



EFFECTS OF ANTI-INFECTION BEHAVIOR ON THE EQUILIBRIUM STATES OF AN INFECTIOUS DISEASE

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Abstract. We propose a mathematical model to analyze the effects of anti-infection behavior on the equilibrium states of an infectious disease. The anti-infection behavior is incorporated into a classical epidemiological SIR model, by considering the behavior adoption rate across the population as an additional variable. We consider also the effects on the adoption rate produced by the disease evolution, using a dynamic payoff function and an additional differential equation. The equilibrium states of the proposed model have remarkable characteristics: possible coexistence of two locally stable endemic equilibria, the coexistence of locally stable endemic and disease-free equilibria, and even the possibility of a stable continuum of endemic equilibrium points. We show how some of the results obtained may be used to support strategic planning leading to effective control of the disease in the long-term.

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1 Introduction

The propagation of an infectious disease can be affected by changes in the population behavior and, at the same time, the population behavior concerning the disease can change due to changes in the perception of the epidemiological situation [11, 6, 32]. Most recently, in the context of the COVID-19 pandemic, has been clear the relevant role played by human behavior on the disease dynamic [14, 8, 5] and also has become evident the changes produced on the population behavior and policymakers due to the increase in the number of infected and death cases [23, 9, 13].

Even before the COVID-19 emergency, there was a well-recognized demand for mathematical models of infectious diseases considering aspects of the population behavior [24, 7].

Many mathematical and computational models for infectious diseases based on SIR models have already considered some type of anti-infection strategies. Some works have incorporated implicitly the possibility of a dynamic preventive behavior, by considering rates of infection or transmission may depend on some of the epidemiological variables S , I , or R [20, 25, 21, 15, 16, 26, 10, 28, 3]. For other models considering behavioral features see [18].

Vaccination, as a form of anti-infection behavior, has been considered assuming that part of the susceptible population goes directly into the removed population or adding additional compartments for partially immune population [31, 27, 1]. For other models considering vaccination see [17, 19, 2].

In [4] a model for vaccination-related behavior is considered using an additional variable corresponding with the rate of vaccination at birth. This new variable interacts with the infection dynamics in the SIR model and is affected by a differential equation that depends on the infected population I . In the present work, we use a similar idea and introduce a behavioral variable related to the adoption rate across the population of some anti-infection behavior. This variable is incorporated into a classical epidemiological SIR model. The dynamics effects on the adoption rate are introduced using an additional differential equation and a dynamic linear payoff depending on the epidemiological variables.

We focus on the study of equilibrium states as an attempt to understand the long-term characteristic and consequences of the interplay between population behavior and disease dynamics.

The equilibrium states of the proposed model have remarkable characteristics: possible coexistence of two locally stable endemic equilibria, the coexistence of locally stable endemic and disease-free equilibria, and even the possibility of a stable continuum of endemic equilibrium points. We will describe how some of the results obtained may be used to support strategic planning leading to effective control of the infectious disease in the long-term.

The paper is organized as follows. In Section 2 we develop the mathematical model and discuss some basic characteristics. In Section 3 we discuss the existence and stability of its equilibrium points, which is the main focus of the present work. We will show that the set of equilibrium points of the proposed model, have some remarkable characteristics in the context of epidemiological models: coexistence of two locally stable endemic equilibria, the coexistence of locally stable endemic and disease-free equilibria, and the possibility of

a stable continuum of endemic equilibrium points. In Section 4 we use some of the results to obtain thresholds for parameters leading to effective long-term control of the epidemic disease. We conclude with some final remarks in Section 5 and an Appendix presenting proofs of some of the results established in the paper.

2 A Mathematical Model for an Infectious Disease with an Anti-Infection behavior

Compartment models, and particularly SIR models, have been extensively used for mathematical modeling of infectious diseases [7]. The main idea behind SIR models is to consider a population divided into three disjoint categories or compartments: susceptible individuals, infected individuals, and removed (recovered or deceased) individuals, denoted by S , I , and R respectively. If N denotes the total population, then we have $N = S + I + R$.

Depending on the modeling approach, the variables S , I , and R may be considered as the absolute numbers of individuals in each group or as the proportion of individuals relative to the total population. In this work, we consider this latter approach. Therefore, considering the time dependency, we have that $S(t) + I(t) + R(t) = 1$ for all t .

Within these considerations, an SIR model with vital dynamics and constant population can be stated as

$$\begin{aligned}\frac{dS}{dt} &= \mu - \beta S I - \mu S \\ \frac{dI}{dt} &= \beta S I - \mu I - \gamma I \\ \frac{dR}{dt} &= \gamma I - \mu R,\end{aligned}\tag{1}$$

with $S(0) + I(0) + R(0) = 1$. The positive real numbers μ , β , and γ can be interpreted as birth-mortality rate, infection rate, and recovery rate respectively. The constant population consideration is implicit into the system, since $N(t) = 1$ is the only solution of

$$\frac{dN}{dt} = \frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = \mu(1 - N)$$

satisfying $N(0) = 1$. For more details about SIR-type models see [17, 19].

Now, consider that there is some behavior or action that can be taken to avoid or reduce the impact of the infection. This behavior can be interpreted as a vaccination initiative, a preventive hygienic measure, a quarantine restraint, or a combination of similar actions. Let x be the proportion of the population following this anti-infection behavior.

When the population is considering this behavior or action, the perception of the benefit obtained by following it, may not always be constant. In fact, depending on the epidemiological state, the benefit may vary. For example, in a situation with a small proportion of infected, the benefit of adopting the anti-infection behavior may be considered irrelevant for some part of the population. On the other hand, in a situation where the

majority of the population has no immunity, the benefits may be considered high. To analyze this kind of situation, we propose to consider that there exists a perceived payoff or benefit obtained from the anti-infection behavior that depends on the epidemiological variables S , I , and R according to a function p given by

$$p(S, I, R) = -a_c + a_I I + a_S S + a_R R, \quad (2)$$

where a_c , a_I , a_S , and a_R are positive constants. The constant a_c can be interpreted as the fixed cost of adopting the anti-infection behavior, and the constants a_I , a_S , and a_R can be interpreted as the behavior-adoption benefit associated with the proportion of infected, susceptible, and removed members of the population, respectively. As we have considered that $S + I + R = 1$, we have that

$$\begin{aligned} -a_c + a_I I + a_S S + a_R R &= -a_c + a_I I + a_S S + a_R (1 - S - I) \\ &= -(a_c - a_R) + (a_I - a_R) I + (a_S - a_R) S \\ &= -a_0 + a_1 I + a_2 S. \end{aligned}$$

Therefore, the payoff functions can be simplified to obtain

$$p(S, I) = -a_0 + a_1 I + a_2 S. \quad (3)$$

Based on the SIR model (1) and the payoff function (3), we propose the following model considering simultaneously the epidemiological variables (S, I, R) and the behavioral state x :

$$\begin{aligned} \frac{dS}{dt} &= \mu - (1 - x)\beta S I - \mu S \\ \frac{dI}{dt} &= (1 - x)\beta S I - \mu I - \gamma I \\ \frac{dR}{dt} &= \gamma I - \mu R \\ \frac{dx}{dt} &= x(1 - x)(-a_0 + a_1 I + a_2 S) \end{aligned} \quad (4)$$

with initial conditions in $[0, 1]$, and $N(0) = S(0) + I(0) + R(0) = 1$. The three initials equations are essentially the SIR model (1) with a variable infection rate depending on the behavioral variable x . If $x = 1$, there is no infection at all. If $x = 0$, the diseases follow the classical SIR dynamics. The fourth equation may be seen as a logistic equation for x with a growth rate depending on the variables S and I and on the cost/payoff parameters a_0, a_1, a_2 . Thus, depending on the interplay between these values over time, the adoption rate x may increase or decrease, leading also to a dynamically decreasing or increasing infection rate. The differential equation for x can also be obtained from the replicator equations in evolutionary game theory (see [29]), applied to a two-behavior game (follow or not follow the anti-infection behavior) with a symmetric payoff given by $-a_0 + a_1 I + a_2 S$.

