A model for ovine brucellosis incorporating direct and indirect transmission

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Abstract

In this work, we construct and analyze an ovine brucellosis mathematical model. In this model the population is divided into susceptible and infected subclasses. Susceptible individuals can contract the disease in two ways: i) direct mode caused by contact with infected individuals; ii) indirect mode related to the presence of virulent organisms in the environment. We derive a net reproductive number and analyze the global asymptotic behavior of the model. We also perform some numerical simulations, and investigate the effect of a slaughtering policy.

1 Introduction

Over the last century, inhabitants of Mediterranean countries were massively exposed to brucellosis, a human disease that appeared in Malta and spread over time throughout the region. Although the disease is not lethal, the consequences for human are serious. This infection is due to brucella, a virus first isolated in 1887 from an infected individual's blood by David Bruce, an army medical officer. In 1905, Zamitt carried out an experiment on goats, numerous in Malta at that time. He discovered that all the subjects were infected, and thus revealed the origin of brucellosis within human population.

Brucellosis still persists today in developing nations of Africa, west Asia and some regions of Latin America [2, 29, 13]. It is transmitted from animals to humans either by ingestion of contaminated products, such as milk or vegetables cultivated on soil containing contaminated manure, or directly via the mucosa upon contact with infected organisms. It is most often characterized as a serious occupational disease, because veterinary surgeons, laboratory assistants, and farmers are predominantly exposed to the virus [12, 15, 22]. At the breeding level, brucella causes genital inflammation, abortion of fetuses, and temporary infertility. Hence the economical losses are significant and have been estimated in Great Britain, to be 32 million dollars in 1962 [11].

Several mathematical models have been proposed to study brucellosis [1, 4, 11, 14, 16]. In the present work, the novelties with respect to the existing literature are the vertical transmission, and the contamination of the environment. Actually, susceptible sheep and cows can contract the disease during the reproduction period by contact with infected individuals. This is the direct mode of transmission. Moreover, infected females eject placenta and fetuses into the environment during the abortion and lambing periods. This is the indirect mode of transmission. These virulent material in the environment is suspected to play an important role in such a context [10, 11].

In sections 3 and 4, we analyze the model and we make some numerical simulations of the model. We will derive the net reproductive number that is the average number of secondary cases produced by an infected individual. We refer to [5, 3, 24, 6] for more details on the subject. By using the net reproductive number, we will derive some results about endemicity and extinction of the disease.

Epidemic models incorporating the contamination of the environment have been used in several other diseases such as H5N1 avian influenza [28], panleucopenia virus within feline populations [7, 8, 9], and salmonella [26, 27, 17, 18, 19]. The model considered here has not been studied previously. Due to the simple structure for infected class individuals and for the contaminant, the model will be reduced to a monotone system of ordinary differential equations on the plan. By using this fact, we will be able to give a global description of the behavior of the model. This has not been done, because the structure of the infected classes was more complicated.

The paper is organized as follows. In section 2, we present the model. In section 3, we analyze the asymptotic behavior of the model. In section 4, we present some numerical simulations. In section 5, we will discuss the results obtained in sections 3 and 4. Moreover, we will discuss a prophylactic method related to the contamination of the environment.

2 The model

The ovine population is decomposed into the susceptible individuals $S(t)$ and infected individuals $I(t)$ at time t. Moreover we introduce $C(t)$ the fraction of contaminated environment. The direct and indirect modes of transmission, as well as the vertical transmission are described in the following model:

$$\begin{cases} \dfrac{dS}{dt} = bS - \left(m + \dfrac{(b-m)}{K}N\right) S + (1-p)bI - a_1 SI - a_2 SC \\ \dfrac{dI}{dt} = pbI - \left(m + \dfrac{(b-m)}{K}N\right) I + a_1 SI + a_2 SC \\ \dfrac{dC}{dt} = k_1 I(1-C) - k_2 C \end{cases} \tag{1}$$

where $b \geq m > 0$, $K > 0$, $p \in [0,1]$, $a_1 \geq 0$, $a_2 \geq 0$, $k_1 > 0$, $k_2 > 0$.

