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A note on the direction of the transcritical bifurcation in epidemic models*

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Abstract. In classical epidemic models, it is common to observe that a disease-free equilibrium looses its stability for $R_0 = 1$ and a transcritical bifurcation takes place. We analyze this aspect from the point of view of the mathematical structure of models, in order to assess which parts of the structure might be responsible of the direction of the transcritical bifurcation. We formulate a general criterion, which gives sufficient (resp. necessary) conditions for the occurrence of forward (resp. backward) bifurcations. The criterion, obtained as consequence of a well known analysis of the centre manifold for general epidemic models, is applied to several epidemic models taken from the literature.

Keywords: epidemic models, forward bifurcation, backward bifurcation.

1 Introduction

One of the main goals of mathematical modelling of epidemics is to understand under which conditions an infectious disease spreading within a host population may be eradicated or will persist. At this aim, very useful insights may come from the qualitative analysis of compartmental models [1, 4, 8, 11, 12, 22, 26] where, as it is well known, a key role is played by the so-called *basic reproduction number*, R_0 [9, 12, 13, 34]. Indeed, assessing the "direction" of the transcritical bifurcation arising at $R_0 = 1$ is a primary issue in epidemic modelling. For many compartmental epidemic models, the sometimes called R_0-*dogma* [28] can be proved: if R_0 is greater than unity, then the disease will spread and possibly persist within the host population; if R_0 is less than the unity, then the infection cannot maintain itself [1, 4, 22]. When this happens, the bifurcation at the criticality is said to be a transcritical *forward* bifurcation (see Fig. 1, left). However, in some cases the dynamics may be more complex than that. This happens, in particular,

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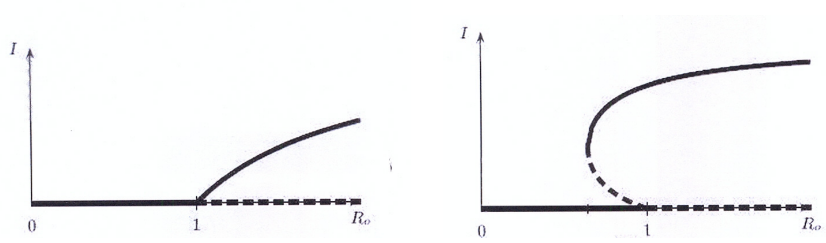

Fig. 1. Qualitative bifurcation diagrams for the forward bifurcation (left) and backward bifurcation (right). The values of infectious at equilibrium are on the vertical axis. The bifurcation parameter, which is the basic reproductive number R_0, is on the horizontal axis. The solid line (–) denotes stability; the dashed line (- -) denotes instability.

when the model exhibits the phenomenon of *backward bifurcation* [3,21]. This occurrence implies that a stable endemic equilibrium may also exist when R_0 is less than unity (see Fig. 1, right). From the epidemiological point of view, this phenomenon has important public health implications because reducing R_0 below the unity is no longer sufficient to guarantee disease elimination; the basic reproduction number must be reduced under a smaller threshold in order to avoid endemic states and get the elimination.

Backward bifurcation has been detected for many epidemic models, both generic compartmental models [3,14,21,33,35] and models for the spread of specific diseases like tuberculosis [10], dengue [17], malaria [7] and sexually-transmitted diseases [29, 30, 36]. For this reason, it is very important to understand the mechanisms that can induce the transcritical bifurcation at $R_0 = 1$ to be forward or backward.

Several investigations on the epidemiological mechanisms leading to backward bifurcation have shown that this phenomenon has been often found for models of vaccine-preventable diseases [2, 3, 5, 6, 24, 25, 30]. The acquired immunity is also a debated cause for its occurrence [28]. In a very recent study, a list of epidemiological causes of backward bifurcation has been provided, based on the review of models from the literature [19]. The list includes (among others): exogenous re-infection (of latently-infected individuals) in models for the spread of tuberculosis; re-infection in general; Host(s) disease-induced mortality in models for the transmission of vector-borne diseases and several mechanisms related to vaccination (imperfect vaccine efficacy; slow vaccine-derived immunity waning, etc.). Furthermore, it has been shown that the introduction of vectored immunoprophylaxis can induce backward bifurcation [36].

As a matter of fact, many compartmental epidemic models given by nonlinear ordinary differential equations have a similar structure and this gives the opportunity to assess which parts of the model structure, independently of their epidemiological meaning, play a major role in inducing a given direction to the transcritical bifurcation.

In [10], a theory was introduced for the analysis of general epidemic models. It settles the question of the existence of equilibria bifurcating from a nonhyperbolic equilibrium. Such theory is based on the general centre manifold theory [18] and extends some similar results previously obtained in [34] and [14].

In this paper, we obtain a criterion, based on the results given in [10, 14, 34], which provides sufficient (resp. necessary) conditions for the occurrence of forward (resp.

backward) bifurcations. When analyzing an epidemic model, after a preliminary analysis on existence and stability of disease-free equilibria, our criterion allows to check, simply looking at the structure of the model, if the direction of the transcritical bifurcation is forward or there is the possibility for the backward bifurcation to occur.

As in [34], the host population is grouped in two general classes, the *infected* and *uninfected* compartments. Under general and common assumptions on the epidemic model, we show that a sufficient condition for a forward bifurcation to occur is that all the following features are included in the model's structure: (i) In the balance equations for the infected compartments, nonlinear terms are present only in the rate of appearance of new infections; (ii) Nonlinear terms are bilinear; (iii) There is no transfer from infected to uninfected compartments. As a corollary, if at least one of these features is not present in the model structure, then a backward bifurcation may occur. For this reason, the criterion is a sufficient condition for the occurrence of forward bifurcation and a necessary condition for the occurrence of backward bifurcation.