The main goal of the present work is to study the long-term behavior of model (4) in terms of its equilibrium points. To achieve this, we will consider a simplified model

obtained by re-scaling some of the parameters. Considering

$$\begin{aligned} \tau = t\mu; \quad \tilde{\beta} = \frac{\beta}{\mu}; \quad \tilde{\gamma} = \frac{\gamma}{\mu}; \quad \tilde{a}_0 = \frac{a_0}{\mu}; \quad \tilde{a}_1 = \frac{a_1}{\mu}; \quad \tilde{a}_2 = \frac{a_2}{\mu} \\ k = 1 + \frac{\gamma}{\mu} = 1 + \tilde{\gamma} \quad \text{and} \quad R_0 = \frac{\beta}{\mu + \gamma} = \frac{\tilde{\beta}}{1 + \tilde{\gamma}} = \frac{\tilde{\beta}}{k}. \end{aligned} \quad (5)$$

and replacing in (4), we obtain

$$\begin{aligned} \frac{dS}{d\tau} &= 1 - (1-x)kR_0SI - S \\ \frac{dI}{d\tau} &= (1-x)kR_0SI - kI \\ \frac{dR}{d\tau} &= (k-1)I - R \\ \frac{dx}{d\tau} &= x(1-x)(-\tilde{a}_0 + \tilde{a}_1I + \tilde{a}_2S), \end{aligned} \quad (6)$$

with initial conditions in $[0, 1]$ and $N(0) = S(0) + I(0) + R(0) = 1$.

Note that the parameter $k > 1$ and the parameter R_0 is also a positive real number. The parameter R_0 is called the basic reproduction number and has a fundamental role in the description of the equilibria stability in the classical SIR model [17, 19]. The parameter R_0 can be interpreted as the number of cases one case generates, on average, in an uninfected population. It represents a measure of the effectiveness of the infection. We introduce below the term R_p , that will be important in the forthcoming analysis of equilibrium points

$$R_p = \frac{\tilde{a}_1 - k\tilde{a}_2}{\tilde{a}_1 - k\tilde{a}_0}.$$

Note that R_p depends both on the payoffs associated with the anti-infection behavior and on the population parameter $k = 1 + \frac{\gamma}{\mu}$. We will see in Section 3 that under the effects of the anti-infection behavior, the constant R_p plays a similar role to the one played by the basic reproduction number R_0 in the classical SIR model.

We end this section proving that the variables in (6) properly represent population proportions, in the sense that S, I, R and x belongs to the interval $[0, 1]$ for all $t \geq 0$, and that $N(\tau) = S(\tau) + I(\tau) + R(\tau) = 1$.

Lemma 1. *The set $\Omega = \{x \in [0, 1], S \geq 0, I \geq 0, R \geq 0 \text{ and } S + I + R = 1\}$ is positively invariant under (6).*

Proof. Since $x(\tau) = 1$ and $x(\tau) = 0$ are stationary solutions of

$$\frac{dx}{d\tau} = x(1-x)(-\tilde{a}_0 + \tilde{a}_1I + \tilde{a}_2S),$$

the uniqueness of solutions ensures that $x(\tau) \in [0, 1]$ for all $\tau \geq 0$, whenever $x(0) \in (0, 1)$. Furthermore, from (6) we have that $\frac{dN}{d\tau} = \mu(1 - N)$. Since $N(0) = 1$, follows that $S(\tau) + I(\tau) + R(\tau) = N(\tau) = 1$ for all $\tau \geq 0$.

To prove that S, I , and R are positives, we analyze the behavior of the solutions with initial conditions at the border of $\mathbb{R}_{\geq 0}^3$.

Case 1. If $S(0) = 0$ then $\frac{dS}{d\tau}(0) = 1 > 0$, therefore S grows locally.

Case 2. If $I(0) = 0$ then $\frac{dI}{d\tau}(0) = 0$, therefore $I(\tau)$ will remain non-negative.

Case 3. If $R(0) = 0$ then $\frac{dR}{d\tau}(0) = (k-1)I(0)$. In this case, if $I(0) = 0$, then $\frac{dR}{d\tau}(0) = 0$, whence R will remain non-negative. On the other hand, if $I(0) > 0$ then $\frac{dR}{d\tau}(0) > 0$ since $k > 1$. Thus R grows locally.

□

3 Equilibrium States

3.1 Existence

In this subsection, we determine all the possible equilibrium points of model (6) and its conditions for existence. The following lemma summarizes the results regarding the six different classes of equilibrium points that can be obtained.

Lemma 2. *Any equilibrium point $P = (\bar{S}, \bar{I}, \bar{R}, \bar{x})$ of model (6) satisfies that $\bar{I} = \frac{1}{k}(1 - \bar{S})$ and $\bar{R} = (1 - \frac{1}{k})(1 - \bar{S})$. Thus all equilibrium points are determined by the values of $\bar{S}$ and $\bar{x}$. Furthermore, all the equilibrium points of model (6) fall into one of the following categories:*

P_1 : $\bar{S} = 1$ and $\bar{x} = 0$;

P_2 : $\bar{S} = 1$ and $\bar{x} = 1$;

P_3 : $\bar{S} = 1$ and $\bar{x} \in [0, 1]$, s.t. $\tilde{a}_0 = \tilde{a}_2$;

P_4 : $\bar{S} = \frac{1}{R_0}$ and $\bar{x} = 0$, s.t. $R_0 > 1$;

P_5 : $\bar{S} = \frac{1}{R_p}$ and $\bar{x} = 1 - \frac{R_p}{R_0}$, s.t. $R_0 > R_p > 1$ and $\tilde{a}_1 \neq k\tilde{a}_0$;

P_6 : $\bar{S} = \frac{1}{R_0(1-\bar{x})}$ and $\bar{x} \in (0, \frac{R_0-1}{R_0})$, s.t. $R_0 > 1$ and $k\tilde{a}_0 = \tilde{a}_1 = k\tilde{a}_2$.