It follows that $N(t) := S(t) + I(t)$ the total number of individuals satisfies the logistic equation

$$\frac{dN(t)}{dt} = (b-m)N(t)\left(1 - \frac{N(t)}{K}\right). \tag{2}$$

In the model (1), p is the proportion of newborns (from an infected mother) which are infected. Thus the parameter p represents the vertical transmission of the disease. Usually p varies from 5% up to 10%. The susceptible and infected individuals have the same demographic parameters, b the birth rate, and m the death rate. Accordingly to Roth et al. [21], we can assume that $0 < m \leq b$. An essential feature of brucella lies in its two different propagation modes. In the model (1), the term $a_1 S(t)I(t)$ corresponds to the direct transmission of Brucellosis by contact between susceptible and infected subjects. In this case, the process of direct transmission follows the mass-action law. The indirect transmission is represented in model (1) by the term $a_2 C(t)I(t)$. Hence, for a fixed fraction of contaminated environment the time necessary to be contaminated is supposed to follow an exponential law, and the time is proportional to $1/C(t)$. Next, the production of contaminant in the environment is described in model (1) by the term $k_1 I(t)(1 - C(t))$ which depends on the remaining fraction of uncontaminated environment $1 - C(t)$. Finally, the contaminant dies out in the environment with a death rate k_2. A schematic representation of the model (1) is given by the diagram flux in Figure 1.

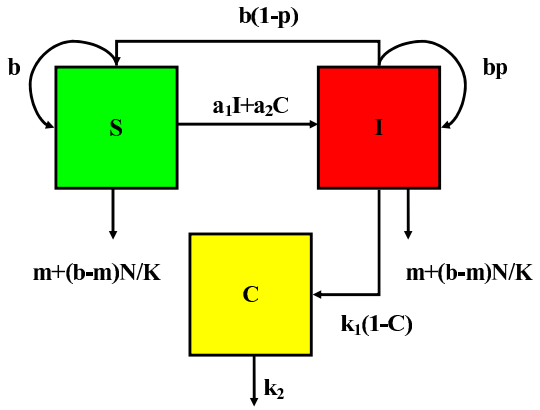

Figure 1: Flux Diagram

3 Asymptotic behavior of the model

By using the logistic equation (2), we can assume, without loss of generality, that

$$N(t) = K, \forall t \geq 0.$$

By replacing $S(t)$ by $K - I(t)$, and N by K in the I-equation of system (1), we derive the following system

$$\begin{cases} \dfrac{dI}{dt} = -(1-p)bI + a_1 (K-I)^+ I + a_2 (K-I)^+ C \\ \dfrac{dC}{dt} = k_1 I(1-C)^+ - k_2 C \end{cases}$$

where $x^+ := \max(0, x)$ is the positive part of x.

Next by considering $i(t) = I(t)/K$ the fraction of infected individuals in the population, we obtain a system of ordinary differential equations on $[0,1] \times [0,1]$

$$\begin{cases} \dfrac{di}{dt} = -(1-p)bi + a_1 K (1-i)^+ i + a_2 (1-i)^+ C \\ \dfrac{dC}{dt} = k_1 K i(1-C)^+ - k_2 C \end{cases} \tag{3}$$

Equilibria: It is clear that $(0,0)$ is an equilibrium of (3), and it corresponds to the disease free equilibrium of system (1). Furthermore, any endemic equilibrium of (3) $(\bar{\imath}, \bar{C}) \in [0,1] \times [0,1] \setminus \{(0,0)\}$ must satisfy

$$\begin{cases} 0 = -(1-p)b\bar{\imath} + a_1 K (1-\bar{\imath})\,\bar{\imath} + a_2 (1-\bar{\imath})\,\bar{C} \\ 0 = k_1 K \bar{\imath}(1-\bar{C})^+ - k_2 \bar{C} \end{cases} \tag{4}$$

