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DENSITY DEPENDENCE IN DISEASE INCIDENCE AND ITS IMPACTS ON TRANSMISSION DYNAMICS

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ABSTRACT. Incidence describes the rate at which new cases of infectious diseases occur. An accurate description of disease incidence is vital to infectious disease modelling. Incidence in epidemic models commonly depends on the size of the infectious and suceptible sub-populations, and may also depend on the size or density of the total population. We show that, even in the simplest SIR models, population dependent incidence can lead to complicated dynamics, including backward bifurcations that result in bistability and Hopf bifurcations that result in periodic oscillations. The types of density dependent incidence we consider can be interpreted as capturing changes in social behaviours as population size changes. Our results demonstrate that density-dependent incidence can be a new mechanism for complex disease dynamics.

1 Introduction For infectious diseases, incidence describes the rate new infections occur. To model the transmission dynamics of an infectious disease, accurately describing and estimating disease incidence are of utmost importance. In classical epidemic models such as those of Kermack-McKendric [**6, 21**], infection occurs through horizontal transmission, and the disease incidence is customarily modelled by a bilinear form, $\beta I(t)S(t)$, which is in proportion to the size or density of the sub-population of susceptible hosts $S(t)$ and that of the sub-population of infectious hosts $I(t)$. The parameter β represents the transmission coefficient and is dependent on the frequency of host-host contact and the probability of a contact being infectious [**1**]. For infections that spread through sexual contacts, as in HIV and other STD transmissions, the incidence is typically modelled by a proportionate form $\beta\frac{I(t)S(t)}{N(t)}$, where $N(t)$ is the total host population and the constant β describes the effec-

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tive contact rate among hosts [**6**]. When the host population is predominantly susceptible or infectious, saturated incidence forms, $\frac{\beta I(t)S(t)}{a+S(t)}$ or $\frac{\beta S(t)I(t)}{b+I(t)}$, respectively, have been used to account for the saturation of contacts [**6, 29**]. Nonlinear incidence of the form $\beta I(t)^p S(t)^q$ is used in [**24**] and shown to lead to complicated behaviours such as multiple endemic equilibria and existence of periodic oscillations. Other general forms of incidence terms have been used and further studied in more recent work [**23, 34**].

Among these common incidence forms, the proportionate incidence $\beta\frac{I(t)S(t)}{N(t)}$ depends explicitly on the total population size $N(t)$, and is said to be density dependent. If $N(t)$ is a constant, it can be combined with β so that the proportionate incidence is equivalent to the bilinear one. However, due to density dependance, the proportionate incidence and the bilinear incidence differ when $N(t)$ varies with time. More general forms of density dependence can be incorporated into the incidence term as $\beta I(t)S(t)f(N(t))$, for certain classes of functions f. A typical example is $f(N) = N^{-\alpha}$, $\alpha \geq 0$. When $\alpha = 0$, we obtain the bilinear incidence, and when $\alpha = 1$, we arrive at the proportionate incidence. It is shown in [**10, 11**] that, if $0 \leq \alpha \leq 1$, the incidence form $\beta\frac{I(t)S(t)}{N(t)^\alpha}$ typically leads to standard threshold behaviour in simple epidemic models: the disease dies out if the basic reproduction number $R_0 < 1$ and the disease becomes endemic and persists at a unique endemic equilibrium when $R_0 > 1$. In the present paper, we show that if $f(N)$ takes more general and yet biologically plausible forms, density-dependent incidence $\beta I(t)S(t)f(N(t))$ can lead to complicated dynamics even in the simplest SIR models.

To introduce and interpret density dependence in disease incidence, we first recall that the disease incidence can be calculated as

$$\lambda(N(t))\frac{S(t)}{N(t)}I(t).$$

In this expression, the contact rate, $\lambda(N)$, is the average number of effective contacts made by a single infectious individual in one unit of time. With probability $S(t)/N(t)$ such a contact is made with a susceptible individual and therefore produces an new infection. Multiplied by the total number $I(t)$ of infectious hosts, the expression gives the total number of new infections per unit time. Density dependence will be introduced through $\lambda(N)$. For bilinear incidence, we have $\lambda(N) = \beta N$, which assumes the number of contacts is linearly proportional to the size of the population. This may be plausible for populations of large urban

centres where, because of limited living space, an increase in population size is likely to increase population density and the frequency of contact. In proportionate incidence, we have that $\lambda(N) = \beta$ and is independent of population size N. This is plausible for populations in rural areas where an increase in population size does not necessarily increase population density and the frequency of contact. In a more general incidence $\beta I(t)S(t)f(N(t))$, we have the contact rate equal to $\lambda(N) = \beta N f(N)$.

The first class of $f(N)$ we consider is $f(N) = BN^{-\alpha},\ \alpha > 1$. In this case, the contact rate $\lambda(N) = \beta B N^{1-\alpha}$. When $\alpha > 1$, an increase in N leads to a decrease of contact. This is plausible for diseases which require a significant number of contact to be transmitted and a culture where people in large urban centres tend to have less contact with their neighbours when population density increases. We demonstrate that, with this incidence form, backward bifurcations can occur in a simple SIR model, namely, multiple endemic equilibria exist when $R_0 < 1$. Backward bifurcations have been investigated in a variety epidemic models and are known to lead to catastrophic effects in terms of disease control [**2, 4, 5, 7, 9, 12, 13, 17, 22, 25, 27, 28, 31, 33**]; when backward bifurcation occurs, the outcome of a disease outbreak not only depends on the parameter values, but also critically depends on the initial conditions. Some known biological mechanisms that may lead to backward bifurcations are imperfect immunity [**9**], a vaccine that is leaky [**2, 22**], and behavioural responses to perceived disease risk [**12**]. In many of these models, backward bifurcation occurs due to asymmetry among different contact groups or multiple routes for transmission. Our result shows that backward bifurcation can result solely from density dependence in the incidence form.