We provide several applications of this result to epidemic models taken from the literature, including transmission of hepatitis, tuberculosis, dengue, West Nile virus and HIV.

The rest of the paper is organized as follows. In Section 2, we give our main result. In Section 3, we give the proof and recall the centre manifold analysis for general compartmental epidemic models as developed in [10, 14, 34]. In Section 4, we illustrate the analysis of a SIS model with vaccination and treatment as specific example. In Section 5, the SIS model is viewed as an application of our criterion together with several more examples taken from the literature. Concluding remarks are given in Section 6. In the Appendix, the normal form of transcritical bifurcation is derived for the sake of completeness.

2 Sufficient conditions for forward bifurcation

We begin by recalling the general compartmental model describing an infectious disease transmission within a heterogeneous population [34]. Then, we will state our main result.

Let us consider a heterogeneous population whose individuals can be grouped into n homogeneous compartments. Let $\mathbf{x} = (x_1, \dots, x_n)^{\mathrm{T}}$ represent the state vector, where each $x_i \geqslant 0$. Suppose that the first m compartments correspond to infected individuals (*infected class*) and the remaining $n - m$ compartments to uninfected individuals (*uninfected class*).

The dynamics of $\mathbf{x}$ is assumed to be given by a system of nonlinear ordinary differential equations

$$\dot{\mathbf{x}} = \mathbf{f}(\mathbf{x}), \quad \mathbf{x} \in \mathbb{R}^n,\ \mathbf{f} \in \mathbb{R}^n, \tag{1}$$

where the upper dot denotes derivative respect to t (time) and $\mathbf{f}$ is continuously differentiable at least twice in $\mathbf{x}$.

It is possible to distinguish new infections from all other changes in population by writing system (1) as

$$\dot{x}_i = f_i(\mathbf{x}) = \mathcal{F}_i(\mathbf{x}) - \mathcal{V}_i(\mathbf{x}), \quad i = 1, \dots, n, \tag{2}$$

where $\mathcal{V}_i = \mathcal{V}_i^- - \mathcal{V}_i^+$. Here $\mathcal{F}_i(\mathbf{x})$ is the rate of appearance of new infections in compartment i; $\mathcal{V}_i^+(\mathbf{x})$ is the rate of transfer of individuals into compartment i by all other means; $\mathcal{V}_i^-(\mathbf{x})$ is the rate of transfer of individuals out of compartment i.

Denote by $\mathbf{X}_s$ the set of all disease free states: $\mathbf{X}_s = \{\mathbf{x} \in \mathbf{R}_n^+\colon\ x_i = 0,\ i = 1, \dots, m\}$. The following conditions, which are commonly satisfied by epidemic models, are assumed to hold:

(A1) In the nonnegative cone ($x_i \geqslant 0$ for all $i = 1, \dots, n$), $\mathcal{F}_i$, $\mathcal{V}_i^+$, $\mathcal{V}_i^-$ are all non negative for $i = 1, \dots, n$;

(A2) If $x_i = 0$ (empty compartment), then $\mathcal{V}_i^- = 0$ (no transfer out of compartment). In particular, if $\mathbf{x} \in \mathbf{X}_s$, then $\mathcal{V}_i^- = 0$ for $i = 1, \dots, m$;

(A3) $\mathcal{F}_i = 0$ if $i > m$ (the incidence of infection for uninfected compartment is zero);

(A4) If $\mathbf{x} \in \mathbf{X}_s$, then $\mathcal{F}_i(\mathbf{x}) = 0$ and $\mathcal{V}_i^+(\mathbf{x}) = 0$ for $i = 1, \dots, m$ (no density dependent immigration of infectives. This ensures that the disease free subspace is invariant).

(A5) If $\mathcal{F}_i(\mathbf{x}) = 0$ for all $i = 1, \dots, n$, then all eigenvalues of $D\mathbf{f}(\mathbf{x}_0)$ have negative real parts, where $\mathbf{x}_0$ denotes a disease-free equilibrium (DFE) and $D\mathbf{f}(\mathbf{x}_0)$ denotes the Jacobian matrix of $\mathbf{f}$ evaluated in the DFE (this means that the DFE is stable in absence of new infections).

The main result of this paper is the following:

Proposition 1. *Assume that conditions* (A1)–(A5) *are satisfied. Furthermore, assume that the following hypotheses are satisfied by system* (2):

(H1) *In the balance equations for the infected compartments, nonlinear terms are present only in the rate of appearance of new infections*;

(H2) *Nonlinear terms are bilinear*;

(H3) *There is no linear transfer from infected to uninfected compartments.*

Then the transcritical bifurcation of system (2) *at* $R_0 = 1$ *is forward.*

Note that (H1) excludes the presence of negative nonlinear terms in the balance equations of infected compartments. We will give the proof at the end of next section.

3 Centre manifold analysis

In this section, we recall some results concerning with the existence and stability of equilibria for system (2) under assumptions (A1)–(A5). The approach is based on the centre manifold analysis.

Proposition 2. (*See* [34].) *If* $\mathbf{x}_0$ *is a DFE of* (2) *and* $f_i(\mathbf{x})$ *satisfies* (A1)–(A5)*, then the derivatives* $D\mathcal{F}(\mathbf{x}_0)$ *and* $D\mathcal{V}(\mathbf{x}_0)$ *are partitioned as*

$$D\mathcal{F}(\mathbf{x}_0) = \begin{pmatrix} F & 0 \\ 0 & 0 \end{pmatrix}, \qquad D\mathcal{V}(\mathbf{x}_0) = \begin{pmatrix} V & 0 \\ J_3 & J_4 \end{pmatrix},$$

where F and V are $m \times m$ matrices defined by

$$F = \left[\frac{\partial \mathcal{F}_i}{\partial x_j}(\mathbf{x}_0)\right] \quad \textit{and} \quad V = \left[\frac{\partial \mathcal{V}_i}{\partial x_j}(\mathbf{x}_0)\right] \quad \textit{with } 1 \leqslant i, j \leqslant m.$$

Further, F is nonnegative, V is a non-singular M-matrix and all the eigenvalues of J_4 have positive real part.

