A SIR-type model for coca crops in Colombia

Proyecto de Grado de Maestría

presentado por

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Contents

Chapter 1

Introduction

Coca cultivation in Colombia has been a major problem for the last 30 years. In the 80's and 90's a migration of coca crops coming from Perú and Bolivia began, as a response to the anti-drug policies [RG11], a phenomenon denominated *efecto globo o balón*. At the beginning of 90's coca cultivation was almost completely concentrated in 4 departments, Guaviare, Caquetá, Putumayo and Bolívar. Comparing this date with data of 2009 it is clear that coca has spread through the Colombian territory [RG11]. Thus, the question is, can we modeled somehow this spreading phenomenon? Is it just a diffusion process? Looking for an answer and based on the rigourous work of Ricardo Rocha García and the *Colombia Coca Cultivation Survey* made by the UNODC, we have found that there exist a form of *contagion* due to the social, economic and even cultural issues that make some territories more *vulnerable* [RG11].

In the following work, we present a new way to analyse coca cultivation in Colombia, by means of a SIR-type model and mathematical epidemiology theory. The first part is a review of the fundamental concepts of ordinary differential equations, dynamical systems and epidemic models that are the theoretical foundations of what follows. In the second part, we present the model in the form of a system of time dependent ordinary differential equations and we develop the classical analysis of equilibria and stability. Based on official data from [UNO] we derive the constants of the model. Then we construct a Lyapunov function for each equilibrium and obtain global properties.

Chapter 2

Preliminaries

We present some of the basic tools about systems of ordinary differential equations and epidemiological models (more specifically, the SIR model) that we are going to need throughout this work. We shall mention some results we need without formal statement or proof. A complete development of such a theory can be found in [Per01] or any classic book in differential equations or non-linear analysis.

2.1 Systems of ordinary differential equations

We begin with a system of ordinary differential equations. Since we are only concerned with the autonomous case, we can write it in the form

$$\dot{x} = f(x) \tag{2.1}$$

where, $\dot{x}(t) := (\frac{dx_1}{dt}, \ldots, \frac{dx_n}{dt})$, $f : E \to \mathbb{R}^n$ a vector field in $C^1(E)$ and $E \subset \mathbb{R}^n$ an open set. A curve ϕ defined on an interval I is called a *solution* of the system (2.1) if ϕ is differentiable on I, $\phi(t) \in E$ for all $t \in I$ and

$$\dot{\phi}(t) = f(\phi(t))$$

for all $t \in I$. If, in addition, for some $x_0 \in E$ there exists $t_0 \in I$ such that

$$\phi(t_0) = x_0$$

then $\phi(\cdot, x_0)$ is called *solution of the initial value problem*

$$\dot{x} = f(x) \tag{2.2}$$
$$x(0) = x_0.$$

3

By the theory of ordinary differential equations and specifically the well-known Existence and Uniqueness Theorem, we know that for each $x_0 \in E$, there exists an $a > 0$ and a unique solution $\phi(\cdot, x_0)^1$ of (2.2) defined on $(-a, a)$. As a corollary this solution can be extended to a maximal interval of existence $I(x_0)$. The set of mappings defined by $\phi_t(x_0) = \phi(t, x_0)$ is called *flow of the system* (2.1) or *flow of the vector field f*. However, there is a stronger theorem which allows us to think that solutions are always defined for all $t \in \mathbb{R}$, but for that, we need to introduce an additional concept.

Definition 1. Let E_1, E_2 be open subsets of $\mathbb{R}^n$, f and g vector fields in $C^1(E_1)$ and $C^1(E_2)$ respectively. Then, the systems of differential equations

$$\dot{x} = f(x)$$

and

$$\dot{x} = g(x)$$

with flows ϕ and ψ are said to be *topologically equivalent* if there exists a homeomorphism $H : E_1 \to E_2$ and for each $x \in E_1$ a continuously differentiable function $t(x, \tau)$ defined for all $\tau \in \mathbb{R}$ such that $\partial t / \partial \tau > 0$ and

$$H \circ \phi_{t(x,\tau)} = \psi_\tau \circ H(x)$$

for all $x \in E_1$ and $\tau \in \mathbb{R}$.

Roughly speaking, two systems are topologically equivalent if there is an time orientation preserving homeomorphism from E_1 to E_2 sending trajectories from the first into trajectories of the second. Now we can state the so-called *global existence theorem*.

Theorem 1 ([Per01], Theorem 3.1.2). *Let f be a vector field in $C^1(\mathbb{R}^n)$. Then, for all $x_0 \in \mathbb{R}^n$ the initial value problem*

$$\dot{x} = \frac{f}{1 + |f|}(x)$$
$$x(0) = x_0,$$

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[1]We make explicit the dependence on x_0 which is guaranteed by uniqueness.

has a unique solution $\phi(\cdot, x_0)$ defined for all $t \in \mathbb{R}$, and it is topologically equivalent to the system

$$\dot{x} = f(x)$$
$$x(0) = x_0.$$

Although the proof of this result is not trivial it relies on a main idea which is to *rescale* time. A similar rescaling argument due to Vinograd can be applied to show that the theorem still holds for systems defined on proper subsets of $\mathbb{R}^n$. See [Per01].

Theorem 2. *Let E be an open subset of $\mathbb{R}^n$ and $f \in C^1(E)$. Then there exists a vector field $F \in C^1(E)$ such that the systems*

$$\dot{x} = f(x)$$

and

$$\dot{x} = F(x)$$

are topologically equivalent and the trajectories of F are defined for all $t \in \mathbb{R}$.

So without restriction, we may assume that for each $x_0 \in E$ there exists a solution $\phi_t(x_0) = \phi(t, x_0)$ defined for all t. It can be shown that the map

$$\phi : \mathbb{R} \times E \to E$$
$$(t, x) \mapsto \phi_t(x)$$

satisfies a one-parameter group condition, namely

1. $\phi_0(x) = x$, for all $x \in E$.

2. $\phi_{t+s}(x) = (\phi_t \circ \phi_s)(x)$, for all $t, s \in \mathbb{R}$ and $x \in E$.

Definition 2. A family of maps $\{\phi_t(\cdot)\}_{t \in \mathbb{R}}$ satisfying the two conditions above is called a *dynamical system on E*.

Remark 1. Note that according to this definition, the first family $\{\phi(t, \cdot)\}_{t \in \mathbb{R}}$ we gave, was just an example of a dynamical system, but since these are the most important ones, we decided to motivate the definition in this way. Moreover, we shall call *dynamical system* to either the system of equations or the family of solution curves without distinction.

2.1.1   Equilibrium points and stability

Let $\phi_t(x)$ be the flow of the system (2.1) and assume it belongs to $C^2(E \times \mathbb{R})$. This means that

$$\frac{d}{dt}\phi_t(x) = f(\phi_t(x)).$$

Differentiating both sides with respect to x, recalling that D_x commutes with d/dt and applying the chain rule we obtain

$$\frac{d}{dt}D_x\phi_t(x) = D_x[f(\phi_t(x))] = D_x f(\phi_t(x)) \cdot D\phi_t(x).$$

If we now fix some $x_0 \in E$ and call $A(t) = D_x f(\phi_t(x_0))$ and $X(t) = D_x\phi_t(x_0)$, what we just write is

$$\dot{X}(t) = A(t)X(t), \tag{2.3}$$

wich is known as the *variational equation*. A matrix Φ satisfying the equation (2.3) is called *fundamental solution* and its columns are n linearly independent solutions of

$$\dot{x} = A(t)x.$$

Given a particular solution passing through x_0, the variational equation measures the behaviour of solutions near the particular one, whether they move away or remain close.

If $x_0 \in E$ is such that $f(x_0) = 0$, x_0 is called *equilibrium* and the function $u_t(x) = x_0$ is an equilibrium solution. Computing the matrix $A(t)$ of the variational equation we get the *linearization at x_0* or *linearized system at x_0* which is given by the linear system

$$\dot{x} = Df(x_0)(x - x_0), \tag{2.4}$$

We shall see that under certain conditions on the spectrum of the matrix $Df(x_0)$ the original system and the linearized one are locally topologically equivalent, i.e., their qualitative behavior near the equilibrium is essentially the same.

Definition 3. Under the notations above, an equilibrium point x_0 is called *hyperbolic* if all eigenvalues of $Df(x_0)$ have non zero real part. If there are at least one eigenvalue with zero real part, x_0 is called *non-hyperbolic*.

Intuitively, an equilibrium point is *stable* if solution curves passing near the equilibrium, remain near the equilibrium when time goes by, and it is asymptotically stable if these curves, in fact, converge to the equilibrium. Formally,

Definition 4. Let $E \subset \mathbb{R}^n$ be an open set, $f \in C^1(E)$ and ϕ the flow of f. If x_0 is an equilibrium for the system $\dot{x} = f(x)$ then,

- x_0 is *stable* if for all $\varepsilon > 0$ there exists a $\delta > 0$ such that for all $t \geq 0$ and all $x \in B(x_0, \delta)$, $\phi(t, x) \in B(x_0, \varepsilon)$.

- x_0 is *asymptotically stable* if there exists $\delta > 0$ such that for all $x \in B(x_0, \delta)$, $\lim_{t \to \infty} \phi(x, t) = x_0$

- x_0 is called *unstable* if it is not stable.

Although we just gave a formal definition of stability, when dealing with linear systems, i.e., systems generated by a linear map, stability can be decided in terms of the sign of the real part of the eigenvalues of such a map. When the real part of all eigenvalues is non-positive, the equilibrium is stable; if there is at least one eigenvalue with positive real part, the equilibrium is unstable. Let us look at some simple examples in order to illustrate this.

Example 1. Consider the following linear systems.

1.
$$\begin{bmatrix} \dot{x} \\ \dot{y} \end{bmatrix} = \begin{bmatrix} -1 & 2 \\ 0 & -2 \end{bmatrix} \begin{bmatrix} x \\ y \end{bmatrix}.$$

   Note that the eigenvalues of the matrix are -1 and -2 so the equilibrium is (asymptotically) stable as Figure (2.1) shows.