A second class of $f(N)$ we investigate is $f(N) = aN^2 + bN + c,\ a > 0$. In this case, the contact rate $\lambda(N) = \beta N\,(aN^2 + bN + c)$ is a cubic function that increases for small or large values of N, and may decrease for intermediate values of N. Such a region of decrease can be the result of adjustment of social behaviours as population size increases. For this class of f, we show that multiple endemic equilibria can exist when $R_0 > 1$. Furthermore, one of the endemic equilibria can undergo stability change, and a Hopf bifurcation occurs, producing stable periodic oscillations. Such dynamical outcomes have been observed in SEIR models of constant total population with nonlinear incidence [**24**]. Our result shows that the same phenomenon can also explained through density dependence in the disease incidence.

We also consider the effect of adding multiple infectious stages to the model with these classes of $f(N)$. Our result shows that endemic equilib-

ria for the multi-stage model can be identified using the same analysis that was used in the single stage model. Furthermore, we determine that the existence of a backward bifurcation depends on the number of infectious stages as well as the model parameters.

Incidence forms that incorporate social behaviour changes have been investigated in epidemic models using nonlinear incidence forms [**12, 28**]. A piecewise incidence function incorporating a sharp change in social behaviours is studied in [**3**] and shown to lead to periodic behaviour. While incidence forms in our study may be considered as social behaviours related, they are different from those in previous studies in that we incorporate social behaviours through nonlinear density dependence, dependence on the total population size N, rather than explicit nonlinear dependence on I or S.

2 The model and preliminaries We consider a simple SIR epidemic model with population dependant incidence. The transfer diagram is depicted in Figure 1. Here, S is the susceptible population, I is the infectious population, and R is the recovered or removed population. The total population $N = S+I+R$. The model is described by a system of differential equations:

$$\begin{aligned} \dot{S} &= \Lambda - \beta I S f(N) - d_S S \\ \dot{I} &= \beta I S f(N) - \gamma I - d_I I \\ \dot{R} &= \gamma I - d_R R. \end{aligned} \tag{1}$$

The average per capita contact rate is given by $\lambda(N) = \beta N f(N)$. The parameter Λ indicates the influx of susceptibles, and γ denotes the rate constant for recovery. Accordingly, $1/\gamma$ is the mean infectious period. We assume that the disease can be fatal and thus death rate d_I for the I compartment may contain both natural and disease-related death. Accordingly, we assume that the death rates $d_S,\ d_I$ and d_R satisfy

$$0 < d_S \leq d_R \quad \text{and} \quad d_S < d_I. \tag{2}$$

This assumption is sufficient for the total population N to be time dependent. In contrast, if $d_S = d_I = d_R = d$, then $N'(t) = \Lambda - dN(t)$, and $N(t) \to \Lambda/d$ as $t \to \infty$ and model (1) can be replaced by a limiting system with $N = \Lambda/d$.

It can be verified that solutions to model (1) with nonnegative initial conditions remain nonnegative and bounded for all $t \geq 0$. Furthermore,

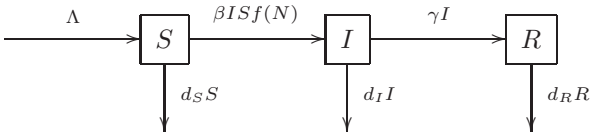


FIGURE 1: The transfer diagram for model (1).

the compact region

$$\Gamma = \left\{ (S, I, R) \in \mathbb{R}^3_+ \;\middle|\; S + I + R \leq \frac{\Lambda}{d_S} \right\}$$

is positively invariant for model (1) and globally attracting. It suffices to investigate the global dynamics of model (1) in Γ.

For all nonnegative parameter values, the model has a disease-free equilibrium $P_0 = (\bar{S}, 0, 0)$, with $\bar{S} = \Lambda/d_S$. The Jacobian matrix of of model (1) at P_0 is given by

$$\begin{bmatrix} -d_S & -\beta\bar{S}f(\bar{S}) & 0 \\ 0 & \beta\bar{S}f(\bar{S}) - (d_I + \gamma) & 0 \\ 0 & \gamma & -d_R \end{bmatrix}$$

and has eigenvalues $\lambda_1 = -d_S < 0$, $\lambda_2 = -d_R < 0$, and $\lambda_3 = \beta\bar{S}f(\bar{S}) - (d_I + \gamma)$. Therefore, the disease free equilibrium P_0 is asymptotically stable if and only if $\beta\bar{S}f(\bar{S}) < d_I + \gamma$. Let

$$R_0 = \frac{\beta}{d_I + \gamma}\bar{S}f(\bar{S}). \tag{3}$$

This is the basic reproduction number for model (1) [**1, 14**]. When $f(N) = 1$, $R_0 = \frac{\beta}{d_I+\gamma}\bar{S}$, which agrees with the basic reproduction number for SIR models with bilinear incidence. When $f(N) = 1/N$, $R_0 = \beta/(d_I + \gamma)$, which agrees with the basic reproduction number of SIR model with proportionate incidence. Note that $R_0 < 1$ if and only if $\beta\bar{S}f(\bar{S}) < d_I + \gamma$. The following threshold result is standard.

Proposition 1. *If $R_0 < 1$, then the disease-free equilibrium P_0 is asymptotically stable. If $R_0 > 1$, then P_0 is unstable, model* (1) *is uniformly persistent, and an endemic equilibrium exists in the interior of* Γ.

Endemic equilibria, (S^*, I^*, R^*) with $I^* > 0$, of model (1) are determined by

$$\begin{aligned} 0 &= \Lambda - \beta I^* S^* f(N^*) - d_S S^* \\ 0 &= \beta S^* f(N^*) - \gamma - d_I \\ 0 &= \gamma I^* - d_R R^*. \end{aligned} \tag{4}$$

From the second equation in (4) we obtain

$$\beta S^* f(N^*) = \gamma + d_I \quad \text{and} \quad N^* = (1 - p d_S) S^* + p\Lambda. \tag{5}$$

Denote

$$p = \frac{1}{d_I + \gamma} + \frac{1}{d_R} \frac{\gamma}{d_I + \gamma} \quad \text{and} \quad \sigma = \frac{\beta}{d_I + \gamma}. \tag{6}$$

The parameter p is the mean life expectancy of those who become infected. The parameter σ is the average number of effective contacts made by an infective in its mean infectious period $\frac{1}{d_I+\gamma}$, and is called the *contact number* in [**14**]. Assumption (2) implies that $pd_S < 1$.