Remark 1. We remark that an M-matrix A is a squared matrix whose off-diagonal entries are less than or equal to zero and one of the twelve properties listed in the theorem by Fiedler and Ptak [16] is satisfied (see also [32, Thm. A.2]). Among these properties, there are the following ones:

- The inverse A^{-1} exists and all its entries are nonnegative;
- The real part of each eigenvalue of A is positive.

Now, let R_0 denote the spectral radius of the *next generation matrix* FV^{-1} [12], i.e.,

$$R_0 = \rho\big(FV^{-1}\big).$$

R_0 is a threshold parameter for the stability of the DFE, as established in the next proposition, and can be taken as *basic reproduction number* [12].

Proposition 3. (*See* [34].) *Under the assumptions* (A1)–(A5)*, $\mathbf{x}_0$ is locally asymptotically stable if $R_0 < 1$, and unstable if $R_0 > 1$.*

We now recall the analysis of the centre manifold near the criticality ($\mathbf{x} = \mathbf{x}_0$, $R_0 = 1$) which allows to clarify the direction of the bifurcation near the bifurcation point.

Let us consider system (1) and take a parameter μ as bifurcation parameter. That is, consider

$$\dot{\mathbf{x}} = \mathbf{f}(\mathbf{x}, \mu), \quad \mathbf{x} \in \mathbb{R}^n,\ \mu \in \mathbb{R},\ \mathbf{f} \in \mathbb{R}^n, \tag{3}$$

where $\mathbf{f}$ is continuously differentiable at least twice in both $\mathbf{x}$ and μ.

Assume that:

(i) $\mathbf{x}_0$ be an equilibrium for all μ, that is: $\mathbf{f}(\mathbf{x}_0, \mu) = 0$ for all μ ($\mathbf{x}_0$ is the DFE);

(ii) $\mathbf{x}_0$ be locally asymptotically stable for $\mu < 0$ and unstable for $\mu > 0$;

(iii) The Jacobian matrix evaluated at $\mathbf{x}_0$ and $\mu = 0$, that is $A = D\mathbf{f}(\mathbf{x}_0, 0)$, where $D\mathbf{f}(\mathbf{x}, \mu)$ denotes the derivative $[\partial f_i/\partial x_j]$, $i, j = 1, \ldots, n$, evaluated in $(\mathbf{x}, \mu)$, admits a single zero eigenvalue, $\lambda_0 = 0$ and all the other eigenvalues have negative real parts.

Note that the properties (i)–(iii) are very common for epidemic models. Conditions (ii)–(iii) mean that $\mathbf{x}_0$ looses its stability and a transcritical bifurcation may take place at $\mu = 0$. In other words, conditions (ii)–(iii) recall Proposition 3 with $R_0 = 1$, replaced by $\mu = 0$.

Let us denote by $\mathbf{v} = (v_1, \ldots, v_n)$ and $\mathbf{w} = (w_1, \ldots, w_n)^{\mathrm{T}}$ the left and right nullvectors, chosen such that $\mathbf{v} \cdot \mathbf{w} = 1$, corresponding to the zero eigenvalue of matrix A.

The normal form of the bifurcation, i.e., the analytic form of the vector field on the center manifold, may be derived by using the centre manifold theorem [18]. More precisely, the following theorem may be proved [10, 14, 34]:

Proposition 4. *In a neighborhood of* $\mu = 0$*, the normal form of the bifurcation of system* (3) *subject to* (i)–(iii) *is given by*

$$\dot{u} = au^2 + b\mu u, \tag{4}$$

where

$$a = \frac{\mathbf{v}}{2} \cdot D_{\mathbf{xx}}\mathbf{f}(\mathbf{x}_0, 0)\mathbf{w}^2 \equiv \frac{1}{2} \sum_{k,i,j=1}^{n} v_k w_i w_j \frac{\partial^2 f_k}{\partial x_i \partial x_j}(\mathbf{x}_0, 0) \tag{5}$$

and

$$b = \mathbf{v} \cdot D_{\mathbf{x}\mu}\mathbf{f}(\mathbf{x}_0, 0)\mathbf{w} \equiv \sum_{k,i=1}^{n} v_k w_i \frac{\partial^2 f_k}{\partial x_i \partial \mu}(\mathbf{x}_0, 0). \tag{6}$$

Note that, in (5) and (6), the f_k's denote the right-hand side of system (3).

A simple proof of this theorem is reported in the Appendix. We refer to [10, 14, 34] for more details.

It is easy to check that the equilibria of (4) are given by $u_1 = 0$ and $u_2 = -b\mu/a$. Note that $b > 0$ due to the hypothesis (ii). As a consequence, we have that:

(a) If $a < 0$, then u_2 is negative and unstable if $\mu < 0$ and positive and stable if $\mu > 0$;

(b) If $a > 0$, then u_2 is positive and unstable if $\mu < 0$ and negative and stable if $\mu > 0$.

These conditions, which characterize the bifurcation locally at $R_0 = 1$, are compatible with the scenarios depicted in Fig. 1. Precisely, condition (a) indicates a forward bifurcation scenario and condition (b) indicates the occurrence of a backward bifurcation.

