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Backward bifurcation for pulse vaccination

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ABSTRACT

We investigate an SIVS model with pulse vaccination strategy. First we compute the disease free periodic solution and prove its global asymptotic stability in the disease free subspace. We identify the corresponding control reproduction number R_c and prove that the disease free periodic solution is locally asymptotically stable if $R_c < 1$, and under some additional conditions it is globally asymptotically stable as well. For $R_c > 1$ we prove the uniform persistence of the disease. Our main result is that nontrivial endemic periodic solutions are bifurcating from the disease free periodic solution as R_c is passing through the threshold value one. A complete bifurcation analysis is provided for the associated nonlinear fixed point equation. We show that backward bifurcation of periodic orbits is possible for suitable parameter values, and give explicit conditions to determine whether the bifurcation is backward or forward. The main mathematical tools are comparison principles and Lyapunov–Schmidt reduction. Finally, we compare the pulse vaccination strategy with continuous vaccination, and illustrate that backward bifurcation occurs in more realistic models as well when pulse vaccination is applied.

1. Introduction

Vaccination is a common and effective strategy to control and to prevent the spread of communicable diseases, thus understanding the impact of various vaccination schemes on the transmission dynamics is of major public health concern. In compartmental models we divide the population being studied into several disjoint classes (Susceptible, Infected, Vaccinated, Recovered, etc.), and use differential equations to describe the transition of individuals among those classes. The basic reproduction number R_0 (corresponds to models of uncontrolled epidemics) and the control reproduction number R_c (corresponds to models where some control measure is applied) are key concepts in mathematical epidemiology, as they express the expected number of secondary infections caused by a single infective introduced into a wholly susceptible (or controlled) population.

Typically, the infection dies out if $R_c < 1$, and the disease remains endemic if $R_c > 1$. In most models, for $R_c < 1$ the disease free equilibrium is the unique steady state and there is a bifurcation at $R_c = 1$, when the disease free equilibrium loses its stability and a stable endemic equilibrium appears for $R_c > 1$. Such a transition of stability is called forward bifurcation. However, in some models the situation is very different: there exist multiple endemic equilibria for $R_c < 1$, even stable one. In this case, there may be a self-sustained epidemic even though the reproduction number is less than one. This situation is called backward bifurcation (see Fig. 1 for a sketch). The nature of this bifurcation has serious implications for disease control: in the first case, it is sufficient to apply a control measure such that R_c becomes less than one to eradicate the disease, while in the second case it is necessary to decrease R_c well below one to ensure that the disease will die out. In various vaccination models, backward bifurcation can appear if the vaccination is imperfect.

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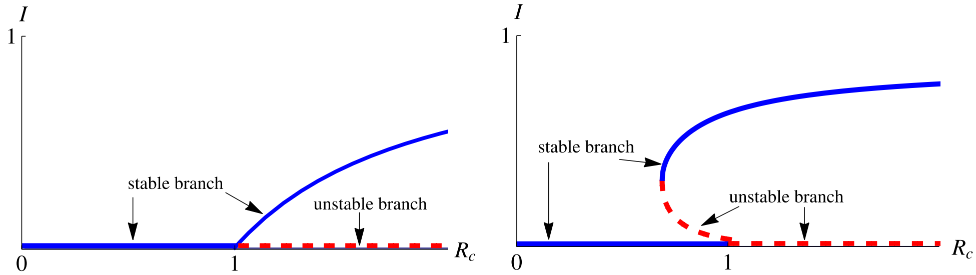

Fig. 1. The types of bifurcation appearing in simple SIVS model.