Define

$$g(S) = S f(N(S)) \tag{7}$$

with

$$N(S) = (1 - p d_S)\, S + p\Lambda.$$

Then, from equation (5), an equilibrium S^* must satisfy

$$g(S^*) = \frac{1}{\sigma}, \quad S^* \in (0, \bar{S}]. \tag{8}$$

In the following two sections, we will show that for different classes of $f(N)$, it is possible for model (1) to have multiple endemic equilibria, which in turn can lead to complicated dynamics.

3 $\mathbf{f(N) = BN^{-\alpha}}$: backward bifurcations In this section, we assume that $f(N) = BN^{-\alpha}$. For $\alpha \leq 1$, it is known that the traditional threshold result holds for model (1) [**10, 11**]: if $R_0 \leq 1$, then the disease-free equilibrium P_0 is globally stable; if $R_0 > 1$, then a unique endemic equilibrium exists and is globally stable in the interior of the feasible region.

In the rest of the section, we assume that $\alpha > 1$. The function $g(S)$ defined in (7) is written as

$$g(S) = \frac{BS}{[(1 - pd_S)S + p\Lambda]^\alpha}. \tag{9}$$

Note that $g(0) = 0$, $g(\bar{S}) = (\Lambda/d_S)^{1-\alpha}$, and $g(S)$ is continuous and positive for $S > 0$. Differentiating $g(S)$ in (9) gives

$$g'(S) = \frac{B\left[S(1 - pd_S)(1 - \alpha) + p\Lambda\right]}{[(1 - pd_S)S + p\Lambda]^{\alpha+1}},$$

and $g(S)$ has a single critical point

$$S_{\text{crit}} = \frac{p\Lambda}{(1 - pd_S)(\alpha - 1)}.$$

When $\alpha \leq \frac{1}{1-pd_S}$, $g(S)$ is monotone in the interval $(0, \bar{S})$, and multiple endemic equilibria can not occur. When $\frac{1}{1-pd_S} < \alpha$, $S_{\text{crit}} \in (0, \bar{S})$, and equation (8) can have two solutions in $(0, \bar{S})$.

The value of g at the critical point is given by

$$g(S_{\text{crit}}) = \frac{g(\bar{S})}{(1 - pd_S)(pd_S)^{\alpha-1}} \frac{(\alpha - 1)^{\alpha-1}}{\alpha^\alpha}. \tag{10}$$

Since the function $h(x) = (1 - x)(x)^{\alpha-1}$ has its maximum value of $\frac{(\alpha-1)^{\alpha-1}}{\alpha^\alpha}$ attained at $\frac{1}{1-x} = \alpha$, we see that, if $\frac{1}{1-pd_S} < \alpha$, then

$$(1 - pd_S)(pd_S)^{\alpha-1} < \frac{(\alpha - 1)^{\alpha-1}}{\alpha^\alpha}. \tag{11}$$

As a consequence, $g(S_{\text{crit}}) > g(\bar{S})$ and $g(S_{\text{crit}})$ is a maximum. We can draw conclusions about the number of solutions of (8) based on the location of $g(S_{\text{crit}})$ and $g(\bar{S})$ relative to $1/\sigma$, as summarized in the next proposition. Figure 2 illustrates the possibilities.

Proposition 2. *Let $f(N) = BN^{-\alpha}$ and assume that $\alpha > \frac{1}{1-pd_S}$. Then system (1) has no endemic equilibria if $g(S_{\text{crit}}) < 1/\sigma$, exactly one endemic equilibria if $g(\bar{S}) > 1/\sigma$, and two endemic equilibria if $g(\bar{S}) < 1/\sigma < g(S_{\text{crit}})$.*

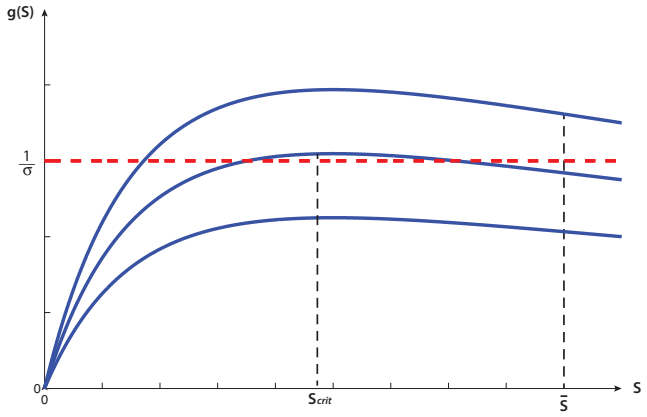


FIGURE 2: Possible solutions of equation $g(S) = 1/\sigma$ with $f(N) = 1/N^{\alpha}$.

We note that $g(\bar{S}) = \bar{S}f(\bar{S})$, and thus $\sigma g(\bar{S}) = 1$ if and only if $R_0 = 1$. Similarly, from (10) we know $\sigma g(S_{\text{crit}}) = 1$ if and only if R_0 agrees with

$$\overline{R}_0 := \frac{\alpha^{\alpha}}{(\alpha-1)^{\alpha-1}}(1 - pd_S)(pd_S)^{\alpha-1}. \tag{12}$$

We see from (11) that $\overline{R}_0 < 1$.

Proposition 2 implies existence of two endemic equilibria when R_0 is in the range $\overline{R}_0 < R_0 < 1$. When this happens, system (1) is said to undergo a *backward bifurcation* at $R_0 = 1$ [**17**]. To complete the bifurcation diagram, we discuss the stability of endemic equilibria. We can show that, in the case when $d_S = d_R$, if two endemic equilibria $P_* = (S_*, I_*, R_*)$ and $P^* = (S^*, I^*, R^*)$ exist, with $S_* < S^*$, then P_* is unstable and P^* is asymptotically stable. See Proposition A in the Appendix for proof. The result is summarized in the following theorem, and the bifurcation diagram using R_0 as a bifurcation parameter is illustrated in Figure 3.