The second equation of (4) implies

$$\bar{C} = \frac{k_1 K \bar{\imath}}{k_2 + k_1 K \bar{\imath}} \tag{5}$$

Hence we consider $\bar{\imath}$ in $(0,1]$, which implies that $\bar{C}$ is strictly positive. By combining the first equation of (4) and (5) we obtain

$$a_1 K (1-\bar{\imath}) + a_2 (1-\bar{\imath}) \frac{k_1 K}{k_2 + k_1 K \bar{\imath}} = (1-p)b. \tag{6}$$

We observe that the first member of equality (6) is monotone strictly decreasing with respect to $\bar{\imath}$. So it follows that there exists at most one positive equilibrium, and this equilibrium exists if and only if

$$a_1K + a_2\frac{k_1}{k_2}K > (1-p)b.$$

Moreover, the positive equilibrium can be explicitly expressed by using (5), and by solving the following second order equation

$$a_1K\left(1-\bar{\imath}\right)\left(k_2+k_1K\bar{\imath}\right)+a_2k_1K\left(1-\bar{\imath}\right)=(1-p)b\left(k_2+k_1K\bar{\imath}\right).$$

Monotonicity property: We observe that system (3) has the form

$$\frac{d}{dt}\begin{pmatrix} i(t) \\ C(t) \end{pmatrix} = F\begin{pmatrix} i(t) \\ C(t) \end{pmatrix}, \tag{7}$$

where $F:\mathbb{R}^2_+\to\mathbb{R}^2$ is the map defined by

$$F\begin{pmatrix} i \\ C \end{pmatrix} = \begin{pmatrix} -(1-p)bi + a_1K\left(1-i\right)^+ i + a_2\left(1-i\right)^+ C \\ k_1Ki(1-C)^+ - k_2C \end{pmatrix},$$

Taking $\lambda > 0$ large enough, $(\lambda I + F)$ maps $\mathbb{R}^2_+$ into itself, and is monotone increasing on $[0,1]\times[0,1]$ for the usual order induced by the positive cone $K=\mathbb{R}^2_+$. We can apply the theory of monotone dynamical system developed by Smith [23] on $[0,1]\times[0,1]$. We observe that

$$F\begin{pmatrix} 1 \\ 1 \end{pmatrix} = \begin{pmatrix} -(1-p)b \\ -k_2 \end{pmatrix} \leq 0,$$

then the solution of system (7) with initial value $\begin{pmatrix} 1 \\ 1 \end{pmatrix}$ converges to either a positive equilibrium, or 0 when there is no positive (endemic) equilibrium. Analysis of the local behavior for the trivial equilibrium $(0,0)$ provides the global asymptotic behavior of system (7).

Linearized equation around $(0,0)$**:** The linearized equation at $(0,0)$ is

$$\frac{d}{dt}\begin{pmatrix} x(t) \\ y(t) \end{pmatrix} = L\begin{pmatrix} x(t) \\ y(t) \end{pmatrix}$$

where

$$L = \begin{bmatrix} a_1K-(1-p)b & a_2 \\ k_1K & -k_2 \end{bmatrix}.$$

F satisfies the following property

$$F\begin{pmatrix} i \\ C \end{pmatrix} \leq L\begin{pmatrix} i \\ C \end{pmatrix}, \forall \begin{pmatrix} i \\ C \end{pmatrix} \in \mathbb{R}^2_+.$$

We defined the net reproductive number as

$$R_0 := \frac{a_1K}{(1-p)b} + \frac{a_2k_1K}{k_2(1-p)b}.$$

From the above analysis it is clear that the system admits a unique positive equilibrium if and only if $R_0 > 1$. When $R_0 \leq 1$ since the system (7) has no positive equilibrium, by using the supremum solution with initial value $\begin{pmatrix} 1 \\ 1 \end{pmatrix}$, we obtain the following results.