The susceptible–vaccinated–infected–removed–susceptible (SVIRS) model

$$\begin{cases} S'(t) = \Lambda(1-\Phi) + \omega_v V(t) + \omega_r R(t) - \dfrac{\beta I(t)}{N(t)} S(t) - \mu S(t), \\ V'(t) = \Lambda\Phi - (1-\psi)\dfrac{\beta I(t)}{N(t)} V(t) - (\omega_v + \mu) V(t), \\ I'(t) = \dfrac{\beta I(t)}{N(t)} S(t) + (1-\psi)\dfrac{\beta I(t)}{N(t)} V(t) - (\sigma_u + \mu) I, \\ R'(t) = \sigma_u I(t) - (\omega_r + \mu) R(t) \end{cases} \tag{1}$$

with waning immunity and imperfect cohort vaccination was analyzed in [1], where one can read the detailed explanation of the terms and parameters.

This model can be simplified if we replace the recruitment term Λ by $\mu N(t)$, then the recruitment and the mortality is balanced and the population size remains constant, what we can normalize to $N(t) = 1$ without loss of generality. The model further reduces if infected individuals do not develop natural immunity, and patients moving immediately to the susceptible class (this is the limit case when the length of immunity $1/\omega_r \to 0$, or equivalently $\omega_r \to \infty$). We replace cohort vaccination by continuous vaccination strategy, that is $\Phi = 0$, and a new parameter ϕ is introduced which describes the vaccination rate at which individuals are moving from the S-class to the V-class. By these simplifying assumptions and modifications, we arrive at the simple SIVS model studied by Brauer [2]:

$$\begin{cases} S'(t) = \mu - \beta S(t) I(t) - \mu S(t) + \gamma I(t) + \theta V(t) - \varphi S(t), \\ I'(t) = \beta S(t) I(t) - (\mu + \gamma) I(t) + \sigma\beta V(t) I(t), \\ V'(t) = \varphi S(t) - \sigma\beta V(t) I(t) - (\mu + \theta) V(t), \end{cases} \tag{2}$$

where we changed the notation ω_v to θ, σ_u to γ and $1 - \psi$ to σ to follow the notation of [2] throughout this paper. In model (2), β is the transmission rate, μ is the birth and death rate, γ is the recovery rate, φ is the vaccination rate. The vaccination may reduce, but not completely eliminate susceptibility to infection: this is modeled by including a factor σ, $0 \le \sigma \le 1$. If $\sigma = 0$, the vaccine is perfectly effective, while $\sigma = 1$ means that the vaccine has zero effect. It is assumed that the vaccination loses effect at rate θ. In this model the constant population size $S(t) + I(t) + V(t) = 1$ is assumed. Brauer investigated this vaccination model and proved the existence of multiple endemic equilibria and backward bifurcation for suitable parameter values [2]. Backward bifurcation has been observed in different epidemic models in various contexts: for malaria [3], influenza [4], HSV-2 [5], Hepatitis B and C [6], chlamydia trachomatis [7], dengue [8], tuberculosis in [9] and general models with treatment [10].

Here we modify model (2), by replacing the continuous vaccination term by a pulse vaccination strategy. We study the resulting system of impulsive differential equations. The pulse scheme is a repeated application of the vaccine at distinct times, so we vaccinate a fraction φ of the susceptible population after each time T. It is known from [11–13], that sometimes pulse vaccination is more effective than continuous vaccination, therefore it is natural to investigate the dynamics and the backward–forward bifurcations of model (2) with pulse vaccination.

2. The model

Consider the following pulse vaccination model, based on (7):

$$\begin{cases} S'(t) = \mu - \beta S(t) I(t) - \mu S(t) + \gamma I(t) + \theta V(t), \\ I'(t) = \beta S(t) I(t) - (\mu + \gamma) I(t) + \sigma\beta V(t) I(t), & \text{if } t \neq nT, \\ V'(t) = -\sigma\beta V(t) I(t) - (\mu + \theta) V(t), \end{cases}$$
$$\begin{cases} S\left(nT^+\right) = (1-\varphi) S\left(nT^-\right), \\ I\left(nT^+\right) = I\left(nT^-\right), & \text{if } t = nT. \\ V\left(nT^+\right) = V\left(nT^-\right) + \varphi S\left(nT^-\right), \end{cases} \tag{3}$$