The parameter a given by (5) may be written in a different way, as stated by the following proposition:

Proposition 5. (*See* [34].) *Assume that conditions* (A1)–(A5) *are satisfied, and* 0 *is a simple eigenvalue of* A*. Then in the nullvectors of* A*,* $v_i \geqslant 0$ *and* $w_i \geqslant 0$ *for* $i = 1, \ldots, m$*,* $v_i = 0$ *for* $i = m+1, \ldots, n$*, and*

$$a = \frac{1}{2} \sum_{i,j,k=1}^{m} v_i w_j w_k \left(\frac{1}{2} \frac{\partial^2 f_i}{\partial x_j \partial x_k}(\mathbf{x}_0, 0) + \sum_{l=m+1}^{n} \alpha_{lk} \frac{\partial^2 f_i}{\partial x_j \partial x_l}(\mathbf{x}_0, 0) \right) \tag{7}$$

with $[\alpha_{lk}]$*,* $l = m+1, \ldots, n$*,* $k = 1, \ldots, m$*, denoting the* $(l-m, k)$ *entry of* $-J_4^{-1}J_3$*, where* J_3 *and* J_4 *are the lower blocks of* A*, as defined in Proposition 2.*

We are now in position to prove the main result of this note.

Proof of Proposition 1. Due to Proposition 3, hypotheses (i)–(iii) are satisfied. Therefore, in order to prove that the transcritical bifurcation is forward, we have to show that the coefficient a of the normal form, given by (7), is negative. Now, (H1)–(H2) imply that the nonlinear terms are bilinear terms involving one infected and one uninfected compartments, so that

$$\frac{\partial^2 f_i}{\partial x_j \partial x_k} = 0, \quad j, k = 1, \ldots, m. \tag{8}$$

Moreover, note that (H1)–(H2) imply also that there are no negative bilinear terms in the equations of infected compartments, so that

$$\frac{\partial^2 f_i}{\partial x_j \partial x_l} \geqslant 0, \quad j = 1, \ldots, m,\ l = m+1, \ldots, n. \tag{9}$$

Now, let us focus on the terms α_{lk}, that is the $(l-m, k)$ entry of $-J_4^{-1}J_3$ (see Proposition 5). Hypothesis (H3) ensures that J_3 has nonnegative entries. On the other hand, taking into account that the functions $\mathcal{F}$ and $\mathcal{V}$ represent directed transfer of individuals and that the entries of J_4, due to hypothesis (H1), are given by the opposites of the coefficients of linear transfers between uninfected compartments, it follows that J_4 is a squared matrix with off diagonal nonpositive entries. Furthermore, from Proposition 2 and Remark 1 it follows that J_4 is a M-matrix and matrix J_4^{-1} has nonnegative entries. Hence, all the terms α_{lk} are nonpositive and this, together with (8) and (9), ensures that coefficient (7), if not zero, is negative. In view of Proposition 4, we can conclude that the bifurcation of system (2) at $R_0 = 1$ is forward. □

4 SIS model with vaccine and treatment

In a recent paper [6], the theory described in the previous section has been applied to an SIS epidemic model which includes a general force of infection, an imperfect preventive vaccine and treatment. We recall the main results obtained in [6] and discuss them in view of the aims of this paper, that is to detect the parts of the model's mathematical structure that might be responsible of a given direction (forward or backward) of the transcritical bifurcation.

The model is given by the following nonlinear ordinary differential equations:

$$\begin{aligned} \dot{S} &= \pi - c\beta_1 F(I)S - (\xi + \mu)S + \alpha I, \\ \dot{V} &= \xi S - c\beta_2 F(I)V - \mu V, \\ \dot{I} &= c\beta_1 F(I)S + c\beta_2 F(I)V - (\alpha + \mu)I. \end{aligned} \tag{10}$$

Here the state variables are the fractions in which the host population is divided: S, V and I denote the size of compartments of susceptible, vaccinated and infectious individuals, respectively. All the parameters are positive constants with the following interpretation: π is the recruitment rate of susceptibles; β_1 and β_2 are the transmission probabilities of susceptibles and vaccinated individuals, respectively; c is the average number of contact partners; ξ is the vaccination rate of susceptibles; α is the therapeutic treatment rate of infectious individuals; μ is the natural death.

The treatment does not confer permanent immunity, so that a linear transfer (at rate α) goes from I to S. The disease transmission is represented by a general force of infection, $F(I) \in C^2(\mathbb{R})$ such that $F(0) = 0$, and $F(I) > 0$ for $I > 0$.

The following assumptions are also considered: (i) $\beta_2 < \beta_1$, due to the fact that vaccination can reduce or eliminate the incidence of infection; (ii) the prevalent disease does not kill infected individuals.

Model (10), with a specific force of infection, has been originally introduced in [20], and later generalized in [5, 6], where the occurrence of backward bifurcations and the effect of nonlinear forces of infection have been studied.

It can be easily checked that model (10) admits the *disease-free* equilibrium

$$E_0 = \left(\frac{\pi}{\xi+\mu}, \frac{\xi\,\pi}{\mu(\xi+\mu)}, 0\right).$$

Taking the contact partners as bifurcation parameter, the following property holds: E_0 is locally stable when $c < c^*$, and unstable when $c > c^*$, where

$$c^* = \frac{\mu(\alpha+\mu)(\xi+\mu)}{\pi F'(0)(\beta_1\mu+\xi\beta_2)}.$$

As a consequence, the critical value $c = c^*$ is a bifurcation value.