Theorem 1 *Assume that* $R_0 \leq 1$. *Then the disease free equilibrium* $\begin{pmatrix} 0 \\ 0 \end{pmatrix}$ *of system (7) is globally asymptotically stable in* $[0,1]\times[0,1]$.

To describe the global asymptotic behavior when $R_0 > 1$, we distinguish two cases: i) $a_2 = 0$; ii) $a_2 > 0$. By using sub- and sup-solutions in the region $i_0 > 0$, we obtain the following result.

Theorem 2 *We assume that $R_0 > 1$, and $a_2 = 0$. Then each solution of (7) with initial value $\begin{pmatrix} i_0 \\ C_0 \end{pmatrix} \in [0,1] \times [0,1]$ with $i_0 > 0$ converges to the endemic equilibrium $\begin{pmatrix} \bar{i} \\ \bar{C} \end{pmatrix}$ which is a stable equilibrium. Furthermore, each solution of (7) with initial value $\begin{pmatrix} i_0 \\ C_0 \end{pmatrix} \in \{0\} \times [0,1]$ converges to the disease free equilibrium $\begin{pmatrix} 0 \\ 0 \end{pmatrix}$.*

Proof. The proof is straightforward. ■

When $a_2 > 0$, the matrix $\lambda I + L$ is positive irreducible for $\lambda > 0$ large enough. So by using sub- and sup-solutions, we also derive the following result.

Theorem 3 *We assume that $R_0 > 1$, and $a_2 > 0$. Then each solution with initial value $\begin{pmatrix} i_0 \\ C_0 \end{pmatrix} \in [0,1] \times [0,1] \setminus \left\{ \begin{pmatrix} 0 \\ 0 \end{pmatrix} \right\}$ converges to the endemic equilibrium $\begin{pmatrix} \bar{i} \\ \bar{C} \end{pmatrix}$ which is locally asymptotically stable.*

Proof. The proof is straightforward. ■

4 Numerical simulations

We start this section by summarizing the parameters of the model and their values taken from the literature (where possible). These values are used for the numerical simulations of the model in figures 2, 3, and 4. The remaining parameters are fixed in order to investigate several scenarios.

parameter	description	value	units
p	Probability of vertical transmission	0.05	
b	Birth rate	0.83	year^{-1}
m	Mortality rate	0.79	year^{-1}
K	Carrying capacity	1.82×10^7	
k_1	Contamination rate	set	
k_2	Disinfection rate	1.82	year^{-1}
a_1	Direct infection rate	set	
a_2	Indirect infection rate	set	

Table 1. Model parameters

In table 1, p the probability of vertical transmission is fixed to 5%. Actually, all newborns coming from an infected mother are infected at birth. But 95% of them recover after a short period of time [10]. Consequently, we neglect this short period of time, and we assume 95% of the newborns are susceptible. The birth rate and the death rate of sheep are fixed according to [21]. Sheep population in Algeria is estimated at 1.82×10^7 individuals because food supply, water, habitat and many other resources are limited [20]. The virus resists in freezing and high environmental temperatures for long periods: at least 75 days in aborted fetuses and more than 200 days in uterine exudate [10]. The virus resists more than half a year in the environment, so we fix the disinfection rate k_2 at $365/200 = 1.82$.

In figure 2, figure 3, and figure 4, we fix $k_1 = 1.5 \times 10^{-7}$. The parameters a_1 and a_2 are fixed in order to describe the direct or indirect transmission. In figure 2, figure 3, and figure 4, we represent the phase diagram of the system (3), and the red dote represents the position of the endemic or disease free equilibrium which attracts the positive orbits. In figure 2, since $a_2 = 0$ the line $i = 0$

is invariant by the flow, so we always use an $i_0 > 0$ for the initial value. In figure 2-(A) we observe the uniform persistence, but when $i_0 > 0$ is small the solution first decreases in C and then increases to converge to the endemic equilibrium. In figures 2-(A) and 3-(A) the disease is endemic, while in the figures 2-(B) and 3-(B) the disease goes extinct. In figure 4-(A) and figure 4-(B), the disease is endemic while in figure 4-(B) we used $a_1 = 10^{-8}$ which is the value used in figure 2-(B) and $a_2 = 0.5$ which is the value used in figure 3-(B). This shows that the combination of both direct and indirect contamination can produce persistency, while if separated the disease goes extinct.

