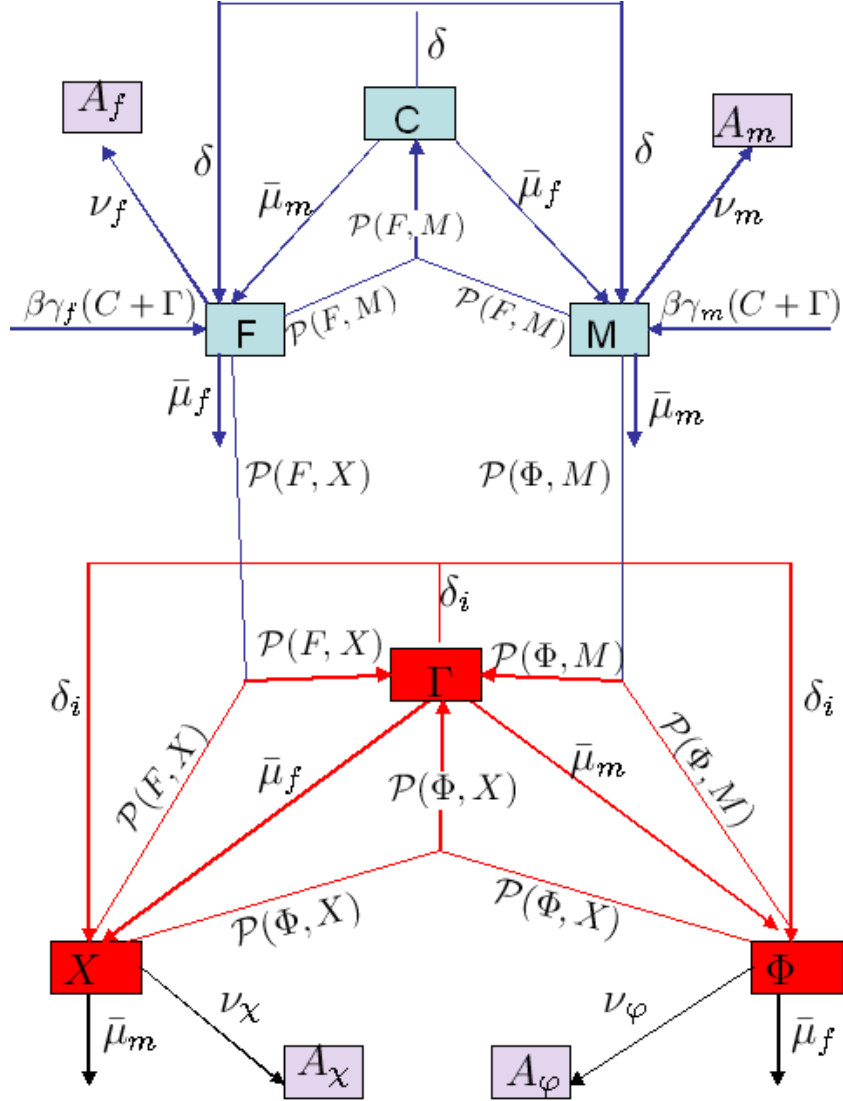


FIGURE 1. The two sex epidemic model with abstained groups.

The total population P is given now by

$$P = F + M + 2C + \Phi + X + 2\Gamma + A_f + A_m + A_\varphi + A_\chi.$$

Remark 4.1. Notice that, in the epidemic model, the concept of “pair formation” includes short lived couples in addition to traditional marriages and implies that these unions are faithful. In other words, we assume that individuals enter a relationship of some sort before engaging in sexual activity. This, of course, is not realistic for communities where casual sexual relations are common but it is appropriate for conservatives cultures where extra marital relations are discouraged or even condemned. Furthermore, even in liberal societies, most people spend some time together before engaging in intimate relations. For these reasons, we consider that the majority of new infections occur among individuals involved in a relationship.

Notice that the disease free equilibrium in the absence of isolation from reproduction is precisely the interior steady state F^* , M^* and C^* of (4) and the one in the presence of the abstained groups is the interior steady state F_s^* , M_s^* , C_s^* , $A_{f_s}^*$ and $A_{m_s}^*$ of (8). The first one is locally asymptotically stable and the second one is also assumed—from the simulations—to be stable. We use this information in order to compute the epidemic reproductive number in both cases mentioned above using a method developed by van den Driessche et al. [7] based on the next-generation matrix.

For an n -dimensional system $x' = f(x)$, we need to write the equations in the form

$$x_i' = \mathcal{G}_i(x) - \mathcal{V}_i(x) \quad i = 1, \dots, n,$$

where \mathcal{G} denotes the rate of appearance of new infections. In our model this is

$$\mathcal{P}(\Phi, M) + \mathcal{P}(F, X).$$

This is because a new infection occurs when there is a marriage between an infected individual and a healthy one. If both partners are already infected they do contribute to the number of infected couples but they do not constitute a new infection. The main result of van den Driessche et al. [7] is that one can compute the epidemic reproductive number by restricting the analysis to the components of \mathcal{G} and \mathcal{V} corresponding to the infected compartments only. For better clarity we change the order of the equations to have the single infected classes first. \mathcal{G} and \mathcal{V} restricted to the infected groups are:

$$\mathcal{G} = \begin{pmatrix} 0 \\ 0 \\ 0 \\ 0 \\ \mathcal{P}(F, X) + \mathcal{P}(\Phi, M) \end{pmatrix},$$

$$\mathcal{V} = \begin{pmatrix} \mathcal{P}(\Phi, X) + \mathcal{P}(\Phi, M) - (\delta_i + \mu_m + b_m P)\Gamma + (\mu_f + b_f P)\Phi + \nu_\varphi \Phi \\ \mathcal{P}(\Phi, X) + \mathcal{P}(F, X) - (\delta_i + \mu_f + b_f P)\Gamma + (\mu_m + b_m P)X + \nu_\chi X \\ (\mu_f + b_f)A_\varphi - \nu_\varphi \Phi \\ (\mu_m + b_m P)A_\chi - \nu_\chi X \\ (\delta_i + \mu_f + \mu_m + (b_f + b_m)P)\Gamma - \mathcal{P}(\Phi, X) \end{pmatrix}.$$

The Jacobians computed below are with respect to the infected classes in the following order: Φ , X and Γ for the system without isolation from sexual activity and Φ , X , A_φ , A_χ and Γ , in the presence of the abstained groups. The basic reproductive number is then defined as being the spectral radius of GV^{-1} where G and V are the Jacobians of \mathcal{G} and \mathcal{V} restricted to the infected classes and evaluated at the disease free equilibrium.

