

A Basic Backward Bifurcation Model in Epidemiology

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Abstract

The existence of a backward bifurcation has important consequences in the strategies and control policies designed to eradicate or control an infectious disease because the policies of public health when this phenomenon appears change from the classically adopted ones. The present work gives a characterization of a big family of models including a wide variety of the models present in the literature which show a backward bifurcation. In addition, it explains how the backward bifurcation can be generated and preserved or eliminated. We define what we call the basic backward bifurcation model, and show that it is contained in all the other models showing a backward bifurcation. We prove that the basic backward bifurcation model is robust under very general modifications of the system. The

general hypotheses we consider are: compartmental models, constant total population, mass-action law type interactions, and susceptible individuals with at least two classes with different susceptibility levels.

Mathematics Subject Classification: 92B05

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1. Introduction

In recent years, theoretical epidemiology has called attention to the existence of multiple endemic equilibria and the necessary conditions for their existence. Some of the cases in the literature that show the existence of multiple endemic states are related to the backward bifurcation phenomena [10].

Backward bifurcations have been found, among others, in models for HIV/AIDS [7 and 19], tuberculosis [9], BRSV [8], influenza [20], dengue [6] and for Chlamydia trachomatis [18]. Backward bifurcations have also been shown due to social groups with different susceptibilities and nonlinear incidences [12],[22], and in metapopulation models where the phenomenon has been associated with relatively high impact of migration on local patch dynamics [11], and models with saturated treatment function [23].

The existence of a backward bifurcation has important consequences in the strategies and control policies designed to eradicate or control an infectious disease because the policies of public health when this phenomenon appears change from the classically adopted ones.

In models that show backward bifurcation, endemic equilibria exist even when the basic reproductive number for the disease is less than one. So, under some conditions on the parameters an epidemic brake out can occur, or an endemic equilibrium can persist even when the threshold parameter is less than one. Furthermore, as R_0 increases through the threshold, there could be a catastrophic increase in the disease incidence. In such case, the existence of a backward bifurcation can be catastrophic for the susceptible population, therefore it is necessary to understand under which hypothesis there exists a backward bifurcation and when and how it can be avoided.

Almost all models found in the literature [1, 2, 3, 4, 5, 12, 13, 14, 15, 16, 17, 21] displaying backward bifurcation have elements in common. Some natural questions arise:

Are there any features common to all these models? If a backward bifurcation appears, which conditions were satisfied in all of them? Is the topological structure of the interactions among classes as important as the parameter values? Which structural and numerical elements of the model can be changed preserving the backward bifurcation? For instance, if the dynamics between classes is delayed (in mathematical terms, we add extra equations to the model), can we still expect to obtain this phenomenon?

These questions arise from the necessity to understand what mathematical and epidemiological mechanisms generate or impede a backward bifurcation.

The present work gives a characterization of a family of models including almost all of the above mentioned, and explains how the backward bifurcation can be generated and preserved or eliminated. We define what we call the basic backward bifurcation model, and show that, in a way defined below; it is contained in all the other models showing a backward bifurcation. We prove that the basic model is robust under very general modifications of the system.

The basic model presented here does not cover all the possible epidemiological models, but it includes the majority of them. Only a few exceptions are left out, due to some very specific structures.

The general hypotheses we consider are: compartmental models, constant total population, mass-action law type interactions, and susceptible individuals with at least two different susceptibility levels.

Along this text, when we refer to a compartmental model, it means either the ordinary differential equations system associated to it or the model itself.

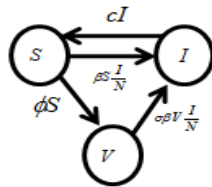
First, we define the basic backward bifurcation model. Then we show that it can be changed in a variety of ways that does not alter its basic topological structure, preserving the existence of multiple endemic states.

2. The Basic Backward Bifurcation Model (BBB-Model)

Let us consider a SIS model for a disease in a constant size closed population with homogeneous mixing, and new infections described in terms of the mass-action law. We also assume a class of individuals with a reduced susceptibility. The choice of a SIS disease framework includes most of the modeling efforts in theoretical epidemiology and we later extend it to include more general cases.

By assuming a constant population size, N , we get three classes; susceptible $S(t)$, infectives $I(t)$ and partially protected individuals $V(t)$.

Definition 1. The BBB-model is the model represented by the following diagram:



The BBB-Model

In which we assume that the number of new infections (from both S and V) is given by the standard incidence ($\beta S \frac{I}{N}$, and $\sigma\beta V \frac{I}{N}$, ($1-\sigma$) being the degree of protection of the class V). Biologically speaking one can think of vaccines or any other way of reducing susceptibility. Infected individuals recover with a fixed rate c . The flow from the susceptible class to the protected one occurs with a fixed rate ϕ .

