# Chapter 5
# Deterministic Compartmental Models: Extensions of Basic Models

P. van den Driessche

**Abstract** The basic compartmental models for disease transmission are extended to include three separate biological features. The first such feature is vertical transmission of disease, for which two ordinary differential equation models (SIR and SEIR) are formulated and analyzed. In particular, vertical transmission is shown to increase the basic reproduction number. Immigration of infective individuals is considered as a second feature, and the resulting model has a unique endemic equilibrium (with no disease-free state). An illustration is provided that includes screening and isolating infectives to reduce the spread of disease. A constant period of temporary immunity is introduced in an SIRS model as the third feature. This results in an integro-differential equation for the fraction of infectives. Analysis shows that, for some parameter values, Hopf bifurcation can give rise to periodic solutions.

## 5.1 Introduction

Basic deterministic compartmental models are introduced and discussed in chapters by Allen [1] and Brauer [2]; the latter also describes models with demographic effects and models with infectivity depending on the age of infection. For some diseases and situations, it is desirable to include other biological features, and to investigate whether these can qualitatively change the model results.

In this chapter three such features are considered separately, namely vertical transmission, immigration of infectives, and temporary immunity upon recovery (which is introduced briefly in Sect. 4.5 of [2]). Models from the

Department of Mathematics and Statistics, University of Victoria, P.O. BOX 3060 STN CSC, Victoria, BC, Canada V8W 3R4
pvdd@math.uvic.ca

literature are summarized: readers are encouraged to consult the original papers for more details and references. These are but a few examples of how the basic models can be extended to better represent certain diseases. More examples are given in subsequent chapters.

## 5.2 Vertical Transmission

### *5.2.1 Kermack–McKendrick SIR Model*

This section is based on a model in the authoritative book on vertically transmitted diseases by Busenberg and Cooke [4, Chap. 2 especially Sect. 2.8]. In the models of the chapter by Brauer [2], disease is transmitted horizontally between infective and susceptible individuals. By contrast, vertical disease transmission is the direct transfer of a disease from an infective parent to an unborn or newly born offspring. The latter can occur, for example, from breast-feeding. Chagas' disease, hepatitis B and HIV/AIDS are examples of diseases that can be transmitted vertically [4, 8]. The SIR model considered here is based on the special simple case of that proposed by Kermack and McKendrick in 1932, but includes input of infectives due to vertical transmission from infective parents.

The model is formulated with the assumptions as in the chapter by Brauer [2] with the following extensions. A fraction $q$ of offspring of infective individuals are assumed infected at birth; thus a fraction $p = 1 - q$ of such offspring are susceptible. The birth and death rate constant for the susceptible and recovered compartments is $b > 0$, whereas $\tilde{b} > 0$ is the birth and death rate constant for the infective compartment. The disease is assumed to be nonfatal, thus the total population size $K = S + I + R$ remains constant, where $S, I, R$ denotes the number in the susceptible, infective, recovered compartment, respectively. Such a model has the form

$$\begin{aligned} S' &= -\beta SI + p\tilde{b}I + b(S + R) - bS \\ I' &= \beta SI + q\tilde{b}I - \tilde{b}I - \gamma I \\ R' &= \gamma I - bR. \end{aligned} \tag{5.1}$$

Recall that mass action incidence is assumed, with each individual making $\beta K > 0$ contacts sufficient to transmit infection per unit time, and that $\gamma$ is the recovery rate constant for infectives.

The variable $R$ can be eliminated from system (5.1), which reduces to the 2-dimensional system

$$S' = -\beta SI + p\tilde{b}I + b(K - S - I)$$
$$I' = \beta SI - p\tilde{b}I - \gamma I \tag{5.2}$$

for which $\{(S, I) \in R_2^+ : S + I \leq K\}$ is invariant. For $p = 1$ (no vertical transmission) and $\tilde{b} = b$, system (5.2) reduces to a model given by Brauer [2, Sect. 2.1].