We introduce first the following notation:

$$\mathcal{R}_f = \frac{\beta\gamma_f}{\mu_f + b_f P^*} - 1, \quad \mathcal{R}_m = \frac{\beta\gamma_m}{\mu_m + b_m P^*} - 1,$$

$$\mathcal{R}_f^{\nu_f} = \frac{\beta\gamma_f + \nu_f}{\mu_f + \nu_f + b_f P_s^*} - 1, \quad \mathcal{R}_m^{\nu_m} = \frac{\beta\gamma_m + \nu_m}{\mu_m + \nu_m + b_m P_s^*} - 1,$$

$$\bar{\mu}_f = \mu_f + b_f P^*, \quad \bar{\mu}_m = \mu_m + b_m P^*,$$

$$\bar{\mu}_f^s = \mu_f + b_f P_s^*, \quad \bar{\mu}_m^s = \mu_m + b_m P_s^*.$$

Without isolation from sexual activity, the Jacobians corresponding to the infected classes, Φ , X and Γ , and evaluated at DFE, are

$$G = \begin{pmatrix} 0 & 0 & 0 \\ 0 & 0 & 0 \\ 2\rho \frac{M^*}{F^*+M^*} & 2\rho \frac{F^*}{F^*+M^*} & 0 \end{pmatrix}$$

and

$$V = \begin{pmatrix} \bar{\mu}_f + 2\rho \frac{M^*}{F^*+M^*} & 0 & -\delta_i - \bar{\mu}_m \\ 0 & \bar{\mu}_m + 2\rho \frac{F^*}{F^*+M^*} & -\delta_i - \bar{\mu}_f \\ 0 & 0 & \delta_i + \bar{\mu}_f + \bar{\mu}_m \end{pmatrix}.$$

The inverse of V is:

$$V^{-1} = \begin{pmatrix} \frac{1}{\bar{\mu}_f + 2\rho \frac{M^*}{F^*+M^*}} & 0 & \frac{\delta_i + \bar{\mu}_m}{(\delta_i + \bar{\mu}_f + \bar{\mu}_m)(\bar{\mu}_f + 2\rho \frac{M^*}{F^*+M^*})} \\ 0 & \frac{1}{\bar{\mu}_m + 2\rho \frac{F^*}{F^*+M^*}} & \frac{\delta_i + \bar{\mu}_f}{(\delta_i + \bar{\mu}_f + \bar{\mu}_m)(\bar{\mu}_m + 2\rho \frac{F^*}{F^*+M^*})} \\ 0 & 0 & \frac{1}{\delta_i + \bar{\mu}_f + \bar{\mu}_m} \end{pmatrix}.$$

The biological interpretation of the entries of V^{-1} is as follows:

- The elements on the main diagonal represent the average time spent by a newly introduced infected single female, male or couple in the Φ , X and Γ classes respectively.
- $\frac{\delta_i + \bar{\mu}_m}{\delta_i + \bar{\mu}_f + \bar{\mu}_m}$ is the fraction of married infected females that move into the single class Φ due to either separation or death of the male partner. Therefore the (1, 3) entry represents the average time spent by an infected married woman into the single class Φ . An analogous interpretation corresponding to the married infected males can be made regarding (2, 3) entry.
- The zero elements on the first two rows of V^{-1} simply mean that there is obviously no transition between single females and single males. The zeros in the last row mean that there is no direct transition from couples to singles. In other words a couple cannot exist as an entity in either Φ or X groups.

The corresponding reproductive number is the spectral radius of GV^{-1} which is

$$\begin{aligned} \mathcal{R}_0 &= 2\rho \frac{M^*}{F^* + M^*} \frac{\delta_i + \bar{\mu}_m}{(\delta_i + \bar{\mu}_f + \bar{\mu}_m) \left(\bar{\mu}_f + 2\rho \frac{M^*}{F^*+M^*} \right)} + \\ &+ 2\rho \frac{F^*}{F^* + M^*} \frac{\delta_i + \bar{\mu}_f}{(\delta_i + \bar{\mu}_f + \bar{\mu}_m) \left(\bar{\mu}_m + 2\rho \frac{F^*}{F^*+M^*} \right)}. \end{aligned}$$

The biological interpretation of the first term of \mathcal{R}_0 is as follows: When a single infected female is introduced in a healthy population she spends and average time in Φ class equal to $\frac{1}{\bar{\mu}_f + 2\rho \frac{M^*}{F^*+M^*}}$.

Hence, $2\rho \frac{M^*}{F^*+M^*} \frac{1}{\bar{\mu}_f + 2\rho \frac{M^*}{F^*+M^*}}$ is the expected number of infected couples generated by a single infected female and $\frac{\delta_i + \bar{\mu}_m}{\delta_i + \bar{\mu}_f + \bar{\mu}_m}$ is the fraction of married

infected females that move back into the single class Φ . In other words, the first term of \mathcal{R}_0 represents the average number of *secondary* cases of infected single females generated by the introduction of a single infected female in a healthy population.