Theorem 1. *Let* $f(N) = BN^{-\alpha}$, $\alpha > \frac{1}{1-pd_S}$. *Assume that* $d_S = d_R$.

(1) *If* $0 < R_0 < \overline{R}_0$, *then the disease-free equilibrium* P_0 *is the only equilibrium in* Γ *and it is asymptotically stable.*

(2) *If* $\overline{R}_0 < R_0 < 1$, *then there exist two endemic equilibria* $P_* = (S_*, I_*, R_*)$ *and* $P^* = (S^*, I^*, R^*)$ *with* $S_* < S^*$. *Equilibrium* P_* *is unstable while* P_0 *and* P^* *are asymptotically stable.*

(3) *If* $R_0 > 1$, *then* P_0 *is unstable, and a unique endemic equilibrium* $P^* = (S^*, I^*, R^*)$ *exists and is asymptotically stable.*

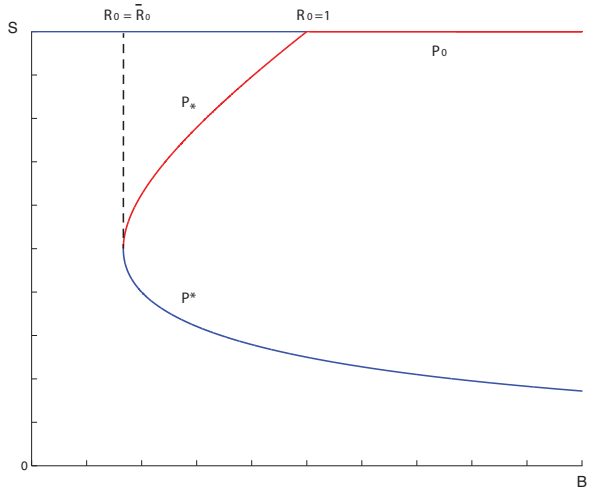


FIGURE 3: Backward bifurcation at $R_0 = 1$ for model (1) when $f(N) = 1/N^\alpha$.

4 Quadratic f(N): Hopf bifurcations In this section, we consider the class of functions

$$f(N) = B(N^2 + aN + b).$$

We will assume that $R_0 = \sigma\, g(\bar{S}) = \frac{\beta}{d_I+\gamma}\bar{S}f(\bar{S}) > 1$ and investigate possibilities of multiple endemic equilibria. As shown in Section 2, an endemic equilibrium $P^* = (S^*, I^*, R^*)$ satisfies equation (8). In this case, the function $g(S)$ is a cubic function

$$g(S) = B_1\, S\, (S^2 + a_1 S + b_1), \tag{13}$$

with

$$B_1 = B(1 - d_S p)^2, \quad a_1 = \frac{a + 2p\Lambda}{1 - pd_S}, \quad b_1 = \frac{(p\Lambda)^2 + ap\Lambda + b}{(1 - pd_S)^2}. \tag{14}$$

We require that $g(S) = 0$ if and only if $S = 0$. This is the case when coefficients in $g(S)$ satisfy relation

$$a_1{}^2 < 4b_1. \tag{15}$$

Function $g(S)$ in (13) has two critical points

$$S_c^{\pm} = \frac{-a_1 \pm \sqrt{a_1{}^2 - 3b_1}}{3}. \tag{16}$$

When these critical points are real, distinct, and located in the interval $(0, \bar{S})$, equation (8) will have three solutions for appropriate values of B_1, resulting in three endemic equilibria. For both critical points to be real, distinct, and positive, it is necessary that

$$a_1 < 0 \quad \text{and} \quad 3b_1 < a_1{}^2. \tag{17}$$

Since $g(\bar{S}) > 1/\sigma$, for all solutions of $g(S) = 1/\sigma$ to belong to $(0, \bar{S})$, it is necessary and sufficient that $g'(\bar{S}) > 0$ and $g''(\bar{S}) > 0$, namely that

$$b_1 > -2a_1\bar{S} - 3(\bar{S})^2 \quad \text{and} \quad a_1 > -3\bar{S}. \tag{18}$$

Figure 4 illustrates the nonempty region in the (a_1, b_1) parameter space defined by conditions (15), (17) and (18), where three endemic equilibria are possible.

Using

$$a_1 = -\frac{3}{2}(S_c^+ + S_c^-) \quad \text{and} \quad b_1 = 3S_c^+ S_c^-,$$

we can rewrite $g(S)$ as

$$g(S) = B_1 S\left[S^2 - \frac{3}{2}(S_c^+ + S_c^-)S + 3S_c^+ S_c^-\right].$$

Then

$$g(S_c^-) = \frac{B_1}{2} S_c^{-2}(3S_c^+ - S_c^-) \quad \text{and} \quad g(S_c^+) = \frac{B_1}{2} S_c^{+2}(3S_c^- - S_c^+). \tag{19}$$

The point S_c^- is a local maximum for the function $g(S)$ while the point S_c^+ is a local minimum. Whether three endemic equilibria occur is determined by relative relations among $g(S_c^{\pm})$, $g(\bar{S})$ and $1/\sigma$.

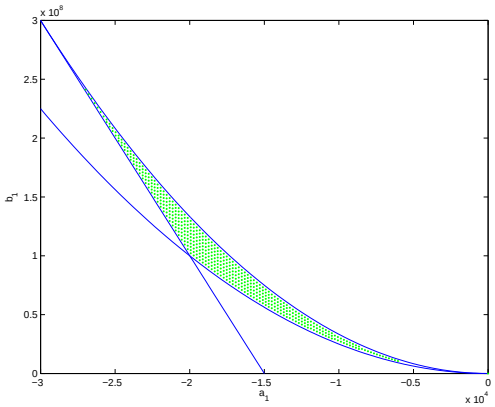


FIGURE 4: Shaded region indicates parameter values (a_1, b_1) for which three endemic equilibria are possible with a quadratic $f(N)$.

Proposition 3. *Let* $f(N) = B(N^2 + aN + b)$. *Assume that* $R_0 = \sigma g(\bar{S}) > 1$, $g'(\bar{S}) > 0$, *and* $g''(\bar{S}) > 0$.