To begin analysis of (5.2), first consider the two equilibria. These are the disease-free equilibrium $(S, I) = (K, 0)$ and the endemic equilibrium $(S_\infty, I_\infty)$ with

$$S_\infty = \frac{p\tilde{b} + \gamma}{\beta}, \quad I_\infty = \frac{b(K\beta - p\tilde{b} - \gamma)}{(\gamma + b)\beta} \tag{5.3}$$

provided that $K > (p\tilde{b} + \gamma)/\beta$. This condition gives a lower bound on the population size needed to sustain the disease. The basic reproduction number $\mathcal{R}_0$ can be easily found from the $I'$ equation as

$$\mathcal{R}_0 = \frac{\beta K + q\tilde{b}}{\gamma + \tilde{b}} \tag{5.4}$$

which satisfies $\mathcal{R}_0 > 1$ if and only if $K > (p\tilde{b} + \gamma)/\beta$, that is the endemic equilibrium exists. The expression for $\mathcal{R}_0$ given in (5.4) comes from accounting for all new infections (due to horizontal and vertical transmission) and multiplying by the average infective period, namely $1/(\gamma + \tilde{b})$. The vertical transmission has the effect of increasing $\mathcal{R}_0$ by a factor of $q\tilde{b}/(\gamma + \tilde{b})$.

It is easy to show that if $\mathcal{R}_0 < 1$, then the disease-free equilibrium is globally asymptotically stable, and the disease dies out. If $\mathcal{R}_0 > 1$, then the disease-free equilibrium is unstable and the endemic equilibrium exists. In this case a special method using a Lyapunov function due to Beretta and Capasso, see [5, page 11] or [4, Theorem 2.8], can be used to show that the endemic equilibrium is globally asymptotically stable, and so the disease remains in the population. Thus $\mathcal{R}_0 = 1$ gives a sharp disease threshold.

Here an alternative method is presented to show that $(S_\infty, I_\infty)$ attracts all solutions with initial values $(S(0), I(0))$ in $\{(S, I) : S \geq 0, I > 0\}$ if $\mathcal{R}_0 > 1$. From (5.2)

$$\frac{\partial}{\partial S}\Big(\frac{S'}{I}\Big) + \frac{\partial}{\partial I}\Big(\frac{I'}{I}\Big) = -\beta - \frac{b}{I} < 0.$$

Thus by the Bendixon–Dulac criterion (see e.g., [4, page 72]) there are no periodic orbits with $I > 0$. An application of the Poincaré- Bendixon Theorem (see e.g., [4, page 72]) completes the proof.

### 5.2.2 SEIR Model

Consider now a more general model that includes vertical transmission and also contains an exposed (latent) compartment. Infected individuals are exposed before becoming infective, and the length of this exposed period depends on the disease. This gives an SEIR model, in which E denotes the exposed compartment.

Li, Smith and Wang [15] formulate such a model that includes a fraction of the offsprings of infected hosts (both exposed and infective) that are infected at birth and so enter the exposed compartment, giving vertical transmission of the disease. They state that their model is appropriate for rubella and the SEI limit (with no recovery) is appropriate for Chagas' disease. Since the total population is constant in their model, they work with *fractions* in each compartment; thus $S, E, I, R$ denote the fraction in the susceptible, exposed, infective, recovered compartment, respectively, with $S + E + I + R = 1$. The natural birth and death rate constant is denoted by $b$, exposed individuals become infective with rate constant $\epsilon$, and infective individuals recover with rate constant $\gamma$. Horizontal incidence is assumed to be of the bilinear mass action form $\beta SI$. A fraction $p \in [0, 1]$ of the offspring from exposed individuals and a fraction $q \in [0, 1]$ of the offspring from infective individuals are born into the exposed compartment. Thus vertical transmission gives a term $pbE + qbI$ entering the exposed compartment and a similar reduction in the birth of susceptibles. The model is given by the following system [15]

$$\begin{aligned} S' &= b - \beta SI - pbE - qbI - bS \\ E' &= \beta SI + pbE + qbI - (\epsilon + b)E \\ I' &= \epsilon E - (\gamma + b)I \\ R' &= \gamma I - bR. \end{aligned} \tag{5.5}$$

Note that if $p = q = 0$, then the system reduces to the classical SEIR model with mass action.