The next step is to investigate the nature of the bifurcation involving E_0 at $c = c^*$. Following the above procedure, in [6], it has been shown that coefficients (5) and (6) for model (10) are given by

$$a = (\mu+\alpha)\left[\frac{F''(0)}{F'(0)} - \frac{2\mu a_0}{\pi(\beta_1\mu+\xi\beta_2)^2}\right], \qquad b = \frac{\pi F'(0)(\beta_1\mu+\xi\beta_2)}{\mu(\xi+\mu)},$$

where

$$a_0 = \xi\beta_2(\beta_1-\beta_2)(\alpha_c-\alpha), \qquad \alpha_c = \frac{\xi^2\beta_2^2+\beta_1^2\mu^2+\xi\mu\beta_1\beta_2+\xi\beta_2^2\mu}{\xi\beta_2(\beta_1-\beta_2)}.$$

The coefficient b, as expected, is always positive so that the local dynamics around E_0 for $c = c^*$ is determined by the sign of the coefficient a.

As a consequence, the following condition ensures the occurrence of a backward bifurcation at $c = c^*$

$$\frac{F''(0)}{F'(0)} > K(\alpha_c-\alpha), \tag{11}$$

where

$$K = \frac{2\xi\beta_2\mu(\beta_1-\beta_2)}{\pi(\beta_1\mu+\beta_2\xi)^2}.$$

On the contrary, condition

$$\frac{F''(0)}{F'(0)} < K(\alpha_c-\alpha) \tag{12}$$

implies that a forward bifurcation occurs at $c = c^*$.

Conditions (11) and (12) put in evidence the interplay between the treatment rate and the force of infection in determining the occurrence of forward or backward bifurcation. In the special case of a linear force of infection, $F(I) = I$, it follows $F'(0) = 1$ and $F''(0) = 0$, so that backward (forward) bifurcation will occur at $c = c^*$ when $\alpha > \alpha_c$ ($\alpha < \alpha_c$).

Note also that $\alpha = 0$ implies forward bifurcation.

In [6], it has been also proved that:

- When the force of infection is a *Michaelis–Menten* functional, $F(I) = I/(1 + I)$, or a non-monotone functional, $F(I) = I/(1 + I^2)$, a threshold value α_c between forward and backward bifurcation still exists;
- When the force of infection is convex, $F(I) = I(1 + I)$, then the backward bifurcation occurs for every $\alpha > 0$.

Summarizing, from conditions (11) and (12) the role played by any single parameter in the occurrence of forward/backward bifurcation can be deduced, as well as the role played by the force of infection. We see that the treatment must be greater than a threshold value, although in some cases such threshold may be zero. In such cases, the backward bifurcation occurs independently of the treatment values. On the other hand, other mechanisms contribute to the occurrence of the phenomenon, as, for example, the level of vaccine protection. In fact, in case of a perfect vaccine, $\beta_2 = 0$, it can be seen that $a > 0$, only if $F''(0) \geqslant (2\mu/\pi)F'(0)$, and the backward bifurcation in several cases, as mass action incidence, will not take place.

From the point of view of the mathematical structure, these results suggest that for this model, a major role in determining the direction of the transcritical bifurcation is given by the nonlinearity of the interaction term (transmission) and the linear transfer from the infected to the susceptibles compartment (treatment).

This is in line with Proposition 1, as it will be underlined in the next section, where several more examples taken from the literature will be also provided.

5 Applications

5.1 SIS model with treatment and imperfect vaccine

We begin with model (10), presented in the previous section. In this case, we can classify the state variables as follows. *Uninfected class*: susceptibles S and vaccinated V. *Infected class*: infectious I.

In the previous section, we have seen that backward bifurcation is possible if the force of infection is nonlinear, or the force of infection is linear and the treatment is not zero ($\alpha > 0$). In the former case, hypothesis (H2) of Proposition 1 is not satisfied; in the latter, hypothesis (H3) is not satisfied. On the other hand, we have also proved that $\alpha = 0$ implies forward bifurcation in case of linear force of infection. Note that, in this case, conditions (H1)–(H3) are satisfied.

We also stress that Proposition 1 is necessary but not sufficient for the occurrence of backward bifurcation. Indeed, if $\beta_2 = 0$, then condition (H3) is not satisfied due to linear transfer from I to S (treatment). However, as we mentioned in the previous section, the transcritical bifurcation is forward.

5.2 Model of hepatitis B and C virus

In [27], the transmission of hepatitis C and B viruses is studied by assuming that the virus is present in two reservoirs, the liver and the blood of host individuals. The model is the

following:

$$\begin{aligned}
\dot{X} &= \lambda_x - \beta_x XV - d_x X,\\
\dot{Y} &= \beta_x XV - a_y Y,\\
\dot{V} &= k_x Y + k_z W - uV - \alpha_x\beta_x XV - \alpha_z\beta_z ZV,\\
\dot{Z} &= \lambda_z - \beta_z ZV - d_z Z,\\
\dot{W} &= \beta_z ZV - a_w W.
\end{aligned} \tag{13}$$

The state variables are the target cells in liver (X) and blood (Z); the infected cells in liver (Y) and blood (W) and the free virus (V). Here X and Z belong to *uninfected class*; Y, V and W belong to the *infected class*. The parameters are described in Table 1. This model extends some previous models on HBV and HCV dynamics because the virions losses when they infect healthy cells is explicitly taken into account (i.e., the terms $\alpha_x\beta_x XV$ and $\alpha_z\beta_z ZV$ in the r.h.s. of the third equation). In order to emphasize the role of these two terms, we have slightly modified the original model by introducing the constants α_x and α_z.

In [27], it is proved that if $\alpha_x = 1$ or $\alpha_z = 1$ (which means that condition (H1) of Proposition 1 is not satisfied), then backward bifurcation occurs if $(k_z - a_w)(k_x - a_y) < 0$, whereas forward bifurcation occurs if the reversed inequality holds. On the other hand, it is also shown that if $\alpha_x = 0$ and $\alpha_z = 0$ (which means that conditions (H1)–(H3) are satisfied), then forward bifurcation occurs.

