



Short communication

Backward bifurcation in epidemic models: Problems arising with aggregated bifurcation parameters

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ABSTRACT

This study addresses problems that have arisen in the literature when calculating backward bifurcations, especially in the context of epidemic modeling. Backward bifurcations are generally studied by varying a bifurcation parameter which in epidemiological models is usually the so-called basic reproduction number R_0 . However, it is often overlooked that R_0 is an aggregate of parameters in the model. One cannot simply vary the aggregate R_0 while leaving all model parameters constant as has happened many times in the literature. We investigate two scenarios. For the incorrect approach we fix all parameters in the aggregate R_0 to constant values, but R_0 is nevertheless varied as a bifurcation parameter. In the correct approach, a key parameter in R_0 is allowed to vary, and hence R_0 itself varies and acts as a natural bifurcation parameter. We explore how the outcomes of these two approaches are substantially different.

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1. Introduction

Epidemiological models have become important tools for helping understand the qualitative dynamics controlling the spread of infectious diseases. Many of these models have strong nonlinearities and therefore exhibit complex population dynamics and possess subtle bifurcation properties. Recently there has been interest in so called “backward bifurcations” because of the unusual thresholds they introduce. In this study we examine an overlooked problem in calculating backward bifurcation diagrams which has led to repeated errors in the literature.

As is well known, the qualitative dynamics of most epidemiological models depends on the threshold quantity known as the basic reproduction number R_0 [1,2]. This quantity represents the average number of secondary infections generated by a typical infected individual during the infectious period, when introduced into an entirely susceptible population. Generally, if $R_0 < 1$ an infected individual will on average be unable to replace himself/herself, and the disease will die out in time. If $R_0 > 1$, an infected individual will on average be able to infect more than one other and thus transmit through the population; as such an equilibrium number of infectives I^* could plausibly be maintained ($I^* > 0$). Thus $R_0 < 1$ corresponds to an infection-free equilibrium ($I^* = 0$), while $R_0 > 1$ corresponds to an endemic equilibrium $I^* > 0$, and this is the usual forward bifurcation scenario shown in Fig. (1).

While the above characterization familiar to most epidemiological modelers is quite general, it has recently been observed that it gives the wrong picture in the presence of a backward bifurcation. Backward bifurcations, which are characterized by multiple coexisting equilibria, allow a disease to persist even though $R_0 < 1$. More specifically, one can find a stable disease free equilibrium coexisting with two endemic equilibria ($I^* > 0$), one being unstable and the other stable even though $R_0 < 1$. A range

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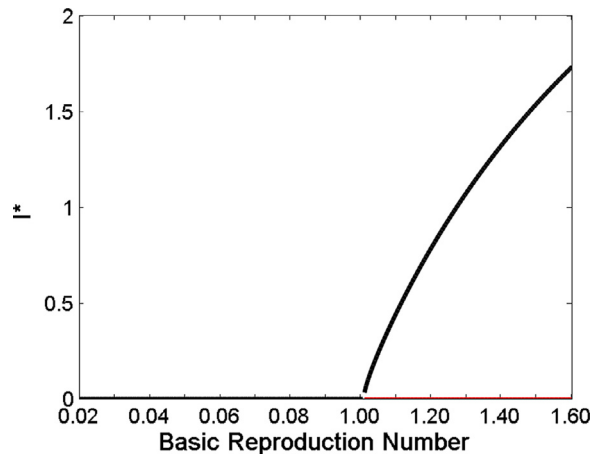


Fig. 1. The equilibrium $I^* = 0$ is stable when $R_0 < 1$ and unstable when $R_0 > 1$. For $I^* > 0$ and $R_0 > 1$ the endemic equilibria is stable. There is a bifurcation and exchange of stability at $R_0 = 1$.

of different epidemiological models have been found to exhibit backward bifurcation, including models that incorporate behavioral responses to perceived risks [3], vaccination [4,5], multiple groups [6], vector-borne diseases [7] and exogenous reinfection [8–10]. The presence of backward bifurcation is important in a practical sense because control programs must reduce R_0 further than below unity to eliminate a disease.

The problem we address here stems from studies of backward bifurcation in the literature where there have been instances where authors illustrate the phenomena by varying R_0 without properly considering the fact that R_0 is an aggregate of parameters in the model. One cannot simply vary the aggregate R_0 while leaving all model parameters constant as has been the practice in a number of important studies [11–15]. To illustrate this problem we examine a (tuberculosis) TB model that incorporates reinfection p as the parameter to induce backward bifurcation, although any other example can be used to exhibit the difference.

2. The model

The model consists of four subpopulations; susceptible (S), exposed (E), infectious (I) and recovered (R) individuals, and may be described by the following equations:

$$\begin{aligned} \frac{dS}{dt} &= \pi - \beta SI - \mu S, \\ \frac{dE}{dt} &= \beta SI - p\beta EI - (\mu + k)E, \\ \frac{dI}{dt} &= p\beta EI + kE - (\mu + r + \mu_d)I, \\ \frac{dR}{dt} &= rI - \mu R. \end{aligned} \quad (1)$$

The numbers of susceptible individuals increase by recruitment through births and immigration at a rate π . Susceptibles who come into contact with infected individuals move straight to the exposed E class but they are not themselves yet infective. The susceptible population is thus diminished due to contact with infected individuals at a rate βSI , where β represents the per-capita effective contact rate of acquiring TB bacteria. Concomitantly, the numbers in the exposed class increase at a rate βSI . Progression to the infectious state occurs when an exposed individual harbors a dormant infection that becomes active due to immune system destabilization. This is the usual “slow TB” which can take years or decades before progression. Exposed individuals move to the infected class I at rate (kE) . In addition, exposed individuals can encounter infectious individuals (I) and be reinfected leading to an acceleration into the infectious class at rate $p\beta EI$. The infected subpopulation is diminished when individuals recover from TB due to treatment at rate r and disease induced death rate μ_d . Finally, the recovered sub-population (R) is generated by recovery of infected individuals (at rate r). The natural death rate decrease all classes at the same rate via the background mortality parameter μ . Though not necessary for our purposes, a more detailed description of the model and parameters can be found in [15].

3. Backward bifurcation

Without going into detailed computation (see [16] for R_0 computation), the basic reproduction number of the model is given as

$$R_0 = \frac{k\beta\pi}{\mu(k + \mu)(\mu + r + \mu_d)}.$$

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