Proof. The equilibrium points of (6) are the solutions in Ω of the non-linear system

$$\begin{aligned} 1 - (1 - \bar{x})kR_0\bar{S}\bar{I} - \bar{S} &= 0 \\ (1 - \bar{x})kR_0\bar{S}\bar{I} - k\bar{I} &= 0 \\ (k - 1)\bar{I} - \bar{R} &= 0 \\ \bar{x}(1 - \bar{x})[-\tilde{a}_0 + \tilde{a}_1\bar{I} + \tilde{a}_2\bar{S}] &= 0. \end{aligned} \tag{7}$$

Note from the first equation that $\bar{S}$ can not be equal to zero. Now, adding the first two equations in (7), we obtain that any equilibrium point must satisfy $1 - \bar{S} = k\bar{I}$. Therefore

$$\bar{I} = \frac{1}{k}(1 - \bar{S}) \tag{8}$$

and thus, from third equation in (7), follows that

$$\bar{R} = \left(1 - \frac{1}{k}\right) (1 - \bar{S}). \quad (9)$$

Thus, if $\bar{S} = 1$, then (8) and (9) implies that $\bar{I} = \bar{R} = 0$ and the expressions for equilibrium types P_1, P_2 and P_3 can be obtain from fourth equation in (7).

If $\bar{S} \neq 1$, then (8) implies that $\bar{I} \neq 0$. Thus, from second equation in (7), we obtain

$$(1 - \bar{x})R_0\bar{S} = 1,$$

which implies that in this case $\bar{x} \neq 1$ and therefore

$$\bar{S} = \frac{1}{R_0(1 - \bar{x})}. \quad (10)$$

Equation (10) implies the expression for equilibrium P_4 but additionally, can be used jointly with equation (8) and the fact that $R_p = \frac{\tilde{a}_1 - k\tilde{a}_2}{\tilde{a}_1 - k\tilde{a}_0}$, obtain by basic manipulations of the fourth equation in (7), the expressions and conditions defining P_5 and P_6 . $\square$

3.2 Comments on Lemma 2

Model (6) has more possible equilibrium points that the classic SIR model. Indeed, the classical SIR model has only two equilibrium points: a disease-free equilibrium and an endemic equilibrium that corresponds precisely to equilibria P_1 and P_4 . In addition, model (6) has other disease-free equilibria (P_2 and P_3) and other endemic equilibria (P_5 and P_6).

The equilibrium points P_1 and P_2 differ only in the last component: in P_1 no one is adopting the anti-infection behavior and in P_2 all population does. Although P_2 seems an ideal scenario, it may not be realistic even if the prevention policy has an insignificant cost.

Equilibrium type P_3 also differs from P_1 only in the last component. However, note that P_3 represents an infinite set of equilibrium, since for each $\bar{x}$ we obtain a different equilibrium point. In particular, P_3 include P_1 and P_2 when $\bar{x} = 0$ and $\bar{x} = 1$, respectively. In fact, P_3 represents a connected path between these two disease-free equilibria.

Note that the family of equilibria P_3 exists only if $\tilde{a}_0 = \tilde{a}_2$. In terms of the original parameters, this is equivalent to $a_c = a_s$, that is, the fixed cost has to be exactly equal to the payoff associated with the proportion of susceptible members of the population. Such equality between parameters may be unrealistic, thus we consider P_3 of minor practical interest. This also applies to equilibrium family P_6 which has also a condition for its existence involving equality between parameters.

As mentioned before, P_4 corresponds to the endemic equilibrium of the classical SIR model and has the same existence condition ($R_0 > 1$) in that context.

In turn, the equilibrium point P_5 does not coincide with any equilibrium of the classic SIR model and can be considered as a more realistic scenario. In the P_5 case, the infection is present ($\bar{I} \neq 0$) and only a part of the population adopted the anti-infection behavior. Note also that the condition $R_p < R_0$, implies that the proportion of the susceptible

population in P_5 is greater than in P_4 . Consequently, the proportion of infected population in P_5 is lower than in P_4 . Therefore, P_5 can be interpreted as a desirable situation where anti-infection behavior reduces the impact of the disease in the long-term.

Note also that in this P_5 scenario, for a fixed value of R_0 , the larger is R_p , the smaller is the proportion of infected people. This relationship between R_0 , a parameter related only to the disease, and R_p , a parameter related to the cost of intervention, allows an analysis of the effects of behavior and cost/payoff changes in the disease dynamic. The best-case scenario would be one with a minimal value for $\bar{I}$, or equivalently, a maximal value for $\bar{x}$. This will occur if R_p tends to 1 and in the limit this will imply $\tilde{a}_2 = \tilde{a}_0$ (existence condition of P_3).

The worst-case scenario for P_5 would be one where R_p goes to R_0 because in this case, $\bar{x}$ goes to zero and P_5 goes to P_4 .

Equilibrium type P_6 represents an infinite set of endemics equilibrium points, one for each $\bar{x} \in \left(0, \frac{R_0-1}{R_0}\right)$. Unlike disease-free equilibria P_3 , in P_6 the value of $\bar{x}$ will affect the value of $\bar{S}$ ($\bar{I}$ and $\bar{R}$ too). Note that if $\bar{x}$ approach $\frac{R_0-1}{R_0}$, then $\bar{S}$ approach 1. This means that if the proportion of the population adopting the prevention behavior increase, the proportion of susceptible population also increases (and the proportion of infected population decrease).

Note that, when $\bar{x}$ goes to 0, P_6 goes to P_4 , and when $\bar{x} = \frac{R_0-1}{R_0}$, the equilibrium P_6 goes to a P_3 equilibrium point. In fact, when $k\tilde{a}_0 = \tilde{a}_1 = k\tilde{a}_2$ both sets of equilibria P_3 and P_6 coexist and have a linking point at $\left(1, 0, 0, \frac{R_0-1}{R_0}\right)$. Lastly, note that equilibrium points P_6 cannot co-exist with equilibrium point P_5 , since its existence conditions are incompatible.

3.3 Jacobian Matrix and its Characteristic Polynomial

We are interested in study the stability of equilibrium points of (6). Then, it will be useful to consider the associated Jacobian matrix given by:

$$J(S, I, R, x) = \begin{bmatrix} -(1-x)IkR_0 - 1 & -(1-x)kR_0S & 0 & IkR_0S \\ (1-x)IkR_0 & (1-x)kR_0S - k & 0 & -IkR_0S \\ 0 & k - 1 & -1 & 0 \\ (1-x)x\tilde{a}_2 & (1-x)x\tilde{a}_1 & 0 & (1-2x)(-\tilde{a}_0 + \tilde{a}_1I + \tilde{a}_2S) \end{bmatrix}.$$

The characteristic polynomial of $J(S, I, R, x)$ can be written as:

$$p(\lambda) = |J(S, I, R, x) - \lambda I| = (-1 - \lambda)q(\lambda) \quad (11)$$

where

$$q(\lambda) = \begin{vmatrix} -(1-x)IkR_0 - 1 - \lambda & -(1-x)kR_0S & IkR_0S \\ (1-x)IkR_0 & (1-x)kR_0S - k - \lambda & -IkR_0S \\ (1-x)x\tilde{a}_2 & (1-x)x\tilde{a}_1 & (1-2x)(-\tilde{a}_0 + \tilde{a}_1I + \tilde{a}_2S) - \lambda \end{vmatrix}.$$

3.4 Stability of P_1 , P_2 , P_4 , and P_5

It is clear from (11) that for any equilibrium point, the Jacobian has at least one negative eigenvalue $\lambda_1 = -1$ and that additional eigenvalues can be studied analyzing the equation $q(\lambda) = 0$. This can be used to establish the following subsection result about the stability of equilibrium points P_1 , P_2 , P_4 , and P_5 whose complete proof is presented in the Appendix.