5.3 Dengue transmission dynamics

Here we consider the model for the transmission dynamics of a strain of dengue disease, including vaccination, studied in [17],

$$\begin{aligned}
\dot{S}_H &= \Pi_H + \omega P_H - \xi S_H - \lambda_H S_H - \mu_H S_H,\\
\dot{P}_H &= \xi S_H - \lambda_H(1-\epsilon)P_H - \omega P_H - \mu_H P_H,\\
\dot{E}_H &= \lambda_H\big[S_H + P_H(1-\epsilon)\big] - \sigma_H E_H - \mu_H E_H,\\
\dot{I}_H &= \sigma_H E_H - \tau_H I_H - \mu_H I_H - \delta_H I_H,\\
\dot{R}_H &= \tau_H I_H - \mu_H R_H,\\
\dot{S}_v &= \Pi_v - \lambda_v S_v - \mu_v S_v,\\
\dot{E}_v &= \lambda_v S_v - \sigma_v E_v - \mu_v E_v,\\
\dot{I}_v &= \sigma_v E_v - \mu_v I_v - \delta_v I_v.
\end{aligned} \tag{14}$$

The state variables are the humans susceptibles (S_H), vaccinated (P_H), exposed (E_H), infectious (I_H), removed (R_H) and the vector susceptibles (S_v), exposed (E_v), infectious (I_v).

Here the variables S_H, P_H, S_v, R_H belong to *uninfected class*; the variables E_H, I_H, E_v and I_v belong to the *infected class*. The parameters are described in Table 2.

Table 1. Description of parameters of model (13).

Parameter	Description
λ_x (λ_z)	Production rate of target cells in liver (blood)
d_x (d_z)	Death rate of target cells in liver (blood)
a_y (a_w)	Death rate of infected cells in liver (blood)
k_x (k_z)	Production rate of virus from infected cells in liver (blood)
β_x (β_z)	Infected cells production rate in liver (blood)
α_x, α_z	Virions decay constants
u	Virus clearance rate

Table 2. Description of parameters of model (14).

Parameter	Description
Π_H (Π_v)	Recruitment rate of humans (vectors)
λ_H (λ_v)	Infection rate of susceptible humans (vectors)
μ_H (μ_v)	Natural death rate of humans (vectors)
σ_H (σ_v)	Progression rate to infectious of exposed humans (vectors)
δ_H (δ_v)	Disease-induced death rate of humans (vectors)
k_H (k_v)	Infection rate of humans (vectors)
τ_H	Recovery rate of humans
ϵ	Vaccination efficacy
ω	Vaccination rate
ξ	Waning rate of vaccination

In [17], it is proved that if the infection rates are given by the following nonlinear terms:

$$\lambda_H = k_H \frac{\eta_v E_v + I_v}{S_H + P_H + E_H + I_H + R_H},$$

$$\lambda_v = k_v \frac{\eta_H E_H + I_H}{S_H + P_H + E_H + I_H + R_H},$$

which means that condition (H2) is not satisfied, then backward bifurcation is possible under certain conditions (see [17, Thm. 7]). However, if the forces of infection are linear, that is:

$$\lambda_H = k_H(\eta_v E_v + I_v), \qquad \lambda_v = k_v(\eta_H E_H + I_H),$$

which means that conditions (H1)–(H3) are satisfied, then forward bifurcation occurs (see [17, Thm. 8]).

5.4 Exogeneous re-infection in TB

The synergistic interaction between HIV and mycobacterium tuberculosis has been investigated in [31] by using a compartmental model, which incorporates many biological and epidemiological features of the two diseases. In particular, as suggested in [15], TB infection is not only seen as progression from primary infection but also as possibility of exogenous reinfection (i.e., acquiring a new infection from another infectious individual).

The model for the transmission dynamics of TB only is given by

$$\begin{aligned}
\dot{S} &= \Pi - \lambda S - \mu S,\\
\dot{L} &= f\lambda S + \rho W - \eta_R \lambda L - (\alpha + \mu)L,\\
\dot{T} &= (1-f)\lambda S + \eta_R \lambda L + \alpha L - (\tau + \mu + \delta)T,\\
\dot{W} &= \tau T - (\rho + \mu)W,
\end{aligned} \tag{15}$$

where state variables are the susceptibles (S), newly-infected with latent-TB (L), infected with active-TB (T) and unprotected treated individuals (W).

Here the variable S belongs to *uninfected class*; the variables L, T and W belong to the *infected class*. The parameters are described in Table 3.

In [31], it is proved that if the force of infection is described by the nonlinear function

$$\lambda = \beta \frac{T + \eta_T W}{S + L + T + W},$$

which means that condition (H2) is not satisfied, then backward bifurcation is possible when η_R is larger than a certain positive quantity [31, Thm. 3.9]. As a consequence, backward bifurcation will not occur if $\eta_R = 0$. In other words, the model will not undergo backward bifurcation in the absence of exogenous re-infection. A further confirm comes from a global stability result for the disease-free equilibrium when the basic reproduction number of model (15) is less than unity [19, Thm. 2].

We note that $\eta_R = 0$ implies that conditions (H1)–(H3) are satisfied, so that, according to our criterion, forward bifurcation occurs.

We finally remark that neglecting the disease-induced mortality, i.e., by setting, $\delta = 0$, it follows that the limiting system has a mass-action incidence, however backward bifurcation may still occur (see [19]). On the other hand, when $\delta = 0$ condition (H1) is not satisfied due to the term $-\eta_R \lambda L$ in the right-hand side of second equation.