The BBB-model is a particular case of the one in Kribs-Zaleta and Velasco-Hernández [15], when $\mu = \theta = 0$. It can be shown that the backward bifurcation phenomenon is preserved, if the birth/death rate μ and the θ rate (which allows a flow from V to S) are omitted. Conversely, it can be shown that once a backward bifurcation appears, adding some migration and birth/death rates does not eliminate it. Furthermore, the structure of the BBB-model suggests that many of the models proposed in the literature which present a backward bifurcation, include in some sense the BBB-model and are not the result of the extra parameters or classes added to the basic models or the dynamics allowed among those classes.

3. Uniqueness of the BBB-Model

In this section we study the family of all three-class models to which the BBB-model belongs. We will show that when a constant population N is divided into three classes $S(t)$, $I(t)$ and $V(t)$, and we use the standard incidence to model new infections, under certain hypotheses (defined in this section), only one single compartmental model of the whole family, the BBB-model, shows a backward bifurcation. The hypotheses are the following:

- G1) all interactions among all three classes are of the type mass-action law or are proportional to the source class.
- G2) two of the classes, S and I , have two flows connecting them. Each of these two classes is connected to V by a single flow.

The family of models satisfying hypotheses G1 and G2 can be reduced to 112 models, grouped in 7 different families, which are sketched here (see proof of theorem 1, below). Note that the handling of all other cases obtained by renaming variables (S instead of I or V , etc.) is analogous to one of the cases presented here and is included in one of the diagrams shown.

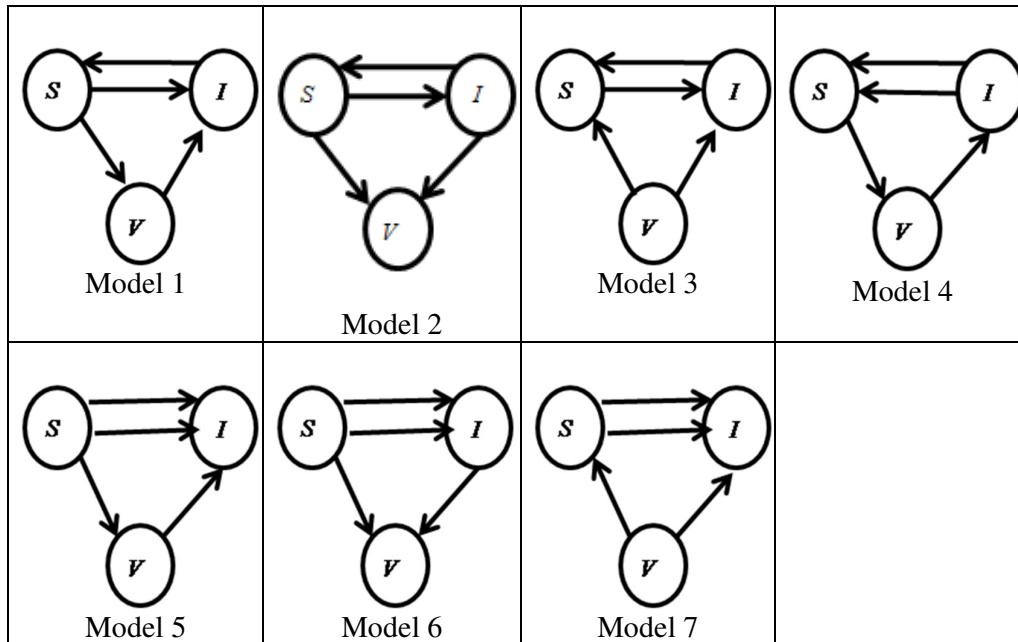
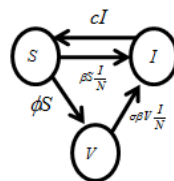


Figure 1

Under these assumptions we have the following result:

Theorem 1. *If the assumptions G1 y G2 are satisfied, then the BBB-model is the unique with backward bifurcation and the model is given by*



BBB- Model

Proof. Without loss of generality, the double interaction in the system occurs between S and I . Let us consider first only the direction of the flows. There are 7 possible configurations which are shown in Figure 1. After selecting either a

mass-action law interaction or a proportional flow, we get 16 combinations for each of the 7 models mentioned before.