An equivalent expression for \mathcal{R}_0 in terms of \mathcal{R}_f and \mathcal{R}_m is

$$\mathcal{R}_0 = \frac{2\rho}{\delta_i + \bar{\mu}_f + \bar{\mu}_m} \left[\frac{\delta_i + \bar{\mu}_m}{2\rho + \bar{\mu}_f(1 + \mathcal{R}_f/\mathcal{R}_m)} + \frac{\delta_i + \bar{\mu}_f}{2\rho + \bar{\mu}_m(1 + \mathcal{R}_m/\mathcal{R}_f)} \right].$$

Finally, in the presence of isolation from sexual activity, G and V , corresponding to the equations for Φ , X , A_φ , A_χ and Γ , are:

$$G_s = \begin{pmatrix} 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 2\rho \frac{M_s^*}{F_s^* + M_s^*} & 2\rho \frac{F_s^*}{F_s^* + M_s^*} & 0 & 0 & 0 \end{pmatrix}$$

and

$$V_s = \begin{pmatrix} \bar{\mu}_f^s + \nu_\varphi + 2\rho \frac{M_s^*}{F_s^* + M_s^*} & 0 & 0 & 0 & -\delta_i - \bar{\mu}_m^s \\ 0 & \bar{\mu}_m^s + \nu_\chi + 2\rho \frac{F_s^*}{F_s^* + M_s^*} & 0 & 0 & -\delta_i - \bar{\mu}_f^s \\ -\nu_\varphi & 0 & \bar{\mu}_f^s & 0 & 0 \\ 0 & -\nu_\chi & 0 & \bar{\mu}_m^s & 0 \\ 0 & 0 & 0 & 0 & \delta_i + \bar{\mu}_f^s + \bar{\mu}_m^s \end{pmatrix},$$

$$V_s^{-1} = \begin{pmatrix} \frac{1}{\bar{\mu}_f^s + \nu_\varphi + 2\rho \frac{M_s^*}{F_s^* + M_s^*}} & 0 & 0 & 0 & \frac{\delta_i + \bar{\mu}_m^s}{(\delta_i + \bar{\mu}_f^s + \bar{\mu}_m^s) \left(\bar{\mu}_f^s + \nu_\varphi + 2\rho \frac{M_s^*}{F_s^* + M_s^*} \right)} \\ 0 & \frac{1}{\bar{\mu}_m^s + \nu_\chi + 2\rho \frac{F_s^*}{F_s^* + M_s^*}} & 0 & 0 & \frac{\delta_i + \bar{\mu}_f^s}{(\delta_i + \bar{\mu}_f^s + \bar{\mu}_m^s) \left(\bar{\mu}_m^s + \nu_\chi + 2\rho \frac{F_s^*}{F_s^* + M_s^*} \right)} \\ \frac{\nu_\varphi}{\bar{\mu}_f^s \left(\bar{\mu}_f^s + \nu_\varphi + 2\rho \frac{M_s^*}{F_s^* + M_s^*} \right)} & 0 & \frac{1}{\bar{\mu}_f^s} & 0 & \frac{\nu_\varphi (\delta_i + \bar{\mu}_m^s)}{\bar{\mu}_f^s (\delta_i + \bar{\mu}_f^s + \bar{\mu}_m^s) \left(\bar{\mu}_f^s + \nu_\varphi + 2\rho \frac{M_s^*}{F_s^* + M_s^*} \right)} \\ 0 & \frac{\nu_\chi}{\bar{\mu}_m^s \left(\bar{\mu}_m^s + \nu_\chi + 2\rho \frac{F_s^*}{F_s^* + M_s^*} \right)} & 0 & \frac{1}{\bar{\mu}_m^s} & \frac{\nu_\chi (\delta_i + \bar{\mu}_f^s)}{\bar{\mu}_m^s (\delta_i + \bar{\mu}_f^s + \bar{\mu}_m^s) \left(\bar{\mu}_m^s + \nu_\chi + 2\rho \frac{F_s^*}{F_s^* + M_s^*} \right)} \\ 0 & 0 & 0 & 0 & \frac{1}{\delta_i + \bar{\mu}_f^s + \bar{\mu}_m^s} \end{pmatrix}.$$

The interpretation of V_s^{-1} is similar to that for V^{-1} . In addition, $\frac{\nu_\varphi}{\bar{\mu}_f^s + \nu_\varphi + 2\rho \frac{M_s^*}{F_s^* + M_s^*}}$

represents the average number of single infected females that move into A_φ class. Hence, the (3,1) entry of V_s^{-1} is the expected time spent in the isolated class by an infected reproductive single female during her life-time. Consequently, the (3,5) entry is the expected time spent in the isolated class by a *married* infected female that moves first into the single reproductive class Φ and then into the isolated class A_φ . A similar interpretation holds for the (4,2) and (4,5) entries.

The epidemic reproductive number in the presence of abstinence is the spectral radius of $G_s V_s^{-1}$:

$$\mathcal{R}_0^s = 2\rho \frac{M_s^*}{F_s^* + M_s^*} \frac{\delta_i + \bar{\mu}_m^s}{\left(\delta_i + \bar{\mu}_f^s + \bar{\mu}_m^s \right) \left(\bar{\mu}_f^s + \nu_\varphi + 2\rho \frac{M_s^*}{F_s^* + M_s^*} \right)} +$$

$$+ 2\rho \frac{F_s^*}{F_s^* + M_s^*} \frac{\delta_i + \bar{\mu}_f^s}{\left(\delta_i + \bar{\mu}_f^s + \bar{\mu}_m^s \right) \left(\bar{\mu}_m^s + \nu_\chi + 2\rho \frac{F_s^*}{F_s^* + M_s^*} \right)}.$$

Just as before, each term represents the gender-specific expected number of secondary infected cases caused by a newly introduced infectious individual in a healthy population. Below we provide an analogous expression for \mathcal{R}_0^s in terms of $\mathcal{R}_f^{\nu_f}$ and $\mathcal{R}_m^{\nu_m}$:

$$\mathcal{R}_0^s = \frac{2\rho}{\delta_i + \bar{\mu}_f^s + \bar{\mu}_m^s} \left[\frac{\delta_i + \bar{\mu}_m^s}{2\rho + (\bar{\mu}_f^s + \nu_\phi)(1 + \mathcal{R}_f^{\nu_f}/\mathcal{R}_m^{\nu_m})} + \frac{\delta_i + \bar{\mu}_f^s}{2\rho + (\bar{\mu}_m^s + \nu_\chi)(1 + \mathcal{R}_m^{\nu_m}/\mathcal{R}_f^{\nu_f})} \right].$$