2.
$$\begin{bmatrix} \dot{x} \\ \dot{y} \end{bmatrix} = \begin{bmatrix} -1 & 2 \\ 0 & 2 \end{bmatrix} \begin{bmatrix} x \\ y \end{bmatrix}.$$

   The eigenvalues here are -1 and 2 so the equilibrium is unstable. See Figure (2.2).

3.
$$\begin{bmatrix} \dot{x} \\ \dot{y} \end{bmatrix} = \begin{bmatrix} 0 & -2 \\ 2 & 0 \end{bmatrix} \begin{bmatrix} x \\ y \end{bmatrix}.$$
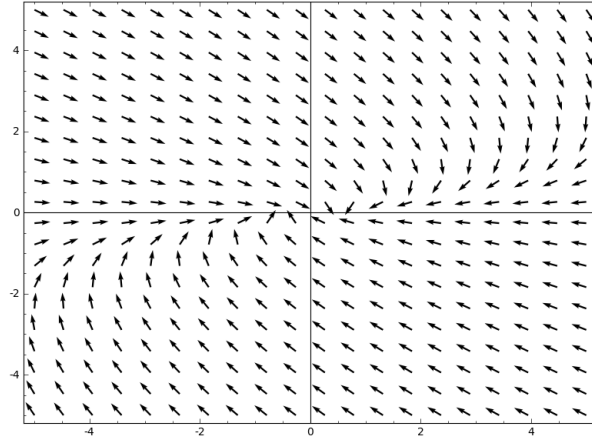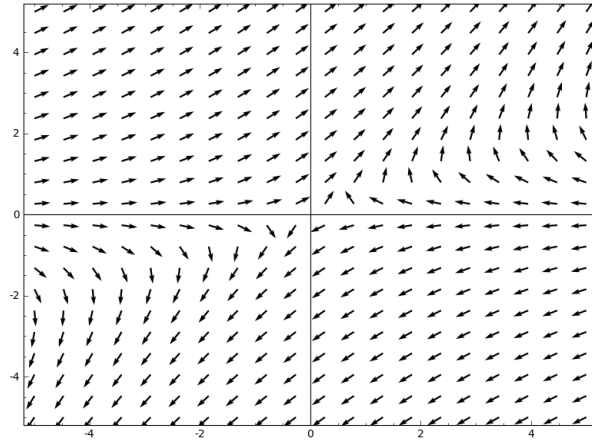
Figure 2.1:

Figure 2.2:

The eigenvalues here are $\pm 2i$ so the equilibrium is stable, but note that in this case, even when the trajectories remain near the equilibrium, they do not converge to the equilibrium. See Figure (2.3).

There are two classical ways to study the stability of a dynamical system. One is to linearize at equilibrium points and make use of Hartman-Grobman theorem unless they are non-hyperbolic. The other possibility, which is in fact more general, is to find Lyapunov functions for the system. We present
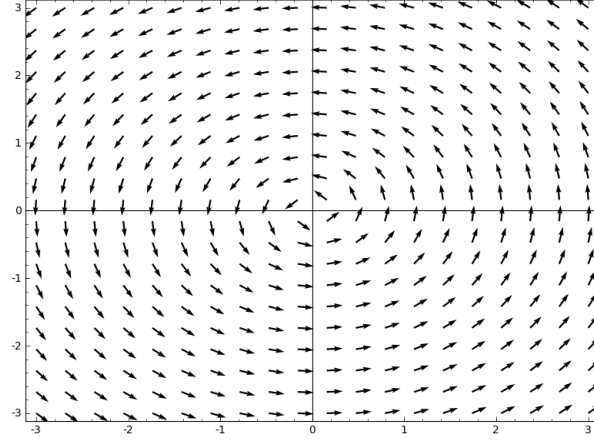
8

Figure 2.3:

both approaches here.

Theorem 3 (Hartman-Grobman). *Consider a dynamical system given by (2.1), ϕ the flow of the system, $0 \in E$ an hyperbolic equilibrium point and let $A := Df(0)$. Then, the systems $\dot{x} = f(x)$ and $\dot{x} = Ax$ are locally topologically equivalent, i.e, there exists an open set U containing 0 and a homeomorphism H of U into an open set V containing the origin such that for every $x_0 \in E$ there exists an open interval $I_0 \subset \mathbb{R}$ containing 0 such that for all $x \in U$ and $t \in I_0$*

$$H \circ \phi_t(x) = e^{tA} H(x)$$

This theorem is classic and the proof could be find in [Per01], for example. The importance of this result is that it ensures that the linearization at hyperbolic equilibrium points describes completely the qualitative structure of the system, at least in a neighbourhood of the equilibrium. Let us look at some examples to understand how the theorem works and when it fails.

Example 2. Consider the two dimensional system

$$\dot{x} = 4x + 2xy - 8$$
$$\dot{y} = 4y^2 - x^2.$$

It has two equilibrium points, namely, $(\pm 2\sqrt{3} - 2, \pm\sqrt{3} - 1)$. A graph

9
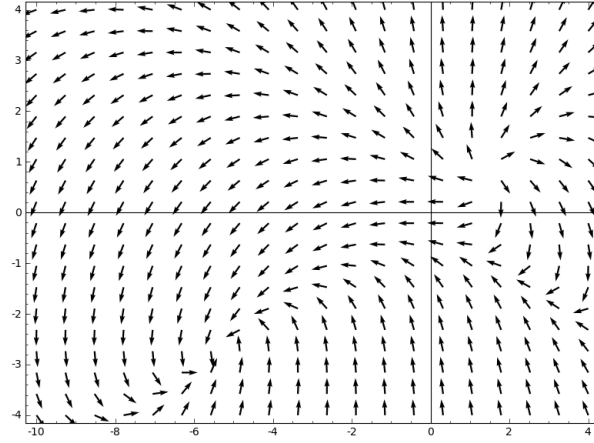
Figure 2.4:

for the vector field that generates the system is shown in Figure 2.4. Now, if we linearize at the equilibrium in the first quadrant, we get, after a change of variables in order to have the equilibrium at zero,

$$\begin{bmatrix} \dot{x} \\ \dot{y} \end{bmatrix} = \begin{bmatrix} 2 + 2\sqrt{3} & 4\sqrt{3} - 4 \\ -4\sqrt{3} + 4 & 8\sqrt{3} - 8 \end{bmatrix} \begin{bmatrix} x \\ y \end{bmatrix}.$$

Figure 2.5:

A phase portrait of this system is shown in Figure 2.5 As the figures show,

the qualitative structure of the non-linear system near the equilibrium is the same as the qualitative structure of the linearized system.

Example 3 (Non-example). Consider the three dimensional system

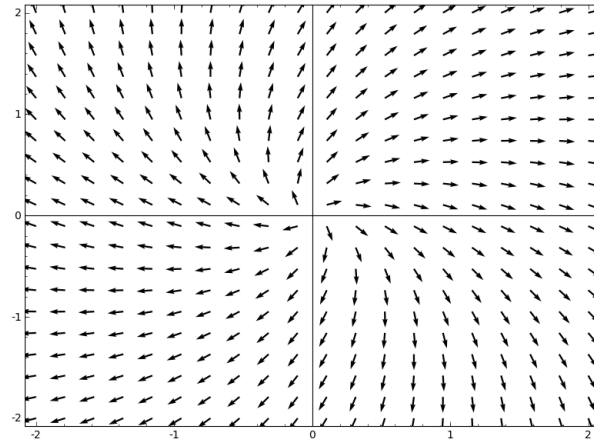$$\dot{x} = -y - xy^2 + z^2 - x^3$$
$$\dot{y} = x + z^3 - y^3$$
$$\dot{z} = -xz - x^2z - z^2y - z^5.$$

It is clear that the origin is an equilibrium point for the system. Linearizing at the origin we get the system

$$\begin{bmatrix} \dot{x} \\ \dot{y} \\ \dot{z} \end{bmatrix} = \begin{bmatrix} 0 & -1 & 0 \\ 1 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix} \begin{bmatrix} x \\ y \\ z \end{bmatrix}.$$

So the eigenvalues are $\pm i$ and 0 and thus, the origin is a non-hyperbolic equilibrium point. Note that taking the exponential of the linearization matrix we obtain

$$\begin{bmatrix} \cos(t) & -\sin(t) & 0 \\ \sin(t) & \cos(t) & 0 \\ 0 & 0 & 1 \end{bmatrix},$$

so the solution curves lie on circles parallel to the plane $z = 0$, and then the origin is a stable equilibrium. However, we shall see soon that for the non-linear system, the origin is in fact an asymptotically stable equilibrium point.

