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Dynamic phenomena arising from an extended Core Group model

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ABSTRACT

In order to obtain a reasonably accurate model for the spread of a particular infectious disease through a population, it may be necessary for this model to possess some degree of structural complexity. Many such models have, in recent years, been found to exhibit a phenomenon known as backward bifurcation, which generally implies the existence of two subcritical endemic equilibria. It is often possible to refine these models yet further, and we investigate here the influence such a refinement may have on the dynamic behaviour of a system in the region of the parameter space near $R_0 = 1$.

We consider a natural extension to a so-called Core Group model for the spread of a sexually transmitted disease, arguing that this may in fact give rise to a more realistic model. From the deterministic viewpoint we study the possible shapes of the resulting bifurcation diagrams and the associated stability patterns. Stochastic versions of both the original and the extended models are also developed so that the probability of extinction and time to extinction may be examined, allowing us to gain further insights into the complex system dynamics near $R_0 = 1$. A number of interesting phenomena are observed, for which heuristic explanations are provided.

1. Introduction

When using a system of deterministic differential equations to model the spread of an infectious disease within a population it is possible, by keeping all but one of the system parameter values fixed, to obtain a diagram showing how the endemic and the disease-free equilibrium solutions change as the remaining parameter, α say, is varied. For some particular value of α this diagram indicates a change in the qualitative behaviour of the system, at which point the disease-free equilibrium (DFE) bifurcates into a branch representing an endemic equilibrium and a further branch of the DFE. The parameter α and its associated graph are, as a consequence, known as a *bifurcation parameter* and *bifurcation diagram*, respectively. The point at which this change in behaviour occurs is termed the *bifurcation point*, and the curve emanating from it the *bifurcation curve*.

By considering the *basic reproduction ratio* R_0 for the system it is straightforward to obtain the location of the bifurcation point. The basic reproduction ratio is defined to be the expected number of secondary cases produced in a population at the DFE by a typical infective individual during his or her entire infectious period. In general R_0 will be a function of the system parameters (see Diekmann et al. [10] for a precise mathematical formulation), and the value of α at the bifurcation point corresponds to $R_0 = 1$.

The bifurcation diagrams of simple epidemic models always display *forward bifurcation*. In this case the bifurcation curve is such that as one moves along it from the bifurcation point, the level of infection increases as R_0 increases, and the disease is able to persist in the population when $R_0 > 1$ but dies out otherwise. In recent years, however, a phenomenon known as *backward bifurcation* has emerged whereby the disease can, for certain parameter values, persist even when $R_0 \leqslant 1$. In this case the initial direction of the bifurcation curve is such that as one moves along it from the bifurcation point, R_0 decreases as the level of infection increases. It seems that the potential for the existence of backward bifurcation in an epidemic model was first noted in similar papers by Castillo-Chavez et al. [5] and Castillo-Chavez et al. [6], and Huang et al. [18]. Some of the more recent papers in this area include those by Castillo-Chavez and Song [7], Brauer [4], Feng et al. [11] and Song et al. [27]. An extensive literature survey of epidemic models exhibiting this phenomenon was carried out by Griffiths [15].

The presence of backward bifurcation indicates the existence of two or more endemic equilibria for $R_0 < 1$, known as *subcritical endemic equilibria*. It has been demonstrated in some models exhibiting backward bifurcation (see Greenhalgh et al. [13], for example) that there is the possibility for subcritical endemic equilibria to be locally asymptotically stable (LAS). This certainly has implications for disease control since the classical requirement for the eradication of the disease is no longer satisfied in such cases. It is now possible for the proportion of infected individuals in the population to remain at a steady level or even invade when $R_0 \leqslant 1$.

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The phenomenon of backward bifurcation tends to arise in relatively complex deterministic epidemic models, often ones possessing some sort of group structure. Such models may, for example, incorporate disease-driven changes in behaviour or take account of the fact that the disease has several stages. Despite their complexity, many of these models may still be regarded as over-simplified representations of the progress of the disease through a population. In such cases it might be possible to extend the model in a natural way, thereby giving a better approximation to the true disease structure. Indeed, Greenhalgh and Griffiths [14] argued that a three-stage model for the spread of bovine respiratory syncytial virus (BRSV) in cattle may be more realistic than the two-stage model studied by Greenhalgh et al. [13]. It might then be asked whether this increase in the complexity of the model provides scope for yet more complicated bifurcation diagrams and hence more complicated system dynamics in the region of the parameter space near $R_0 = 1$. Subsequent investigation of the three-stage BRSV model revealed that this was in fact the case.

In this paper we study, in connection with the points made above, the *Core Group* model (CG model) for the spread of a sexually transmitted disease as described by Hadeler and Castillo-Chavez [17]. The CG model is able to exhibit backward bifurcation, although we note here that there is a distinct structural difference between the CG and BRSV models. While the latter models a disease that passes through several stages, the CG model incorporates disease-driven changes in behaviour. After outlining the main features of this model, we carry out an analytic study of the local asymptotic stability of the endemic equilibria with the purpose of seeing whether a general result emerges relating the stability of endemic equilibria to their positions on the bifurcation curve. The CG model is then extended in a natural way in order to explore the possibility that more complicated bifurcation diagrams and stability patterns might appear, as was found when the BRSV model was extended from two to three stages.