In the diagrams given by the models 3, 5, 6 and 7 there is a class without incoming flows; therefore such class tends to 0, reducing asymptotically the dimension of the system to two. In Model 2, the classes S and I taken together do not receive any flow from V , tending therefore to 0. This impedes the appearance of any possible backward bifurcation.

In what follows we analyze only the BBB-model. Model 4 and the remaining cases of models 1 only is need verified that there are two (or less than two) nonnegative equilibria for the system. In some cases it is a consequence of the constant term in the quadratic polynomial to be negative. Note that when the system is linear only the trivial equilibrium exists, and in this case no backward bifurcation can occur.

The BBB-model has associated the system

$$\begin{aligned}\dot{S} &= -\beta S \frac{I}{N} - \phi S + cI, \\ \dot{I} &= \beta S \frac{I}{N} + \sigma\beta V \frac{I}{N} - cI, \\ \dot{V} &= -\sigma\beta V \frac{I}{N} + \phi S.\end{aligned}$$

Substituting S , we get:

$$\begin{aligned}\dot{I} &= \beta(N - I - (1 - \sigma)V) \frac{I}{N} - cI, \\ \dot{V} &= -\sigma\beta V \frac{I}{N} + \phi(N - I - V).\end{aligned}$$

The equilibria associated to this model are the trivial equilibrium and the solutions of the equation $xf(x) = 0$, where $f(x) = Ax^2 + Bx + C$.

The parameters are given by $A = -\sigma\beta$, $B = \sigma(\beta - (\phi + c))$, $C = \sigma\phi\left(1 - \frac{1}{R_\phi}\right)$, and $R_\phi = \frac{\sigma\beta}{c}$.

Therefore, the equilibria are $(0, N)$ and the solutions of $f(x) = 0$.

This can be summarized in the following

Theorem 2. Let $R_\phi = \frac{\sigma\beta}{c}$. The existence of equilibria for the BBB-model is given by the following conditions:

- i) When $R_\phi > 1$, the system presents a unique non trivial equilibrium.
- ii) When $R_\phi < 1$, the system presents two nontrivial equilibria if and only if $B < 0$, and $B^2 - 4AC > 0$.
- iii) When $R_\phi < 1$, the system presents one double non trivial equilibrium if and only if $B < 0$, and $B^2 - 4AC = 0$.
- iv) When $R_\phi < 1$, the system does not present equilibria if and only $B < 0$, and $B^2 - 4AC < 0$.

In particular, this shows that when $R_\phi < 1$ there exists not only the disease free equilibrium, but also one endemic one.

Next, to find the direction of the bifurcation when $R_\phi = 1$, we use the central manifold theory and normal forms. We use the methodology applied by [14].

Let us define $\bar{V} = V - N$ and $\rho = R_\phi - 1$.

The normal form associated to the system is:

$$\dot{x} = c\rho x - \frac{\sigma\beta((1-\sigma)\beta - \phi)}{N(\sigma\beta + \phi)}x^2 + \frac{(1-\sigma)\beta c}{N\phi}x^2\rho + O(3).$$

Therefore, the bifurcation in the trivial equilibrium and $R_\phi = 1$ is transcritical if $h(\sigma) = (1-\sigma)\beta + \phi \neq 0$, and backward in I if and only if $h > 0$. So, the trivial equilibrium is locally asymptotically stable and the endemic equilibrium is unstable.

4. Generalization of the BBB-model

Once knowing that the BBB-model is the only three-class model presenting backward bifurcation, one naturally wants to know how robust its structure is. What can be changed or added without losing the backward bifurcation?

In order to answer this question we define what we will call the extension of a flow.

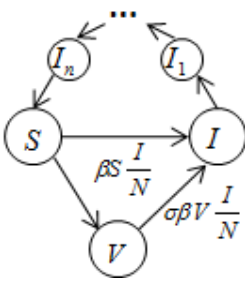
Definition 2. Given the BBB-model, we call a model **an extension** of the original one, if the new one was obtained by any subset of following processes:

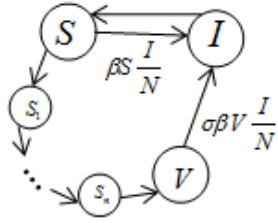
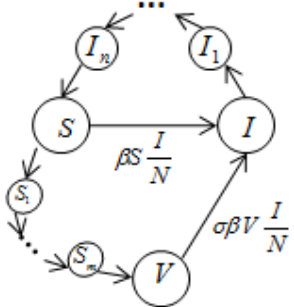
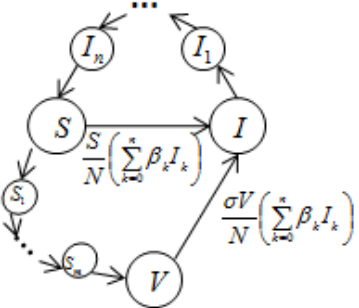
1) We substitute the flow between S and V by any number of consecutive classes S_1, S_2, \dots, S_n , and flows proportional to the source class from S to S_1, S_i to S_{i+1} , for $i=1, \dots, n$, and from S_n to V .