Let

$$\Omega : \left\{(S, E, I, R) \in R^4_+ : S + E + I + R = 1\right\}.$$

Any solution starting in $\Omega$ does not leave $R^4_+$ by crossing one of its faces. Since also $(S + E + I + R)' = 0$, the solution remains in $\Omega$ for all $t \geq 0$. Thus $\Omega$ is a positively invariant set that is biologically feasible. Using the relation $R = 1 - S - E - I$, (5.5) can be reduced to the equivalent 3-dimensional system, given by the first three equations in (5.5) on the closed invariant set

$$\Gamma : \left\{(S, E, I) \in R^3_+ : S + E + I \leq 1\right\}.$$

The 3-dimensional system has the disease-free equilibrium $(S, I, R) = (1, 0, 0)$ and an endemic equilibrium $(S_\infty, I_\infty, R_\infty)$ with

$$S_\infty = \big((\epsilon+b)(\gamma+b) - pb(\gamma+b) - qb\epsilon\big)/\beta\epsilon$$

provided this is less than one. In this case $I_\infty = \epsilon b(1-S^\infty)/((\epsilon+b)(\gamma+b))$ and $E_\infty = (\gamma+b)I_\infty/\epsilon$.

The authors define a basic reproduction number [15, equation(2.3)]

$$\mathcal{R}_0(p,q) = \frac{\beta\epsilon}{(\epsilon+b)(\gamma+b) - pb(\gamma+b) - qb\epsilon} \tag{5.6}$$

and show that if $\mathcal{R}_0(p,q) \le 1$, then the disease-free equilibrium is globally stable in $\Gamma$; whereas if $\mathcal{R}_0(p,q) > 1$, then the unique endemic equilibrium is globally stable in the interior of $\Gamma$. Thus $\mathcal{R}_0(p,q)$ is a sharp threshold, determining whether the disease dies out or persists at an endemic level. The interesting and highly nontrivial proof in [15] for $\mathcal{R}_0(p,q) > 1$ employs a geometric approach introduced by Li and Muldowney [14]. The authors [15] state that a key step in their proof is the construction of a suitable Lyapunov function for the second additive compound of the Jacobian matrix of the system. Interested readers please consult [15, Sect. 4] for details of the proof.

The contribution to $\mathcal{R}_0(p,q)$ in (5.6) of vertical transmission is given in [15, Sect. 5]. However, we present here an alternate basic reproduction number, denoted by $\mathcal{R}_0$, that is derived from the next generation matrix method [6] as elaborated in [16]. From the 3-dimensional system taking $E$ and $I$ as infecteds, and horizontal and vertical transmission as giving new infecteds, the matrices $F$ and $V$ defined in [16] (which should be consulted for more details) are

$$F = \begin{bmatrix} pb & qb+\beta \\ 0 & 0 \end{bmatrix}, \qquad V = \begin{bmatrix} \epsilon+b & 0 \\ -\epsilon & \gamma+b \end{bmatrix}.$$

Then $\mathcal{R}_0 = \rho(FV^{-1})$, where $\rho$ denotes the spectral radius, is easily found (since $F$ has rank 1) as

$$\mathcal{R}_0 = \frac{\beta\epsilon + pb(\gamma+b) + qb\epsilon}{(\epsilon+b)(\gamma+b)}. \tag{5.7}$$

Here the first term in the numerator comes from horizontal transmission and the second and third terms come from vertical transmission, which increases the value of $\mathcal{R}_0$. The term $pb/(\epsilon+b)$ accounts for vertical transmission from exposed individuals with $1/(\epsilon+b)$ the average exposed period. The term $qb\epsilon/(\epsilon+b)(\gamma+b)$ accounts for vertical transmission from infected individuals with $\epsilon/(\epsilon+b)$ giving the fraction surviving the exposed compartment, and $1/(\gamma+b)$ the average time in the infective compartment. Comparing (5.6) and (5.7) it follows that $\mathcal{R}_0(p,q) = 1$ precisely where $\mathcal{R}_0 = 1$. Thus the sharp threshold is given by either number, but the biological interpretation and the dependence on the model parameters is better given by $\mathcal{R}_0$ in (5.7).