The following result indicates that there exists a DFE induced by the abstained groups:

PROPOSITION 4.1. *There exists a threshold on the abstinence rates, ν_f , ν_m , ν_ϕ and ν_χ such that the DFE is unstable in the absence of the sexually isolated groups and locally asymptotically stable in the presence of them.*

Proof. Notice the following dependency of \mathcal{R}_0^s on the non-reproductive transition rates:

$$\mathcal{R}_0^s = \mathcal{R}_0^s(P_s^*(\nu_f, \nu_m), \nu_\phi, \nu_\chi).$$

Furthermore, \mathcal{R}_0^s is a decreasing function with respect to the transition rates, ν_ϕ and ν_χ , into the abstained groups coming from the infected singles and, in fact, it is easy to see that

$$\mathcal{R}_0^s \rightarrow 0 \text{ as } \nu_\phi \rightarrow \infty \text{ or } \nu_\chi \rightarrow \infty.$$

We can, therefore, establish conditions on the parameters so that

$$\mathcal{R}_0 > 1 \quad \text{and} \quad \mathcal{R}_0^s < 1.$$

□

The next two pictures show two numerical examples for the disease persistence in the absence of the abstained groups and one where the DFE is stable in the presence of the abstained groups. The values of the parameters were chosen to illustrate the mathematical result and do not correspond to real data.

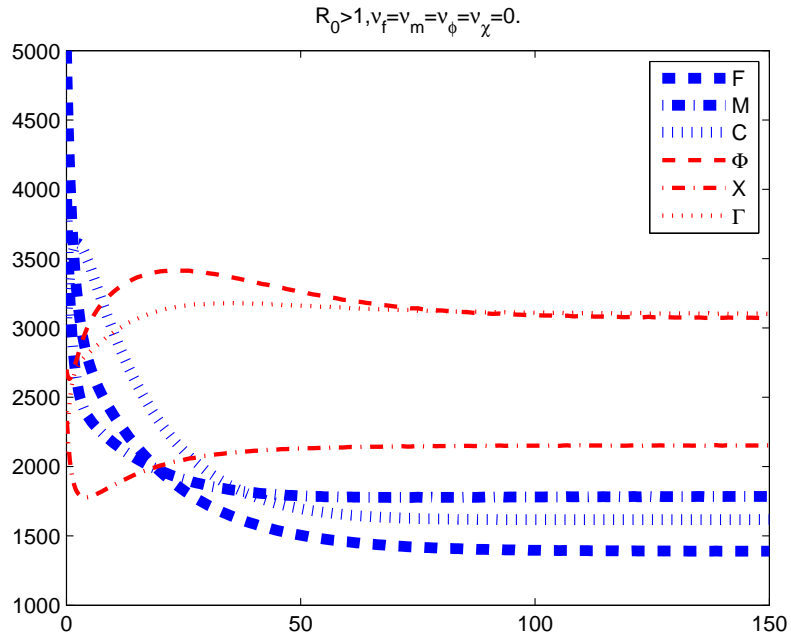


FIGURE 2. The endemic case.

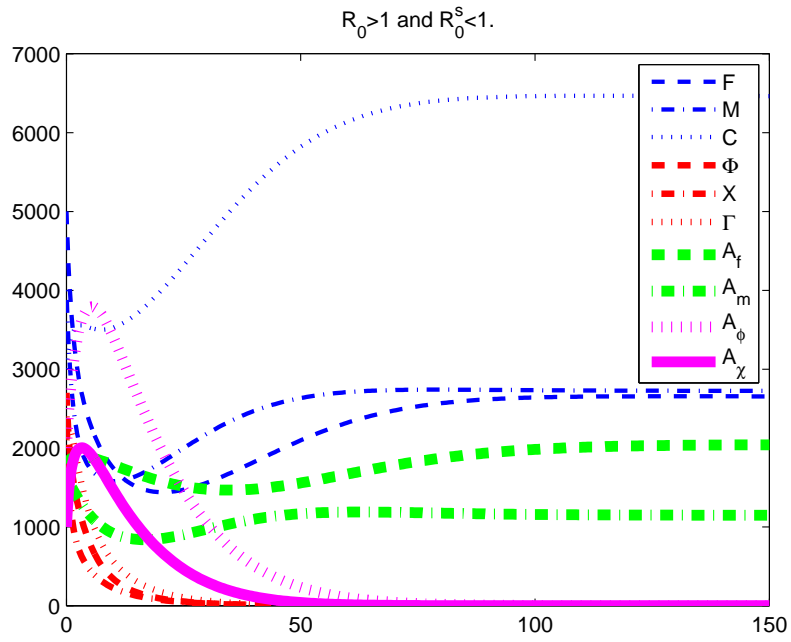


FIGURE 3. DFE induced by the abstained groups.

This result is similar to the one obtained in our previous paper [8] involving SI -type one-sex models. In that case the transmission process involved only one parameter, λ , the force of infection coefficient. We managed then to provide a range for λ where the disease is eliminated by the sexually inactive groups:

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

where $\nu_1 = \nu_f = \nu_m$ and $\nu_2 = \nu_\varphi = \nu_\chi$. The left inequality means that the disease persists in the absence of the abstained groups, that is $\nu_1 = \nu_2 = 0$, while the right inequality denotes the condition that leads to the elimination of the disease by the introduction of an abstained group in an otherwise endemic population. Similarly, $\mathcal{R}_0 > 1$ means that the disease is endemic, while $\mathcal{R}_0^s < 1$ is the condition for the disease-free steady state to be induced by the abstained classes.