We now proceed to show another tool to study the stability of a system. Suppose x_0 is an equilibrium point of the (2.1). In order to study its stability we may take any other point x close to x_0 and a hyperplane containing x but not x_0. Then look at the angle between the vectors $f(x)$ and the normal to such a hyperplane. Depending on this angle we can know if a solution curve passing through x is moving away from x_0 or not. Since we should do this for every x in a neighbourhood of x_0, it turns out that there is a natural way to obtain such a hyperplane for each x, by considering the tangent spaces of level sets of some function. See Figure 2.6. Surprisingly, if we take some real valued function on a neighbourhood of x_0 and compose it with the flow of the system, we obtain another real valued function, whose derivative w.r.t.
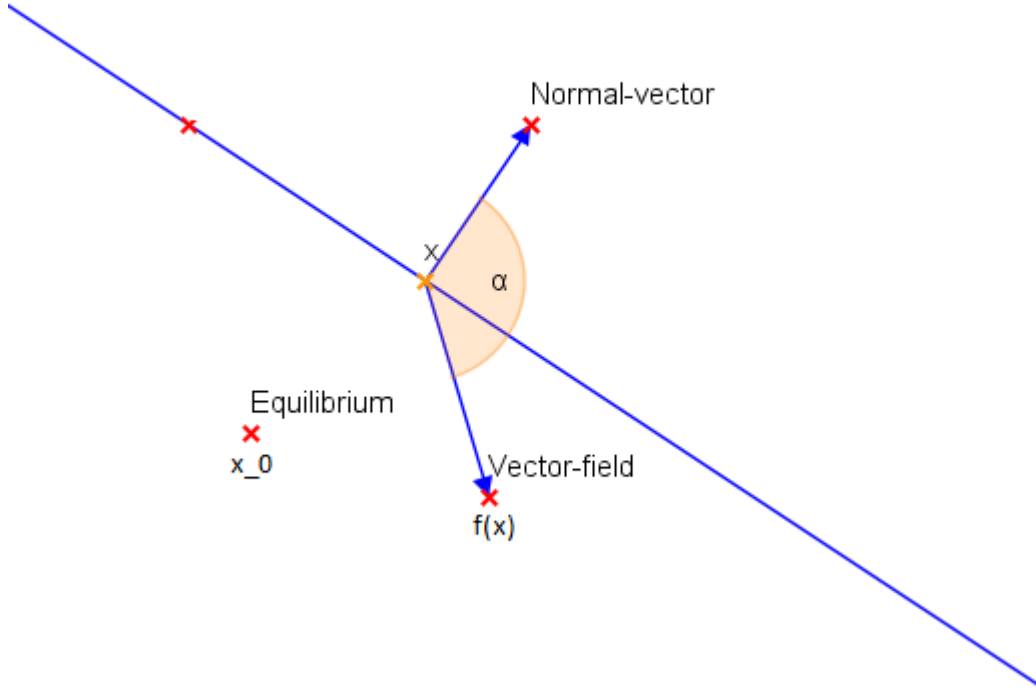
Figure 2.6: The idea behind the Lyapunov's direct method

the time, avaluated in $t = 0$ is exactly what we are describing. Of course this is just an idea to illustrate the idea behind the following definition and theorem.

Definition 5. Consider the system (2.1), and assume that $x_0 \in E$ is an equilibrium point. A function $V : E \to \mathbb{R}$ satisfying

- $V(x_0) = 0$,

- $V(x) > 0$ for all x in some neighbourhood of x_0

is called *Lyapunov function for (2.1)* at x_0. If such a neighbourhood is the whole E, V is called *global Lyapunov funtion*. Also, we define the *orbital derivative* of V or derivative of V along solution curves of 2.1 as

$$\dot{V}(x) := \frac{d}{dt}\Big|_{t=0} (V(\phi(x,t))) = DV(x)f(x) = \nabla V(x)^t f(x),$$

12

where the last equality holds because of the chain rule.

Although it seems to be a naive definition, it is the only thing we need to check stability of an equilibrium point. This is stated as follows,

Theorem 4 (Lyapunov's Direct Method). *If V is a Lyapunov function for 2.1 at x_0 then,*

1. *if $\dot{V}(x) \leq 0$ for all $x \in E$, then x_0 is stable.*

2. *If $\dot{V}(x) < 0$ for all $x \in E$, $x \neq x_0$, then x_0 is asymptotically stable.*

3. *If $\dot{V}(x) \geq 0$ for all $x \in E$, then x_0 is unstable.*

Proof. For the first two parts, we follow the proof of [Per01]. Take $\varepsilon > 0$ such that $\overline{B_\varepsilon(x_0)} \subset E$. Since the boundary of this set is compact, V attains a minimum $m > 0$ by the continuity of V. Now take $U = \{x \in B_\varepsilon(x_0) | V(x) < m\}$. If $\dot{V}(x) \leq 0$, then V is decreasing along solution curves. Therefore, for any $x \in U$ the corresponding solution curve passing through x can not leave U and this means that x_0 is stable.

Now, assume that $\dot{V} < 0$ and take a trajectory $\phi(t, x) \in U \setminus \{x_0\}$. Since $\overline{B_\varepsilon(x_0)}$ is compact, there exists a sequence of times $t_n \to \infty$ such that $\phi(t_n, x) \to \bar{x}$. We must show that $\bar{x} = x_0$. If $\bar{x} \neq x_0$, there exists a $\delta > 0$ such that $\bar{x} \notin B_\delta(x_0)$. As before, there exists an open set $\tilde{U} \subset B_\delta(x_0)$ such that trajectories starting on U can not leave U. Therefore, the sequence $\phi(t_n, x)$ is eventually outside $B_\delta(x_0)$. Moreover, we can assume that $\phi(t_n, x)$ do not enter $B_\delta(x_0)$. Then there is an $\alpha > 0$ such that $\dot{V} \leq -\alpha$ for all $x \in U \setminus \tilde{U}$. Since $\phi(t_n, x)$ does not enter $\tilde{U}$ we can apply this estimate to such (t_n, x) so that

$$V(\phi(t_n, x)) - V(x) = \int_0^{t_n} \dot{V}(\phi(s, x))dt$$
$$\leq -\alpha t_n.$$

Hence, for sufficiently large n, $V(\phi(t_n, x)) \leq V(x) - \alpha t_n \leq 0$, which contradicts the definition of V.

Finally we consider the case $\dot{V} > 0$. Here we follow the proof of [Kha92][2] Let M be the maximum of V on $\overline{B_\varepsilon(x_0)}$. Take any $\delta > 0$, $x \in B_\delta(x_0) \setminus \{x_0\}$ and $a := V(x)$. Since $\dot{V} > 0$, V is strictly increasing on trajectories and so $V(\phi(t, x)) \geq a$ for all $t \geq 0$. By the positive definiteness of $\dot{V}$ and the compatness of $\{x \in \overline{B_\varepsilon(x_0)}, \ V(x) \geq a\}$,

$$m := \inf\{\dot{V}(x)|x \in \overline{B_\varepsilon(x_0)}, \ V(x) \geq a\} > 0.$$

Then, $V(\phi(t, x) - V(x)) \geq mt$ for all $t \geq 0$, so for a sufficiently large t, $V(\phi(t, x)) > M$, this is, $\phi(t, x)$ leaves $B_\varepsilon(x_0)$ and hence x_0 is . $\qquad \square$

Example 4. Consider the system of Example (3). Let $V(x, y, z) = \frac{1}{2}(x^2 + y^2 + z^2)$. This is clearly a Lyapunov function for the system at the origin. Computing the orbital derivative of V we get,

$$\begin{aligned}
\dot{V}(x, y, z) &= -xy - x^2y^2 + xz^2 - x^4 + xy + yz^3 - y^4 - xz^2 - x^2z^2 - yz^3 - z^6 \\
&= -x^4 - 2x^2y^2 - y^4 - z^6 < 0
\end{aligned}$$

for every $(x, y, z) \neq (0, 0, 0)$. Then, the origin is an asymptotically stable equilibrium point.

2.1.2 Some considerations about two dimensional systems

There exists some strong results concerning two dimensional systems wich are useful in order to study the asymptotic behaviour of solutions, the existence of periodic orbits, clasification of α/ω-limit sets and so on. First of all, let give some definitions. In what follows E is an open subset of $\mathbb{R}^n$ as before.

Definition 6. Let $x \in E$ and $\phi(\cdot, x)$ be a solution of the system (2.1). A point $p \in E$ is called ω-*limit point* of the solution if there exists a sequence $(t_n)_n \subset \mathbb{R}$ such that

$$\lim_{n \to \infty} \phi(t_n, x) = p.$$

In case we have a point q with a similar property but with $n \to -\infty$, it is called α-*limit point*. The set of α-limit (resp. ω-limit) points is called the α-limit (resp ω-limit) set.

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[2]This is just because the proof of [Kha92] illustrates in a clearer way the need of compactness of $\overline{B_\varepsilon(x_0)}$

Remark 2. By $\omega(p)$ we mean the ω-limit set of the solution curve passing through p wich by uniqueness, is equivalent to the ω-limit of p.

Definition 7. A subset $M \subset E$ is called *positively invatiant* under the vector field f if given a point $x \in M$, $\phi_t(x) \in M$ for all $t \geq 0$.

The following theorems hold for $n = 2$ and their proof can be found in [Wig03] or [Kha92].

Theorem 5 (Bendixson-Dulac Criterion). *Let* $B \in C^1(E, \mathbb{R})$ *and assume that E is simply connected. If $\nabla \cdot Bf$ is not identically zero and does not change in sign, then (2.1) does not have closed periodic solution curves lying in E.*

Theorem 6 (Poincaré-Bedixson Theorem). *If M is a positively invariant set containing a finite number of equilibrium points of (2.1), the one of the following is true,*

- $\omega(p)$ *is an equilibrium point.*

- $\omega(p)$ *is a closed periodic curve.*

- $\omega(p)$ *consists of a finite set of equilibrium points S, and finite number of closed curves with their α/ω-limits in S.*

2.2 Epidemic Models

2.2.1 Basic features of SIR model

The epidemic models we are going to deal with belong to the class of compartmental models. This approach is mainly due to A.G. McKendrick and W.O. Kermack in the beginning of 1900's [BCC12]. The idea behind these kind of models is to divide the affected population in groups of similar features or *stages* of illness, and model the dynamic between the groups by time dependent ordinary differential equations.

The simplest epidemic model is the *Kermack-McKendrick* model which divides the population in three compartments, the susceptible (S), the infected (I) and the recovered (R). We explain here the basic properties and
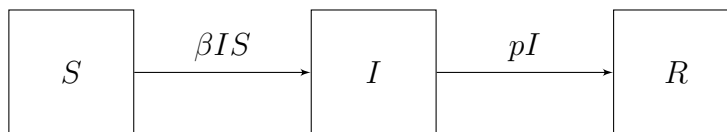
Figure 2.7: SIR diagram

important quantities associated to this model.