## 5.3 Immigration of Infectives

In the previous section, newborn infecteds enter the infected population. Consider now a communicable disease introduced into a population by infectives immigrating from outside. Given such a situation, a model can be formulated to describe the dynamical spread of disease and to suggest possible control strategies. The SIS models considered here are related to the basic models described in the chapter by Brauer [2, Sect. 2.2] and are taken from [3]. Consider a constant flow $A$ into the population per unit time with a fraction $p \in (0, 1]$ infective. The per capita natural death rate constant is denoted by $d > 0$. Letting $S, I$ denote the number of susceptible, infective individuals, respectively, the total population $N = S + I$ varies with time. Taking mass action incidence and denoting the recovery rate constant and the disease death rate constant by $\gamma$ and $\alpha$, respectively, the model equations are

$$\begin{aligned} S' &= (1-p)A - \beta SI - dS + \gamma I \\ I' &= pA + \beta SI - (d + \gamma + \alpha)I \\ N' &= A - dN - \alpha I. \end{aligned} \tag{5.8}$$

For nonnegative initial values, the model is well posed with $N \le A/d$. From the second equation, it follows that with immigration of infectives there is no disease-free equilibrium. Working in $I, N$ variables, and eliminating $N$, at an endemic equilibrium

$$G(I) = \beta(d + \alpha)I^2 - \sigma I - pdA = 0$$

where $\sigma = \beta A - d(d + \gamma + \alpha)$. Thus there is a unique equilibrium given by

$$I_\infty = \frac{\sigma + \sqrt{\sigma^2 + 4\beta Adp(d + \alpha)}}{2\beta(d + \alpha)}, \qquad N_\infty = \frac{A - \alpha I_\infty}{d}. \tag{5.9}$$

This model can be generalized by replacing mass action incidence by the assumption that each individual makes $\beta(N)N$ contacts sufficient to transmit infection per unit time; see [2]. It is biologically reasonable to assume that $\beta(N)N$ is a nondecreasing function of $N$ and $\beta(N)$ is a nonincreasing function of $N$. These assumptions are satisfied by mass action incidence ($\beta(N) = \beta$), standard incidence ($\beta(N) = \lambda/N$) and saturating incidence ($\beta(N) = a/(1 + bN)$). The model equations are now as in system (5.4) with $\beta$ replaced by $\beta(N)$. It is more convenient to write the equilibrium equation in terms of $N$, namely

$$[(d + \alpha)N - A]\,\beta(N) = -\frac{\alpha^2 pA}{A - dN} + \alpha(d + \gamma + \alpha).$$

The left side of this equation is zero at $N_1 = A/(d + \alpha)$ and is increasing, whereas the right side is positive at $N_1$, decreases and is zero at

$$N = N_0 = \frac{A(d+\gamma+\alpha(1-p))}{d(d+\gamma+\alpha)}.$$

Thus there is a unique endemic equilibrium given by $N_\infty \in [N_1, N_0]$, and $I_\infty > I_0 = pA/(d+\gamma+\alpha)$.

To investigate the stability, linearize system (5.8) about this equilibrium to give the Jacobian matrix

$$\begin{bmatrix} -\frac{pA}{I} - I\beta(N) & (N\beta(N))'I - \beta'(N)I^2 \\ -\alpha & -d \end{bmatrix}$$

at $(I_\infty, N_\infty)$. By considering the signs of each entry (noting that the $(1,2)$ entry is nonnegative), this matrix is sign stable; see, e.g., [12]. Thus for any values of the parameters, the endemic equilibrium is locally asymptotically stable. A Bendixson–Dulac calculation as in Sect. 2.1 shows that there are no period orbits with $I > 0$. The Poincaré–Bendixson theorem then completes the proof that the endemic equilibrium is globally asymptotically stable, so solutions of the SIS model with immigration of infectives converge to the endemic equilibrium $(I_\infty, N_\infty)$. For mass action incidence, this equilibrium is given explicitly by (5.9).