The next result shows that the presence of the sexually isolated groups may have the surprising effect of causing the total population to settle at higher values than in the absence of them.

PROPOSITION 4.2. *If $\mathcal{R}_0^s < 1$, a greater separation rate δ_i of the infected couples combined with a low isolation into the isolated groups of healthy singles leads to*

$$\lim_{t \rightarrow \infty} P(t) < P_s^*.$$

Proof. To see why this happens, notice that, if $\delta_i = \delta$ and $\nu_f, \nu_m, \nu_\varphi$ and ν_χ are zero, then the disease will not affect the general dynamics of the population meaning that the singles and the couples, are modeled precisely by the same system as (4):

$$\begin{aligned} (12) \quad (F + \Phi)' &= -(\mu_f + b_f P)(F + \Phi) + (\beta\gamma_f + \delta + \mu_m + b_m P)(C + \Gamma) - \mathcal{M}(F + \Phi, M + X), \\ (M + X)' &= -(\mu_m + b_m P)(M + X) + (\beta\gamma_m + \delta + \mu_f + b_f P)(C + \Gamma) - \mathcal{M}(F + \Phi, M + X), \\ (C + \Gamma)' &= \mathcal{M}(F + \Phi, M + X) - (\delta + \mu_f + \mu_m + (b_f + b_m)P)(C + \Gamma), \end{aligned}$$

whose interior steady state is P^* , the solution of (6), as we know from the analysis in the previous section. If $\delta_i > \delta$, then it is clear that P^* is eventually an upper bound for the total population size $P(t)$ as $t \rightarrow \infty$. On the other hand, we also now that

$$P_s^* < P^* \quad \text{and} \quad P_s^* \rightarrow P^* \quad \text{as} \quad (\nu_f, \nu_m) \rightarrow (0, 0).$$

It follows that, for sufficiently large δ_i, ν_φ , and ν_χ , and sufficiently small ν_f and ν_m ,

$$\lim_{t \rightarrow \infty} P(t) < P_s^*.$$

□

Remark 4.2. *The situation described above can be explained by the fact that, while the infected groups are present, a higher separation rate of the infected couples means that the reproductive number of the paired individuals is lowered significantly. On the other hand, there is no recovery from the disease, which means that the infection transmission acts as a drain of*

reproductive people from a group with high reproductive rate to a group with higher separation rate δ_i , resulting in an overall smaller population size at steady state. In contrast, if the disease is eliminated, then the entire population is governed by a low separation rate δ and the isolated groups do not manage to decrease it too much if ν_f and ν_m are small.

Remark 4.3. Having greater separation and isolation rates for infected individuals can be justified in cases where people become aware of their infection. In the context of mild and non-lethal diseases it is reasonable to assume that these rates are the same for both healthy and infected. On the other hand, if a certain individuals become aware of their infection, they may choose to refrain from sexual activity. Intuitively, this increases the likelihood of couple separation or transition into the abstained groups.

In the next picture we show one numerical example in support for this result.

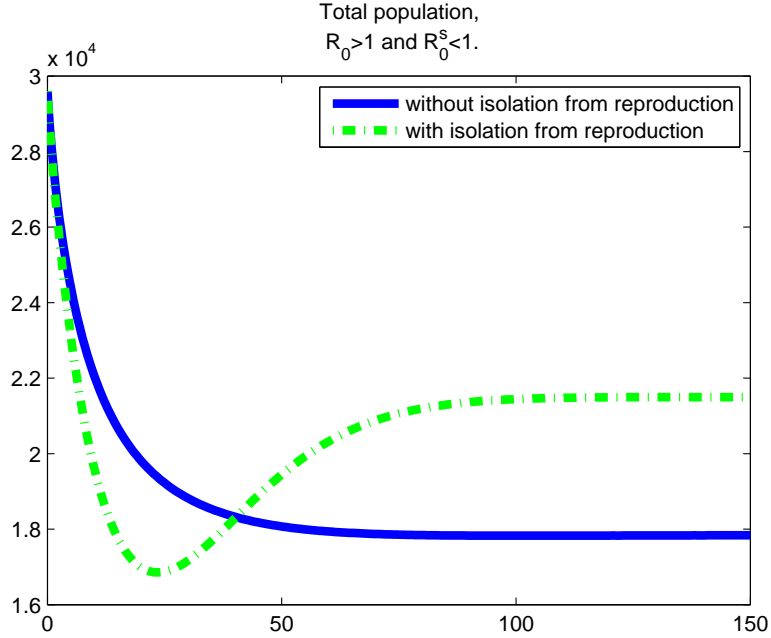


FIGURE 4. Comparison of the total population size.

5. THE CASE OF GENDER INDEPENDENT PARAMETERS

In this section we compute the reproductive numbers derived before in the case of equal gender-related parameters. In doing so we will reduce the dimension of the system to 4 and we will be able to compute explicitly the interior steady states since they will be roots of quadratics. This will give us the opportunity to identify a range on the key parameters—aside from ν_φ and ν_χ —that induce the stability of DFE.