Theorem 1. *Consider system (6). Assume that $\tilde{a}_0 \neq \tilde{a}_2$, $\tilde{a}_0 \neq \tilde{a}_1/k$, $R_0 \neq 1$, and $R_0 \neq R_p$.*

1. *If $R_0 < 1$ then*

- i. P_1 is locally asymptotically stable if $\tilde{a}_0 > \tilde{a}_2$;*
- ii. P_2 is locally asymptotically stable if $\tilde{a}_0 < \tilde{a}_2$,*
- iii. P_4 and P_5 do not exist.*

2. *If $R_0 > 1$ and $R_0 < R_p$, then*

- i. P_4 is locally asymptotically stable if $\tilde{a}_0 > \tilde{a}_2$;*
- ii. P_2 is locally asymptotically stable if $\tilde{a}_0 < \tilde{a}_2$;*
- iii. P_1 is not stable;*
- iv. P_5 do not exist.*

3. *If $R_0 > 1$ and $R_0 > R_p$,*

- i. P_5 is locally asymptotically stable if $\tilde{a}_0 > \tilde{a}_2$, and $\tilde{a}_0 < \tilde{a}_1/k$;*
- ii. P_4 is locally asymptotically stable if $\tilde{a}_0 > \tilde{a}_2$, and $\tilde{a}_0 > \tilde{a}_1/k$;*
- iii. P_2 is locally asymptotically stable if $\tilde{a}_0 < \tilde{a}_2$, and $\tilde{a}_0 < \tilde{a}_1/k$;*
- iv. P_2 and P_4 are locally asymptotically stable if $\tilde{a}_0 < \tilde{a}_2$, and $\tilde{a}_0 > \tilde{a}_1/k$;*
- v. P_1 is not stable.*

3.5 Comments on Theorem 1

In the classic SIR model (1), when the basic replication rate is sufficiently low ($R_0 < 1$), the disease-free equilibrium point is stable, so the infection does not become an epidemic. As described in Theorem 1, this phenomenon also occurs in system (6) but in this case, there are two possible disease-free equilibrium: P_1 (zero behavior adoption) and P_2 (complete behavior adoption). The values of $\tilde{a}_0$ and $\tilde{a}_2$ determine which one is stable.

When the disease is more infectious ($R_0 > 1$), the classic SIR model admits only one possibility: the endemic equilibrium is stable and the disease-free equilibrium is unstable. Cases (2i) and (3ii) of the Theorem 1 are equivalent to this situation, since P_4 is equivalent to the endemic equilibrium of the classical SIR model. However, in model (6) some more realistic behaviors may occur. Note for example that it is possible that a disease-free equilibrium P_1 and the endemic equilibrium P_4 coexist simultaneously, both being locally

stable (Theorem 1 (3iii)). Figure 1(a) illustrates this interesting case. Note also that in this situation, equilibrium points P_1 and P_5 also exist but are not stable.

From Theorem 1 (2ii) and (3ii) another remarkable behavior can be observed, even if $R_0 > 1$, it is possible that the system has a disease-free and unique stable equilibrium. Figure 1(b) illustrates this situation. In this case, the equilibrium P_1 exists and is unstable and equilibrium P_5 does not exit.