A schematic figure of the SIR model is shown in figure (2.7)
From this diagram we get the following system of equations,

$$\frac{dS}{dt} = -\beta IS$$
$$\frac{dI}{dt} = \beta IS - pI$$
$$\frac{dR}{dt} = pI.$$

Here, β and p are positive constants representing the infection rate, and the removal or recovery rate respectively. Note that from these we derive a first obvious assumption of the model which is that it considers immunity to re-infection. The other assumption which is clear from the equations is that the total population remains constant. This is usually explained by the fact that the time scale of the study of the disease is usually faster than the time scale of births and deaths so population dynamics might be ignored [BCC12]. Now let us analyze this equations in some more detail.

Note that I is decreasing if $S < p/\beta$ (and increasing if we have the other inequality), but since $\dot{S} < 0$, S is always decrasing from an initial amount $S_0 = S(0)$. Thus, if $S_0 < p/\beta$, the infective compartment disappear eventually, and in the other case, it increases to a maximum value when S approach the value p/β or equivalently when $\beta S_0/p$ reaches the value 1. Therefore, $R_0 := \beta S_0/p$ is a *threshold value* for the system in the sense that if $R_0 < 1$ the epidemic will disappear, while if $R_0 > 1$ there will be an epidemic. The case $R_0 = 1$ is inconclusive and requires more considerations depending on the problem. R_0 is known as the *basic reproduction number* becasue it measures the number of secondary infections caused by a single infective.

16

Now, since the population remains constant, we can reduce the system to a two dimensional system by dropping the equation for R. For, in case I or S depend on R we just replace every occurrence of it by $N - S - I$ where N is the total population. The resulting system is

$$\frac{dS}{dt} = -\beta I S$$

$$\frac{dI}{dt} = \beta I S - p I.$$

This consideration makes easier to identify the solution curves, but more generally, it allows us to use Poincaré-Bendixson-Dulac theory in order to study the asymptotic behavior of the solutions. As a way to know at least where the solution curves lie, we divide the two equations above and we obtain

$$\frac{\dot{I}}{\dot{S}} = \frac{dI}{dS} = \frac{\beta S I - p I}{-\beta S I} = -1 + \frac{p}{\beta S}.$$

So we get an ordinary separable equation with solution,

$$I(S) = -S + \frac{p}{\beta} \ln(S) + c,$$

and then $I + S - \frac{p}{\beta} \ln(S)$ is constant for solutions of the system. Then the solution curves lie on contour lines of the function

$$V(S, I) = I + S - \frac{p}{\beta} \ln(S).$$

2.2.2   Qualitative Analysis

We first compute the *isoclines* of the system (the the resulting curves taking one of the equations equal to 0) and we get that if $dS/dt = 0$ then the isoclines are the S and I axis. If $dI/dt = 0$ we get again the S axis and the line $S = p/\beta$. Taking the intersection of these isoclines we get the line of disease free equilibria $I = 0$.

Now we take $f(S, I) = [-\beta I S \ \beta I S - p I]^t$. With $B \equiv 1$ we have that

$$\nabla \cdot B f = \beta(s - i) - p$$

which is larger than 0 iff $I < S - p/\beta$. Thus, in order to apply Bendixson-Dulac Criterion we need that $D = \{(S, I) |\ S \geq 0,\ I \geq 0,\ S + I \leq N\}$ does not intersect the line $I = S - p/\beta$, but this is equivalent to say that $p/\beta > N$ or $\beta N/p < 1$ and in this case $R_0 < 1$. Altogether, if $R_0 < 1$ Bendixson-Dulac Criterion implies that there are no periodic solutions.

Chapter 3

A SIR model for coca crops in Colombia

Illicit crops in Colombia and more specifically coca crops have shown a geographical behaviour similar to the outbreak of an infectious disease in a population. There are some territories with social, political and economical features which are determinant in their vulnerability to the emergence of coca crops. Moreover, there exists certain propagation phenomena which allows us to think that there is a form of *contagion*. In [RG11] this phenomena is denoted by *efecto globo o balón*, a term used in the 90's to describe the migration of coca crops form Perú and Bolivia, to Colombia. In the same book, Rocha García shows some data concerning the space dynamics of coca crops and deduce that there is a mixture of coalescence and fragmentation in Colombia. He talks about coca *clusters* that rather than being static, have the ability to move, even to quite distant places. During the 90's, for example, there were 4 big reported clusters in Guaviare, Caquetá, Putumayo and Bolívar. Almost twenty years later in 2009, there were coca crops in 23 of the 32 departments of Colombia, with some similarities in the distribution of the old ones, but with a big reduction in departments like Putumayo, Caquetá and Meta followed by the rise of new clusters in the west side of the country.

These economic information has suggested us that there is a possibility to model the problem of coca crops in Colombia as an epidemic, and use all the machinery of ODE modelling in order to make predictions and find quantitative evidence of what strategies could be more effective in reducing the hectares of coca crops.
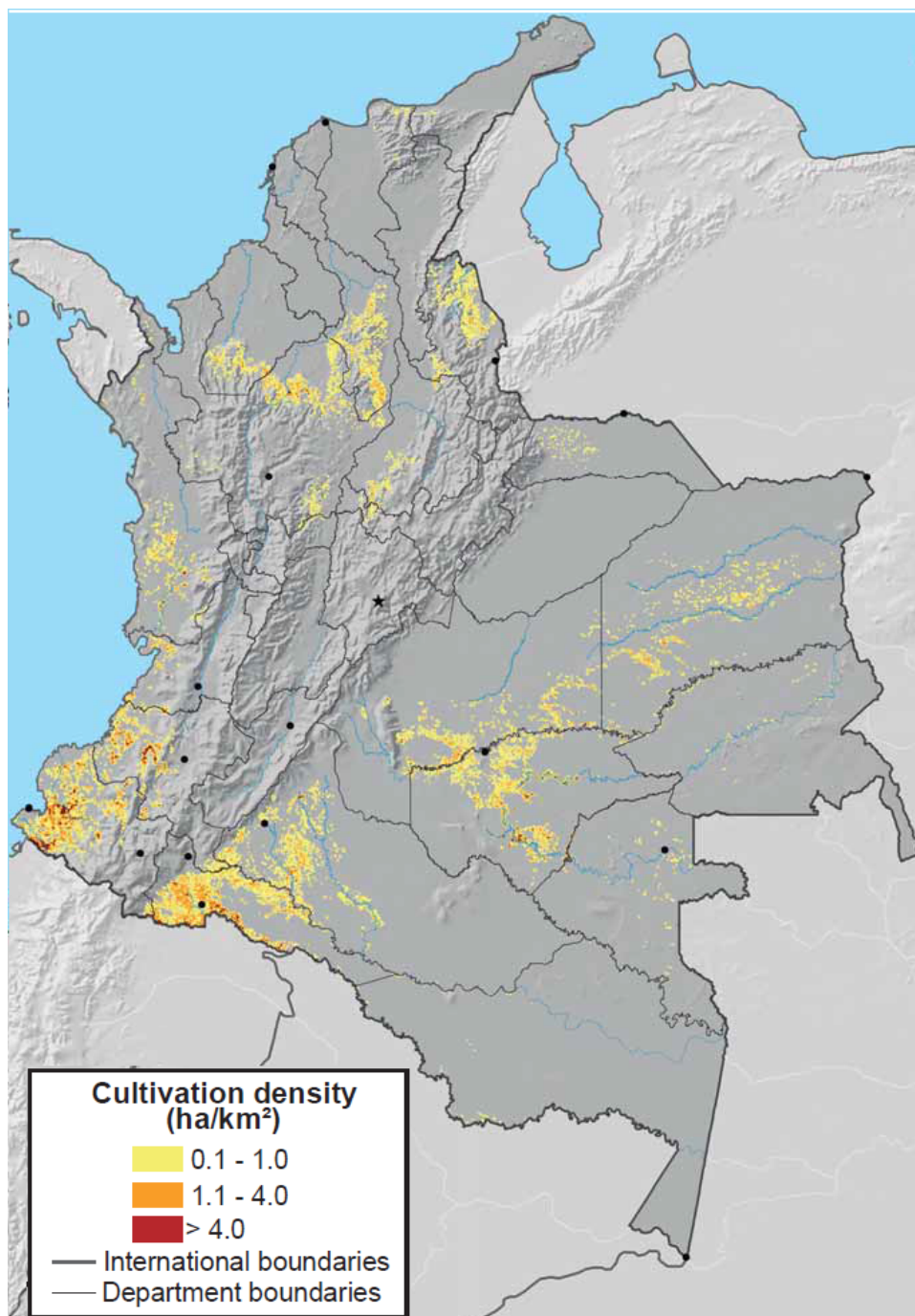
Figure 3.1: Coca Cultivation Density in Colombia in 2011. Source: UNODC, 2011

3.1 SIR model and some preliminary comments

We present here a SIR-type model for coca crops in Colombia where the population is composed by territorial divisions. Our model differs from the classic SIR on the fact of reinfection. However, this occurs with a different rate and that is why we do not use a SIS model. The SIRS is a model that allows reinfection, but only by transfer of recoverder individuals into the susceptible compartment. Based on the data of [UNO] we decided that this model will not be so appropiate because here, a recovered territory shows even more vulnerability to return into the infective compartment, see Figure(**??**). We have also based on the work of [WC07] and [MS09] A diagram of the dynamics is shown in Figure 3.3.

In equations,

$$
\begin{aligned}
\frac{dS}{dt} &= -\beta_1 \frac{I}{N} S \\
\frac{dI}{dt} &= \beta_2 \frac{I}{N} S + \beta_2 \frac{I}{N} R - pI \\
\frac{dR}{dt} &= pI - \beta_2 \frac{I}{N} R.
\end{aligned}
$$

The constants and the assumptions of the model are the following:

- Here, S, I and R are not individuals but can be departments municipalities, or any division of the territory. In our case we will use division by departments.

- β_1 is the probability that a department become infected after *contact* with a infectious one. Here *contact* means presence of new croppers coming eventually from other departments they may have been forced to leave as in the *efecto globo* mentioned in [RG11], or new croppers from the same department searching for new opportunities influenced by the evidence of better profitability of coca cultivation.