(1) *If* $1/\sigma < g(S_c^+)$, *then model* (1) *has exactly one endemic equilibrium.*
(2) *If* $g(S_c^+) = 1/\sigma$, *then model* (1) *has two endemic equilibria.*
(3) *If* $g(S_c^+) < 1/\sigma < g(S_c^-)$, *then model* (1) *has three endemic equilibria.*
(4) *If* $g(S_c^-) = 1/\sigma$, *then model* (1) *has two endemic equilibria.*
(5) *If* $g(S_c^+) < 1/\sigma$, *then model* (1) *has exactly one endemic equilibrium.*

Proposition 3 is illustrated in Figure 5. Using (14) and (19) we can rewrite conditions in Proposition 3 in terms of ranges for parameter B_1. For instance, the range of B_1 for model (1) to have three endemic equilibria is

$$\frac{2}{{S_c^-}^2(3S_c^+ - S_c^-)} < B_1 < \frac{2}{{S_c^+}^2(3S_c^- - S_c^+)}.$$

To investigate secondary bifurcations when multiple endemic equilibria exist, we examine the stability of endemic equilibria. Routh-Hurwitz conditions for all eigenvalues of the Jacobian matrix F at an endemic equilibrium to have negative real parts are

1. $T = \text{trace}(F) < 0$,

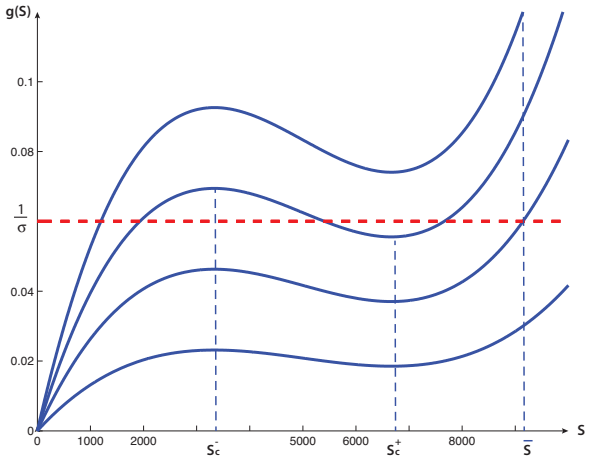


FIGURE 5: Number of solutions of equation of $g(S) = 1/\sigma$ in $[0, \bar{S})$ with a quadratic $f(N)$.

2. $D = \det(F) < 0$, and
3. $C = TM - D < 0$,

where M is the sum of the second-order principle minors of F. It can be verified that

$$T = -If(N) - d_S - d_R < 0,$$

and that

$$\begin{aligned} D &= -\frac{d_R}{\beta} If(N) + ISf'(N)[d_R d_S + \gamma d_S - d_R(d_I + \gamma)] \\ &= -d_R(d_I + \gamma)[If(N) + ISf'(N)(1 - pd_S)] \\ &= -d_R(d_I + \gamma)\frac{dg(S)}{dS}. \end{aligned}$$

Then, whenever $\frac{dg(S)}{dS} < 0$, D is positive and the equilibrium will be unstable. As shown in Figure 5, when there are three endemic equilibria, the equilibrium with intermediate S^* value will always be unstable. When $\frac{dg(S)}{dS} > 0$, the stability is determined by the sign of $C = TM - D$. This allows the possibility for one of the branches to undergo stability change, and possibility for Hopf bifurcation.

Numerical computation using Matlab reveals that the sign of C at the endemic equilibrium with the largest value of S^* can change as values of parameters change. Since $\frac{dg(S^*)}{dS} > 0$ at this equilibrium, a sign change in C indicates that a pair of complex eigenvalues cross the imaginary axis and the occurrence of a Hopf bifurcation.

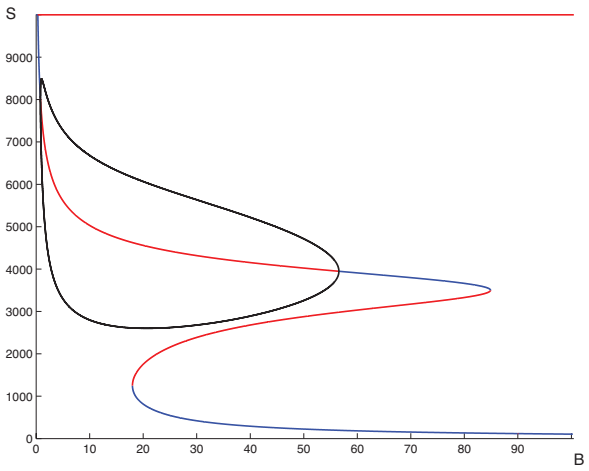
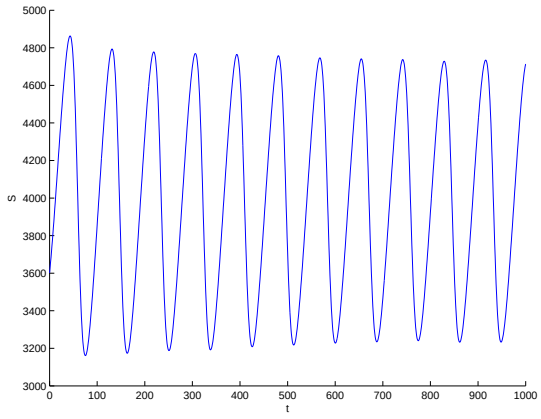
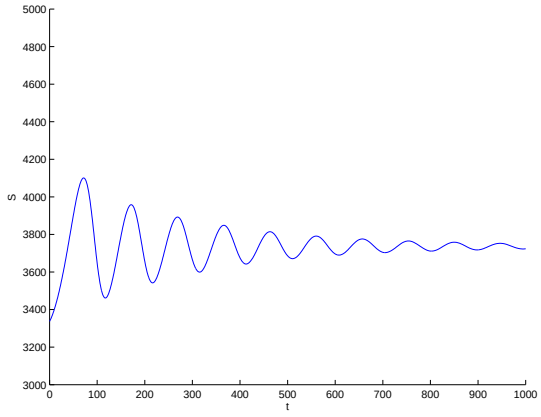


FIGURE 6: Bifurcation diagram when $f(N)$ is quadratic. A supercritical Hopf bifurcation occurs when B decreases through $B = 55$. The dark closed loop indicates stable periodic solutions, and they exist for B in the range $(0.5, 55)$.