If $\mathcal{R}_0$ is defined in the usual way with mass action incidence as

$$\mathcal{R}_0 = \frac{\beta A}{(d+\gamma+\alpha)d}$$

then for $p$ close to 0

$$I_\infty \approx \begin{cases} \frac{Ad}{|\sigma|}p & \text{if } \mathcal{R}_0 < 1 \ (\sigma < 0) \\ \frac{Ad}{\sigma}p + \frac{\sigma}{\beta(d+\alpha)} & \text{if } \mathcal{R}_0 > 1 \ (\sigma > 0). \end{cases}$$

The limiting infective population is a smooth function of $\mathcal{R}_0$, with the threshold $\mathcal{R}_0 = 1$ not as sharp as in the classical case (except in the limit as $p \to 0^+$).

Gani et al. [7, Sect. 2] formulated models for the spread of HIV in a constant population prison, and considered a program of screening with quarantining of prisoners found to be HIV positive. Note that quarantining is used here to mean the isolation of infective individuals. A continuous analog of their SI model is formulated in [3, Sect. 5]. This simple model indicates that such a program can reduce the infective population size, but a more detailed model including more realistic assumptions and data on HIV is needed to give quantitative predictions.

Consider model (5.8) in the limit with $\gamma = 0$ and $\alpha > 0$ (since HIV is a fatal disease). The demographics now refer to incarceration (at rate $A$ with a fraction $p$ infective) and release of prisoners (with rate constant $d$). Taking one month as the time unit, $A = 25$, $d = 1/24$, $p = 0.1$ giving a prison population

carrying capacity as 600. The mean infective period is assumed to be ten years (so $\alpha = 1/120$). With $\beta = 1/3000$ (1 contact every 5 months/infective), $I_\infty = 391$ and $N_\infty = 521$. Thus 75% are infective at equilibrium, which (by numerical simulation) is reached in 2.5 years.

For constant $\tau$ with $0 \le \tau \le 1$, $\tau(S+I)$ prisoners are screened in unit time and the $\tau I$ found to be infective are moved to a quarantined compartment. The number in this compartment is denoted by $Q(t)$. This gives the model [3, Sect. 5]

$$\begin{aligned} S' &= (1-p)A - \beta SI - dS \\ I' &= pA + \beta SI - (d+\alpha+\tau)I \\ Q' &= \tau I - (d+\alpha)Q. \end{aligned} \tag{5.10}$$

The total population $N = S + I + Q$ thus satisfies

$$N' = A - dN - \alpha I - \alpha Q.$$

Analysis of this model is similar to that of (5.8) and shows that there is a unique endemic equilibrium $(S_\infty, I_\infty, Q_\infty)$ with

$$I_\infty = \frac{\sigma\sqrt{\sigma^2 + 4\beta A dp(d+\alpha+\tau)}}{2\beta(d+\alpha+\tau)}$$

with $\sigma = \beta A - d(d+\alpha+\tau)$, and that this equilibrium is locally asymptotically stable. For global stability, note that the first two equations of (5.10) do not contain $Q$, and so by analogy with (5.8) it follows that $(S, I) \to (S_\infty, I_\infty)$ as $t \to \infty$. The third equation then shows that $Q \to Q_\infty$.

Taking parameters as for the prison population above, if $\tau = 0.1$ (so 42 prisoners screened per month), then $I_\infty = 71$; whereas if $\tau = 0.2$ (so 95 prisoners screened per month), then $I_\infty = 25$. It takes about two years to reach these equilibria. Thus, from this model, a considerable reduction of infectives occurs with screening and quarantining of infectives.

## 5.4 General Temporary Immunity

For diseases that confer only temporary immunity, for example strains of influenza, an SIRS model is appropriate. If the SIR Kermack–McKendrick model is assumed with the addition of a recovered period that is exponentially distributed, then an ordinary differential equation model results. For this model, the basic reproduction number gives a sharp threshold, determining whether the disease dies out or goes to an endemic value.