- β_2 is the probability of emergence of coca crops in a department which had become free of crops.
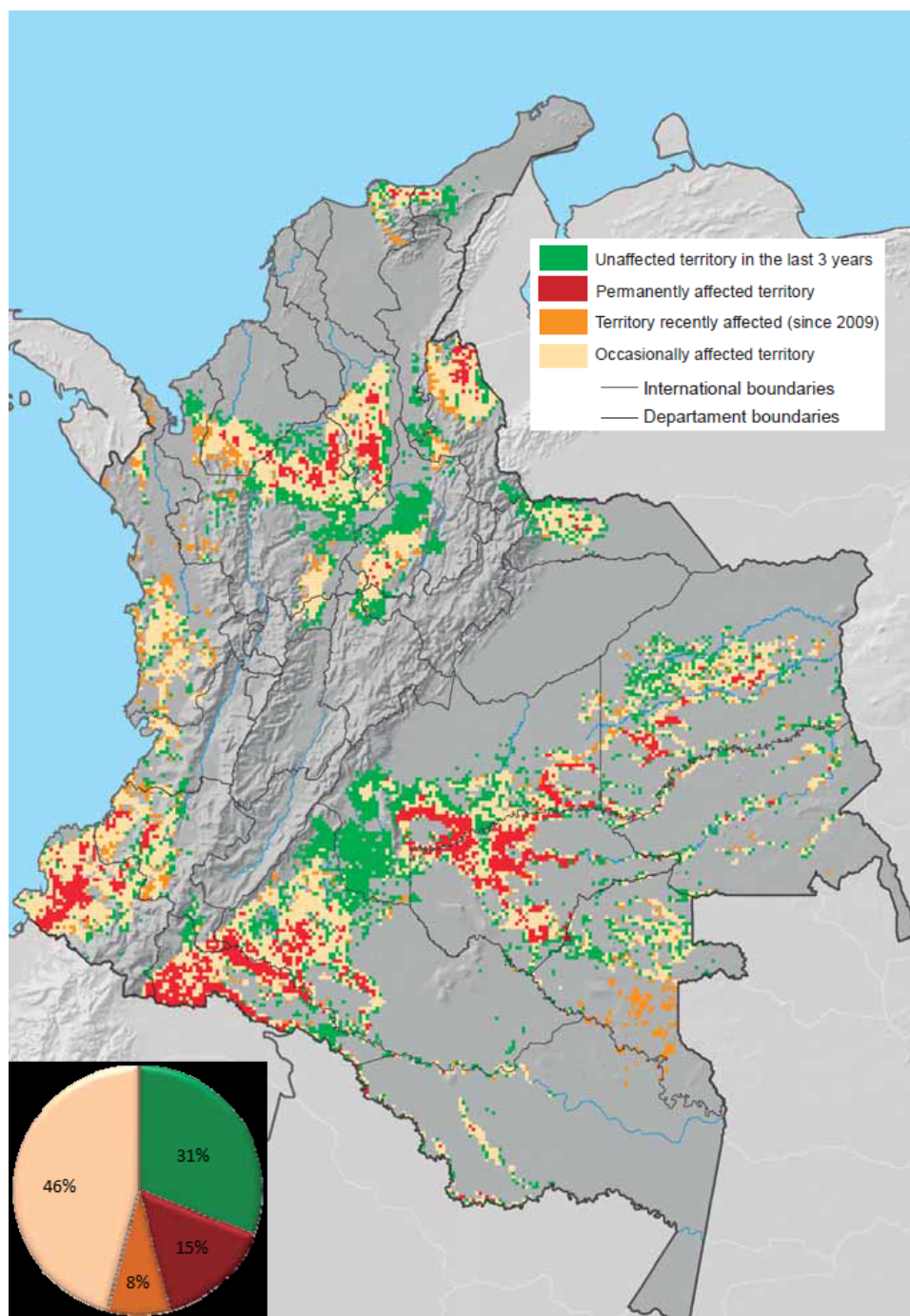
Figure 3.2: Regional stability of coca cultivation in Colombia, 2001 - 2011.
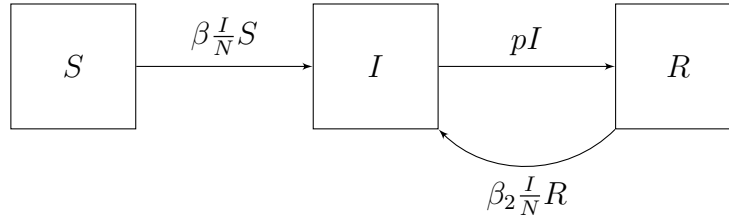Source: UNODC, 2011

Figure 3.3: Model diagram

- p is the removal rate, in this case due to manual eradication, aerial spraying or volunteer desertion.

- The population remains constant. This is quite obvious since no department will disappear.

- There exists homogeneous mixing. This comes from social and quantitative studies and specifically the work of [RG11]. Coca croppers from Guaviare, for example, are disposed to go to Norte de Santander if the conditions force them to do so. Moreover, although Orinoquía and Amazonía which are supposed to be non-suitable places to cultivate, there are in fact crops there. In [RG11] Rocha García describes som aspects of this space dynamics, se Figure 3.4.

3.2 Qualitative analysis of the model

3.2.1 First approach to identify solution curves

Here we use a very simple idea to find a surface whose contour line are solution curves of the system. This approach does not work in order to study stability but at least give some clues about the behavior of solution curves.

We first use a common simplification of the model using the fact that the population is constant and so $R = N - S - I$. Therefore, the resulting two dimensional system is,
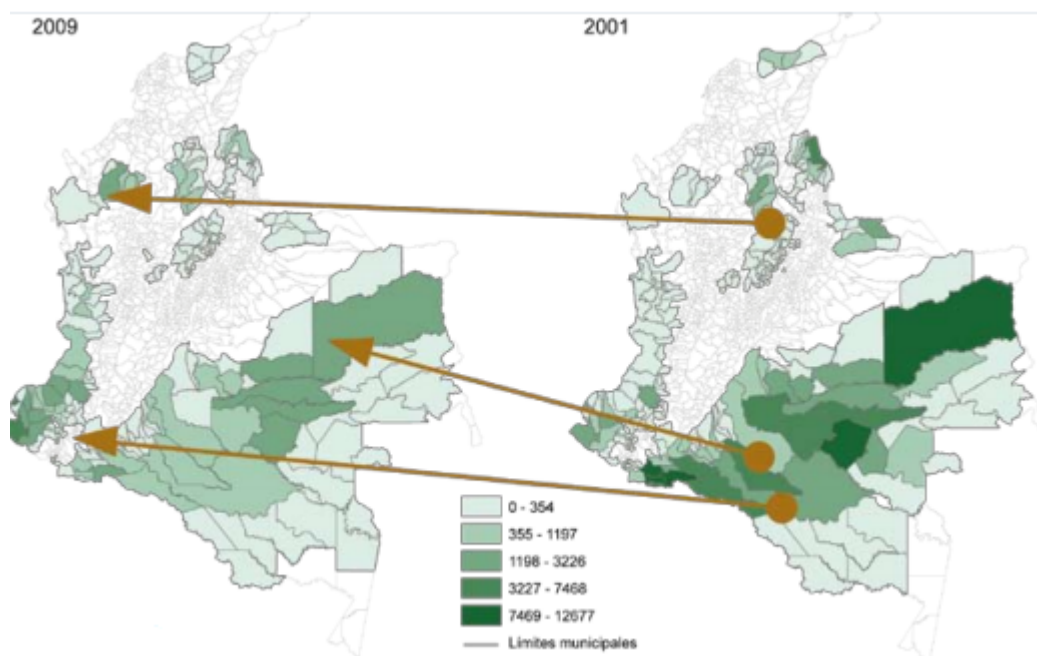
Figure 3.4: Changes in the cultivation area in 2001 - 2009. Source: [RG11]

$$\frac{dS}{dt} = -\beta_1 \frac{I}{N} S \tag{3.1}$$

$$\frac{dI}{dt} = \beta_1 \frac{I}{N} S + \beta_2 I - \beta_2 \frac{I}{N} S - \beta_2 \frac{I^2}{N} - pI. \tag{3.2}$$

The idea is the same we have used to find solution curves of the classic SIR model. In order to obtain the desired contours we divide the equation for I by the equation of S in order to get a single ODE,

$$\frac{dI}{dS} = \frac{(\beta_1 - \beta_2)IS + (\beta_2 - p)IN - \beta_2 I^2}{-\beta_1 IS}$$

$$= -1 + \frac{\beta_2}{\beta_1} + \left(\frac{p - \beta_2}{\beta_2}\right) N \frac{1}{S} + \frac{\beta_2}{\beta_1 S} I.$$

So we obtain a linear ODE. An integrating factor for this equation is

$$e^{\frac{-\beta_2}{\beta_1} \int \frac{dS}{S}} = S^{-\beta_2/\beta_1}.$$

Let us call $\alpha := \beta_2/\beta_1$. Therefore,

$$\left(IS^{-\alpha}\right)' = (\alpha - 1)S^\alpha + \left(\frac{p - \beta_2}{\beta_1}\right) NS^{-\alpha-1}$$

$$\Rightarrow IS^{-\alpha} = \frac{(\alpha - 1)S^{-\alpha}}{-\alpha + 1} + \left(\frac{p - \beta_2}{\beta_1}\right) N \frac{S^{-\alpha}}{-\alpha} + C$$

$$= -S^{1-\alpha} + \left(\frac{\beta_2 - p}{\alpha p}\right) NS^{-\alpha} + C$$

$$\Rightarrow I = -S + \left(\frac{\beta_2 - p}{\beta_2}\right) N + CS^{\beta_2/\beta_1}.$$