2) We substitute the flow between I and S by any number of consecutive classes I_1, I_2, \dots, I_m , and flows proportional to the source class from I to I_1, I_i to I_{i+1} , for $i=1, \dots, m-1$, and from I_m to S . We change the infection flow from S to I for the expression $\left(\frac{S}{N} \sum_{k=0}^m \beta_k I_k\right)$ which models infection not only with the I class, but with all or any of the I_i 's classes.

3) We change the infection flow from V to I for the expression $\left(\frac{\sigma V}{N} \sum_{k=0}^m \beta_k I_k\right)$ which models infection not only with the I class, but with all or any of the I_i 's classes.

The biological interpretation of case 1 includes situations in which there are one or more time delays for moving from S to V . Analogously for case 2. The extensions described in cases 3 and 4 would allow infections from some or all of the infected classes. For simplicity we use in the following table the convention $S_0 = S, I_0 = I$.

Case I	
$\dot{S} = -\beta S \frac{I}{N} - \phi S + c_n I_n,$ $\dot{I} = \beta S \frac{I}{N} + \sigma \beta V \frac{I}{N} - cI,$ $\dot{I}_k = c_{k-1} I_{k-1} - c_k I_k,$ $\dot{V} = \phi S - \sigma \beta V \frac{I}{N}.$ <p>For $k = 0, \dots, n$.</p>	

<p>Case II</p> $\dot{S} = -\beta S \frac{I}{N} - \phi S + c_n I_n,$ $\dot{I} = \beta S \frac{I}{N} + \sigma \beta V \frac{I}{N} - cI,$ $\dot{S}_j = \phi_{j-1} S_{j-1} - \phi_j I_j,$ $\dot{V} = \phi_m S_m - \sigma \beta V \frac{I}{N}.$ <p>For $j = 0, \dots, m$.</p>	
<p>Case III</p> $\dot{S} = -\beta S \frac{I}{N} - \phi S + c_n I_n,$ $\dot{I} = \beta S \frac{I}{N} + \sigma \beta V \frac{I}{N} - cI,$ $\dot{I}_k = c_{k-1} I_{k-1} - c_k I_k,$ $\dot{S}_j = \phi_{j-1} S_{j-1} - \phi_j I_j,$ $\dot{V} = \phi_m S_m - \sigma \beta V \frac{I}{N}.$ <p>For $j = 0, \dots, m, k = 0, \dots, n$.</p>	
<p>Case IV</p> $\dot{S} = -\frac{S}{N} \left(\sum_{k=0}^n \beta_k I_k \right) - \phi S + c_n I_n,$ $\dot{I} = \frac{S}{N} \left(\sum_{k=0}^n \beta_k I_k \right) + \sigma \frac{V}{N} \left(\sum_{k=0}^n \beta_k I_k \right) - cI,$ $\dot{I}_k = c_{k-1} I_{k-1} - c_k I_k,$ $\dot{S}_j = \phi_{j-1} S_{j-1} - \phi_j I_j,$ $\dot{V} = \phi_m S_m - \sigma \frac{V}{N} \left(\sum_{k=0}^n \beta_k I_k \right).$ <p>For $j = 0, \dots, m, k = 0, \dots, n$.</p>	

Next, we analyze these systems to conclude that by adding n classes between classes \mathbf{S} and \mathbf{V} from the basic model, all of which are related in a linear way, the system preserves the nontrivial equilibria even when the trivial equilibrium is stable, which means that the bifurcation phenomenon is still present in all these systems.

Since the results showing the presence of a backward bifurcation are proved in a similar way for all cases, only the first case is presented here.

The first step is to find expressions for the equilibria in order to show the existence of multiple endemic states.

Notice that we have an $n+m+3$ ordinary differential equations system, which since

$$N \text{ is constant, can be reduced in one dimension. } S = N - \sum_{k=0}^n I_k - \sum_{j=1}^m S_j - V.$$

The trivial equilibrium is $(0, \dots, 0, N)$ always exists for all the parameter values.