We assume now

$$\mu = \mu_f = \mu_m, \quad b = b_f = b_m, \quad \gamma_f = \gamma_m = \frac{1}{2},$$

$$\nu_1 = \nu_f = \nu_m, \quad \nu_2 = \nu_\varphi = \nu_\chi.$$

Then,

$$\mathcal{R}_f = \mathcal{R}_m \quad \text{and} \quad \mathcal{R}_f^{\nu_f} = \mathcal{R}_m^{\nu_m}.$$

In addition, to simplify the expressions, we denote

$$\bar{\mu} = \mu + bP^* \quad \text{and} \quad \bar{\mu}_s = \mu + bP_s^*.$$

The epidemic reproductive numbers become

$$\mathcal{R}_0 = \frac{2\rho(\delta_i + \bar{\mu})}{(\rho + \bar{\mu})(\delta_i + 2\bar{\mu})} \quad \text{and} \quad \mathcal{R}_0^s = \frac{2\rho(\delta_i + \bar{\mu}_s)}{(\rho + \nu_2 + \bar{\mu}_s)(\delta_i + 2\bar{\mu}_s)},$$

where $\bar{\mu}$ and $\bar{\mu}_s$ are computed solving explicitly (6) and (10), respectively, having the following unique positive values:

$$\bar{\mu} = \frac{-(\delta + \rho) + \sqrt{(\delta + \rho)^2 + 4\rho\beta}}{4},$$

$$\bar{\mu}_s = \frac{-(\delta + \rho + 2\nu_1) + \sqrt{(\delta + \rho + 2\nu_1)^2 + 4(\rho\beta - 2\delta\nu_1)}}{4}.$$

The existence condition of a positive steady state becomes

$$(13) \quad \frac{\beta}{2} > \mu + \frac{(\delta + 2\mu)(\mu + \nu_1)}{\rho}.$$

$\mathcal{R}_0 > 1$ becomes

$$(14) \quad \delta_i(\rho - \bar{\mu}) > 2\bar{\mu}^2,$$

and $\mathcal{R}_0^s < 1$ is equivalent to

$$(15) \quad \delta_i(\rho - \nu_2 - \bar{\mu}_s) < 2\bar{\mu}_s^2 + 2\nu_2\bar{\mu}_s.$$

Notice that (14) requires $\rho > \bar{\mu}$, which is equivalent to

$$3\rho + \delta > \frac{\beta}{2}.$$

Remark 5.1. *The condition above explains the double role—demographic and epidemiological—played by the pair formation coefficient ρ and by the separation rate δ . On one hand, the existence condition (13) provides a lower bound for ρ and an upper bound for δ meaning that marriages need to compensate couple separations in order to sustain a positive stable population. On the other hand, both ρ and δ as well as δ_i must be large enough because three factors must be satisfied in order for an epidemic to occur: a large ρ means that there are enough contacts between infected and healthy people, a large δ provides enough healthy singles which become later on new infections and, finally, a large δ_i supplies single infected individuals. As it is expected, condition (15) is either trivially satisfied if $\rho - \bar{\mu}_s < \nu_2$ or if $\delta_i < \frac{2\bar{\mu}_s^2 + 2\nu_2\bar{\mu}_s}{\rho - \nu_2\bar{\mu}_s}$ and it says that the disease is eliminated either due to the large segregation rate of single infected people or due to a lack of separation of infected couples. The last one essentially has the same effect of reducing the size of single infected groups.*

Remark 5.2. What is the effect of separating because of infection?

From the above remark we see that a higher separation rate of infected couples $\delta_i > \delta$ increases the chance for an epidemic because it combines the unwanted demographic effect of fewer healthy newborns (since we assume no vertical transmission) with the epidemiological effect of having more single infected in the population. This also explains biologically the mathematical result in the previous section when one can obtain a larger population size in the presence of isolation from reproduction.

According to our simulations we conjecture that the stability of both the endemic and the disease free equilibrium are global. In the following particular case we can prove this assertion:

PROPOSITION 5.1. *If the separation rate is independent of the presence of infection, i.e. $\delta = \delta_i$, the endemic equilibrium in the absence of the abstained groups is globally asymptotically stable.*

Proof. Assuming $\nu_1 = \nu_2 = 0$ the original system (11) becomes

$$(16) \quad \begin{cases} F' &= -(\mu + bP)F + \frac{\beta}{2}(C + \Gamma) + (\delta + \mu + bP)C - \rho \frac{F^2}{F+\Phi} - \rho \frac{F\Phi}{F+\Phi}, \\ \Phi' &= -(\mu + bP)\Phi + (\delta + \mu + bP)\Gamma - \rho \frac{F\Phi}{F+\Phi} - \rho \frac{\Phi^2}{F+\Phi}, \\ C' &= \rho \frac{F^2}{F+\Phi} - (\delta + 2\mu + 2bP)C, \\ \Gamma' &= 2\rho \frac{F\Phi}{F+\Phi} + \rho \frac{\Phi^2}{F+\Phi} - (\delta + 2\mu + 2bP)\Gamma. \end{cases}$$

where $P = 2(F + \Phi + C + \Gamma)$.

Denoting $x = F + \Phi$ and $y = C + \Gamma$ we obtain the following planar system:

$$(17) \quad \begin{cases} x' &= -(\rho + \mu + 2bx)x + \left(\frac{\beta}{2} + \delta + \mu + 2by\right)y &:= \bar{f}_1(x, y), \\ y' &= \rho x - (\delta + 2\mu + 4bx + 4by)y &:= \bar{g}_1(x, y). \end{cases}$$

Notice now that, just as in Proposition 3.2, we have

$$\begin{aligned} & \frac{\partial}{\partial x} \left[\frac{1}{xy} \bar{f}_1(x, y) \right] + \frac{\partial}{\partial y} \left[\frac{1}{xy} \bar{g}_1(x, y) \right] = \\ &= -\frac{1}{xy} \left[2bx + 2\mu + \left(\frac{\beta}{2} + \delta + \mu + 2by \right) \frac{y}{x} + \rho \frac{x}{y} \right] < 0 \end{aligned}$$

on the positive quadrant. Using Poincare-Bendixson theory and the Dulac's criterion as in Proposition 3.2 we conclude that the unique interior equilibrium of this system is globally asymptotically stable:

$$x^* = \frac{\bar{\mu} - \mu}{2b} \frac{\delta + 2\bar{\mu}}{\rho + \delta + 2\bar{\mu}} \quad \text{and} \quad y^* = \frac{\bar{\mu} - \mu}{2b} \frac{\rho}{\rho + \delta + 2\bar{\mu}}.$$

Using now the fact that $F(t) + \Phi(t) \rightarrow x^*$ and $C(t) + \Gamma(t) \rightarrow y^*$, we can use results on asymptotically autonomous systems—such as the ones derived

by Thieme in [10]—in order to compute the limits of each of the 4 groups of people that appear in the model.