Stochastic aspects of the CG models are also studied here. In particular, we explore the interaction between the deterministic phenomenon of backward bifurcation and the probability of extinction for the corresponding stochastic version of each model. Our main purpose here is to compare the theoretical probabilities of extinction for stochastic formulations of the model with the corresponding probabilities obtained via an extensive series of stochastic simulations. We would hope to be able to offer explanations for any observed discrepancies. Our investigations were carried out using analytical and numerical methods, and also by way of computer simulations. We have indeed found interesting links between the presence of backward bifurcation in the deterministic models and the probability of extinction in the stochastic versions. Furthermore, the expected time to extinction for the CG model is considered in order to see whether, in certain circumstances, it is possible to observe significant discrepancies between theoretical and simulated values, in contrast to the rather inconclusive results of Griffiths [15] for the two-stage BRSV model. Some more unusual bifurcation diagrams are then obtained by using the full epidemic model (i.e. the model for the population as a whole rather than just that for the isolated sexually active core group).

When investigating backward bifurcation and associated phenomena in the two and three-stage BRSV models, Greenhalgh and Griffiths [14] obtained, both from the deterministic and the stochastic point of view, a number of potentially interesting results. It cannot be assumed however, that such results, obtained by studying one model in isolation, will automatically carry over to other epidemic models. Although detailed analysis revealed a number of phenomena that were noteworthy in their own right, it may be that these were in fact particular to the model that was being considered. Thus, in the light of the findings for the BRSV models, we would like to see which of these phenomena do actually transfer to other epidemic models.

2. The basic Core Group model

Hadeler and Castillo-Chavez [17] consider the spread of a sexually transmitted disease. The population P is split into two classes; a sexually active and relatively small core group C and a weakly connected and sexually inactive remainder non-core group A. The core group is further subdivided into susceptible S, educated (or vaccinated) V and infected I individuals with $C = S + V + I$ and $P = A + C$. Members of the core group are recruited from the non-core group.

This scenario is modelled by way of a general set of differential equations. In order to be able to draw some conclusions about the behaviour of this rather complex model, the following system of differential equations, modelling an isolated core population of constant size C, is studied in detail:

$$\frac{dS}{dt} = \mu C - \beta\frac{SI}{C} - \psi S + \alpha(1-\gamma)I - \mu S, \tag{2.1}$$

$$\frac{dV}{dt} = \psi S - \tilde{\beta}\frac{VI}{C} + \alpha\gamma I - \mu V \tag{2.2}$$

$$\text{and} \quad \frac{dI}{dt} = \frac{\beta SI + \tilde{\beta}VI}{C} - \alpha I - \mu I, \tag{2.3}$$

where μ is the (per capita) common birth and death rate, β is the transmission rate from infected to susceptible individuals, $\tilde{\beta}$ is the transmission rate from infected to educated (vaccinated) individuals (with $0 \leqslant \tilde{\beta} \leqslant \beta$), α is the recovery rate, γ is the proportion of recovered individuals passing into the educated class and ψ is the rate of direct transition from the susceptible class to the educated class. Since the above system is homogeneous it can be normalised by setting $C = 1$, meaning that S, V and I then represent population proportions rather than numbers of individuals.

The reproduction ratios for initial populations consisting entirely of susceptible and educated individuals, respectively, are

$$R = \frac{\beta}{\alpha + \mu} \quad \text{and} \quad \tilde{R} = \frac{\tilde{\beta}}{\alpha + \mu}$$

and the basic reproduction ratio is given by

$$R_0(\psi) = \frac{\mu}{\mu + \psi}R + \frac{\psi}{\mu + \psi}\tilde{R} = \frac{\mu\beta + \psi\tilde{\beta}}{(\alpha + \mu)(\mu + \psi)},$$

where R_0 is written as a function of ψ in order to indicate that ψ is to be utilised as the bifurcation parameter. We note here that R and $\tilde{R}$ given above are denoted R_0 and $\tilde{R}_0$, respectively, in the paper. We make this change in order to avoid confusion over the commonly accepted notation for the basic reproduction ratio that we have adopted here. The authors make the point that education is not necessary when $R < 1$, while if $\tilde{R} > 1$ then education is not effective, so the interesting situation is $\tilde{R} < 1 < R$, and we shall assume that this is the case. When $\tilde{R} < 1 < R$ the unique education rate unique education rate $\psi$for which $R_0(\psi) = 1$ is given by

$$\psi^* = \frac{R - 1}{1 - \tilde{R}}\mu > 0.$$

3. Locally asymptotically stable endemic equilibria and the bifurcation curve

In their detailed analysis of the endemic equilibria of the two-stage BRSV model, Greenhalgh et al. [13] found that when backward bifurcation was present the upper subcritical endemic equilibrium was always LAS while the lower one was always