So the solution curves lie in contour lines of the form

$$I + S - \left(\frac{\beta_2 - p}{\beta_2}\right) N = CS^{\beta_2/\beta_1}.$$

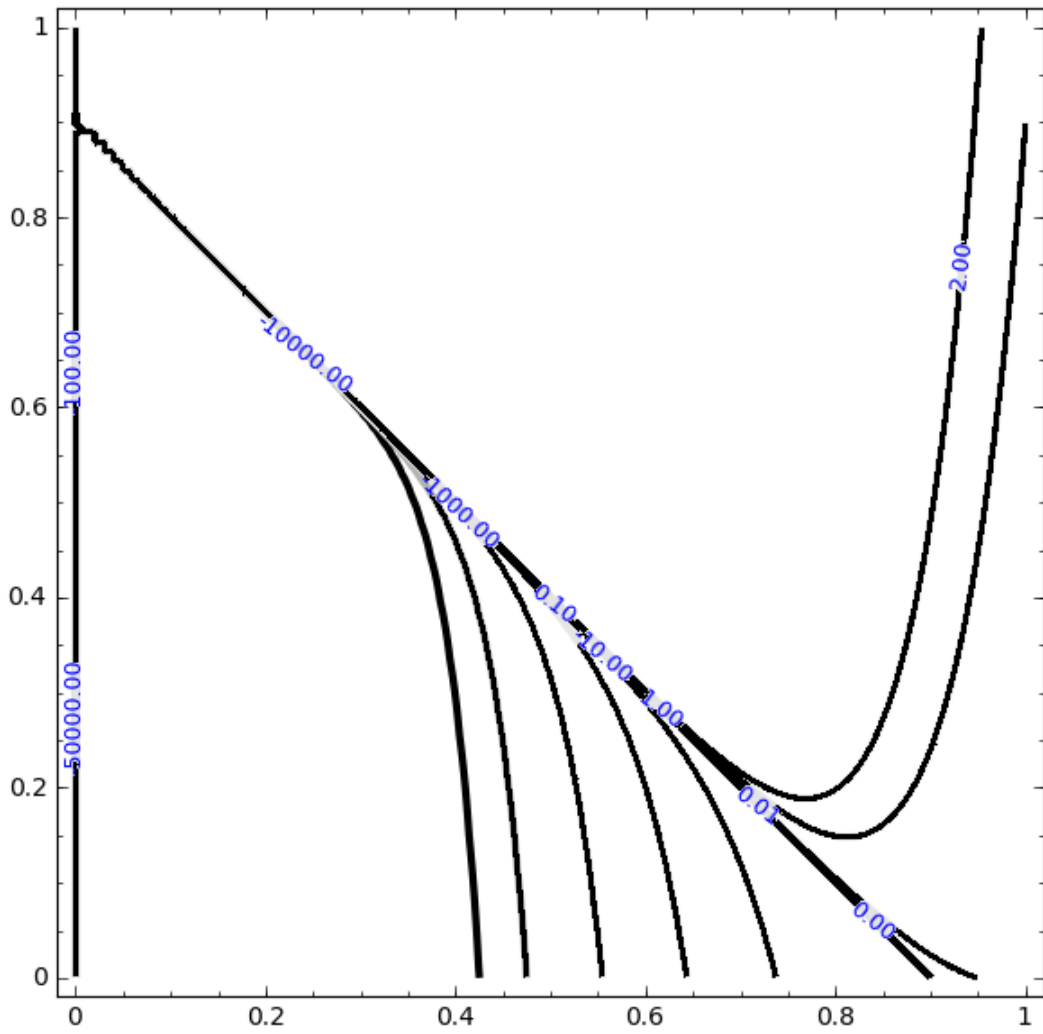Figure 3.5: Some of the trayectories obtained by dividing the equations

26

3.2.2   Equilibria and linear stability

Now we use the tools of the theory of ODE modelling to study the qualitative structure of the model and we demonstrate the global asymptotic stability of the endemic equilibrium.

We first make a usual change of variables

$$s = \frac{S}{N}, \ i = \frac{I}{N}, \ r = \frac{R}{N}$$

in order to work with proportions instead of quantities and avoid the dependence on N. The resulting system is the following

$$\dot{s} = -\beta_1 i s$$
$$\dot{i} = \beta_1 i s + \beta_2 i r - p i$$
$$\dot{r} = p i - \beta_2 i r,$$

and taking into account that $s + i + r = 1$ we reduce the system to

$$\dot{s} = -\beta_1 i s \tag{3.3}$$
$$\dot{i} = (\beta_2 - p)i + (\beta_1 - \beta_2)is - \beta_2 i^2. \tag{3.4}$$

From this we get the following isoclines:

- $s' = 0 \Rightarrow i = 0$ or $s = 0$. So the s and i axis are isoclines.

- $i' = 0 \Rightarrow i(\beta2 - p + (\beta_1 - \beta_2)s - \beta_2 i) = 0 \Rightarrow i = 0$ or
  $i = \dfrac{\beta_2 - p}{\beta_2} + (\dfrac{\beta_1 - \beta_2}{\beta_2})$.

Taking the intersection of them we get the following equilibrium points:

- The s axis, or crop free line equilibria (CFE).

- The endemic equilibrium $\left(0, \frac{\beta_2 - p}{\beta_2}\right)$, provided $\beta_2 > p$

The linearisation matrix of the system is

$$
\begin{bmatrix}
-\beta_1 i & -\beta_1 s \\
(\beta_1 - \beta_2)i & \beta_2 - p + (\beta_1 - \beta_2)s - 2\beta_2 i
\end{bmatrix}.
$$

Then, the linearisation matrix at the CFE line is

$$
J(s,0) = \begin{bmatrix}
0 & -\beta_1 s \\
0 & \beta_2 - p + (\beta_1 - \beta_2)s
\end{bmatrix},
$$

from what we get that the eigenvalues are $\lambda_1 = 0$ and $\lambda_2 = \beta_2 - p + (\beta_1 - \beta_2)s$. For the sign of λ_2 we have two cases:

- Case 1: $\beta_2 > \beta_1$. Here, $\lambda_2 > 0$ iff $s < \dfrac{\beta_2 - p}{\beta_2 - \beta_1}$, and this point belongs to our region of interest iff $\beta_1 < p < \beta_2$

- Case 2: $\beta_1 > \beta_2$. Here, $\lambda_2 > 0$ iff $s > \dfrac{\beta_2 - p}{\beta_2 - \beta_1}$, and this point belongs to our region of interest iff $\beta_2 < p < \beta_1$.

The linearisation matrix at the endemic equilibrium point is

$$
J\left(0, \frac{\beta_2 - p}{\beta_2}\right) = \begin{bmatrix}
-\beta_1 \dfrac{\beta_2 - p}{\beta_2} & 0 \\
\dfrac{(\beta_1 - \beta_2)(\beta_2 - p)}{\beta_2} & p - \beta_2
\end{bmatrix},
$$

so the endemic equilibrium is hyperbolic if $\beta_2 \neq p$ and by the by the Hartman-Grobman theorem, the linearized system would have the same quality structure as the nonlinear one. The eigenvalues are $-\beta_1 \frac{\beta_2 - p}{\beta_2}$ and $p - \beta_2$ which are both negative provided $\beta_2 - p > 0$ so the endemic equilibrium point is locally asymptotically stable. The i axis is a stable curve for the endemic equilibrium and it is in fact invariant because if $s = 0$, $s' = 0$, and if $i(0) \lessgtr \frac{\beta_2 - p}{\beta_2}$ then $i' \gtrless 0$. Now if we consider $s + i$, we get that

$$
s' + i' = i(\beta_2 - p - \beta_2(i + s)).
$$

Then $s' + i' \lessgtr 0$ if $i + s \gtrless \dfrac{\beta_2 - p}{\beta_2}$. Thus, the triangle formed by the positive axis and the line $s + i = \dfrac{\beta_2 - p}{\beta_2}$ is positively invariant.The line is also

28

invariant because there $s' + i' = 0$ and it is a joining curve of an unstable equilibrium point $\left(\dfrac{\beta_2 - p}{\beta_2}, 0 \right)$ and a stable one $\left(0, \dfrac{\beta_2 - p}{\beta_2} \right)$, so it is a *heterocline* curve.

Altogether, we have that the interior of the triangle is positively invariant so by the Poincaré-Bendixson theorem, the omega limit of any point is the endemic equilibrium or a periodic orbit.

3.2.3   A Lyapunov function for the system

We make use of a well known function [1] in order to construct Lyapunov functions for SIR models with non-linear incidence.

$$\tilde{V}(s, i) = s - \bar{s}\ln(s) + i - \bar{i}\ln(i),$$

where $(\bar{s}, \bar{i})$ is an equilibrium point. It is not hard to guess where does it come from when we remember the construction of a curve to identify the solution curves of the classic SIR model. The Lyapunov function will be

$$V(s, i) = s - \bar{s}\ln(s) + i - \bar{i}\ln(i) - \tilde{V}(\bar{s}, \bar{i}),$$

which is just the previous one minus the evaluation of itsef in the equilibrium in order to impose it the condition that $V(\bar{s}, \bar{i}) = 0$. With such a function we are going to show the instability of the crop-free equilibrium $(1, 0)$ and the asymptotic stability of the endemic equilibrium.

For the crop-free equilibrium the Lyapunov function is

$$V_{CFE}(s, i) = s + i - \ln(s) - 1.$$

Let us convince ourselves that it is a Lyapunov function:

- $V_{CFE}(1, 0) = 0$ and,

- $\dfrac{\partial V}{\partial i} = 1$, so the function is constant along lines paralel to the i axis.
  $\dfrac{\partial V}{\partial s} = 1 - \dfrac{1}{s} < 0$ since $0 < s \leq 1$, so the function is decreasing in the

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[1]This a commonly used function in mathematical Ecology and Epidemiology. For general Lyapunov function for these kind of models see [Kor06] or [KW02].

positive s direction. Now, for "small" $r > 0$, $V(r, 0) = r - \ln(r) > 0$ and $V(1, 0) = 0$. Thus, the function is indeed, postive in the desired region.