The following system obtained from (16)

$$(18) \quad \begin{cases} \Phi' &= -(\mu + bP)\Phi + (\delta + \mu + bP)\Gamma - \rho \frac{F\Phi}{F+\Phi} - \rho \frac{\Phi^2}{F+\Phi}, \\ \Gamma' &= 2\rho \frac{F\Phi}{F+\Phi} + \rho \frac{\Phi^2}{F+\Phi} - (\delta + 2\mu + 2bP)\Gamma. \end{cases}$$

is asymptotically autonomous and by replacing F with $x^* - \Phi$ and C with $y^* - \Gamma$ we can obtain its limiting system:

$$(19) \quad \begin{cases} \Phi' &= -(\bar{\mu} + \rho)\Phi + (\delta + \bar{\mu})\Gamma &:= \bar{f}_2(\Phi, \Gamma), \\ \Gamma' &= 2\rho\Phi - \frac{\rho}{x^*}\Phi^2 - (\delta + 2\bar{\mu})\Gamma &:= \bar{g}_2(\Phi, \Gamma). \end{cases}$$

The interior equilibrium of (19) is

$$\Phi^* = \frac{\rho\delta - \delta\bar{\mu} - 2\bar{\mu}^2}{\rho(\delta + \bar{\mu})} \quad \text{and} \quad \Gamma^* = \frac{(\bar{\mu} + \rho)(\rho\delta - \delta\bar{\mu} - 2\bar{\mu}^2)}{\rho(\delta + \bar{\mu})^2}$$

which exists whenever

$$\delta(\rho - \bar{\mu}) > 2\bar{\mu}^2.$$

As it is expected this is precisely $\mathcal{R}_0 > 1$. Seeking now a similar argument as above for the global stability of the solution of (19) we apply again Dulac's Criterion to rule out the possibility of periodic solutions:

$$\begin{aligned} & \frac{\partial}{\partial \Phi} \left[\frac{1}{\Phi\Gamma} \bar{f}_2(\Phi, \Gamma) \right] + \frac{\partial}{\partial \Gamma} \left[\frac{1}{\Phi\Gamma} \bar{g}_2(\Phi, \Gamma) \right] = \\ &= \frac{1}{\Phi\Gamma} \left[-(\delta + \bar{\mu}) \frac{\Gamma}{\Phi} - 2\rho \frac{\Phi}{\Gamma} + \rho \frac{\Phi}{\Gamma} \frac{\Phi}{x^*} \right] < 0 \end{aligned}$$

because, in the limiting system, $\frac{\Phi}{x^*} < 1$.

Thus, our system satisfies the Poincaré-Bendixson type trichotomy established by Thieme in [10] for asymptotically autonomous systems. Therefore the only possibility is that any solution of (18) will converge to an equilibrium of the limiting system (19). \square

In the next pictures we illustrate the interplay between the marriage and the separation rate with the dynamics of the disease and show how, under some conditions, the isolation from sexual activity increases the likelihood of having a disease free equilibrium in an endemic population. For some of the parameters we will use the data from the 2000 U.S. Census. In that year, the birth rate *per couple* was $\beta = 0.07338$. The mortality rates, computed as reciprocals of life expectancy at birth were

$$\mu_f = 0.01258 \quad \text{and} \quad \mu_m = 0.01350.$$

Since in this simulation we are going to use a common death rates for both genders, we will consider an average value $\mu = 0.01304$. We restrict also the range of the other parameters to the interval $[0, 0.2]$. In the first picture we show the feasible region of the possible values taken by the marriage and separation rate so that we have a positive stable population. In the second

graph we add the restriction that the disease is endemic, i.e. the region defined by

$$\mathcal{R}_0 > 1 \quad \text{and condition (13)}.$$

Finally, in all other pictures we add the condition for the stability of the disease free equilibrium induced by the abstained groups, i.e. we plot the region defined by

$$\mathcal{R}_0 > 1, \quad \mathcal{R}_0^s < 1 \quad \text{and condition (13)},$$

for several values of the isolation rate ν .

In the first figure we can see how the the endemic condition $\mathcal{R}_0 > 1$ imposes lower bounds on both the marriage and the separation rate.

Remark 5.3. *As it is expected, if the isolation rate ν is very small, for a given value of the marriage rate ρ the interval of existence for the separation rate δ is very small as well. This is because the two thresholds \mathcal{R}_0 and \mathcal{R}_0^s are equal if $\nu = 0$. As ν increases, the interval for δ becomes larger up to a maximum, however, if ν continues to increase, the condition of existence of a stable positive population becomes more restrictive and, eventually, the population becomes extinct due to the lack of reproduction. One can see in the last figure that the left boundary of the (δ, ρ) domain is shifted to the right and its slope becomes smaller with larger values of ν meaning that the existence condition (13) becomes more restrictive.*

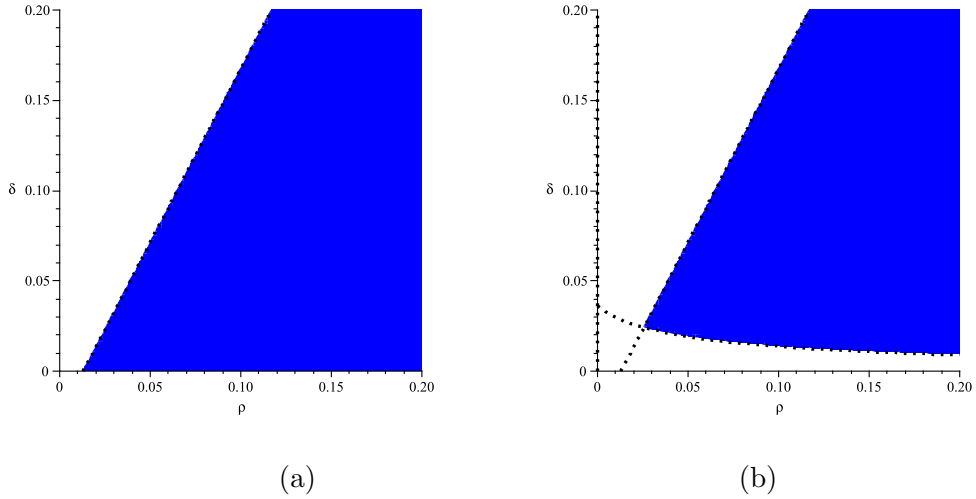


FIGURE 5. (a) Existence of the positive interior equilibrium, (b) the endemic case $\mathcal{R}_0 > 1$.