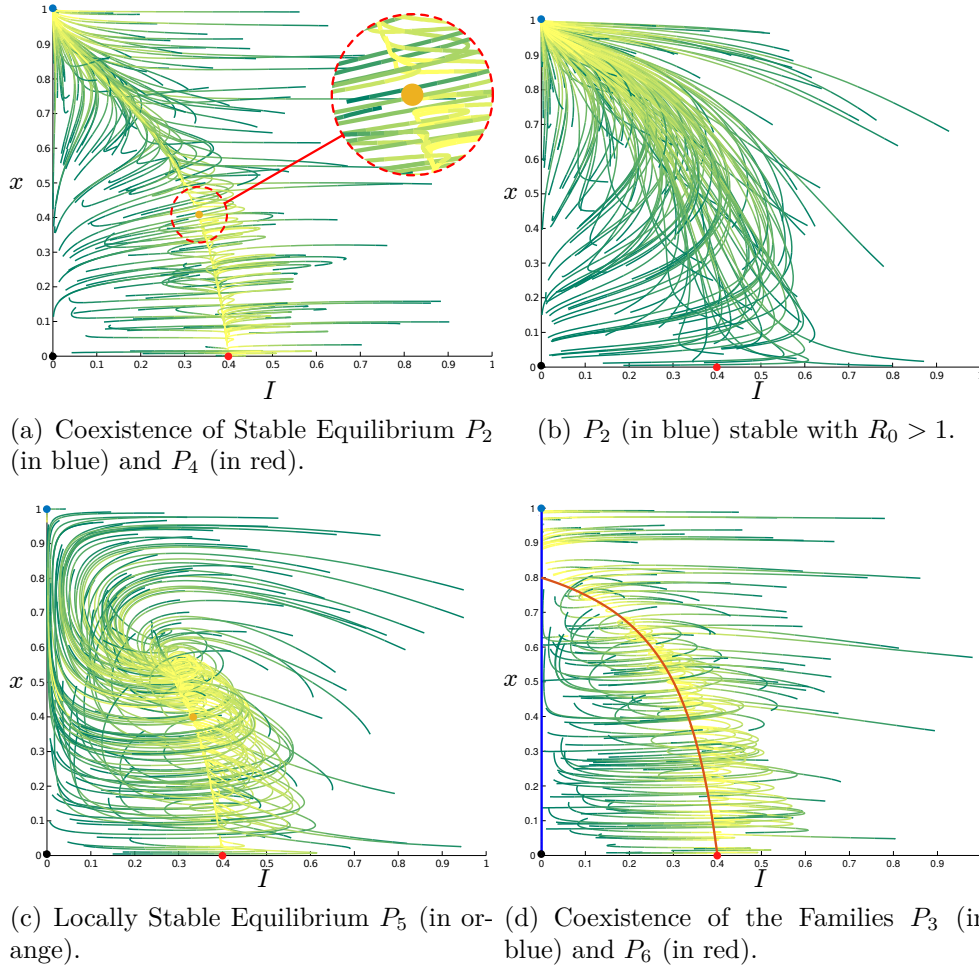


Figure 1: **Solution curves $I(\tau) \times x(\tau)$ of system (6).** Numerical simulations of solutions with different initial conditions. Temporal evolution is represented using dark green for initial trajectory points and a gradual variation to yellow as time increase. The equilibrium points P_1 , P_2 , P_4 , and P_5 are denoted by the dots in the color black, blue, red, and orange, respectively, while the families of equilibria P_3 and P_6 are denoted by the lines in the color blue and red, respectively (when they exist). In all cases pictured $k = 2$ and $R_0 = 5$. In 1(a) $\tilde{a}_0 = \tilde{a}_1 = 1$ and $\tilde{a}_2 = 2$. Thus $R_p = 3$ and $R_0 > \max\{1, R_p\}$, ensuring that P_2 and P_4 are both locally stable, while P_1 and P_5 are unstable (the instability of P_5 is highlighted in zoom). In 1(b) $\tilde{a}_0 = 1$, $\tilde{a}_1 = 7$, and $\tilde{a}_2 = 2$. Thus $R_p = 0.6$ and $R_0 > \max\{1, R_p\}$, ensuring that P_2 are locally stable, while P_1 and P_4 are unstable. In 1(c) $\tilde{a}_0 = 3$, $\tilde{a}_1 = 7$, and $\tilde{a}_2 = 2$. Thus $R_p = 3$, $R_0 > \max\{1, R_p\}$, and $\tilde{a}_1/k > \tilde{a}_0 > \tilde{a}_2$, ensuring that P_5 are locally stable, while P_1 , P_2 , and P_4 are unstable. In 1(d) $\tilde{a}_0 = \tilde{a}_2 = 1$ and $\tilde{a}_1 = 2$. Thus, Theorem 1 ensures that whole family P_6 is stable.

Finally, besides P_4 , we have the possibility of another endemic stable equilibrium: the equilibrium point P_5 . Assuming that conditions of Theorem 1 (3i) are satisfied, equilibria P_1 , P_2 , and P_5 exists, but only the last one is stable. This equilibrium is particularly interesting because it represents a more favorable epidemiological situation than the equilibrium point P_4 . Indeed, as $R_p < R_0$, the value of $\bar{I}$ at P_5 is smaller than the value of $\bar{I}$ at P_4 .

3.6 On the stability of equilibria family P_6

As mentioned before, the existence conditions for equilibrium families P_3 and P_6 involve equality between some parameters which can be unrealistic. The corresponding stability analysis can not be done using the standard approach based on the Jacobian matrix as in Theorem 1, because in this cases, the corresponding Jacobian matrix have a null eigenvalue. In fact, solving equation (11) for equilibrium P_3 equilibrium lead us to

$$\lambda_1 = -1, \quad \lambda_2 = -1, \quad \lambda_3 = 0 \quad \text{and} \quad \lambda_4 = k(R_0(1 - \bar{x}) - 1),$$

and in a similar fashion, the P_6 equilibrium points also have a null eigenvalue ^{*}.

It can be noted however that some points in the equilibrium family P_3 may be locally stable, as illustrated in the Figure 1(d). When $\bar{x} = \frac{R_0-1}{R_0}$, then P_6 becomes $(1, 0, 0, \bar{x})$, so this point is a linking point between P_6 and P_3 . Note that this point acts as the threshold between stable and unstable equilibrium points in P_3 .

Nevertheless, a closer look at system (6) and to the conditions for the existence of P_6 , allow us to determine some stability conditions for equilibria P_6 presented in the following theorem.

Theorem 2. *Assume that in model (6) we have $R_0 > 1$ and $k\tilde{a}_0 = \tilde{a}_1 = k\tilde{a}_2$, so the family of equilibria P_6 exists. If $-\frac{R_0k}{(R_0-1)(k-1)} < \tilde{a}_0$, then the family of equilibria P_6 is stable.*

Proof. Note first that if $-\frac{R_0k}{(R_0-1)(k-1)} < \tilde{a}_0$ then for all $\bar{x} \in \left(0, \frac{R_0-1}{R_0}\right)$ we have that

$$-\frac{(1 - \bar{x})R_0k}{\bar{x}(k - 1)} < \tilde{a}_0, \tag{12}$$

because $0 < \bar{x} < \frac{R_0-1}{R_0}$ implies that $-\frac{1-\bar{x}}{\bar{x}} < -\frac{1}{R_0-1}$. Now, if $k\tilde{a}_0 = \tilde{a}_1 = k\tilde{a}_2$, we have from third and fourth equation of the system (6) that

$$\begin{aligned} \frac{dx}{d\tau} &= x(1 - x)[- \tilde{a}_0 + k\tilde{a}_0 I + \tilde{a}_0 S] \\ &= \tilde{a}_0 x(1 - x)[(k - 1)I - R] \\ &= \tilde{a}_0 x(1 - x) \frac{dR}{d\tau}. \end{aligned}$$

Thus, we have that

$$\frac{dx}{dR} = \tilde{a}_0 x(1 - x),$$

^{*}Null eigenvalues appears also for P_1 if $\tilde{a}_2 = \tilde{a}_0$ or $R_0 = 1$, and for P_2 when $\tilde{a}_2 = \tilde{a}_0$

and we can express x in terms of R as

$$x(R) = \frac{e^{\tilde{a}_0 R}}{e^{\tilde{a}_0 R} + C_1}.$$

This consideration allows us to eliminate the differential equation for x in (6) and using that $S = 1 - I - R$, we can reduce model (6) to a simplified epidemic model with a recovered-dependant infection described as

$$\begin{aligned} \frac{dI}{d\tau} &= I[f(R)(1 - I - R) - k] \\ \frac{dR}{d\tau} &= (k - 1)I - R, \end{aligned} \tag{13}$$

where $f(R) = (1 - x(R))kR_0$. Recovered-dependent epidemic models as (13) were considered by the authors in [3]. In particular, Theorem 4.3 in [3] establish the following result: *If f is positive function, differentiable on $[0, 1]$ and (I^*, R^*) is an endemic equilibrium point of (13) such that $\frac{df}{dR}(R^*) < \frac{1}{k-1}f^2(R^*)$ then (I^*, R^*) is a locally stable equilibrium point.* Note that if $f(R) = (1 - x(R))kR_0$, f is in fact a positive differentiable function on R . Additionally, the following inequalities equivalences holds:

$$\begin{aligned} \frac{df}{dR}(R^*) &< \frac{1}{k-1}f^2(R^*) \\ -kR_0 \frac{dx}{dR} &< \frac{1}{k-1}f^2(R^*) \\ -kR_0 \tilde{a}_0 \bar{x}(1 - \bar{x}) &< \frac{(1 - \bar{x})^2 k^2 R_0^2}{k-1} \\ -\tilde{a}_0 \bar{x} &< \frac{(1 - \bar{x})kR_0}{k-1} \\ -\frac{(1 - \bar{x})R_0 k}{\bar{x}(k-1)} &< \tilde{a}_0, \end{aligned}$$

which we already showed in (12) is valid when $-\frac{R_0 k}{(R_0 - 1)(k - 1)} < \tilde{a}_0$. Therefore, we conclude that the whole family of equilibria P_6 is stable. $\square$

4 Controlling the infection through population behavior: Choosing the right payoffs

In this section, we use the results in Theorem 1 to find conditions on the behavioral payoffs, that produce a diminishing on the infected population at a stable equilibrium. This can be interpreted as specific policy actions leading to reduce and control the infection in the long-term.