Numerical bifurcation analysis using XPPAUTO confirms that the system has a Hopf bifurcation at the endemic equilibria with the largest value of S^*. We show in the bifurcation diagram in Figure 6 that, as a bifurcation parameter B decreases, the equilibrium changes from being stable to unstable, and a supercritical Hopf bifurcation occurs, creating a stable periodic orbit. Matlab simulations also confirm that model (1) has a stable periodic orbit in the range of B given in the bifurcation diagram. In Figure 7(a), a solution of (1) is shown to converge to a stable periodic solution when $B = 50$. In Figure 7(b), we show that solutions converge to an endemic equilibrium at a $B = 75$, before the Hopf bifurcation occurs. We remark that, since the incidence form is $\beta ISB(N^2 + aN + b)$, bifurcation observed as we vary parameter B can also be observed if we vary parameter β.



(a) A solution converges to a sable periodic solution when $B = 50$.



(b) A solution converges to an endemic equilibrium when $B = 75$.

FIGURE 7: Matlab simulations for $B = 50$ and $B = 75$.

5 Multiple infectious stages Similar results and analysis in Sections 3 and 4 can be carried out for epidemic models with more complex structures than the simple SIR model. We consider a multiple-stage model that describes the transmission dynamics of infectious diseases progressing through a long infectious period such as HIV/AIDS

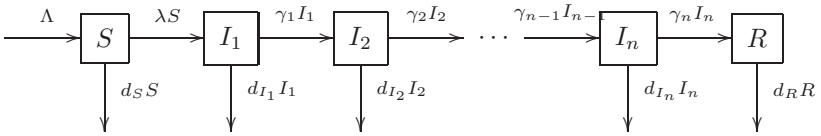


FIGURE 8: Transfer diagram for the n-stage model (20). Incidence term is given by $\lambda S = \sum_{j=1}^{n} \beta_j I_j f(N) S$.

[**8, 10, 11, 18, 19, 20, 26**]. The n-stage model as depicted in Figure 8 is a generalization of the single-stage SIR model (1). The infectious period is partitioned into n distinct stages with $I_j(t)$ individuals in the j-th infectious stage. Individuals in the j-th infectious stage are assumed to have a transmission coefficient β_j and the transfer rate from the j-th stage to the next is given by γ_j, $j = 1, \cdots, n$. We assume that all parameter values are nonnegative and, as in the preceding sections, that $0 < d_S \leq d_R$, and $d_S < d_{I_j}$, $j = 1, \cdots, n$. The model is described by a system of $n + 2$ differential equations

$$
\begin{aligned}
S' &= \Lambda - \bar{\lambda} S f(N) - d_S S, \\
I_1' &= \bar{\lambda} S f(N) - \gamma_1 I_1 - d_{I_1} I, \\
I_i' &= \gamma_{i-1} I_{i-1} - \gamma_i I - d_{I_i} I, \quad \text{for} \quad i = 2 \cdots n, \\
R' &= \gamma_n I_n - d_R R,
\end{aligned}
\tag{20}
$$

where the force of infection is given by

$$
\bar{\lambda} = \sum_{j=1}^{n} \beta_j I_j f(N). \tag{21}
$$

Adding the equations in (20) we obtain

$$
N^{'} = \Lambda - d_S S - d_{I_1} I_1 - \cdots - d_{I_n} I_n - \gamma_n I_n \leq \Lambda - d_S N.
$$

It follows that $\lim\limits_{t \to \infty} \sup N(t) \leq \Lambda / d_S$. The global dynamics of model (20) can be investigated in the positively invariant compact subset of $\mathbb{R}_+^{n+2}$

$$
\Delta = \{(S, I_1, \cdots, I_n, R) \in \mathbb{R}_+^{n+2} \ : \ 0 \leq S + I_1 + \cdots + I_n \leq \Lambda / d_S\}.
$$

Let

$$A = \begin{bmatrix} d_{I_1}+\gamma_1 & 0 & 0 & \cdots & & \\ -\gamma_1 & d_{I_2}+\gamma_2 & 0 & \cdots & & \\ 0 & -\gamma_2 & d_{I_3}+\gamma_3 & \cdots & & \\ \vdots & \vdots & \vdots & \ddots & & \\ & & & & d_{I_n}+\gamma_n & 0 \\ & & & & -\gamma_n & d_R \end{bmatrix}. \tag{22}$$

Then A is an M-matrix and diagonally dominant in columns. Therefore, A is invertible and $A^{-1} > 0$ [**16**]. In particular,

$$\sigma_n = (\beta_1, \cdots, \beta_n, 0)A^{-1}(1, 0, \cdots, 0)^t > 0, \tag{23}$$

and that

$$p_n = (1, \cdots, 1)A^{-1}(1, 0, \cdots, 0)^t > 0, \tag{24}$$

where the superscript t denotes the matrix transposition. The inverse A^{-1} of the triangular and bidiagonal matrix A can be computed to give the explicit expressions for σ_n and p_n

$$\sigma_n = \sum_{j=1}^{n} \frac{\beta_j}{d_{I_j}+\gamma_j}\delta_{j-1}, \tag{25}$$

and

$$p_n = \left(\sum_{j=1}^{n} \frac{1}{d_{I_j}+\gamma_j}\delta_{j-1}\right) + \frac{1}{d_R}\delta_n, \tag{26}$$

where δ_k is given by

$$\delta_k = \prod_{j=1}^{k} \frac{\gamma_j}{d_{I_j}+\gamma_j}.$$

Notice that when $n = 1$, the values given in (25) and (26) agree with σ and p in Section 2. Thus σ_n can be regarded as the contact number for the n-staged model (20) and p_n can be interpreted as the mean remaining life expectancy of those who become infected. The quantity δ_k represents the proportion of those who become infected who survive to reach the $(k+1)$-th stage of infection.