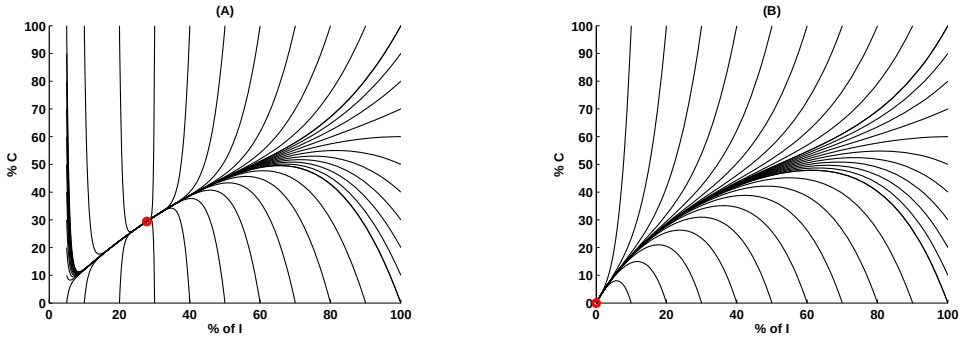

Figure 2: *(Direct transmission only)* For both figures (A) and (B) we fix $a_2 = 0$ and $k_1 = 1.5 \times 10^{-7}$. Moreover we fix $a_1 = 0.6 \times 10^{-7}$ in figure (A) and $a_1 = 10^{-8}$ in figure (B). In figure (A) the disease is endemic (i.e. $R_0 > 1$), while in figure (B) the disease goes to extinct (i.e. $R_0 < 1$).

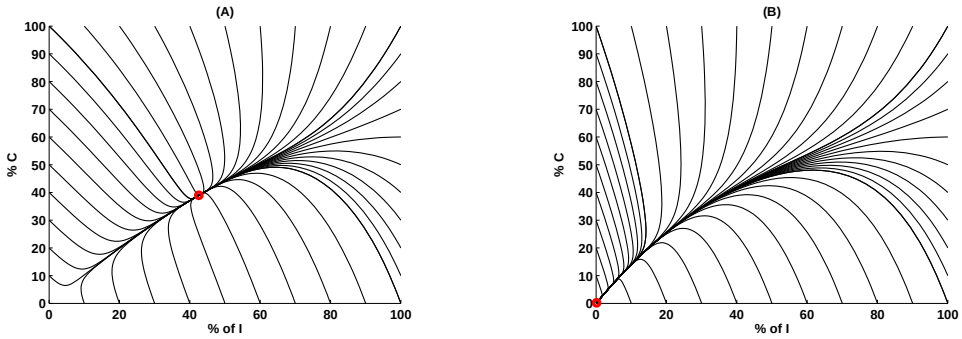

Figure 3: *(Indirect transmission only)* For both figures (A) and (B) we fix $a_1 = 0$ and $k_1 = 1.5 \times 10^{-7}$. Moreover we fix $a_2 = 1.5 \times 10^{-7}$ in figure (A) we fix $a_2 = 1.5$, and in figure (B) we fix $a_2 = 0.5$. In figure (A) the disease is endemic (i.e. $R_0 > 1$), while in figure (B) the disease goes to extinct (i.e. $R_0 < 1$).