According to system (6), an infectious disease with a small replication rate ($R_0 < 1$), requires no anti-infection behavior to be eradicated, since the possible stable points P_1 and P_2 are both disease-free. Nevertheless, the stability conditions in part 1. of Theorem 1 can be rewritten in terms of the original parameters as follows: if $a_c > a_s$, then P_1 is

locally asymptotically stable; if $a_c < a_s$, then P_2 is locally asymptotically stable. This can be interpreted in terms of public policies, as a quantification of how much reduction on the fixed cost a_c is necessary to achieve full adoption of an anti-infection behavior; **if a_c is smaller than a_s , then in the long-term everyone tends to follow the prevention behavior, even if the disease is poorly infectious ($R_0 < 1$).**

We focus now on the situation when $R_0 > 1$ and therefore, the infectious disease may became endemic. We aim to determine, in terms of R_p , a_c , a_s , a_I , and a_R , successful intervention strategies to control the disease. We consider two scenarios:

Scenario 1: Assume that $a_c < a_s$ and therefore $\tilde{a}_0 < \tilde{a}_2$. In this case, from parts 2. and 3. in Theorem 1 we have two possibilities: only the disease-free equilibrium P_2 is stable (cases (2ii) and (3iv)), or P_2 and the endemic equilibrium P_4 are stables (case (3iii)).

From the epidemiological point of view, we would like to avoid the case of stability of an endemic equilibrium. **Therefore, to avoid the stability of P_4 , we must ensure that $\tilde{a}_0 < \tilde{a}_1/k$, that is, besides $a_c < a_s$, we need that $a_c < \frac{a_I}{k} + a_R \left(1 - \frac{1}{k}\right)$.**

This is an ideal scenario that can be interpreted as disease eradication in the long-run.

Scenario 2: Consider now that $a_c > a_s$ (so $\tilde{a}_0 > \tilde{a}_2$), and still $R_0 > 1$.

In this case, the locally stable points will always be endemic: P_4 (cases (2i) and (3ii)) or P_5 (case (3i)). Note however that, if P_5 exists ($R_p < R_0$), this equilibrium will represent a better situation than P_4 , since the proportion of infected in P_5 will be lower than in P_4 . Although R_0 does not depend on the payoff parameters, R_p does, therefore **in order to obtain a lower proportion of infected, we must seek strategies such that the payoff parameters imply $R_p < R_0$. Furthermore, it is not enough that P_5 exists, we want P_5 to be stable. Then, in addition to $\tilde{a}_0 > \tilde{a}_2$ and $R_p < R_0$, we must also be sure that $\tilde{a}_0 < \tilde{a}_1/k$.**

Note also that the components of P_5 depend on the value of R_p and if R_p goes to 1, the proportion of infected persons predicted by this equilibrium decrease. Given an infectious disease with $R_0 > 1$, whereas it is not possible to change the inequality $\tilde{a}_0 > \tilde{a}_2$, it is possible to decrease the number of infected people ensuring that $\tilde{a}_0$ be less than $\tilde{a}_1/k$ (so P_5 is stable) and as close as possible to $\tilde{a}_2$.

In this scenario, it is possible to quantify precisely the percentage of reduction on the infected population, produced by changes in the payoff parameters, as described in the following proposition.

Proposition 1. *Consider system (6) and assume that $R_0 > 1$ and $\tilde{a}_2 < \tilde{a}_0 < \tilde{a}_1/k$. A reduction of $p\%$ in $\tilde{a}_0$ produce a reduction of $\left(\frac{\tilde{a}_0}{\tilde{a}_1 - k\tilde{a}_2}\right)p$ percentage points in the infected population on the endemic equilibrium state P_5 and a relative reduction of $\frac{\tilde{a}_0 - \tilde{a}_2}{\tilde{a}_0 - \tilde{a}_2}p\%$.*

Proof. We can compute the percentage point reduction by computing the difference between the old value of the proportion of the infected population at the equilibrium point P_5 (denoted by $\bar{I}$) and the new value (denoted by $\hat{I}$) obtained after the reduction on a_0 . Note that

$$\bar{I} = \frac{1}{k} \left(1 - \frac{1}{R_p}\right) = \frac{1}{k} \left(1 - \frac{\tilde{a}_1 - k\tilde{a}_0}{\tilde{a}_1 - k\tilde{a}_2}\right) = \frac{\tilde{a}_0 - \tilde{a}_2}{\tilde{a}_1 - k\tilde{a}_2},$$

so we have that

$$\begin{aligned}\bar{I} - \hat{I} &= \frac{\tilde{a}_0 - \tilde{a}_2}{\tilde{a}_1 - k\tilde{a}_2} - \frac{(1 - \frac{p}{100})\tilde{a}_0 - \tilde{a}_2}{\tilde{a}_1 - k\tilde{a}_2} \\ &= \frac{\tilde{a}_0}{\tilde{a}_1 - k\tilde{a}_2} \frac{p}{100}.\end{aligned}$$

Therefore, the reduction of $p\%$ in $\tilde{a}_0$ can be interpreted as a reduction, in the long-term, of $\left(\frac{\tilde{a}_0}{\tilde{a}_1 - k\tilde{a}_2}\right) p$ percentage points in the proportion of infected population.

The corresponding relative reduction can be obtained as

$$\begin{aligned}\frac{(\bar{I} - \hat{I})100}{\bar{I}} &= \frac{\tilde{a}_0}{\tilde{a}_1 - k\tilde{a}_2} \frac{\tilde{a}_1 - k\tilde{a}_2}{\tilde{a}_0 - \tilde{a}_2} p \\ &= \frac{\tilde{a}_0}{\tilde{a}_0 - \tilde{a}_2} p.\end{aligned}$$

So, a reduction of $p\%$ in $\tilde{a}_0$ can be interpreted as a reduction, in the long-term, of $\frac{\tilde{a}_0}{\tilde{a}_0 - \tilde{a}_2} p\%$ in the proportion of infected population. $\square$

Example. Recent measles outbreaks have been associated with a lack of effective vaccination, mainly due to misinformation on the inherent risks of vaccines [30]. In terms of the model proposed in this paper, erroneously high valuations on vaccination risk could be interpreted as a high value for a_c or equivalently, a high value for $\tilde{a}_0$. In this context, it is relevant to ask how much $\tilde{a}_0$ must be reduced to obtain, for example, a reduction of 1 percentage point on the infected population in the long-term. Under conditions on Proposition 1, this desired one percentage point reduction can be obtained by a reduction of $\left(\frac{\tilde{a}_1 - k\tilde{a}_2}{\tilde{a}_0}\right) \%$ in $\tilde{a}_0$.

To obtain useful insights from the last expression, besides considering the limitations and partial validity of using the proposed model for this specific disease, one should also be able to have an estimation of k , $\tilde{a}_0$, $\tilde{a}_1$, and $\tilde{a}_2$. These last parameters were just introduced in the present paper and as such, there are no estimations available yet.

For illustration purposes, we present in Figure 4 a heat map for p , the percentage reduction on a_0 , depending on the values of $\tilde{a}_1$ and $\tilde{a}_2$, that would be necessary to obtain a 1 percentage point reduction on the infected population in the long-term, considering the value of a_0 as a normalized quantity equals to 1 and an estimated[†] value of k equals to 3.8.