To allow for a more general recovered period, let $P(t)$ be the fraction of recovered individuals remaining in the recovered class $t$ units after

recovery from infection. It is reasonable to assume that $P(t)$ is nonincreasing, $P(0^+)=1$, $\lim_{t\to\infty} P(t) = 0$ and the average period of immunity $\int_0^\infty P(v)dv = \omega$ is finite. Assuming that the average infectious period is $1/\gamma$ and neglecting demographics, gives the system for the fractions in the infective, recovered and susceptible compartment as

$$\begin{aligned} I(t) &= I(0)e^{-\gamma t} + \int_0^t \beta S(x)I(x)e^{-\gamma(t-x)}dx \\ R(t) &= R_0(t) + \int_0^t \gamma I(x)P(t-x)dx \\ S(t) &= 1 - I(t) - R(t) \end{aligned} \tag{5.11}$$

where $R_0(t)$ is the number initially removed and still removed at $t$, with $R_0(\infty) = 0$. This model is formulated and analyzed in [11], and has richer dynamics than the corresponding ordinary differential equation SIRS model.

System (5.11) is equivalent to the integrodifferential equation

$$I'(t) = \gamma I(t) + \beta I(t)[1 - I(t) - R_0(t) - \gamma \int_0^t I(t+u)P(-u)]du. \tag{5.12}$$

By standard theorems on retarded functional differential equations [10, 13], there exists a unique solution of (5.12) for all $t \geq 0$. Here $\mathcal{R}_0 = \beta/\gamma$, and it is shown in [11] that if $\mathcal{R}_0 \leq 1$, then all solutions tend to the disease-free equilibrium; but if $\mathcal{R}_0 > 1$, the disease-free equilibrium is unstable and a unique endemic equilibrium $(S_\infty, I_\infty)$ exists that is given by

$$S_\infty = \frac{1}{\mathcal{R}_0}, \qquad I_\infty = \frac{1 - 1/\mathcal{R}_0}{1 + \omega\gamma}.$$

For further analysis with $\mathcal{R}_0 > 1$, assume a constant period of temporary immunity, thus

$$P(t) = \begin{cases} 1 \text{ for } 0 \leq t < \omega \\ \\ 0 \text{ for } t \geq \omega. \end{cases}$$

Then for $t \geq \omega$, equation (5.12) becomes

$$I'(t) = -\gamma I(t) + \beta I(t)[1 - I(t) - \gamma \int_{-\omega}^0 I(t+u)du].$$

Translating $I_\infty$ to the origin by using $I(t) = I_\infty(1 + X(t))$ and letting $t = \omega\tau$ gives

$$X'(\tau) = \frac{-\omega\gamma(\mathcal{R}_0 - 1)}{1 + \omega\gamma}(X(\tau) + 1)[X(\tau) + \omega\gamma \int_{-1}^0 X(\tau + v)dv].$$

Linearizing about $X = 0$ and setting $X(\tau)$ proportional to $e^{z\tau}$ yields the quasi-polynomial characteristic equation

$$z + \frac{\omega\gamma(\mathcal{R}_0 - 1)}{1 + \omega\gamma}[1 + \omega\gamma \int_{-1}^{0} e^{zv} dv] = 0. \tag{5.13}$$

The assumption of a constant recovery period (through the step function $P(t)$) has resulted in a difficult stability problem, even for the linearized equation about the endemic equilibrium. However, it is possible to find purely imaginary roots of (5.13) by setting $z = i\mu$ for $\mu > 0$, which on equating real and imaginary parts becomes

$$\frac{\sin\mu}{\mu} = -\frac{1}{\omega\gamma} \quad \text{and} \quad \mu^2 = \frac{(\omega\gamma)^2(\mathcal{R}_0 - 1)(1 - \cos\mu)}{1 + \omega\gamma}.$$