A graph of the contour lines of function V_{CFE} is shown in Figure 3.6.
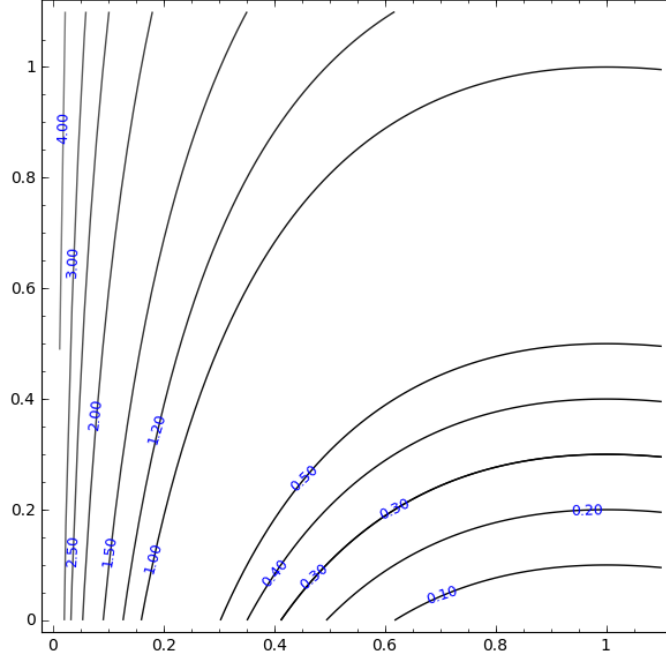
Figure 3.6: Contour lines of the Lyapunov function at the CFE equilibrium

Now, computing the derivative of V along solution curves we get,

$$\dot{V}(s, i) = \begin{bmatrix} 1 - \frac{1}{s} & 1 \end{bmatrix} \begin{bmatrix} -\beta_1 si \\ (\beta_2 - p)i + (\beta_1 - \beta_2)is - \beta_2 i^2 \end{bmatrix}$$
$$= -\beta_1 si + \beta_1 i + (\beta_2 - p)i + (\beta_1 - \beta_2)is - \beta_2 i^2$$
$$= (\beta_2 + \beta_1 - p)i - \beta_2 is - \beta_2 i^2,$$

which is positive if and only if

$$i + s < 1 + \frac{\beta_1 - p}{\beta_2},$$

and this actually holds for every feasible (s, i), provided $\beta_1 > p$. Here the word $feasible$ means $s \leq 0$, $i \leq 0$ and $i + s \leq 1$. Therefore, by theorem 4

30

$(1, 0)$ is an unstable equilibrium point.

For the endemic equilibrium point, the appropiate Lyapunov function is

$$V_{END}(s, i) = i + s - \frac{\beta_2 - p}{\beta_2} \ln(i) - \frac{\beta_2 - p}{\beta_2} + \frac{\beta_2 - p}{\beta_2} \ln \left(\frac{\beta_2 - p}{\beta_2} \right).$$

A graph of the contour lines of function V_{CFE} is shown in Figure 3.7.
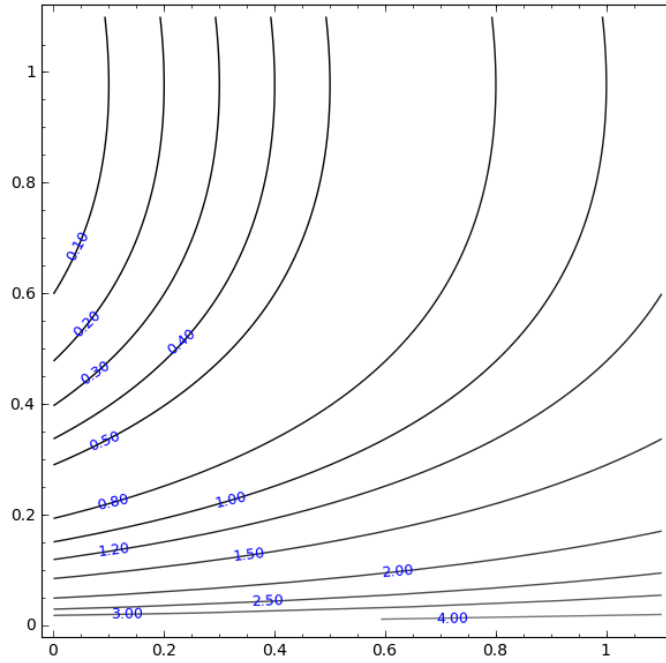
Figure 3.7: Contour lines of the Lyapunov function at the endemic equilibrium

Again, since $\ln(i) < 0$ for $i \in (0, 1]$ the function is positive in the region of interest. Computing the derivative along solution curves we get,

$$\dot{V}(s, i) = \begin{bmatrix} 1 & 1 - \frac{\beta_2 - p}{\beta_2 i} \end{bmatrix} \begin{bmatrix} -\beta_1 s i \\ (\beta_2 - p)i + (\beta_1 - \beta_2)is - \beta_2 i^2 \end{bmatrix}$$
$$= -\frac{(\beta_2 - p)^2}{\beta_2} + 2(\beta_2 - p)i + \frac{(\beta_2 - p)(\beta_2 - \beta_1)}{\beta_2}s - \beta_2 is - \beta_2 i^2.$$

31

We want to proof that this is negative. To do so, we will show that the maximum is negative.

First, we look for local maxima inside the feasible region.

$$\nabla \dot{V}(s,i) = \begin{bmatrix} \frac{(\beta_2-p)(\beta_2-\beta_1)}{\beta_2} - \beta_2 i \\ 2(\beta_2-p) - \beta_2 s - 2\beta_2 i \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \end{bmatrix}$$

$$\Longleftrightarrow i = \frac{(\beta_2-p)(\beta_2-\beta_1)}{\beta_2^2} \ , \qquad s = \frac{2\beta_1(\beta_2-p)}{\beta_2^2},$$

and since,

$$s + i = \frac{(\beta_2-p)(\beta_1+\beta_2)}{\beta_2^2}$$

$$= \left(1 - \frac{p}{\beta_2}\right)\left(1 + \frac{\beta_1}{\beta_2}\right),$$

which is larger than 1 provided $\frac{\beta_2}{p} > 1$. Thus, there are no extremal values in the feasible region. For the boundary we restrict the function for each of the three parts [2].

- $s = 0 : \Rightarrow \dot{V}(0,i) = \frac{(\beta_2-p)^2}{\beta_2} + 2(\beta_2-p)i - \beta_2 i^2$, which is cuadratic in i and attains a maximum at $\frac{\beta_2-p}{\beta_2}$ with value 0. But note that the point $(0, \frac{\beta_2-p}{\beta_2})$ is exactly the equilibrium point.

- $i = 0 : \Rightarrow \dot{V}(s,0) = -\frac{(\beta_2-p)^2}{\beta_2} + \frac{(\beta_2-p)(\beta_2-\beta_1)}{\beta_2}s$ which is linear in s with positive slope so it attains a maximum in $s = 1$ with value $\frac{(\beta_2-p)(p-\beta_1)}{\beta_2}$, which is negative provided the same condition as before, $\frac{\beta_2}{p} > 1$.

- $s + i = 1 :$

$$\dot{V}(s,i) = -\frac{(\beta_2-p)^2}{\beta_2} + 2(\beta_2-p)i + \frac{(\beta_2-p)(\beta_2-\beta_1)}{\beta_2}(1-i)$$

$$- \beta_2 i(1-i) - \beta_2 i^2$$

$$= -\frac{(\beta_2-p)(\beta_1-p)}{\beta_2} + \frac{\beta_2\beta_1 - \beta_2 p - \beta_1 p}{\beta_2}i.$$

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[2]We decided to do it by hand because it is easy and we make zero the probability of numerical noise.

Note that the slope of this line is $\beta_1 - p(1 + \beta_1/\beta 2)$ which is positive if $\frac{\beta_1}{p} > 1 + \frac{\beta_1}{\beta_2}$. In this case, it attains a maximum at $i = 1$ with value $\frac{-p^2}{\beta_2} < 0$!

Finally, we have shown that $\dot{V}(s, i) < 0$ for all feasible (s, i) except the equilibrium point. Then, the endemic equilibrium $(0, \frac{\beta_2 - p}{\beta_2})$ is globally asymptotically stable.

Chapter 4

Conclusions and further investigation

4.1 Conclusions

We have proposed an epidemic SIR model for coca cultivation in Colombia. It differs from the classical SIR model in the reinfection term. A justification to propose such a model is based on social and technical studies we found in [RG11] and [UNO]. In the former, Rocha García use terms like coalescence, fragmentation and contagion, to describe the space dynamics of coca crops. He talks about coca *clusters* that have the ability to move to even far places when conditions are adverse. We found out that, as a system of ordinary differential equations, the model has two equilibrium points, a crop free equilibrium, when there are no department with coca crops, and an endemic equilibrium, which is basically the current situation in Colombia, with the majority of the departments with coca crops. A Lyapunov function has been constructed to show that the former is an unstable equilibrium and the latter is globally asymptotically stable. This means that, according to the model, the current dynamic of coca crops shows a trend towards the endemic equilibrium with any initial conditions. It is also worth to emphasise a characteristic of this model that is possibly the reason for the existence of such a *strong* endemic equilibrium, and is the value of β_2 which is so larger than the other parameters. This tells us that, different from almost any other infection where partial recovery means partial immunity, here the probability of reinfection is so much larger to even the probability of become infected

for the firs time. Mathematically speaking, this tells also that the parameter worthy of been reduced is β_2.

We have not given so much importance to the basic reproduction number R_0, which in this case is $\frac{\beta_1}{p}$, because it is a threshold value that tells us whether there is going to exist an epidemic or not. In our case $R_0 > 1$. Since the situation in Colombia is already in an endemic state, we thought that it was more important to analyse the endemic equilibrium in the sense that we already know the situation at the beginning with the growth of coca crops during the 80's and 90's [RG11], [UNO].