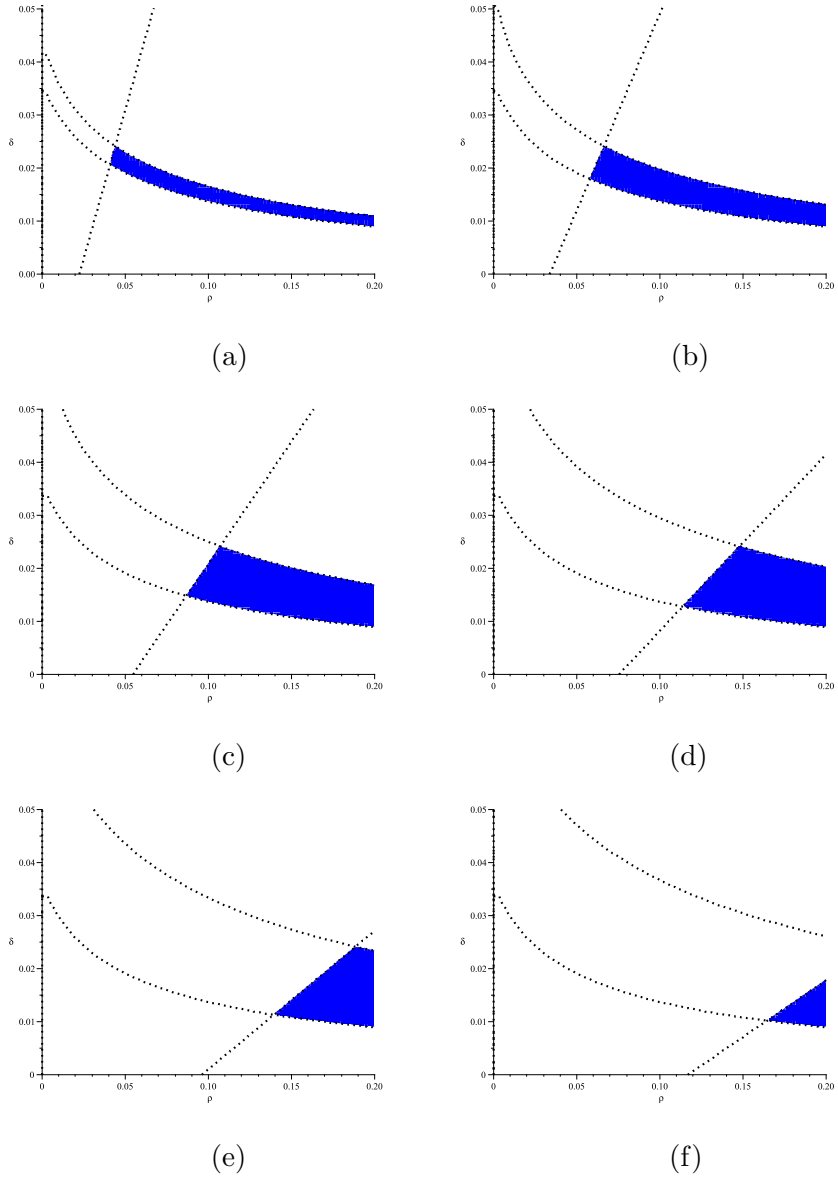


FIGURE 6. (a) $\nu = 0.009$, (b) $\nu = 0.02$, (c) $\nu = 0.04$,
 (d) $\nu = 0.06$, (e) $\nu = 0.08$, (f) $\nu = 0.1$.

6. CONCLUSIONS

We introduced a two-sex logistic model with non-linear mortality and used it to study the influence of the non-reproductive groups on the population dynamics as a continuation of the work initiated by Milner in [6]. We found that the conditions that need to be imposed on the parameters to ensure the logistic behavior are similar to the ones derived by Castillo-Chavez and Huang for a similar model with non-linear birth and separation rate. This is true for both the demographic model that includes only the females males

and couples as well as for the demographic model with the non-reproductive groups. In the latter case we proved only the global stability of the extinction equilibrium. For the interior equilibrium we run approximately one thousand numerical examples based on the Latin hypercube sampling in order to be able to conjecture that it is also locally asymptotically stable. We used the demographic model with isolation from reproduction to analyze the impact of abstaining from sexual activity on the evolution of a persistent sexually transmitted disease. This was a continuation of our previous work using one-sex S-I type models [8]. We found that, just as in the one-sex case, the isolation from sexual activity has both a demographic and an epidemiological impact in the sense that the isolated group can induce a stable disease free equilibrium in an otherwise endemic population. For several particular cases we managed to prove that the stability is also global. We also found that, under some conditions, the total population size may be greater in the presence of the isolated groups, provided that they do manage to eliminate the disease and that the reproductive number of the infected couple is very low. This is of course a consequence of having a disease without recovery and having the mechanism of couple formation/separation responsible for both the population growth and the disease transmission.

One limitation of the epidemic model is that it does not include people who are non-reproductive but sexually active. We omitted this class to keep our model as simple as possible and to compare the results with those from one-sex models analyzed in [8]. The distinction between sexually active and non-reproductive and sexually inactive will be treated in an upcoming paper using both one-sex and two-sex models. Future research may also take into consideration age structure, treatment, vertical transmission, or recovery from the disease.

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