To find any nontrivial equilibria, we substitute values of V^* , I_i^* and S_j^* in the equations for I , and solve for $\dot{I} = 0$ to get I^* . The coordinates of V^* , I_i^* and S_j^* are the result of solving $\dot{V} = 0$, $\dot{S}_j = 0$ and $\dot{I}_k = 0$, $k = 1, \dots, n$, $j = 0, \dots, m$.

The equation that has to be solved to find nontrivial equilibria is:

$$xf(x) = x(Ax^2 + Bx + C) = 0, \text{ where } x = \frac{I^*}{N}.$$

In the next table we show the coefficients A, B and C in $f(x) = Ax^2 + Bx + C$ for each case

Case I $R_\phi = \frac{\sigma\beta}{c}$.
$A = \sigma\beta \left(\sum_{l=0}^n \sum_{\substack{s=0 \\ s \neq l}}^n c_s \right) \prod_{s=1}^n c_s,$ $B = \sigma \prod_{s=1}^n c_s \left(-\beta \left(\prod_{s=1}^n c_s \right) \prod_{j=1}^m \phi_j + \phi \left(\sum_{l=0}^n \prod_{s=1}^n c_s \right) + \prod_{s=0}^n c_s \right),$ $C = -\sigma\phi \left(\prod_{s=1}^n c_s \right)^2 \left(1 - \frac{1}{R_\phi} \right).$

Case II $R_\phi = \frac{\sigma\beta}{c}$.

$$A = \left(\prod_{\substack{k=0 \\ k \neq j}}^n \phi_k \right) \frac{\sigma\beta}{\phi_0},$$

$$B = \sigma \left(-\beta \left(\prod_{j=1}^m \phi_j \right) + \prod_{j=0}^m \phi_j + \phi \left(\sum_{l=0}^n \prod_{s=1}^n c_s \right) + \left(\sum_{\substack{j=0 \\ r \neq j}}^m \prod_{r=0}^m \phi_r \right) \right),$$

$$C = -\sigma \left(\prod_{k=0}^n \phi_k \right)^2 \left(1 - \frac{1}{R_\phi} \right).$$

Case III $R_\phi = \frac{\sigma\beta}{c}$.

$$A = \sigma\beta \prod_{j=1}^m \phi_j \left(\sum_{\substack{l=0 \\ s \neq l}}^n \sum_{s=0}^n c_s \right) \prod_{s=1}^n c_s,$$

$$B = \sigma \prod_{s=1}^n c_s \left(-\beta \left(\prod_{s=1}^n c_s \right) \prod_{j=1}^m \phi_j + \prod_{j=0}^m \phi_j \left(\sum_{\substack{l=0 \\ s \neq l}}^n \prod_{s=0}^n c_s \right) + \prod_{s=0}^n c_s \left(\sum_{\substack{j=0 \\ r \neq j}}^m \prod_{r=0}^m \phi_r \right) \right),$$

$$C = -\sigma \prod_{j=0}^m \phi_j \left(\prod_{s=1}^n c_s \right)^2 \left(1 - \frac{1}{R_\phi} \right).$$

Case IV $R_\phi = \sum_{k=0}^n \frac{\sigma\beta_k}{c_k}$.

$$A = \sigma \prod_{j=1}^m \phi_j \left(\sum_{\substack{l=0 \\ s \neq l}}^n \sum_{s=0}^n c_s \right) \left(\sum_{\substack{l=0 \\ s \neq l}}^n \prod_{s=0}^n c_s \beta_l \right),$$

$$B = \sigma \prod_{s=1}^n c_s \left(- \left(\sum_{\substack{l=0 \\ s \neq l}}^n \prod_{s=0}^n c_s \beta_l \right) \prod_{j=1}^m \phi_j + \prod_{j=0}^m \phi_j \left(\sum_{\substack{l=0 \\ s \neq l}}^n \prod_{s=0}^n c_s \right) + \prod_{s=0}^n c_s \left(\sum_{\substack{j=0 \\ r \neq j}}^m \prod_{r=0}^m \phi_r \right) \right),$$

$$C = -\sigma \prod_{j=0}^m \phi_j \left(\prod_{s=1}^n c_s \right)^2 \left(1 - \frac{1}{R_\phi} \right).$$

Here we get that if $R_\phi < 1$, then $C > 0$, and if $R_\phi > 1$ we have $C < 0$. Notice that in each case the function $f(x)$ has only one positive solution if $C < 0$, and two when $C > 0$, $B < 0$ and $B^2 - 4AC > 0$. From here, we conclude that under certain conditions, there are nonnegative equilibria for all extensions of the BBB-model.

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