4.2 Further investigation

This is a first attempt to model coca crops via mathematical epidemiology and several things to do are proposed for future work. One of them is to implement a stochastic component to the model including the information of coca crops per municipalities instead of departments. Moreover, a more precise model would partition the territory in cells rather than political boundaries. Such a model could also implement a stochastic variable to each cell that measures its vulnerability to the existence of coca crops, based on Rocha's analysis of the coalescence-fragmentation intensity and his table of space correlation of certain variables like area of coca crops, vulnerability, environmental conflict in the use of water and ground, and roads density [RG11] (Anexo A: Análisis espacial de la coca).

It will be also interesting to combine the model with an SIRS model, additioning a rate of transfer of individuals from the recovered compartment into de susceptible one. Moreover, since there exists a new policy of territorial consolidation, it will be appropiate to try a vaccination model if this policy show positive results in the protection of the recovered territories.

Chapter 5

Appendices

5.1 Bifurcation at $\beta_2 = p$

In Figure (5.1) we show a bifurcation diagram to illustrate the changes in the stability of the endemic equilibrium depending on β_2.

5.2 Calculation of the constants β_1, β_2, and p

In order to compute the constants of the model we use data from the *Coca Cultivation Survey* implemented by the UNODC (United Nations Office on Drugs and Crime) and some standard technics of regression. It is important to take into account that these official and technical data exist since 2002 which was the first year when satellite photographs were taken in order to estimate the area of coca crops, by the SIMCI (Sistema Integrado de Monitoreo de Cultivos Ilícitos). The number of hectares in each department from 2002 to 2011 is shown in Table 5.2. In order to compute de desired constants, we first count the number of territories in each compartment per year. With these data we construct three rows with the information of migration from one compartment to another, this is, one for S to$I$, one for I to R and one for R to I. Then we construct two rows: in one row we write on each entry, the value # of susceptibles times # of infected/total number of territories. In the other one, we put # of susceptibles times # of recovered/total number of territories. With the former row and the row corresponding to the migration from S to I we compute the coefficient of the linear regression,
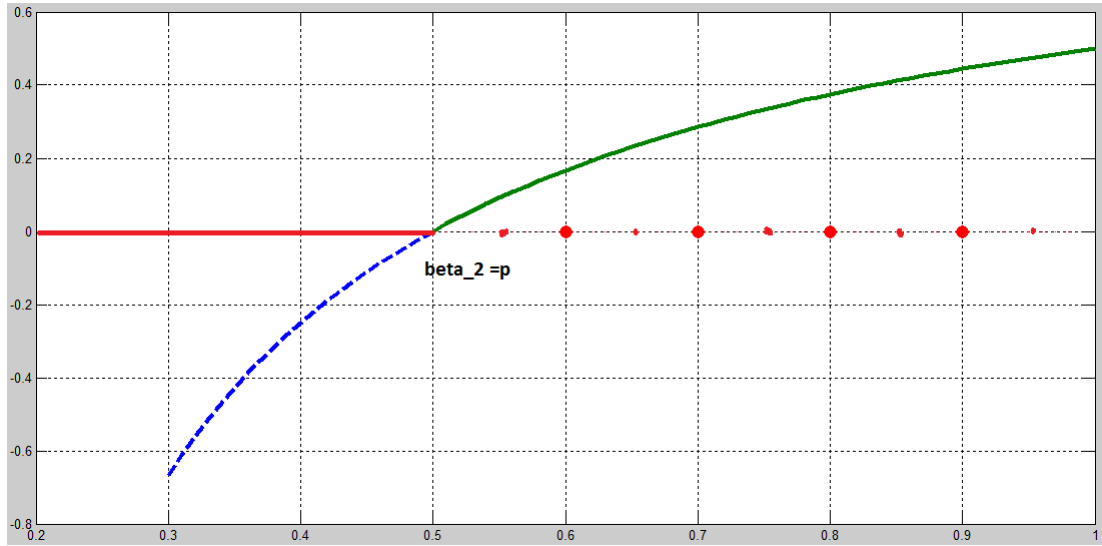
Figure 5.1: Bifurcation diagram. The vertical axis corresponds to the endemic equilibrium and the horizontal one corresponds to β_2.

and we repeat the same for the latter row and the row concerning migrations from R to I. This procedure gives us the coefficients β_1 and β_2 respectively. For p we compute the linear regression between the row I to R and the row with the number of infectives (since this value depends only on the number of infectives).

With this procedure, we derive the constants of the model, $\beta_1 = 0.036$, $\beta_2 = 0.693$ and $p = 0.014$.

Figure 5.2: Evolution of model vs. reality

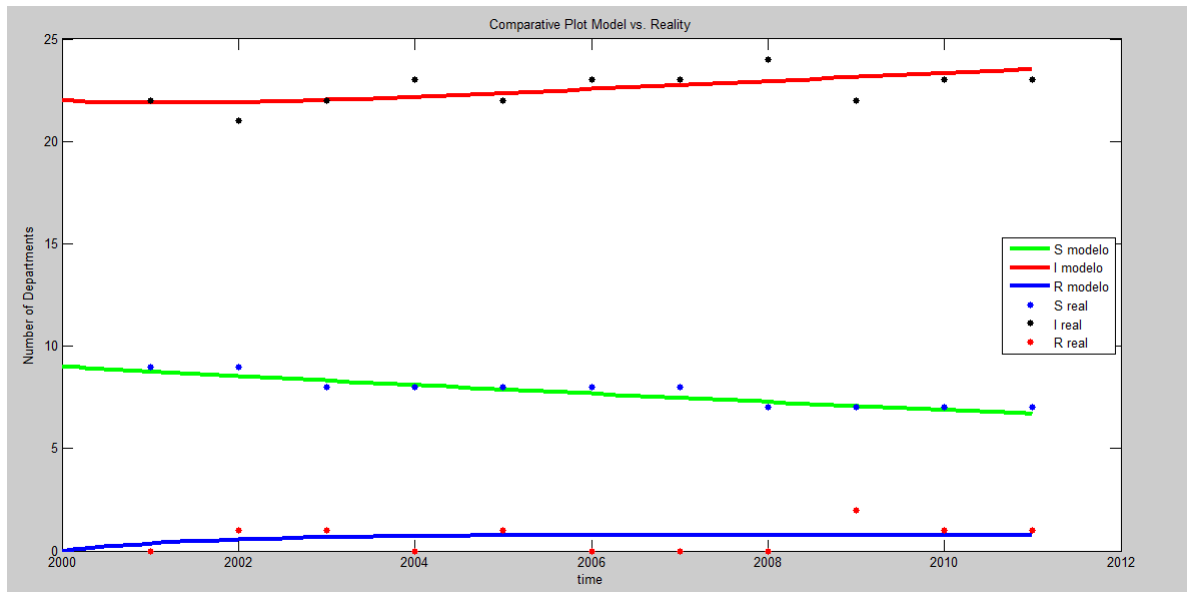| Departamento	Área	2001	2002	2003	2004	2005
Nariño	33268	7494	15131	17628	14154	13875
Guaviare	53460	25553	27381	16163	9769	8658
Cauca	29308	3139	2120	1443	1266	2705
Putumayo	24885	47120	13725	7559	4386	8963
Antioquia	63612	3171	3030	4273	5168	6414
Córdoba	25020	652	385	838	1536	3136
Chocó	46530	354	0	453	323	1025
Meta	85635	11425	9222	12814	18740	17305
Bolívar	25978	4824	2735	4470	3402	3670
Vichada	100242	9166	4910	3818	4692	7826
Caquetá	88965	14516	8412	7230	6500	4988
Norte de Santander	21658	9145	8041	4471	3055	844
Vaupés	54135	1918	1485	1157	1084	671
Valle del Cauca	22140	184	111	37	45	28
Santander	30537	415	463	632	1124	981
Guainía	72238	1318	749	726	721	752
Amazonas	109665	532	784	625	783	897
Arauca	23818	2749	2214	539	1552	1883
La Guajira	20848	385	354	275	556	329
Magdalena	23188	480	644	484	706	213
Boyacá	23189	245	118	594	359	342
Caldas	7888	0	0	54	358	189
Cundinamarca	24210	22	57	57	71	56
Cesar	22925	0	0	0	0	0
Atlántico	3388	0	0	0	0	0
Sucre	10670	0	0	0	0	0
Risaralda	4140	0	0	0	0	0
Quindío	1845	0	0	0	0	0
Tolima	23562	0	0	0	0	0
Huila	19890	0	0	0	0	0
Casanare	44640	0	0	0	0	0

Departament	2006	2007	2008	2009	2010	2011
Nariño	15606	20259	19612	17639	15951	17231
Guaviare	9477	9299	6629	8660	5701	6839
Cauca	2104	4168	5422	6597	5908	6066
Putumayo	12254	14813	9658	5633	4785	9951
Antioquia	6157	9926	6096	5096	5350	3104
Córdoba	1216	1858	1710	3113	3889	1088
Chocó	816	1080	2794	1789	3158	2511
Meta	11063	10386	5525	4469	3008	3004
Bolivar	2382	5632	5847	5346	3324	2207
Vichada	5523	7218	3174	3228	2743	2264
Caquetá	4967	6318	4303	3985	2578	3327
Norte de Santander	488	1946	2886	3037	1889	3490
Vaups	460	307	557	395	721	277
Valle del Cauca	281	453	2089	997	665	981
Santander	866	1325	1791	1066	673	595
Guaina	753	623	625	606	446	318
Amazonas	692	541	836	312	338	122
Arauca	1306	2116	447	430	247	132
La Guajira	166	87	160	182	134	16
Magdalena	271	278	391	169	121	46
Boyacá	441	79	197	204	105	93
Caldas	461	56	187	186	46	46
Cundinamarca	120	131	12	0	32	18
Cesar	0	0	5	0	0	0
Atlántico	0	0	0	0	0	0
Sucre	0	0	0	0	0	0
Risaralda	0	0	0	0	0	0
Quindo	0	0	0	0	0	0
Tolima	0	0	0	0	0	0
Huila	0	0	0	0	0	0
Casanare	0	0	0	0	0	0

Table 5.1: Number of infected hectares per department

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