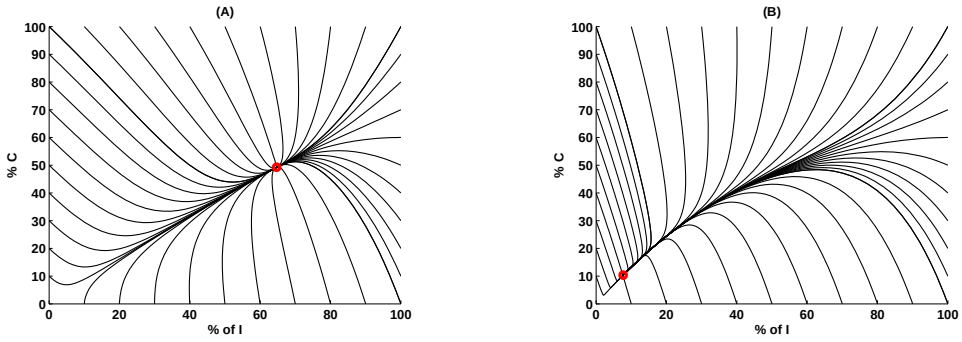

Figure 4: *(Both direct and indirect transmission)* For both figures (A) and (B) we fix $k_1 = 1.5 \times 10^{-7}$. In figure (A) we fix $a1 = 0.6 \times 10^{-7}$ and $a_2 = 1.5$, and in figure (B) we fix $a1 = 10^{-8}$ and $a_2 = 0.5$. In both figures (A) and (B) the disease is endemic (i.e. $R_0 > 1$).

5 Discussion

In this article, we have formulated a model for Brucellosis including vertical transmission and direct and indirect contamination of individuals. Moreover, we were able to describe the global dynamic of the model. In particular we obtained the net reproductive number

$$R_0 := \underbrace{\frac{a_1 K}{(1-p)b}}_{\text{direct transmission}} + \underbrace{\frac{a_2 k_1 K}{k_2(1-p)b}}_{\text{indirect transmission}} .$$

In the above formula, the contribution of the direct transmission is $R_0^{direct} = a_1 K/((1-p)b)$, and the contribution of the indirect transmission is $R_0^{indirect} = a_2 k_1 K/(k_2(1-p)b)$. Refai [20] mentions a controversy about the use of mass vaccination or the use of slaughter policy in the near east region. One may note that Brucellosis is an asymptomatic disease [10], so it is difficult (if not impossible) to isolate the infected individuals from the susceptible.

In practice, vaccination is not used. So we consider an annual slaughtering policy. Here we assume that every year a fraction $(1-f)$ is killed and look at the consequences of the policy over 10 years. We assume that we choose randomly the individuals in the population so a fraction $(1-f)$ of susceptible and infected individuals is killed every year. In order to represent this slaughtering policy, we use the model (1) to describe the dynamic of the disease within the year, and we use the rule $S(t^+) = fS(t^-)$ and $I(t^+) = fI(t^-)$ at the end of each year, that is for $t = 1, 2, ..., 10$. Figure 5 presents the dynamics of the disease without slaughtering (so with $f = 1$). In figure 6 we use the same value as in figure 5 for k_1, $a1$, and a_2, but we assume that one half of the individuals are killed at the end of each year. We observe that this policy is efficient to recover from this disease over a period of 10 years. In figure 7, we use the same policy as in figure 6, but we assume there is contamination of the environment (i.e. with fix a_2 at 0). In this case, we observe that the slaughtering policy is much more efficient, since the population recovers from the disease over a period of 7 years only. We conclude that the contamination of the environment can play an important role in the persistence of the disease (i.e. when $R_0^{indirect} > 1$), but also to control the epidemic.

To conclude this article, we would like to mention some possibilities for further investigations in the context of brucellosis. One can first note that here we neglect the fact that the infected mothers abort during the first year of infection. This suggests that in order to better understand such a disease one would need to incorporate the age of infection (or/and the chronological age). Another

important aspect in the context of Brucellosis is the spatial distribution of both the individuals and the contaminant. These questions will be further investigated in some future works.