5.5 West Nile virus transmission

The following model for the transmission of the West Nile virus within the mosquito, bird (intermediate host) and human population has been considered in [23]:

$$\begin{aligned}
\dot{M}_S &= \lambda_M - b_1 \Lambda_M M_S - \mu_M M_S,\\
\dot{M}_I &= b_1 \Lambda_M M_S - \mu_M M_I,\\
\dot{B}_S &= \lambda_B - b_1 \Lambda_B B_S - (\mu_B + \delta_B) B_S,\\
\dot{B}_I &= b_1 \Lambda_B B_S - (\mu_B + \delta_B) B_I - d_B B_I,\\
\dot{S} &= \lambda_H - b_2 \Lambda_H S - \mu_H S,\\
\dot{E} &= b_2 \Lambda_H S - \alpha E - \mu_H E,\\
\dot{I} &= \alpha E - \delta I - (d_I + r + \mu_H) I,\\
\dot{H} &= \delta I - d_H H - \tau H - \mu_H H,\\
\dot{R} &= \tau H + r I - \mu_H R,
\end{aligned} \tag{16}$$

Table 3. Description of parameters of model (15).

Parameter	Description
Π	Recruitment rate
β	Effective contact rate
μ	Natural death rate
α	Progression rate to active TB of individuals with latent TB
ρ	Progression rate to latent TB of treated individuals
η_T	Weight parameter
η_R	Probability of (exogeneous) re-infection of latently-infected individuals
f	Fraction of newly-infected individuals with latent TB
$1-f$	Fraction of newly-infected individuals with active TB
τ	Treatment rate
δ	Disease-induced death rate

Table 4. Description of parameters of model (16).

Parameter	Description
λ_B (λ_H, λ_v)	Recruitment rate of birds (humans, mosquitoes)
μ_B (μ_H, μ_v)	Death rate of birds (humans, mosquitoes)
b	Average biting rate of mosquitoes
$b_1\beta_1$ ($b_1\beta_2$)	Transmission rate from birds to mosquitoes (from mosquitoes to birds)
$b_2\beta_3$	Transmission rate from mosquitoes to humans
d_B (d_I, d_H)	Disease-induced death rate of birds (infectious humans, hospitalized)
δ_B	Migration rate of birds
α	Progression rate of humans from latent to infectious
δ	Hospitalization rate of humans
r (τ)	Recovery rate of infectious (hospitalized) humans

where state variables are the susceptible (M_S) and infected (M_I) mosquitoes; the susceptible (B_S) and infected (B_I) birds; the susceptible (S), exposed (E), infectious (I), hospitalized (H) and recovered (R) humans.

In this case, the variables M_S, B_S, S, H and R belong to *uninfected class*; the variables M_I, B_I, E, I belong to the *infected class*. The parameters are described in Table 4.

The forces of infection are nonlinear (so that condition (H2) is not satisfied) and given by

$$\Lambda_M = \beta_1 \frac{B_I}{B_S + B_I}, \qquad \Lambda_B = \beta_2 \frac{M_I}{B_S + B_I}, \qquad \Lambda_H = \beta_3 \frac{M_I}{S + E + I + H + R}.$$

In [23], it is proved that backward bifurcation occurs under certain conditions. However, when the disease-induced deaths are neglected ($d_B = d_I = d_H = 0$) the limiting system has a mass-action incidence (so that conditions (H1)–(H3) are satisfied) and the forward bifurcation occurs.

5.6 HIV infection model

In [36], a mathematical model for the HIV infection was developed based on vectored immunoprophylaxis experiments. The major novelty of the model, compared to previous HIV models, is that it includes the production and losses of antibodies in humoral immune

Table 5. Description of parameters of model (17).

Parameter	Description
λ	Recruitment rate of uninfected cells
d	Natural death rate of healthy cells
β	Infection coefficient
δ	Death rate of infected cells
N	Total number of free virus particles released by each productively infected cells over its lifespan
c	Clearance rate of virus particles
p	Killing rate of antibodies
q	Loss rate of antibodies
a	Production rate of antibodies
b	Clearance rate of antibodies

response. It is shown that the introduction of vectored immunoprophylaxis can induce backward bifurcation. The model is the following:

$$\begin{aligned} \dot{T} &= \lambda - dT - \beta TV, \\ \dot{T}^* &= \beta TV - \delta T^*, \\ \dot{V} &= N\delta T^* - cV - pAV, \\ \dot{A} &= \mu - bA - qAV, \end{aligned} \tag{17}$$

where state variables are the healthy cells T, the antibodies in humoral immune response A, the infected cells T^* and the virus V. Here, the variables T and A belongs to *uninfected class*; the variables T^*, V belong to the *infected-class*. The parameters are describedin Table 5.

In [36], it has been proved that backward bifurcation occurs if $\beta < pdq\mu/(b(cb+p\mu))$. On the other hand, condition (H1) is not satisfied because of the negative bilinear term $-pAV$ in the third equation. However, if the virus losses are neglected ($p = 0$), so that conditions (H1)–(H3) are fulfilled, then forward bifurcation occurs.

6 Concluding remarks

In this paper, we give a criterion in form of sufficient conditions for the occurrence of forward bifurcation and necessary conditions for the occurrence of backward bifurcation in epidemic models.

We provide several applications to models from the literature, including transmission of hepatitis, tuberculosis, dengue, West Nile virus and HIV.

Our result comes as a corollary of the theory developed in [10,14,34] and gives a direct way to evaluate the direction of the transcritical bifurcation by simply looking at the model structure.

We stress that the criterion does not include the possibility of nonlinearities other than transmission, as for example the nonlinear treatment term considered in [35], which results in backward bifurcation from an endemic (disease-present) equilibrium.