The basic reproduction number of (20) is derived in [**10**] as

$$R_0 = \sigma_n \, \bar{S} \, f(\bar{S}), \tag{27}$$

where $\bar{S} = \Lambda/d_S$, using the method of next generation matrix [**32**]. We see that, when $n = 1$, the expression for R_0 in (27) reduces to that for the single stage model in Section 2. For $f(N) = N^{-\alpha}$ and $0 < \alpha \leq 1$, it is also established in [**10**] that if $R_0 \leq 1$ then the disease-free equilibrium $P_0 = (\bar{S}, 0, \cdots, 0)$ is globally asymptotically stable in Δ; if $R_0 > 1$, then P_0 is unstable and the model (20) is uniformly persistent. As a consequence, an endemic equilibrium $P^* = (S^*, I_1^*, \cdots, I_n^*, R^*)$ exists in the interior $\overset{\circ}{\Delta}$ of Δ. Furthermore, it is shown in [**10**] that P^* is unique and globally asymptotically stable in $\overset{\circ}{\Delta}$ when $R_0 > 1$. We show in this section that when $f(N)$ is chosen from a wider class functions, more complicated dynamics are possible.

In the following, we investigate the number of endemic equilibria following the presentation of [**10**]. An endemic equilibrium $(S^*, I_1^*, \cdots, I_n^*, R^*)$ of (20) satisfies

$$\begin{aligned}
0 &= \Lambda - d_S S^* - \bar{\lambda}^* \, S^*, \\
0 &= \bar{\lambda}^* \, S^* - (d_{I_1} + \gamma_1) I_1^*, \\
0 &= \gamma_{i-1} I_{i-1}^* - (d_{I_i} + \gamma_i) I_i^*, \quad i = 2, \ldots, n-1, \\
0 &= \gamma_{n-1} I_{n-1}^* - (d_{I_n} + \gamma_n) I_n^*, \\
0 &= \gamma_n I_n^* - d_R R^*
\end{aligned} \tag{28}$$

where

$$\bar{\lambda}^* = \sum_{j=1}^{n} \beta_j I_j^* f(N^*) \tag{29}$$

is the force of infection at an endemic equilibrium P^*. We write the equations in (28) for $I_1^*, \cdots, I_n^*$ and R^* in the form

$$(I_1^*, \cdots, I_n^*, R^*)^t = \bar{\lambda}^* \, S^* A^{-1} (1, 0, \cdots, 0)^t, \tag{30}$$

where A is the matrix in (22). Multiplying the row vector $(\beta_1, \cdots, \beta_n, 0)$

to (30) and using (21) and (23), we obtain

$$\begin{aligned}\sum_{i=1}^{n}\beta_i I_i^* &= (\beta_1,\cdots,\beta_n,0)\,(I_1^*,\cdots,I_n^*,R^*)^t\\ &= (\beta_1,\cdots,\beta_n,0)A^{-1}(1,0,\cdots,0)^t\bar{\lambda}^*S^*\\ &= \sigma_n\bar{\lambda}^*\,S^* = \sigma_n f(N^*)S^*\sum_{j=1}^{n}\beta_j I_j^*.\end{aligned}$$

Since $\sum_{i=1}^{n}\beta_i I_i^* \neq 0$ at an endemic equilibrium, it follows that

$$\sigma_n\,S^*\,f(N^*) = 1. \tag{31}$$

Similarly, multiplying row vector $(1,\cdots,1)$ to (30) and applying (24) we have

$$\sum_{i=1}^{n} I_i^* + R^* = (1,\cdots,1)(I_1^*,\cdots,I_n^*,R^*)^t = p_n f(N^*)S^*\sum_{j=1}^{n}\beta_j I_j^*, \tag{32}$$

where $p_n > 0$ is defined in (24). From the first equation of (28) we get

$$f(N^*)S^*\sum_{j=1}^{n}\beta_j I_j^* = \Lambda - d_S S^*,$$

which, together with (32), implies

$$\sum_{i=1}^{n} I_i^* + R^* = p_n(\Lambda - d_S S^*),$$

and thus,

$$N^* = S^* + \sum_{i=1}^{n} I_i^* + R^* \;=\; S^* + p_n(\Lambda - d_S S^*) = (1 - p_n d_S)S^* + p_n\Lambda. \tag{33}$$

Substituting (33) into (31) we obtain the following equation for an endemic equilibrium $P^* = (S^*, I_1^*,\cdots,I_n^*,R^*)$

$$g_n(S^*) := S^* f((1 - p_n d_S)S^* + p_n\Lambda) = \frac{1}{\sigma_n}. \tag{34}$$

Comparing equation (34) to the equilibrium equation (8) for the single stage model, we see that the number of endemic equilibria for the n-stage model (20) can be determined in exactly the same way as in Sections 2–4. As a consequence, results in Sections 3 and 4, Theorem 1 and Proposition 3 in particular, hold for the n-stage model, with p and σ replaced by p_n and σ_n, respectively.

We now consider the effects on the dynamical outcomes described in the preceding sections of adding additional infective stages to an SIR model. To simplify the discussion, we assume that $\beta_j = \beta$, $d_{I_j} = d_I$, and $\gamma_j = n\gamma$ for all j. In other words, we chose all the stages of the disease to be identical and assume that individuals move through the stages at a constant rate. The choice of $\gamma_j = n\gamma$ means that adding stages will not change the average length of infection for those who recover.