From this estimations, we have for example that, if in comparison with $\tilde{a}_0$, $\tilde{a}_1$ is 10 times greater and $\tilde{a}_2$ is a half, then, to obtain a 1 percentage point reduction on the infected population in the long-term it is necessary at least a reduction of 8.1% on $\tilde{a}_0$.

[†]An estimation of k could be obtained from the equality $R_0 = \frac{\beta}{\mu + \gamma} = \frac{\beta}{\mu k}$ in (5) so $k = \frac{\beta}{R_0 \mu}$. For measles, R_0 is commonly considered between 12-18, and in this example we consider it equals to 18. As discussed in [12], this estimation may not be adequate for all kinds of populations. The risk of transmission of an infectious disease is closely related to the infection rate β and we consider the worst-case scenario where both parameters are equals. For measles, we consider this value equal to 90% [22] The constant μ can be estimated as the inverse of the mean life expectancy and we are considering $\mu = \frac{1}{76}$

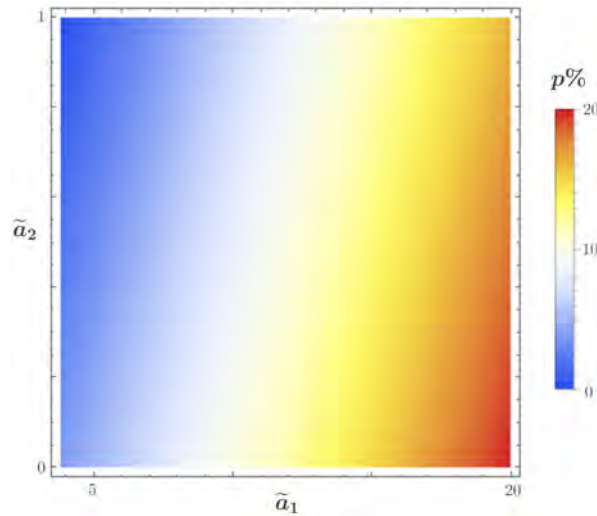


Figure 2: **Heat map for p .** Necessary percentage reduction on a_0 (p), depending on the values of $\tilde{a}_1$ and $\tilde{a}_2$, to obtain a reduction of 1 percentage point on the measles infected population in the long-term

5 Final Comments

The main contribution of this paper is the introduction of a mathematical model to analyze the interplay between infectious disease and anti-infection behavior adoption across the population. We focused on equilibrium states (Lemma 2) and showed the appearance of remarkable characteristics in the context of epidemiological models (Theorem 1), such as the coexistence of two locally stable endemic equilibria, the coexistence of a locally stable endemic and a disease-free equilibrium, and even the possibility of a stable continuum of endemic equilibrium points (Theorem 2). We determine also the effects of some payoff reduction on the infected population size in an endemic equilibrium (Proposition 1). The expressions obtained in Proposition 1 could be used as a threshold to estimate costs/payoff policies leading to long-term effective control of an epidemic infection through anti-infection behavior. Note that the relative reduction index obtained, depends only on the payoff parameters and not on the epidemiological parameters of the disease, therefore, it would be necessary to develop methods to estimate these payoff parameters for specific diseases and model validation from real data.

Other directions may be followed after the present work, to achieve real practical applicability of this kind of behavioral epidemiology modeling. It would be reasonable to consider that the payoff function for the behavioral variable x , for the epidemiological variables, may not be linear. Also, it would be reasonable to consider that the payoff parameters are not necessarily constants and may vary on time. Different ways to model the variation and the effects of the behavioral variable x can also be considered. Other models different from SIR can be suitable for specific situations, including models considering delay differential equations to incorporate delayed effects/variations on the behavior adoption rate. We consider that the results obtained in the present work open valuable paths of research.

A Proof of Theorem 1

In this Appendix, we present the proof of Theorem 1 based on the Jacobian matrix and characteristic polynomial (11).

As mentioned before, any equilibrium point has at least one eigenvalue $\lambda_1 = -1$, and the other eigenvalues can be studied by analyzing the equation $q(\lambda) = 0$ for P_1 , P_2 , P_4 , and P_5 . This is described as follows.

Case: $P_1 = (1, 0, 0, 0)$

In this case, we have

$$q(\lambda) = \begin{vmatrix} -1 - \lambda & -kR_0 & 0 \\ 0 & kR_0 - k - \lambda & 0 \\ 0 & 0 & -\tilde{a}_0 + \tilde{a}_2 - \lambda \end{vmatrix}.$$

Thence, the additional eigenvalues are

$$\lambda_2 = -1, \quad \lambda_3 = k(R_0 - 1) \quad \text{and} \quad \lambda_4 = \tilde{a}_2 - \tilde{a}_0.$$

Therefore, if $R_0 < 1$ and $\tilde{a}_2 < \tilde{a}_0$, then all eigenvalues will be negative and, consequently, P_1 is locally asymptotically stable. If $R_0 > 1$ or $\tilde{a}_2 > \tilde{a}_0$, then P_1 is not stable.

Case: $P_2 = (1, 0, 0, 1)$

In this case, we obtain

$$q(\lambda) = \begin{vmatrix} -1 - \lambda & 0 & 0 \\ 0 & -k - \lambda & 0 \\ 0 & 0 & \tilde{a}_0 - \tilde{a}_2 - \lambda \end{vmatrix}.$$

Thence, the additional eigenvalues are

$$\lambda_2 = -1, \quad \lambda_3 = -k, \quad \text{and} \quad \lambda_4 = \tilde{a}_0 - \tilde{a}_2.$$

Therefore, it is sufficient that $\tilde{a}_0 < \tilde{a}_2$ for P_2 to be locally asymptotically stable. If $\tilde{a}_0 > \tilde{a}_2$, then P_2 is not stable.

Case: $P_4 = \left(\frac{1}{R_0}, \frac{1}{k} \left(1 - \frac{1}{R_0} \right), \left(1 - \frac{1}{k} \right) \left(1 - \frac{1}{R_0} \right), 0 \right)$

In this case, we have that

$$q(\lambda) = \begin{vmatrix} -\left(1 - \frac{1}{R_0}\right)R_0 - 1 - \lambda & -k & 1 - \frac{1}{R_0} \\ \left(1 - \frac{1}{R_0}\right)R_0 & -\lambda & \frac{1}{R_0} - 1 \\ 0 & 0 & -\tilde{a}_0 + \frac{\tilde{a}_1\left(1 - \frac{1}{R_0}\right)}{k} + \frac{\tilde{a}_2}{R_0} - \lambda \end{vmatrix} = q_1(\lambda)q_2(\lambda),$$

where

$$q_1(\lambda) = \frac{R_0(\tilde{a}_1 - \tilde{a}_0 k) - \tilde{a}_1 + \tilde{a}_2 k}{k R_0} - \lambda \text{ and}$$

$$q_2(\lambda) = \lambda^2 + \lambda \left(\left(1 - \frac{1}{R_0} \right) R_0 + 1 \right) + k \left(1 - \frac{1}{R_0} \right) R_0.$$

Thence, the additional eigenvalues are $\lambda_2 = \frac{R_0(\tilde{a}_1 - \tilde{a}_0 k) - \tilde{a}_1 + \tilde{a}_2 k}{k R_0}$ (the root of q_1) and the roots of the quadratic polynomial q_2 . If $R_0 > 1$, then the coefficients of q_2 are all positives and therefore from the Routh–Hurwitz criterion, we conclude that eigenvalues associated with this polynomial must have negative real part. Note also that in this case $\lambda_2 < 0$, if and only if $R_0(\tilde{a}_1 - \tilde{a}_0 k) - \tilde{a}_1 + \tilde{a}_2 k < 0$ or, equivalently, $R_0(\tilde{a}_1 - \tilde{a}_0 k) < \tilde{a}_1 - \tilde{a}_2 k$.