This gives a family of imaginary root curves for $\mu \in ((2k-1)\pi, 2k\pi)$, $k = 1, 2, ....$ For $\omega\gamma < 1$, all roots have negative real parts, so the endemic equilibrium is locally asymptotically stable below the lowest imaginary root curve $k = 1$. Assume $\mathcal{R}_0 > 1$ is fixed and that $z = i\mu_c$ solves (5.13) when $\omega\gamma = c$, then there is a *Hopf bifurcation* from $X = 0$ for small $|\omega\gamma - c|$ of the form

$$X(\tau) = |A(\mu_c)(\omega\gamma - c)|^{\frac{1}{2}} [\cos(\mu_c\tau) + o(|\omega\gamma - c|^{\frac{1}{2}})]$$

where $\omega\gamma > c$ and $A \neq 0$. If the bifurcation point $(\mathcal{R}_0, c)$ is on the lowest imaginary root curve, then the periodic solution is locally asymptotically stable and has period between $\omega$ and $2\omega$. If the bifurcation point is on a higher curve ($k = 2, 3, ...$), then the periodic solution is unstable. Details of the Hopf bifurcation theorem can be found in [9] and [13].

Thus a constant period of temporary immunity can lead, for some parameter values, to solutions of this SIRS model that oscillate about the endemic equilibrium. For more details of this and oscillatory solutions for an ordinary differential equation model that has at least three removed classes (corresponding to a gamma-distributed time delay in the recovered class), please consult [11]. It is interesting to note that an alternate SIRS model with an arbitrarily distributed time delay in the infectious compartment and an exponentially distributed delay in the removed compartment does not exhibit periodic solutions [11, Sect. 5]. For epidemic models that include delays and vertical transmission see [4, Chap. 4].

Mechanisms that can lead to oscillatory solutions either autonomously or through external forcing in epidemic models are discussed in [10]. In addition to delays in the recovered compartment, these mechanisms include nonlinear incidence, age structure and periodic incidence. Such oscillations are often seen in disease incidence data; thus models that predict this phenomenon are useful in understanding disease spread and suggesting possible control measures.

## References


1. Allen, L.J.S.: An introduction to stochastic epidemic models. Chapter 3 of Mathematical Epidemiology (this volume)
2. Brauer, F.: An introduction to compartmental models in epidemiology. Chapter 2 of Mathematical Epidemiology (this volume)
3. Brauer, F. and van den Driessche, P.: Models for transmission of disease with immigration of infectives. Math. Biosci. **171**, 143–154 (2001)
4. Busenberg, S. and Cooke, K.: Vertically Transmitted Diseases. Biomath. **23**, Springer, Berlin Heidelberg New York (1993)
5. Capasso, V.: Mathematical Structures of Epidemic Systems. Lect. Notes Biomath. **97**, Springer, Berlin Heidelberg New York (1993)
6. Diekmann, O. and Heesterbeek, J.A.P.: Mathematical Epidemiology of Infectious Diseases. Model Building, Analysis and Interpretation, Wiley (2000)
7. Gani, J. Yakowitz, S. and Blount, M.: The spread and quarantine of HIV infection in a prison system. SIAM J. Appl. Math. **57**, 1510–1530 (1997)
8. Hart, C.A.: Microterrors. Firefly Books. Axis (2004)
9. Hale, J.K. and Verduyn Lunel, S.M.: Introduction to Functional Differential Equations. Springer, Berlin Heidelberg New York(1993)
10. Hethcote, H.W., and Levin, S.A.: Periodicity in epidemiological models. In: Levin, S.A., Hallam, T.G., Gross, L.J. (eds) Applied Mathematical Ecology, Biomath. Texts. **18**, Springer, Berlin Heidelberg New York 193–211 (1989)
11. Hethcote, H.W., Stech, H.W., and van den Driessche, P.: Non-linear oscillations in epidemic models. SIAM J. Appl. Math. **40**, 1–9 (1981)
12. Jeffries, C., Klee, V., and van den Driessche, P.: When is a matrix sign stable? Can. J. Math. **29**, 315–326 (1977)
13. Kuang, Y.: Delay Differential Equations with Applications in Population Dynamics. Academic (1993)
14. Li, M.Y., and Muldowney, J.S.: A geometric approach to global- stability problems. SIAM. J. Math. Anal. **27**, 1070–1083 (1996)
15. Li, M.Y., Smith, H.L., and Wang, L.: Global dynamics of an SEIR epidemic model with vertical transmission. SIAM. J. Appl. Math. **62**, 58–69 (2001)
16. van den Driessche, P., and Watmough, J.: Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission. Math. Bios. **180**, 29–48 (2002)