We feel that once that many investigations on the same phenomena for models with a similar structure are available from the literature, the necessity of general criterion based on the mathematical common aspects arises. This paper is therefore intended to give a contribution, albeit small, in this direction.

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Appendix: Derivation of the normal form

It is well know that the centre manifold theorem ensures the existence of the manifold [18]

$$W^c = \big\{(x_c, y)\colon\ y = h(x_c)\big\},$$

where $x_c \in E^c = \mathbb{R}$, $y \in E^s = \mathbb{R}^{(n-1)}$, and

$$h\colon\ U_{x_0} \subset \mathbb{R} \to \mathbb{R}^{(n-1)}, \quad h(x_0) = 0, \quad Dh(x_0) = 0.$$

Introduce now $\mathbf{v}_\alpha$ and $\mathbf{w}_\alpha$, left and right eigenvectors of A corresponding to the αth eigenvalue λ_α with $\alpha = 1, \dots, n$ (denote by $\mathbf{v}_n := \mathbf{v}$ and $\mathbf{w}_n := \mathbf{w}$ the eigenvectors corresponding to the zero eigenvalue, taken such that $\mathbf{v} \cdot \mathbf{w} = 1$).

Since in our setting $\mathbb{R}^n$ can be decomposed as $\mathbb{R}^n = E^c \oplus E^s \equiv \operatorname{span}(\mathbf{v}) \oplus E^s$, the center manifold may be parameterized by $u(t)$ and decomposed into E^c and E^s to give

$$W^c = \big\{\mathbf{x} = \mathbf{x}_0 + u(t)\mathbf{w} + \mathbf{z}(u, \mu)\big\},$$

where $\mathbf{z}(u, \mu) = \sum_{\alpha=1}^{n-1} \beta_\alpha \mathbf{w}_\alpha$ is orthogonal to $\mathbf{v}$ and is second order in both u and μ.

Moreover, the center manifold W^c is invariant under $\dot{\mathbf{x}} = \mathbf{f}(\mathbf{x}, \mu)$ so that

$$\dot{\mathbf{x}} = \dot{u}\mathbf{w} + \frac{\mathrm{d}\mathbf{z}}{\mathrm{d}t} = \mathbf{f}\big(\mathbf{x}_0 + u(t)\mathbf{w} + \mathbf{z}(u, \mu), \mu\big).$$

Multiplying by $\mathbf{v}$, we get

$$\mathbf{v} \cdot \dot{u}\mathbf{w} + \mathbf{v} \cdot \frac{\mathrm{d}\mathbf{z}}{\mathrm{d}t} = \mathbf{v} \cdot \mathbf{f}.$$

Observe that $\mathbf{v} \cdot \dot{u}\mathbf{w} = \dot{u}\mathbf{v} \cdot \mathbf{w} = \dot{u}$; and $\mathbf{v} \cdot \mathbf{z} = 0 \Rightarrow \mathbf{v} \cdot \mathrm{d}\mathbf{z}/\mathrm{d}t = 0$, so that

$$\dot{u} = \mathbf{v} \cdot \mathbf{f}\big(\mathbf{x}_0 + u(t)\mathbf{w} + \mathbf{z}(u, \mu), \mu\big).$$

By expanding in Taylor series, we obtain

$$\begin{aligned}\dot{u} = \mathbf{v} \cdot \Big[&\mathbf{f}(x_0, 0) + D_\mu \mathbf{f}(x_0, 0)\mu + D_{\mathbf{x}}\mathbf{f}(0, 0)(\mathbf{x} - \mathbf{x}_0) + \frac{1}{2} D_{\mu\mu}\mathbf{f}(x_0, 0)\mu^2 \\ &+ D_{\mathbf{x}\mu}\mathbf{f}(x_0, 0)\mu(\mathbf{x} - \mathbf{x}_0) + \frac{1}{2} D_{\mathbf{xx}}\mathbf{f}(x_0, 0)(\mathbf{x} - \mathbf{x}_0)^2 + O(3)\Big],\end{aligned}$$

where $O(3)$ denotes terms that are third order or higher. In this last equality, several terms vanish to give

$$\dot{u} = \mathbf{v} \cdot D_{\mathbf{x}\mu}\mathbf{f}(\mathbf{x}_0, 0)\mu(\mathbf{x} - \mathbf{x}_0) + \mathbf{v} \cdot \frac{1}{2} D_{\mathbf{xx}}\mathbf{f}(\mathbf{x}_0, 0)(\mathbf{x} - \mathbf{x}_0)^2 + O(3).$$

Recall that $\mathbf{x} - \mathbf{x}_0 = u(t)\mathbf{w} + \mathbf{z}(u, \mu)$, so that we have

$$\dot{u} = \mathbf{v} \cdot D_{\mathbf{x}\mu}\mathbf{f}(\mathbf{x}_0, 0)\mu(u\mathbf{w} + \mathbf{z}) + \mathbf{v} \cdot \frac{1}{2} D_{\mathbf{xx}}\mathbf{f}(x_0, 0)(u^2\mathbf{w}^2 + \mathbf{z}^2 + 2u\mathbf{w} \cdot \mathbf{z}) + O(3).$$

Since $\mathbf{z}$ is second order in both u and μ, it follows:

$$\dot{u} = \frac{\mathbf{v}}{2} \cdot D_{\mathbf{xx}}\mathbf{f}(x_0, 0)\mathbf{w}^2\, u^2 + \mathbf{v} \cdot D_{\mathbf{x}\mu}\mathbf{f}(\mathbf{x}_0, 0)\mathbf{w}\, \mu u + O(3).$$

Consider now quantities (5) and (6). Then, for $|\mu| < \delta$, the normal form (4) follows.

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