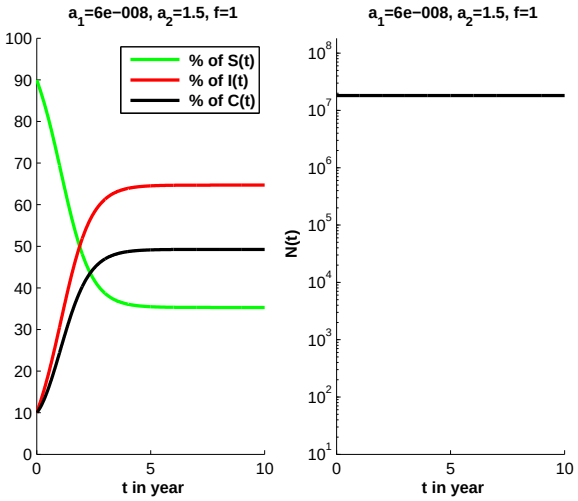

Figure 5: We fix $k_1 = 1.5 \times 10^{-7}$, $a1 = 0.6 \times 10^{-7}$, $a_2 = 1.5$, and $f = 1$. The figure on the left represents the susceptible, the infected, and the contamination of the environment in the function of the time t. The figure on the right represents the total number of individuals in the population.

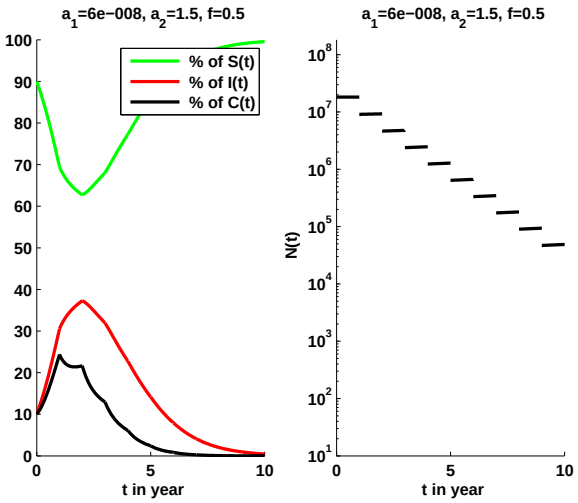

Figure 6: We fix $k_1 = 1.5 \times 10^{-7}$, $a1 = 0.6 \times 10^{-7}$, $a_2 = 1.5$, and $f = 0.5$. The figure on the left represents the susceptible, the infected, and the contamination of the environment in the function of the time t. The figure on the right represents the total number of individuals in the population.

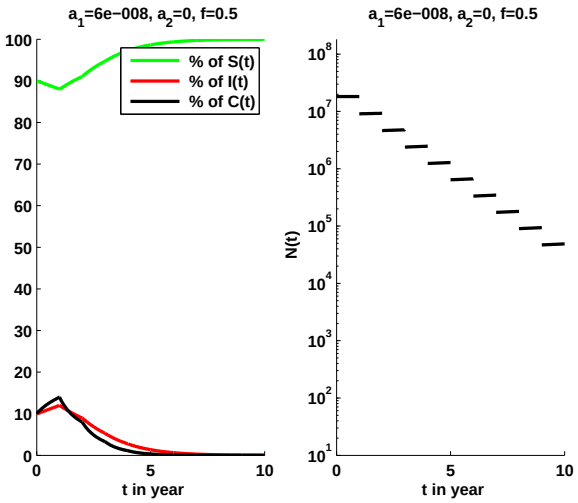

Figure 7: We fix $k_1 = 1.5 \times 10^{-7}$, $a1 = 0.6 \times 10^{-7}$, $a_2 = 0$, and $f = 0.5$. The figure on the left represents the susceptible, the infected, and the contamination of the environment in the function of the time t. The figure on the right represents the total number of individuals in the population.

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