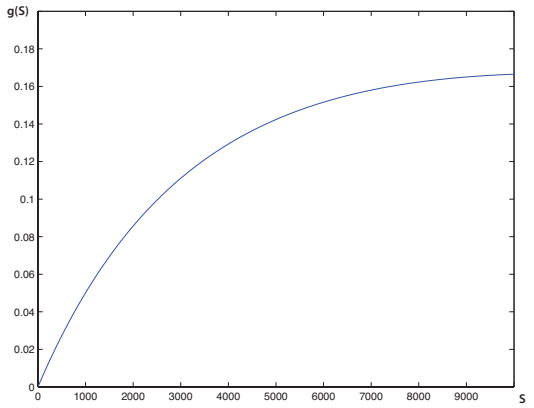
In such a case, the expression for p_n is simplified to

$$\begin{aligned} p_n &= \frac{1}{d_I}\left[1 - \left(\frac{n\gamma}{d_I + n\gamma}\right)^n\right] + \frac{1}{d_R}\left(\frac{n\gamma}{d_I + n\gamma}\right)^n \\ &= \frac{1}{d_I} + \left(\frac{1}{d_R} - \frac{1}{d_I}\right)\left(\frac{n\gamma}{d_I + n\gamma}\right)^n \end{aligned}$$

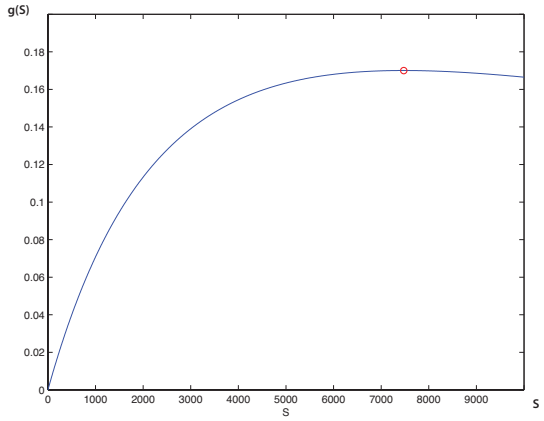
The quantity p_n depends on n only through the term $\delta_n = \left(\frac{n\gamma}{d_I+n\gamma}\right)^n$, which is a decreasing function of n. Since we assume that $d_I > d_R$, we know p_n and $\frac{1}{1-d_S p_n}$ decrease as n increases. As a result, the range of α values for which backward bifurcation occurs (Theorem 1) becomes larger as n increases; adding more infective stages to a simple SIR model with $f(N) = N^{-\alpha}$, $\alpha > 1$, will increase the chance for backward bifurcation and the associated catastrophic behaviours.

For example, Figures 9(a) and 9(b) show the function $g_n(S)$ for $n = 1$ and $n = 5$, respectively. With only a single stage, $g_1(S)$ is monotonic and has no critical points; only one sub-threshold endemic equilibrium is possible. With five stages, $g_5(S)$ has a critical point in the feasible region; two sub-threshold endemic equilibria and backward bifurcation are possible for suitable range of parameter values.

6 Conclusions It is known that complicated dynamics can occur through backward bifurcation or Hopf bifurcation in epidemic models with nonlinear incidence [**15, 24**], or complex group structures [**12, 17**], or with time delays [**30**]. In this paper, we have shown that nonlinear density dependence in disease incidence can also give rise to backward bifurcations and Hopf bifurcations, in simplest models of SIR type.



(a) Function $g_n(S)$ with $n = 1$



(b) Function $g_n(S)$ with $n = 5$

FIGURE 9: Graphs of function $g_n(S)$ for $n = 1$ and $n = 5$.

For incidence functions of the form $\frac{\beta IS}{N^\alpha}$, $\alpha > 1$, we proved that backward bifurcation and bi-stability can occur for $R_0 < 1$. We have also shown that incidence functions of the form $\beta ISf(N)$ with $f(N)$ being quadratic can lead to periodic oscillations through Hopf bifurcation. On the one hand, our results provide a new mechanism for complicated dynamics to occur in simple epidemic models. On the other, they indicate

that, by restricting incidence terms to traditional bilinear form (βIS) or standard form ($\frac{\beta IS}{N}$), we may have unintentionally eliminated the possibility of many complicated but interesting dynamics.

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Appendix: stability of endemic equilibria We consider the special case when recovered class suffers no disease-related fatality (full recovery), namely $d_S = d_R$.

Proposition 4. *Assume that $d_S = d_R = d$. Let $P^* = (S^*, I^*, R^*)$ be an endemic equilibrium of* (1)*. Then P^* is asymptotically stable if $\frac{dg(S^*)}{dS} > 0$, and unstable if $\frac{dg(S^*)}{dS} < 0$.*

Proof. The Jacobian matrix J at P^* is given by

$$\begin{bmatrix} -\beta If(N) - \beta SIf'(N) - d & -\beta Sf(N) - \beta SIf'(N) & -\beta ISf'(N) \\ \beta If(N) + \beta SIf'(N) & \beta Sf(N) + \beta SIf'(N) - (d_I + \gamma) & \beta ISf'(N) \\ 0 & \gamma & -d \end{bmatrix}$$

with superscripts suppressed. Since $\beta S^* f(N^*) = d_I + \gamma$

$$J = \begin{bmatrix} -\beta If(N) - \beta SIf'(N) - d & -(d_I + \gamma) - \beta SIf'(N) & -\beta ISf'(N) \\ \beta If(N) + \beta SIf'(N) & \beta SIf'(N) & \beta ISf'(N) \\ 0 & \gamma & -d \end{bmatrix}.$$

Therefore,

$$\det(J - \mu I) = (-d - \mu)[\mu^2 + (d + \beta If(N))\mu + \beta(If(N)(d_I + \gamma) + (d_I - d)ISf'(N))]. \tag{35}$$

One eigenvalue is $\mu_1 = -d < 0$, while the remaining two eigenvalues are the solutions of the quadratic equation

$$\mu^2 + \big(d + \beta If(N)\big)\mu + \beta If(N)(d_I + \gamma)(d_I + \gamma) + (d_I - d)\beta ISf'(N) = 0.$$

Since $d + \beta I f(N) > 0$, a necessary and sufficient condition for both solutions to have negative real parts is that

$$\beta I f(N) + \sigma(d_I - d) I S f'(N) > 0.$$

Using the facts that $\sigma(d_I - d) = 1 - pd$ and

$$\frac{dg(S)}{dS} = f(N(S)) + S f'(N(S))(1 - pd),$$

we obtain

$$\beta I f(N) + \sigma(d_I - d) I S f'(N) = (d_I + \gamma) I \frac{dg(S)}{dS}.$$

Therefore, if $\frac{dg(S)}{dS} > 0$, then all the eigenvalues have negative real parts, and the endemic equilibrium is stable. If $\frac{dg(S)}{dS} < 0$, then one of the eigenvalues is positive, and the endemic equilibrium is unstable. □

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