Therefore, $\lambda_2 < 0$ if and only if

- $\tilde{a}_1 - \tilde{a}_0 k > 0$ and $R_0 < \frac{\tilde{a}_1 - \tilde{a}_2 k}{\tilde{a}_1 - \tilde{a}_0 k} = R_p$, or
- $\tilde{a}_1 - \tilde{a}_0 k < 0$ and $R_0 > \frac{\tilde{a}_1 - \tilde{a}_2 k}{\tilde{a}_1 - \tilde{a}_0 k} = R_p$, or
- $\tilde{a}_1 - \tilde{a}_0 k = 0$ and $\tilde{a}_1 - \tilde{a}_2 k > 0$.

If any of these conditions are satisfied, then P_4 is locally asymptotically stable.

Case: $P_5 = \left(\frac{1}{R_p}, \frac{1}{k} \left(1 - \frac{1}{R_p} \right), \left(1 - \frac{1}{k} \right) \left(1 - \frac{1}{R_p} \right), 1 - \frac{R_p}{R_0} \right)$

In this case we obtain

$$q(\lambda) = \begin{vmatrix} -R_p - \lambda & -k & \frac{R_0}{R_p^2}(R_p - 1) \\ R_p - 1 & -\lambda & -\frac{R_0}{R_p^2}(R_p - 1) \\ \frac{\tilde{a}_2(R_0 - R_p)R_p}{R_0^2} & \frac{\tilde{a}_1(R_0 - R_p)R_p}{R_0^2} & -\lambda \end{vmatrix} = -\lambda^3 - C_2\lambda^2 - C_1\lambda - C_0,$$

where

$$C_2 = R_p$$

$$C_1 = \frac{(R_p - 1)}{R_0 R_p} ((R_0 - R_p)(\tilde{a}_1 - \tilde{a}_2) + k R_0 R_p), \text{ and}$$

$$C_0 = \frac{(\tilde{a}_1 - \tilde{a}_2 k)(R_0 - R_p)(R_p - 1)}{R_0 R_p}.$$

According to the Routh–Hurwitz criterion, the roots of $-q$ (also roots of q) will have the negative real part if, and only if,

$$C_2 > 0, \quad C_0 > 0 \quad \text{and} \quad C_2 C_1 - C_0 > 0.$$

If $1 < R_p < R_0$, then we have immediately that $C_2 = R_p > 0$. Furthermore, in this case for $C_0 > 0$ it is necessary and sufficient that

$$\tilde{a}_1 - \tilde{a}_2 k > 0. \tag{14}$$

Additionally, note that

$$C_2C_1 - C_0 = \frac{(R_p - 1)(R_0 - R_p)}{R_0} \left[(\tilde{a}_0k - \tilde{a}_2) + \frac{kR_0R_p}{R_0 - R_p} \right]$$

since $(\tilde{a}_1 - \tilde{a}_0k)R_p = (\tilde{a}_1 - \tilde{a}_0k)\frac{\tilde{a}_1 - \tilde{a}_2k}{\tilde{a}_1 - \tilde{a}_0k} = \tilde{a}_1 - \tilde{a}_2k$.

Considering that $R_0 > 0$, $R_p > 1$ and $R_0 > R_p$, then

$$\begin{aligned} C_2C_1 - C_0 > 0 &\Leftrightarrow (\tilde{a}_0k - \tilde{a}_2) + \frac{kR_0R_p}{R_0 - R_p} > 0 \\ &\Leftrightarrow \tilde{a}_2 < k \left(\tilde{a}_0 + \frac{R_0R_p}{R_0 - R_p} \right). \end{aligned} \quad (15)$$

That is, P_5 is locally asymptotically stable, if and only if, (14) and (15) are satisfied (s.t. the conditions of P_5 existence).

Remember that the existence conditions for P_5 are

$$\tilde{a}_1 \neq k\tilde{a}_0 \quad (16)$$

$$1 < R_p < R_0. \quad (17)$$

Since $R_p = \frac{\tilde{a}_1 - k\tilde{a}_2}{\tilde{a}_1 - k\tilde{a}_0}$, to analyze inequality (17) we separate (16) in two cases:

Case 1: $\tilde{a}_1 - k\tilde{a}_0 > 0$.

Multiplying (17) by $\tilde{a}_1 - k\tilde{a}_0$ we have

$$\begin{aligned} \tilde{a}_1 - k\tilde{a}_0 &< \tilde{a}_1 - k\tilde{a}_2 < R_0(\tilde{a}_1 - k\tilde{a}_0) \\ \Rightarrow -k\tilde{a}_0 &< -k\tilde{a}_2 < R_0(\tilde{a}_1 - k\tilde{a}_0) - \tilde{a}_1 \\ \Rightarrow k\tilde{a}_0 &> k\tilde{a}_2 > -R_0(\tilde{a}_1 - k\tilde{a}_0) + \tilde{a}_1. \end{aligned}$$

Joining the last inequality with the hypothesis considered in this case we have

$$\tilde{a}_1 > k\tilde{a}_0 > k\tilde{a}_2 > -R_0(\tilde{a}_1 - k\tilde{a}_0) + \tilde{a}_1. \quad (18)$$

Case 2: $\tilde{a}_1 - k\tilde{a}_0 < 0$.

Analogously to the previous case, we will have

$$\tilde{a}_1 < k\tilde{a}_0 < k\tilde{a}_2 < -R_0(\tilde{a}_1 - k\tilde{a}_0) + \tilde{a}_1.$$

Note that, in order to ensure P_5 stability, is necessary that $\tilde{a}_1 > \tilde{a}_2k$ (condition (14)), which only occurs in (18). However, if (18) is satisfied, since $k > 1$ and $R_0 > R_p$ we have that

$$\tilde{a}_2 < k\tilde{a}_2 < k\tilde{a}_0 < k\tilde{a}_0 + k \frac{R_0R_p}{R_0 - R_p}.$$

That is, in the case (18) the condition (15) is always satisfied.

Summarizing:

- If $\tilde{a}_1 > k\tilde{a}_0 > k\tilde{a}_2 > -R_0(\tilde{a}_1 - k\tilde{a}_0) + \tilde{a}_1$, then P_5 exists and is locally asymptotically stable.
- If $\tilde{a}_1 < k\tilde{a}_0 < k\tilde{a}_2 < -R_0(\tilde{a}_1 - k\tilde{a}_0) + \tilde{a}_1$, then P_5 exists but is not stable.
- In other cases P_5 does not exist.

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